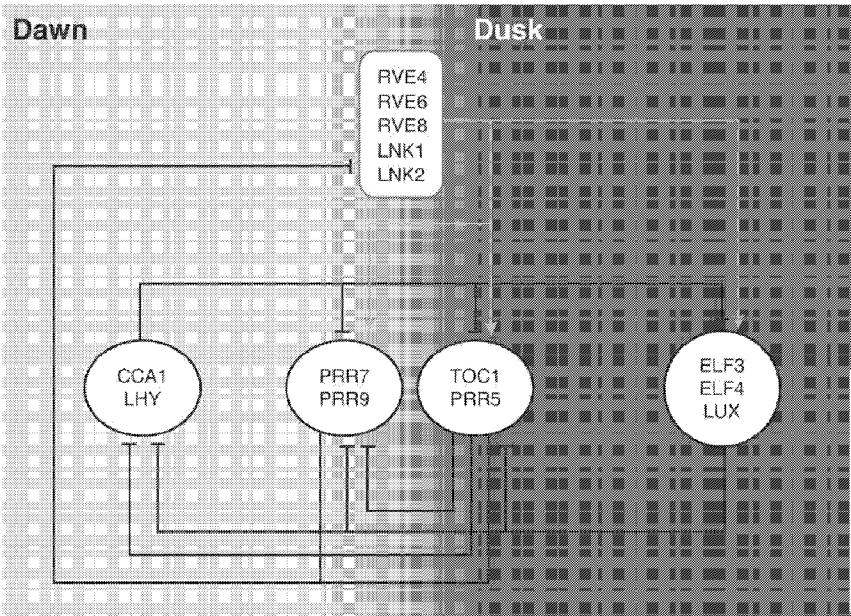




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(54) Title: PLANTS WITH REDUCED PLASTICITY



(57) Abstract: Plants modified to exhibit reduced plasticity and related methods and compositions are disclosed. The plants have reduced developmental plasticity in response to changes in light and temperature conditions, and exhibit additional features such as earlier, more consistent and uniform flowering regardless of changes in day length and temperature, and reduced listing in the field.

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PLANTS WITH REDUCED PLASTICITY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority from Provisional Application number 63/391,651, filed July 22, 2022, the entire contents of which are hereby incorporated by reference.

SEQUENCE LISTING

[0002] This application contains a Sequence Listing that has been submitted in .XML format via PatentCenter and is hereby incorporated by reference in its entirety. The .XML is named 077875_767246_Sequence_Listing, and is 735 kilobytes in size.

FIELD OF THE INVENTION

[0003] The present disclosure relates to modified plants, and methods and compositions for modifying plants, plant tissues, parts thereof, and seeds exhibiting reduced plasticity compared to wild type.

BACKGROUND OF THE INVENTION

[0004] One goal of modern breeding programs is to increase the uniformity of crops so that harvesting time is more predictable and quality is consistent. This is true for intensive, precision outdoor farming and Total Controlled Environment Agriculture (TCEA, or vertical farming). However, plants are developmentally plastic and respond to changes in light and temperature to optimize their growth. Developmental plasticity is advantageous in natural conditions where resources and environmental stresses vary across seasons and location, but is disadvantageous in modern crop monoculture where fertilizers, pesticides, irrigation, etc., can be provided. Climate change offers additional challenges, with more varied weather and increasing temperatures disrupting plant development. Importantly, flowering in many crops is dependent on day length and

highly influenced by ambient temperatures. This is disruptive to farmers who can only harvest at defined times of the year.

[0005] Accordingly, there is a need for plants with reduced developmental plasticity suitable for intensive, precision outdoor farming practices and TCEA or vertical farming.

SUMMARY OF THE INVENTION

[0006] One aspect of the instant disclosure encompasses a modified plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity. The modified plant or part thereof, plant cell, or seed comprises (a) a modification of an endogenous polynucleotide sequence encoding a component of the circadian clock; and (b) an exogenous polynucleotide sequence encoding an environmental signal sensor. The modification of the endogenous polynucleotide sequence encoding the component of the circadian clock modifies expression of the component of the circadian clock; and the modification of the endogenous polynucleotide encoding the environmental signal sensor modifies expression of the environmental signal sensor. The modified expression of the component of the circadian clock and of the environmental signal sensor causes the plant to exhibit (i) reduced developmental plasticity in response to changes in environmental conditions during growth and (ii) modified circadian function.

[0007] The component of the circadian clock can be a component of the evening complex (EC). For instance, the component of the circadian clock is selected from EARLY FLOWERING 3 (ELF3), EARLY FLOWERING 4 (ELF4), LUX ARRHYTHMO (LUX), or any combination thereof. In some aspects, the component of the circadian clock is an ELF3 protein. In some aspects, the modification of a polynucleotide encoding the ELF3 protein is a loss-of-function mutation.

[0008] In some aspects, the plant or part thereof, plant cell, or seed is *Arabidopsis thaliana* (*A. thaliana*). When the plant is *A. thaliana*, the ELF3 protein can comprise an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an

amino acid sequence of SEQ ID NO: 2. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 1 and an ELF3 loss-of-function mutation comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof.

[0009] In some aspects, the plant or part thereof, plant cell, or seed is *Thlaspi arvense* (*T. arvense*). When the plant is *T. arvense*, the ELF3 protein can comprise an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 21. In some aspects, the polynucleotide encoding the ELF3 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20. The modification of the polynucleotide encoding the ELF3 protein can comprise a deletion of a nucleic acid segment in the polynucleotide encoding the ELF3 protein, wherein the nucleic acid segment can comprise about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof.

[0010] In some aspects, the modification of the polynucleotide encoding the ELF3 protein comprises a modification introduced by a programmable nucleic acid modification system comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA). In some aspects, the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof. An expression construct expressing the Cas9 protein can

comprise a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.

[0011] In some aspects, the plant or part thereof, plant cell, or seed is basil. When the plant is basil, the polynucleotide encoding ELF3 can comprise a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13. In some aspects, the modification of the polynucleotide encoding the ELF3 protein comprises a modification introduced by a programmable nucleic acid modification system comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA). The Cas9 protein can be encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof. In some aspects, an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.

[0012] The environmental signal can comprise photoperiod, light intensity and quality, temperature, chemicals, gravity, moisture, biotic or abiotic stress, oxygen and carbon dioxide concentrations, carbohydrate availability, or any combination thereof. For instance, the environmental signal sensor can be a photoreceptor, temperature sensor, CO₂ sensor, O₂ sensor, ethylene sensor, gravitropic sensor, or any combination thereof.

[0013] In some aspects, the environmental signal sensor is a photoreceptor. The photoreceptor can be a phytochrome; a cryptochrome, a phototropin, an F-box containing Flavin binding proteins; UVR8, or any combination thereof. In some aspects, the photoreceptor is a phytochrome photoreceptor. The polynucleotide encoding an

environmental signal sensor can encode a phytochrome B photoreceptor. In some aspects, the phytochrome B photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 6 or SEQ ID NO: 28. In other aspects, the polynucleotide encoding the phytochrome B photoreceptor comprises least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 5 or SEQ ID NO: 28.

[0014] The phytochrome B photoreceptor can be overexpressed, constitutively expressed, or constitutively active. In some aspects, the modification of a polynucleotide encoding a phyB photoreceptor encodes a constitutively active phyB photoreceptor. When the modification of the polynucleotide encoding a phyB photoreceptor encodes a constitutively active phyB photoreceptor, the phytochrome B photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof. In some aspects, the polynucleotide encoding the phytochrome B photoreceptor comprises least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof.

[0015] In some aspects, the plant or part thereof, plant cell, or seed is *Arabidopsis thaliana* (*A. thaliana*). When the plant is *A. thaliana*, the modified *A. thaliana* plant can comprise a genetic modification of a polynucleotide encoding PhyB, wherein the polynucleotide comprising the genetic modification encodes a constitutively active PhyB photoreceptor. The constitutively active PhyB photoreceptor can comprise an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination

thereof. In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof. In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 12, or both. In other aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or both.

[0016] In some aspects, the plant or part thereof, plant cell, or seed is *T. arvense*. The modified *T. arvensis* plant can comprise a genetic modification of a polynucleotide encoding PhyB, wherein the polynucleotide comprising the genetic modification encodes a constitutively active PhyB photoreceptor. In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof. In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or SEQ ID NO: 27. In other aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 26. The constitutively active PhyB photoreceptor can be encoded by a nucleic acid sequence comprising at least about 75% or more, at

least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25.

[0017] In some aspects, the modified plant or part thereof, plant cell, or seed of can comprise (a) a modification of a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation; and (b) a modification of a polynucleotide encoding a phyB photoreceptor wherein the polynucleotide encodes a constitutively active PhyB photoreceptor. In some aspects, the modified plant comprises constitutively inactivated temperature input to the circadian clock and a constitutively activated light input to the circadian clock. In some aspects, the modified plant is not etiolated, flowers earlier and consistently regardless of changes in day length and has a reduced cellular elongation response to increasing temperature thereby reducing listing in the field, and any combination thereof.

[0018] In some aspects, the modified plant is plant is *A. thaliana*. The modified *A. thaliana* can comprise (a) a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof; and (b) a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof.

[0019] In other aspects, the modified plant is plant is *T. arvensis* comprising (a) a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an

amino acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof; and (b) a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25.

[0020] Another aspect of the instant disclosure encompasses a system for modifying a component of the circadian clock, an environmental signal sensor, or both in a plant. The system can comprise a nucleic acid construct comprising at least one or both of: (a) a programmable nucleic acid modification system comprising a targeting nucleic acid sequence targeting a nucleic acid sequence in a polynucleotide sequence encoding a component of the circadian clock; and (b) an expression construct comprising a promoter operably linked to a polynucleotide encoding a polynucleotide encoding an environmental signal sensor; wherein (a) introduces a loss of function mutation into the polynucleotide sequence encoding the component of the circadian clock, and wherein (b) increases expression of the environmental signal sensor, thereby causing the plant to exhibit reduced developmental plasticity in response to changes in environmental conditions during growth and modified circadian function.

[0021] In some aspects, the programmable nucleic acid modification system introduces a loss of function mutation into a polynucleotide encoding an ELF3 protein. In some aspects, the programmable nucleic acid modification system comprises a CRISPR/Cas nuclease system comprising a CAS9 protein (dCAS9) and a guide RNA (gRNA).

[0022] The plant can be *T. arvense*. When the plant is *T. arvense*, the Cas9 protein can be encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or both.

[0023] The plant can also be basil. When the plant is basil, the Cas9 protein can be encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA can comprise a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.

[0024] In some aspects, the expression construct comprises a promoter operably linked to a polynucleotide encoding a polynucleotide encoding a PhyB photoreceptor, wherein the expression construct increases expression of PhyB. In some aspects, the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a 35S promoter operably linked to a polynucleotide encoding the PhyB photoreceptor and the construct constitutively expresses the PhyB photoreceptor. In some aspects, the PhyB photoreceptor is constitutively active. When the PhyB photoreceptor is constitutively active, the expression construct can comprise a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 24. In some aspects, the expression construct comprises a nucleic acid sequence comprising a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19.

[0025] Another aspect of the instant disclosure encompasses a modified plant or part thereof, plant cell, or seed comprising one or more systems for modifying a plant exhibiting reduced developmental plasticity. The systems can be as described herein above.

[0026] Yet another aspect of the instant disclosure encompasses one or more expression constructs for modifying a plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity, the one or more expression constructs comprising at least one or both of: (a) an expression construct for modifying the expression of a component of the circadian clock; and (b) an expression construct for modifying the expression of an environmental signal sensor.

[0027] The expression construct for modifying the expression of a component of the circadian clock can comprise a promoter operably linked to a polynucleotide encoding a programmable nucleic acid modification system targeted to a nucleic acid sequence in a polynucleotide encoding a component of the circadian clock. In some aspects, the programmable nucleic acid modification system comprises a CRISPR/Cas nuclease system and wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA). In some aspects, an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.

[0028] In some aspects, the plant is *T. arvense*. When the plant is *T. arvense*, the polynucleotide encoding a component of the circadian clock can encode ELF3, wherein the polynucleotide encoding ELF3 can comprise a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20 and the gRNA can comprise a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or both. In some aspects, the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base 254 to base 1287 of SEQ ID NO: 32.

[0029] The plant can also be Basil. When the plant is basil, the polynucleotide encoding a component of the circadian clock can encode ELF3, the polynucleotide encoding ELF3 can comprise a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13, and the gRNA can comprise a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof. In some aspects, an expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises a nucleic acid sequence comprising about 75% or more, at least about 85%

or more, at least about 95% or more, or 100% sequence identity with the gRNA expression construct of SEQ ID NO: 37. In some aspects, an expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 23. In some aspects, the expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 695 to base 2799 of SEQ ID NO: 37.

[0030] In some aspects, the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a constitutive expression promoter operably linked to a polynucleotide encoding a PhyB photoreceptor. In some aspects, the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a 35S promoter operably linked to a polynucleotide encoding a constitutively active PhyB photoreceptor. The constitutively active PhyB photoreceptor can be encoded by a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or both. In some aspects, the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 24. In some aspects, the expression construct comprising a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19.

[0031] An additional aspect of the instant disclosure encompasses a modified plant or part thereof, plant cell, or seed comprising one or more expression constructs for modifying a plant exhibiting reduced developmental plasticity. The constructs can be as described herein above.

[0032] One aspect of the instant disclosure encompasses a method of improving performance of a plant or part thereof, plant cell, or seed grown under intensive, precision outdoor farming conditions, Total Controlled Environment Agriculture (TCEA), or vertical farming. The method comprises obtaining or having obtained a modified plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity; and cultivating the plant under intensive, precision outdoor farming conditions, TCEA, or vertical farming.

[0033] A yet additional aspect of the instant disclosure encompasses a method of reducing developmental plasticity of a plant or part thereof, plant cell, or seed. The method comprises generating a modified plant comprising one or more expression constructs for modifying a plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity. The plant or part thereof, plant cell, or seed can be as described herein above. The plant can be resistant to changes in growth conditions of the plant. In some aspects, the growth conditions comprise daylength and temperature.

[0034] One aspect of the instant disclosure encompasses a method of reducing a plastic response to competition among a co-cultivated group of plants or parts thereof, plant cells, or seeds. The method comprises, co-cultivating a group of modified plants or parts thereof, plant cells, or seeds exhibiting reduced developmental plasticity. The of plants or parts thereof, plant cells, or seeds can be as described herein above.

[0035] Another aspect of the instant disclosure encompasses a method of stabilizing production of a metabolite, nucleic acid, or protein in a plant or part thereof, plant cell, or seed. The method comprises obtaining or having obtained a modified plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity; cultivating the plant for a time sufficient to generate the metabolite, nucleic acid, or protein; and harvesting the metabolite, nucleic acid, or protein from the plant or part thereof, plant cell, or seed. In some aspects, the plant is grown under intensive, precision outdoor farming conditions, TCEA, or vertical farming. In some aspects, stabilizing production of a metabolite, nucleic acid, or protein can comprise equal

production of the metabolite, nucleic acid, or protein irrespective of light period, temperature variation or both.

[0036] Another aspect of the instant disclosure encompasses a kit for modifying a plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity. The kit comprises: (a) one or more modified plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity; (b) one or more expression constructs for modifying a plant or part thereof, plant cell, or seed to exhibit reduced developmental plasticity; (c) one or more modified plants or parts thereof, plant cells, or seeds comprising one or more expression constructs for modifying a plant or part thereof, plant cell, or seed to exhibit reduced developmental plasticity; or any combination of (a) to (c). The plants or parts thereof, plant cells, or seeds and the constructs can be as described herein above.

BRIEF DESCRIPTION OF THE FIGURES

[0037] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0038] **FIG. 1** is a simplified representation of the plant circadian regulatory network. Similar genes operating at similar times during the day in a similar manner are grouped together in white circles. Black lines with blunt ends indicate genes function as repressors in the negative feedback loops. Gray lines and arrows indicate genes acting as activators in the regulatory network.

[0039] **FIG. 2A** is a schematic representation of how light signaling pathways integrate with the circadian clock regulatory network. The underlying clock network is the same as **FIG. 1** with the light-signaling pathway linking to points in the circadian regulatory network. Red and blue pathways indicate how these different wavelengths of light are integrated into the clock at different points via independent pathways.

[0040] **FIG. 2B** is a schematic representation of how temperature signaling pathways integrate with the circadian clock regulatory network. The underlying clock

network is the same as **FIG. 1** with the temperature-signaling pathway linking to points in the circadian regulatory network. Different temperatures influence the same pathway (blue to orange shaded box), with cooler temperatures stabilizing complex formation and warmer temperatures releasing growth factors such as PIFs.

[0041] **FIG 3A** is a plot showing the accumulation of PHYB and YHB transcript in wild-type, YHB, *elf3-2*, and PHYB::YHB(*elf3*) seedlings determined using qRT-PCR.

[0042] **FIG 3B** is a photo of seedlings of WT, *elf3-2*, YHB, and YHB (*elf3-2*) E269.11 grown in constant darkness.

[0043] **FIG 3C** is a plot showing hypocotyl elongation of seedlings grown under either constant darkness, short day (8:16) or long day (16:8) light:dark cycles for 6 days.

[0044] **FIG 3D** is a plot showing hypocotyl elongation in response to temperature. Seedlings were grown in short day (8:16) light:dark cycles at the indicated temperature for 6 days.

[0045] **FIG 3E** are photographs of plants showing the rosette phenotype of adult PHYB::YHB seedlings following growth under short day conditions.

[0046] **FIG 3F** is a plot showing flowering phenotype of PHYB::YHB seedlings grown under short- or long-day conditions.

[0047] **FIG. 4A** is a plot showing the hypocotyl elongation response of wild type, *elf3-1*, *phyb-9*, *elf3-1 phyb-9*, and *elf3-1 phyb-9* YHB plants when combined in response to daylength. Seedlings were grown under either short day (8 light :16 dark), day neutral (12 light :12 dark) or long day (16 light :8 dark) cycles for 6 days at 22 °C at ~80 $\mu\text{mol m}^{-2} \text{s}^{-1}$.

[0048] **FIG. 4B** is a plot showing the hypocotyl elongation response of wild type, *elf3-1*, *phyb-9*, *elf3-1 phyb-9*, and *elf3-1 phyb-9* YHB plants when combined in response to temperature. Seedlings were grown under day neutral (12 light :12 dark) cycles at ~80 $\mu\text{mol m}^{-2} \text{s}^{-1}$ at either 16 °C, 22 °C, or 28 °C for 6 days before measurement.

[0049] **FIG. 5A** is a plot showing the circadian rhythms of wild type, *elf3-2*, PHYB::YHB and PHYB::YHB *elf3-2* plants in constant darkness, measured by luciferase bioluminescence driven by the circadian *CCA1* promoter. White boxes indicate periods

of light irradiation in light:dark cycles prior to transfer to constant darkness. Dark grey segments indicate periods of darkness; light grey segments highlight periods of subjective daytime when held in constant darkness. Zeitgeber time is hours since last dawn.

[0050] **FIG. 5B** is a plot showing the circadian rhythms of wild type, *elf3-1*, *elf3-1 phyb-9*, and *elf3-1 phyb-9 35S::YHB* plants in constant darkness, measured by luciferase bioluminescence driven by the circadian *CCA1* promoter. White boxes indicate periods of light irradiation in light:dark cycles prior to transfer to constant darkness. Dark grey segments indicate periods of darkness; light grey segments highlight periods of subjective daytime when held in constant darkness. Zeitgeber time is hours since last dawn.

[0051] **FIG. 6A. *The combination of YHB and elf3 alleles alters gene expression additively compared to either allele alone.*** Heatmap showing fold change of transcript abundance ($\log_2FC$) for each core circadian clock gene (list of circadian genes taken from Hsu and Harmer, 2014) in dark treated *elf3-2*, *YHB*, and *YHB(elf3-2)* seedlings respective to the expression in wild type (Col-0).

[0052] **FIG. 6B. *The combination of YHB and elf3 alleles alters gene expression additively compared to either allele alone.*** Venn diagram of highly differentially expressed ($\log_2FC > 1.0$, $p < 0.05$) circadian genes in one or more mutant genotypes with respect to wild type.

[0053] **FIG. 6C. *The combination of YHB and elf3 alleles alters gene expression additively compared to either allele alone.*** Heatmap showing highly differentially expressed ($\log_2FC > 1.0$, $p < 0.05$) genes associated with photomorphogenesis (list of photomorphogenesis genes taken from TAIR keywords in either of dark treated *YHB*, *YHB(elf3-2)* or *elf3-2* seedlings respective to the expression in wild type (Col-0).

[0054] **FIG. 6D. *The combination of YHB and elf3 alleles alters gene expression additively compared to either allele alone.*** Venn diagram of highly differentially expressed ($\log_2FC > 1.0$, $p < 0.05$) genes associated with

photomorphogenesis in one or more mutant genotypes with respect to wild type. Normalized transcript abundance in wild type samples was used to calculate fold change difference of transcript abundance. Data shows the average of the three independent biological replicates.

[0055] **FIG. 6E. *ELF3* is required to enable *YHB*-driven circadian rhythms of *GIGANTEA (GI)* in constant darkness.** Real-time reverse transcription polymerase chain reaction showing steady-state accumulation of *GI* transcripts in wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Seedlings were grown for 12 days under 12hrs:12hrs light:dark cycles on 0.5MS plates before transfer to constant darkness at ZT12. RNA was extracted from pools of ca. 20 seedlings for each genotype and used to synthesise cDNA. qRT-PCR data was normalised to the expression of three internal control genes (*APA1*, *APX3* and *IPP2*), and shows the average expression from three independent experiments.

[0056] **FIG. 6F. *ELF3* is required to enable *YHB*-driven circadian rhythms of *PRR9* in constant darkness.** Real-time reverse transcription polymerase chain reaction showing steady-state accumulation of *PRR9* transcripts in wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Seedlings were grown for 12 days under 12hrs:12hrs light:dark cycles on 0.5MS plates before transfer to constant darkness at ZT12. RNA was extracted from pools of ca. 20 seedlings for each genotype and used to synthesise cDNA. qRT-PCR data was normalised to the expression of three internal control genes (*APA1*, *APX3* and *IPP2*), and shows the average expression from three independent experiments.

[0057] **FIG. 6G. *ELF3* is required to enable *YHB*-driven circadian rhythms of *CCA1* in constant darkness.** Real-time reverse transcription polymerase chain reaction showing steady-state accumulation of *CCA1* transcripts in wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Seedlings were grown for 12 days under 12hrs:12hrs light:dark cycles on 0.5MS plates before transfer to constant darkness at ZT12. RNA was extracted from pools of ca. 20 seedlings for each genotype and used to synthesise cDNA. qRT-PCR data was normalised to the expression of three internal control genes

(*APA1*, *APX3* and *IPP2*), and shows the average expression from three independent experiments.

[0058] **FIG. 6H. *ELF3* is required to enable *YHB*-driven circadian rhythms of *LHY* in constant darkness.** Real-time reverse transcription polymerase chain reaction showing steady-state accumulation of *LHY* transcripts in wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Seedlings were grown for 12 days under 12hrs:12hrs light:dark cycles on 0.5MS plates before transfer to constant darkness at ZT12. RNA was extracted from pools of ca. 20 seedlings for each genotype and used to synthesise cDNA. qRT-PCR data was normalised to the expression of three internal control genes (*APA1*, *APX3* and *IPP2*), and shows the average expression from three independent experiments.

[0059] **FIG. 7A. Characterisation of additional *YHB elf3* alleles.** Relative gene expression of wild type *PHYB* and *YHB* transcript in 6 day old Col-0 (Wild type), *PHYB::YHB*, *elf3-2*, and four independently-transformed *PHYB::YHB(elf3-2)* lines.

[0060] **FIG. 7B. Characterisation of additional *YHB elf3* alleles.** Relative gene expression of wild type *PHYB* and *YHB* transcript in 6 day old Col-0 (Wild type), *phyb-9*, *elf3-1*, and a *35S::YHB(phyb-9 elf3-1)* line.

[0061] **FIG. 7C. Characterisation of additional *YHB elf3* alleles.** Assessment of circadian rhythms following transfer to constant darkness in additional *PHYB::YHB(elf3-2)* transformed lines. White boxes indicate periods of light irradiation in light:dark cycles prior to transfer to constant darkness. Dark grey segments indicate periods of darkness; light grey segments highlight periods of subjective daytime when held in constant darkness. Zeitgeber time is hours since last dawn.

[0062] **FIG. 7D. Characterisation of additional *YHB elf3* alleles.** Assessment of circadian rhythms following transfer to constant darkness in *35S::YHB(phyb-9 elf3-1)* seedlings. White boxes indicate periods of light irradiation in light:dark cycles prior to transfer to constant darkness. Dark grey segments indicate periods of darkness; light grey segments highlight periods of subjective daytime when held in constant darkness. Zeitgeber time is hours since last dawn.

[0063] **FIG. 8A. Venn diagram highlighting circadian-regulated promoters bound by phyB or ELF3.** Promoters bound by either phyB (red) or ELF3 (blue) are highlighted. 'Core' circadian gene list taken from Hsu and Harmer 2014.

[0064] **FIG. 8B. Patterns of gene expression correlate with reported binding patterns for phyB and ELF3.** Binding patterns of phyB (red) and ELF3 (blue) at *CCA1*, *LHY*, *PRR9* and *GI* loci at different temperatures (phyB data) or throughout the day (ELF3 data).

[0065] **FIG. 9A. *YHB elf3* plants retain daily variation of gene expression in light:dark cycles.** Luciferase bioluminescence reporting activity of the circadian-regulated *CCA1* promoter in transgenic Arabidopsis (*CCA1::LUC2*). Rhythms are maintained in all genotypes in driven light:dark cycles (indicated by black bars), but are lost in constant light (subjective night indicated by grey bars).

[0066] **FIG. 9B. *YHB elf3* plants retain daily variation of gene expression in light:dark cycles.** Daily patterns of gene expression (represented by *CCA1*- driven bioluminescence) are maintained in square-wave light conditions. White box indicates relative light intensity (right hand axis).

[0067] **FIG. 9C. *YHB elf3* plants retain daily variation of gene expression in light:dark cycles.** Daily patterns of gene expression (represented by *CCA1*- driven bioluminescence) are maintained in fluctuating light conditions. White box indicates relative light intensity (right hand axis).

[0068] **FIG. 10A. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Quantification of hypocotyl length of plants grown in constant darkness, short days, long days, or varied light cycles. Asterisks indicate a significantly different hypocotyl length than plants of the same genotype grown in constant darkness ($p < 0.05$). Short days describes daily cycles of 8hrs:16hrs light:dark (square-form), long days describes daily cycles of 16hrs:8hrs light:dark (square-form), varied light describes daily cycles of 1hrs 10 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 8hrs 40 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 5hrs 30 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 4hrs 10 $\mu\text{mol m}^{-2} \text{s}^{-1}$ white light followed by 6hrs of darkness.

[0069] **FIG. 10B. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Representative images of wild type (Col-0), *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings grown for 21 days under long days. Short days describes daily cycles of 8hrs:16hrs light:dark (square-form), long days describes daily cycles of 16hrs:8hrs light:dark (square-form), varied light describes daily cycles of 1hrs 10 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 8hrs 40 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 5hrs 30 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 4hrs 10 $\mu\text{mol m}^{-2} \text{s}^{-1}$ white light followed by 6hrs of darkness.

[0070] **FIG. 10C. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Rosette diameter at flowering of *Arabidopsis* plants grown under either long days or short days light. Short days describes daily cycles of 8hrs:16hrs light:dark (square-form), long days describes daily cycles of 16hrs:8hrs light:dark (square-form).

[0071] **FIG. 10D. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Flowering time of wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* plants grown under long (16 hr:8 hr light:dark) or short (8 hr:16 hr light:dark) days. Asterisks indicate a significant difference in flowering time between plants of the given genotype grown in long and short days ($p < 0.0001$). Short days describes daily cycles of 8hrs:16hrs light:dark (square-form), long days describes daily cycles of 16hrs:8hrs light:dark (square-form).

[0072] **FIG. 10E. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Flowering time of plants grown under 12:12 light dark cycles with 160 $\mu\text{mol m}^{-2} \text{s}^{-1}$ white light. After germination and establishment for 7 days at 22°C, plants were transferred to a constant temperature of either 22°C or 27°C as indicated.

[0073] **FIG. 10F. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Average rosette area over time of *Arabidopsis* plants grown under short days. Short days describes daily cycles of 8hrs:16hrs light:dark (square-form),

[0074] **FIG. 10G. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Average rosette area over time of plants grown under long days. Long days describes daily cycles of 16hrs:8hrs light:dark (square-form).

[0075] **FIG. 10H. *YHB elf3* plants demonstrate less developmental plasticity in response to varying environmental cues.** Expanded graph of FIG. 10F shows reduced growth in *YHB elf3* during the first 35 days of growth in short day conditions. Short days describes daily cycles of 8hrs:16hrs light:dark (square-form).

[0076] **FIG. 11A. *YHB* and *YHB (elf3)* seedlings retain responses to light and temperature.** Phase response curves of Col-0, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Seedlings were held in constant light for the indicated time (y axis) prior to release into constant darkness for imaging. Phase is reported relative to CT0 (dawn for entrained plants) and was defined as the time until maximal *CCA1*-driven bioluminescence.

[0077] **FIG. 11B. *YHB* and *YHB (elf3)* seedlings retain responses to light and temperature.** Circadian free running period estimates of plants transferred to varied intensities of white light at different constant temperatures. Wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings expressing a *CCA1::LUC2* reporter, entrained for 7 days under 12 hr:12 hr light:dark cycles at 22°C before transfer to constant light at a temperature of 12°C. Plants were imaged every 2 hours after transfer to constant light at the intensity indicated on the x-axis of each plot. Data shows the average free running periods from two independent experiments.

[0078] **FIG. 11C. *YHB* and *YHB (elf3)* seedlings retain responses to light and temperature.** Circadian free running period estimates of plants transferred to varied intensities of white light at different constant temperatures. Wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings expressing a *CCA1::LUC2* reporter, entrained for 7 days under 12 hr:12 hr light:dark cycles at 22°C before transfer to constant light at a temperature of 17°C. Plants were imaged every 2 hours after transfer to constant light at the intensity indicated on the x-axis of each plot. Data shows the average free running periods from two independent experiments.

[0079] **FIG. 11D. *YHB* and *YHB (elf3)* seedlings retain responses to light and temperature.** Circadian free running period estimates of plants transferred to varied intensities of white light at different constant temperatures. Wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings expressing a *CCA1::LUC2* reporter, entrained for 7 days under 12 hr:12 hr light:dark cycles at 22°C before transfer to constant light at a temperature of 22°C. Plants were imaged every 2 hours after transfer to constant light at the intensity indicated on the x-axis of each plot. Data shows the average free running periods from two independent experiments.

[0080] **FIG. 11E. *YHB* and *YHB (elf3)* seedlings retain responses to light and temperature.** Circadian free running period estimates of plants transferred to varied intensities of white light at different constant temperatures. Wild type, *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings expressing a *CCA1::LUC2* reporter, entrained for 7 days under 12 hr:12 hr light:dark cycles at 22°C before transfer to constant light at a temperature of 27°C. Plants were imaged every 2 hours after transfer to constant light at the intensity indicated on the x-axis of each plot. Data shows the average free running periods from two independent experiments.

[0081] **FIGs. 12A-12D. Additional description of data presented in FIGs. 11B-11E.** Data from FIGs. 11B-11E is replotted as temperature response curves.

[0082] **Fig 13.** Diagrammatic representation of a nucleic acid modification in a polynucleotide encoding an *elf3* protein in pennycress generated using CRISPR editing. Two independent editing events resulting in either a 7 bp or 1683 bp deletion are shown as a comparison of the sequencing chromatogram (below) to the genomic sequence (above) starting from the start of translation in exon 1. The gene structure of pennycress *ELF3* is represented by exons as thick black rectangles and introns as thin black lines.

DETAILED DESCRIPTION

[0083] The present disclosure is based in part on the surprising demonstration of reduced developmental plasticity obtained when a combination of two or more genetic modifications in the environmental sensing and circadian clock mechanisms of the plant

provides advantages over each genetic modification individually. More specifically, the inventors surprisingly discovered that ability of the plant to sense and respond to environmental cues, when combined with a modification of a circadian function of the plant, can reduce the plasticity of the plant in response to changes in environmental conditions during growth all while exhibiting improved agronomic traits regardless of changing environmental conditions. For instance, plants comprising both genetic modifications can flower consistently and uniformly regardless of differences in day length, at varied latitudes, in the face of climate change, increasing temperatures and disrupting weather patterns, or any combination thereof. The genetic modifications increase the uniformity of crops so that harvesting time is more predictable and quality is consistent in intensive, precision outdoor farming practices and Total Controlled Environment Agriculture (TCEA, or vertical farming).

I. Genetically modified plants

[0084] One aspect of the present disclosure encompasses a genetically modified plant, plant tissues, part thereof, plant cell, or seed (hereinafter referred to as “genetically modified plants” or “modified plants”) having reduced developmental plasticity and improved agronomic traits. The modified plants comprise at least two genetic modifications that modify the expression of two or more components of the circadian system. The main components of a circadian system are the central oscillator (the circadian clock) that controls circadian functions by maintaining a roughly 24-h rhythm even in the absence of input signals, the input signals from the environment that reset the clock, and the output signals that generate daily rhythms in pathways associated with development, physiology, and metabolism. As used herein, the term “circadian function” is defined as the effect on plant growth and development resulting from the circadian system in response to sensed environmental factors. Non-limiting examples of circadian functions include transitions from shoot elongation, regulation of root gravitropism, altered flowering time, growth cessation of leaves, and timing of germination, the synthesis of chlorophyll, de-etiolation (when a seedling emerges into

the light and starts its photo-autotrophic life style), stomata development, transition to flowering, senescence, shade avoidance, elongation of seedlings, size, shape, number, and movement of leaves, and the timing of flowering in adult plants

[0085] In some aspects, the modified plants comprise a nucleic acid modification in a polynucleotide encoding a component of the circadian clock and a nucleic acid modification of a polynucleotide encoding an environmental signal sensor. The nucleic acid modifications modify the expression of the component of the circadian clock and the environmental signal sensor. As used herein, “expression” includes but is not limited to one or more of the following: transcription of a gene into precursor mRNA; splicing and other processing of the precursor mRNA to produce mature mRNA; mRNA stability; translation of the mature mRNA into protein (including codon usage and tRNA availability); production of a mutant protein comprising a mutation that modifies the activity of the protein; and glycosylation and/or other modifications of the translation product, if required for proper expression and function.

[0086] Components of the circadian clock and genetic modifications in components of the circadian clock are described in **Section I(a)**. Environmental signal sensors and genetic modifications that modify expression of environmental signal sensors are described in **Section I(b)**.

(a) Circadian clock

[0087] A modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a component of the circadian clock. The genetic modification modifies a function of the circadian system. In some aspects, the modification that modifies a function of the circadian system comprises a modification of an endogenous polynucleotide sequence encoding a component of the circadian clock.

[0088] In plants, the circadian clock is a complex gene regulatory network of repressors and activators that form multiple interlocking feedback loops (**FIG. 1**). These clock genes are expressed at specific times of the day, regulate each other's expression, and influence multiple pathways and mechanisms of development,

physiology, and metabolism. The circadian clock ensures that a plant is most responsive to light during daylight hours, to growth hormones during the night, and to environmental stresses at times when adverse conditions are most likely. To appropriately regulate plant responses to external factors, the clock is directly linked with the light and temperature-signaling pathways, which also ensures synchronicity between the external and internal rhythms (See **Section I(b)** herein below). The cross talk between these regulatory pathways also provides seasonal information to the plant, allowing for example the determination of day length for the appropriate control of the transition to flowering.

[0089] A genetic modification of the instant disclosure that modifies a function of the circadian clock can modify any component of the circadian clock. The network of intertwined feedback loops of the plant circadian clock comprises repressor and activator transcription factors among other factors. Levels of these proteins are in constant flux, each peaking at a specific time of day and feeding back to regulate each other's expression. In *Arabidopsis*, the morning-expressed MYB-like transcription factors CCA1 (CIRCADIAN CLOCK ASSOCIATED1) and LHY (LATE ELOGATED HYPOCOTYL) repress the afternoon expressed PSEUDO-RESPONSE REGULATOR (PRR) genes, including PRR1/TOC1 (TIMING OF CAB EXPRESSION 1), PRR5, PRR7, and PRR9. TOC1, along with the other PRR proteins, in turn, repress the expression of CCA1 and LHY, closing this feedback loop. CCA1/LHY are themselves primarily repressors of transcription and bind to a cis-motif termed the evening element (EE) found in the regulatory regions of many clock genes, including the PRRs. Other direct targets of CCA1/LHY activity include genes that encode members of the transcriptional regulatory evening complex, ELF3 (EARLY FLOWERING3), ELF4, and LUX (LUX ARRHYTHMO). These three genes are expressed at night, at which time the evening complex feeds back to repress multiple morning- and afternoon-expressed genes to complete another feedback loop in the network (**FIG. 1**).

[0090] The circadian regulatory network in plants also comprises a second set of midday-expressed MYB-like transcription factors, REVEILLE4 (RVE4), RVE6, and

RVE8, have been shown to activate expression of several clock genes including TOC1, the PRRs and the evening complex genes. To activate gene expression, RVE8 forms a complex with LNK1 (NIGHT LIGHT-INDUCIBLE AND CLOCK-REGULATED1) and LNK2 and associates with the promoters of TOC1 and PRR5. The RVE activator proteins are not simply a second layer of regulation on top of the core circadian clock but are connected and embedded into the clock regulatory network (**FIG. 1**). RVE8 expression is repressed by TOC1 and the PRRs, forming yet another negative feedback loop in this network.

[0091] Land plants contain an additional family of LOV UV-A/blue light photoreceptors/clock proteins comprising ZEITLUPE (ztl), FLAVIN-BINDING, KELCH REPEAT, F-BOX (fkl1) and LOV KELCH PROTEIN 2 (lkp2) proteins (collectively referred to as Zeirlupes). In contrast to the phototropins, Zeirlupes contain a single FMN-binding LOV domain followed by an F-box and six Kelch repeats. As suggested by their domain organization, Zeirlupes form SCF E3 ubiquitin ligase complexes directly controlling light-mediated protein degradation. LOV domains are also found associated with other output domains including DNA binding b-ZIP in aureochromes from photosynthetic stramenopile algae. Therefore, LOV domains are versatile light absorption modules mediating different biochemical outputs.

[0092] ZEITLUPE (ZTL) is unique in being both a component of the plant clock and a blue-light photoreceptor. ZTL interacts directly with GIGANTEA (GI), another clock component, and this interaction is stabilized by blue light via the photosensory LOV domain of ZTL. This ZTL–GI complex can maintain circadian rhythms by influencing the stability of both TOC1 and GI proteins. GI stability is also affected by a second protein complex that includes ELF3 and COP1 (CONSTITUTIVE PHOTOMORPHOGENIC1) that acts downstream from the blue light photoreceptor CRY2. The ELF3–COP1 complex targets GI for degradation and represents yet another point at which light signals are integrated into the circadian clock network. The LNK2 and RVE8 complex also appears to play a role in the integration of the clock and light-signaling pathways (**FIG. 2A**). It is possible that clock entrainment relies on the induction

of LNK expression by phytochromes in conjunction with the early morning expression of CCA1 and LHY.

[0093] A modified plant of the instant disclosure can comprise nucleic acid modifications that modify expression of any protein or factor that functions in the circadian clock of a plant. Accordingly, a modified plant of the instant disclosure can comprise a genetic modification of a polynucleotide encoding an MYB-like transcription factor, a PSEUDO-RESPONSE REGULATOR (PRR) protein, a protein of the evening complex (EC), a zeitlupe protein, or any combination thereof. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding an MYB-like transcription factor that modifies the expression of the MYB-like transcription factor. In other aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a PRR protein that modifies the expression of the MYB-like transcription factor PRR protein. In yet other aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a protein of the evening complex that modifies the expression of the protein of the evening complex. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a zeitlupe protein that modifies the expression of the zeitlupe protein.

[0094] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding CCA1, LHY, PRR1/TOC1, PRR5, PRR7, PRR9, ELF3, ELF4, LUX, ZTL, FKF1, LKP2, GI, COP1, LNK2, REV4, REV6, RVE8, LNK1, LNK2, TOC1, or any combination thereof. In other aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding ELF3, ELF4, LUX, or any combination thereof. In some aspects, the modified plant comprises a genetic modification of a polynucleotide encoding ELF4. In some aspects, the modified plant comprises a genetic modification of a polynucleotide encoding LUX.

[0095] In some aspects, the modified plant comprises a genetic modification of a polynucleotide encoding ELF3. In some aspects, a genetic modification of a

polynucleotide encoding ELF3 modifies expression of ELF3. In some aspects, a genetic modification of a polynucleotide encoding ELF3 reduces expression of ELF3. Methods of reducing expression of a protein or RNA in a plant are known in the art and include, without limitation, introducing a genetic modification in an endogenous nucleic acid sequence that regulates expression of the protein, introducing a programmable transcription regulation system, or modifying the protein to generate a defective protein. In some aspects, expression of the ELF3 protein is reduced. In some aspects, expression of the ELF3 protein is reduced by introducing into the plant a loss of function mutation in an endogenous polynucleotide expressing ELF3.

[0096] In some aspects, the modified plant is a modified *Arabidopsis thaliana* (*A. thaliana*). When the plant is *A. thaliana*, the polynucleotide encoding ELF3 can comprise a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 1. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 1. In some aspects, the polynucleotide encoding ELF3 comprises an amino acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 2. In some aspects, the polynucleotide encoding ELF3 comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 2.

[0097] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide comprising a loss-of-function mutation in a nucleic acid sequence encoding ELF3. In some aspects, a nucleic acid sequence encoding ELF3 and comprising a loss-of-function mutation comprises about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 3, SEQ ID NO: 4, or a combination thereof. In some aspects, a nucleic acid sequence encoding ELF3 and comprising a loss-of-function mutation comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 3, SEQ ID NO: 4, or a combination thereof.

[0098] In some aspects, the modified plant is a modified *Thlaspi arvense* (*T. arvense*; pennycress). In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20.

[0099] In some aspects, the polynucleotide encoding ELF3 comprises an amino acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 21. In some aspects, the polynucleotide encoding ELF3 comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 21.

[00100] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide comprising a loss-of-function mutation in a nucleic acid sequence encoding ELF3. In some aspects, the genetic modification of the polynucleotide encoding the ELF3 protein comprises a deletion of a nucleic acid segment in the polynucleotide encoding the ELF3 protein, wherein the nucleic acid segment comprises about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 22, a sequence

comprising the AGCGCTA nucleic acid sequence, or a combination thereof. In some aspects, the genetic modification of the polynucleotide encoding the ELF3 protein comprises a deletion of a nucleic acid segment in the polynucleotide encoding the ELF3 protein, wherein the nucleic acid segment comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof.

[00101] In some aspects, the genetic modification of the polynucleotide encoding the ELF3 protein comprises a genetic modification introduced by a programmable nucleic acid modification system comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA). In some aspects, the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof. In some aspects, the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof.

[00102] In some aspects, the modified plant is a modified basil plant. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13.

[00103] In some aspects, the genetic modification of the polynucleotide encoding the ELF3 protein comprises a genetic modification introduced by a programmable nucleic acid modification system comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA). In some aspects, the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof. In some aspects, the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.

(b) Environmental signal

[00104] A modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a component of the circadian clock. The genetic modification of the polynucleotide encoding a component of the circadian clock modifies the ability of a plant to receive environmental signal, respond to a received environmental signal, or both. In some aspects, a genetic modification of the polynucleotide encoding a component of the circadian clock modifies expression of the environmental signal sensor. In some aspects, the modification of a polynucleotide encoding a component of the circadian clock comprises a modification of an endogenous polynucleotide sequence encoding an environmental signal sensor. In some aspects, modification of the endogenous polynucleotide encoding the environmental signal sensor modifies expression of the environmental signal sensor. In some aspects, the modification of a polynucleotide encoding a component of the circadian clock comprises an introduced exogenous polynucleotide sequence encoding

an environmental signal sensor. In some aspects, the introduced exogenous polynucleotide sequence encoding an environmental signal sensor modifies expression of the environmental signal sensor.

[00105] Circadian clocks must be continually adjusted by environmental cues so that the processes they control are appropriately timed even as temperature, day-length, and other environmental cues change throughout the life of the plant. Non-limiting examples of environmental signals that can influence the circadian clock include photoperiod, light intensity and quality, temperature, chemicals, gravity, moisture, biotic or abiotic stress, oxygen and carbon dioxide concentrations, carbohydrate availability, , or any combination thereof.

[00106] The plant clock uses multiple mechanisms to sense and integrate external environmental signals into the feedback loops described above (**FIG. 2A-B**). Non-limiting examples of environmental signal sensors through which plants sense and communicate the environmental signal to the circadian clock include photoreceptors, temperature sensors, CO₂ sensors, O₂ sensors, ethylene sensors, gravitropic sensors, or any combination thereof. Accordingly, a modified plant of the instant disclosure can comprise a genetic modification of a polynucleotide encoding one or more of a photoreceptor, a temperature sensor, or any combination thereof.

A. Photoreceptors

[00107] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a photoreceptor, wherein the nucleic acid modification modifies the expression of the photoreceptor and the response of the plant to changes in photoperiod, intensity, and quality, or any combination thereof. Photoreceptors can sense environmental cues, such as irradiance, day-night transition, photoperiods, and light quality. Non-limiting examples of photoreceptors include phytochromes, phototropins, cryptochromes, F-box containing Flavin binding proteins (e.g., *ZEITLUPE*, *FKF1/LKP2*), UV-B resistance 8 (UVR8), or any combination thereof.

[00108] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a phototropin. Phototropins are photoreceptor proteins (more specifically, flavoproteins) that mediate phototropism responses in higher plants. Phototropins can be important for the opening of stomata and the movement of chloroplasts. These blue light receptors are seen across the entire green plant lineage. Phototropins are part of the phototropic sensory system in plants that causes various environmental responses in plants. Phototropins specifically will cause stems to bend towards light and stomata to open. Phototropins have been shown to impact the movement of chloroplast inside the cell. In addition, phototropins mediate the first changes in stem elongation in blue light prior to cryptochrome activation. Phototropins are also required for blue light mediated transcript destabilization of specific mRNAs in the cell. Non-limiting examples of phototropins include PHOT1 and PHOT2, or any combination thereof. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding PHOT1 that modifies the expression of PHOT1. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding PHOT2 that modifies the expression of PHOT2.

[00109] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a cryptochrome, wherein the nucleic acid modification modifies the expression of the cryptochrome. Cryptochromes (CRY) are UV-A/blue photoreceptors ubiquitously found in bacteria, fungi, animals, and plants sharing a common evolutionary ancestor with DNA photolyases. Cryptochromes regulate growth and development in plants and the circadian clock in plants and animals. The *Arabidopsis* genome encodes three cryptochrome genes, CRY1, CRY2, and CRY3. CRY1 and CRY2 act primarily in the nucleus, whereas CRY3 likely functions in chloroplasts and mitochondria. *Arabidopsis* CRY1 and CRY2 mediate primarily blue light regulation of de-etiolation and photoperiodic control of flowering, respectively. In addition, these two photoreceptors regulate other aspects of plant growth and development, including entrainment of the circadian clock, guard cell development and

stomatal opening, root growth, plant height, fruit and ovule size, tropic growth, apical dominance, apical meristem activity, programmed cell death, the high-light stress response, osmotic stress response, shade avoidance, and responses to bacterial and viral pathogens. *Arabidopsis* CRY3 belongs to the CRY-DASH clade of the photolyase/cryptochrome superfamily, and it is known to act as a single-stranded DNA repairing enzyme. However, CRY-DASH of some organisms have been reported to possess both DNA-repairing enzyme activity and photosensory activity. *Arabidopsis* CRY3 can also act as a dual function photoreceptor in mitochondria and chloroplasts. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding CRY1 that modifies the expression of CRY1. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding CRY2 that modifies the expression of CRY2. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding CRY3 that modifies the expression of CRY3.

[00110] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a ZEITLUPE (ZTL) protein that modifies the expression of zeitlupe protein. Zeitlupes can be as described in **Section I(a)** herein above.

[00111] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a UVR8 protein that modifies the expression of the phytochrome UVR8 protein. UVR8 is a UV-B – sensing protein found in plants. It is responsible for sensing ultraviolet light in the range 280-315 nm and initiating the plant stress response. UVR8 has also been shown to be functionally linked with the circadian clock in plants.

[00112] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a phytochrome that modifies the expression of the phytochrome. The phytochrome-signaling pathway is one of the main mechanisms through which plants sense and respond to changes in red light availability and is directly linked to the clock regulatory network. Phytochromes (phys) are the

primary red and far-red light photoreceptors in plants and consist of a five-member protein family in *Arabidopsis*; PhyA, PhyB, PhyC, PhyD, and PhyE. Phys reversibly switch between P_r and P_{fr} forms upon absorption of red or far-red light, respectively, and the ratio of these forms within the cell controls the shade avoidance response and contributes to light perception. PhyA is the most divergent phy, with a specialized role as a far-red light sensor, whereas phyB is the predominant red light sensor in *Arabidopsis*. Although oscillation of circadian transcripts is dampened under constant far-red light, phyA retains photoregulatory control of these and other genes under these conditions. By contrast, phyA, phyB, phyC, and phyD each appear to contribute to maintenance of circadian rhythms under constant red light. PhyD single mutants have a wild-type circadian phenotype but have an additive effect when introgressed into a phyB background.

[00113] Of the phytochrome receptors, phytochrome B (phyB) is the main red-light receptor and its effects on plant growth and development have been extensively studied. PhyB photoconverts from an inactive form (P_r) to an active form (P_{fr}) on absorption of red light. P_{fr} interacts with the PHYTOCHROME-INTERACTING FACTORS (PIFs) and targets these transcription factors for degradation during the day to limit cell elongation to the nighttime hours. PIF proteins have been established as transcriptional regulators of morning expressed LHY and CCA1, directly linking the light and clock regulatory networks. Recently, PIFs have also been shown to mediate metabolic signals to the circadian oscillator. Another link between the clock- and light-signaling pathways occurs via interactions between phyB and the evening complex protein ELF3. ELF3 also binds to PIF4 independently of the other evening complex components to repress PIF4 function, thus regulating a light-signaling component controlling hypocotyl elongation. Similarly, TOC1 and other PRR proteins have been shown to bind directly to PIF3 and PIF4 and inhibit their ability to activate transcription. Thus, the association of PRR factors with PIFs on the G-box elements of target promoters serves to limit PIF transactivation function to the predawn hours. The PRRs and the evening complex have also been shown to regulate transcription of PIF genes.

Thus, both ELF3 and the PRR proteins limit the function and expression of the important growth regulatory PIF factors and provide further links between clock and light regulation of growth (**FIG. 2A**).

[00114] Accordingly, a modified plant of the instant disclosure can comprise a genetic modification of a polynucleotide encoding one or more of phyA, phyB, phyC, phyD, phyE, a PIF protein, or any combination thereof. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding phyA. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding phyC. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding phyD. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding phyE.

[00115] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding PhyB. In some aspects, the genetic modification of the polynucleotide encoding the PhyB photoreceptor modifies expression of the PhyB photoreceptor. In some aspects, the polynucleotide encoding PhyB comprises a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 5 or SEQ ID NO: 27. In some aspects, the polynucleotide encoding PhyB comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 5 or SEQ ID NO: 27. In some aspects, the polynucleotide encoding PhyB comprises an amino acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 6 or SEQ ID NO: 28. In some aspects, the polynucleotide encoding PhyB comprises an amino acid sequence comprising at least

about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 6 or SEQ ID NO: 28.

[00116] In some aspects, a genetic modification of a polynucleotide encoding PhyB increases expression of PhyB. For instance, a genetic modification can increase expression of PhyB by, without limitation, overexpressing PhyB, constitutively expressing PhyB, expressing a constitutively active PhyB photoreceptor, or any combination thereof. In some aspects, a genetic modification can increase expression of PhyB by overexpressing PhyB. Methods of overexpressing a protein or RNA in a plant are known in the art and include, without limitation, introducing an expression construct expressing the protein to thereby generate a modified plant comprising multiple copies of the polypeptide encoding the protein, introducing an expression construct expressing the protein under the control of a constitutive promoter, introducing a genetic modification in an endogenous nucleic acid sequence that regulates expression of the protein, introducing a programmable transcription regulation system, or modifying the protein to generate a constitutively active protein. In some aspects, the phytochrome B photoreceptor is overexpressed, constitutively expressed, or constitutively active, or any combination thereof. In some aspects, the phytochrome B receptor is overexpressed, constitutively expressed, and constitutively active.

[00117] In some aspects, a genetic modification of a polynucleotide encoding a phyB photoreceptor encodes a constitutively active phyB photoreceptor. In some aspects, a genetic modification of a polynucleotide encoding a phyB photoreceptor encodes a constitutively expressed and constitutively active phyB photoreceptor.

[00118] The constitutively active phyB photoreceptor can be encoded by a polynucleotide comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof. In some aspects, the constitutively active phyB photoreceptor is encoded by a polynucleotide comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or

100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, ~~SEQ ID NO: 32~~, or any combination thereof. The constitutively active phyB photoreceptor can comprise an amino acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof. In some aspects, the constitutively active phyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.

[00119] In some aspects, the modified plant is a modified *A. thaliana*. When the plant is *A. thaliana*, the plant can comprise a genetic modification of a polynucleotide encoding a phyB photoreceptor comprising a modified activity. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a constitutively active phyB photoreceptor. In some aspects, the constitutively active phyB photoreceptor is YHB and is encoded by a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof. In some aspects, the constitutively active phyB photoreceptor is YHB and is encoded by a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, SEQ ID NO: 27, or any combination thereof. In some aspects, the amino acid sequence of the constitutively active YHB comprises about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any

combination thereof. In some aspects, the amino acid sequence of YHB comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.

[00120] In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a phyB photoreceptor comprising a modified activity. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a constitutively active phyB photoreceptor. In some aspects, the constitutively active phyB photoreceptor is YHB and is encoded by a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof. In some aspects, the constitutively active phyB photoreceptor is YHB and is encoded by a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof. In some aspects, the amino acid sequence of the constitutively active YHB comprises about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, or a combination thereof. In some aspects, the amino acid sequence of YHB comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, or a combination thereof.

[00121] In some aspects, the modified plant is a modified *T. arvense*. In some aspects, the modified plant is *Thlaspi arvensis* (*T. arvensis*). In some aspects, the modified *T. arvensis* plant comprises a genetic modification of a polynucleotide encoding PhyB, wherein the polynucleotide comprising the genetic modification encodes a constitutively active PhyB photoreceptor.

[00122] In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof. In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.

[00123] In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof. In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof.

[00124] In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 26. In some aspects, the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 26.

[00125] In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25. In some aspects, the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25.

B. Temperature sensors

[00126] Temperature is another environmental signal that is integrated into the clock network (**FIG. 2B**). Accordingly, a modified plant of the instant disclosure can comprise a modified response to temperature changes.

[00127] A temperature sensor can be a photoreceptor as plant photoreceptors can also function as temperature receptors. One such receptor is phyB, with the rate of reversion from the active P_{fr} form to the inactive P_r form increasing at higher temperatures.

[00128] In some aspects, a modified plant of the instant disclosure comprising a modified response to temperature changes comprises a genetic modification in a polynucleotide encoding a phyB protein that modifies the activity of the phyB protein, thereby modifying the response of the modified plant to temperature changes. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a phyB photoreceptor comprising a modified activity. In some aspects, a modified plant of the instant disclosure comprises a genetic modification of a polynucleotide encoding a constitutively active phyB photoreceptor. PhyB photoreceptors, genetic modifications of polynucleotides encoding PhyB photoreceptors, and modified plants comprising the polynucleotides can be as described in **Section I(b)(A)** herein above.

[00129] PIF4 has also been shown to respond to changes in temperature to alter plant development and morphology. Because degradation of PIF4 is promoted by P_{fr} , the increased rate of P_{fr} to P_r reversion at higher temperatures may account for the warm temperature-induced posttranscriptional accumulation of PIF4 protein.

Accordingly, a modified plant of the instant disclosure comprising a modified response to temperature changes can comprise a genetic modification in a polynucleotide encoding a PIF4 protein that modifies the expression of the PIF4 protein thereby modifying the response of the modified plant to temperature changes.

[00130] Temperature has also been shown to regulate the activity of the evening complex. At higher temperatures, association of ELF3 with target promoters is reduced. Thus, in warm conditions, evening-complex mediated repression of targets such as the clock genes PRR7, PRR9, GI, LUX, and the growth regulating PIF4 is relieved, leading to elevated levels of these transcripts during warm nights. Integration of cold temperature cues into the clock network can occur via CBF1/DREB1a (COLD-INDUCIBLE C-REPEAT/DROUGHT-RESPONSIVE ELEMENT-BINDING FACTOR). CBF1 expression is highly induced by cold, and this factor has been shown to bind directly to the promoter of the evening complex component LUX and promote its high-amplitude rhythmic expression at cold temperatures. Intriguingly, phyB and PIF proteins have been reported to repress CBF1 expression, suggesting links between distinct temperature-sensing pathways. Finally, expression of CBF1 is regulated by a number of clock components including the PRRs, the evening complex, and CCA1/LHY, providing yet another example of the ubiquitous feedback loops found in the circadian system. Accordingly, a modified plant of the instant disclosure comprising a modified response to temperature changes can comprise a genetic modification in a polynucleotide encoding any of the above cited proteins thereby modifying the response of the modified plant to temperature changes.

(c) Genetically modified plants

[00131] As sessile organisms, plants are unable to seek out environmental conditions optimal for their growth and development. Instead, plants rely on their remarkable developmental plasticity to adapt to their environment throughout the life of the plant. By integrating environmental information into the regulation of growth and developmental processes, plant can modulate growth and development according to the

environment in which the plant is growing. In this way, the final morphology of the plant depends on the environment, defining it as plastic. Plant development starts with a seedling lacking most species-specific characteristics of the adult as a result of plant embryogenesis. Spreading developmental decisions throughout the life cycle provides the opportunity to integrate environmental information into the regulation of these growth and developmental processes, to thereby tune body form and function to the changing environment. For instance, when faced with a spell of unusually elevated temperatures before or during flower initiation and/or development, a plant may respond by reducing the number of flowers or seeds in anticipation of further scarcity of resources.

[00132] While this is advantageous in natural conditions where resources and environmental stresses vary across seasons, location, and in response to unusual weather patterns, plasticity can be disadvantageous under cultivated conditions, resulting in at least reduced yields. In modern crop monoculture, plants are grown under intensive agricultural practices, a plant may not need to adjust in anticipation of harsh conditions as the plant is provided with sufficient resources. In at least that sense, plants with reduced plasticity such as plants of the instant disclosure are well suited for intensive, precision outdoor farming, TCEA, and/or vertical farming). For instance, in one aspect, the modified plants of the instant disclosure flower consistently and uniformly regardless of differences in day length, at varied latitudes, in the face of climate change, increasing temperatures and disrupting weather patterns, or any combination thereof. Importantly, genetically modified plants of the instant disclosure comprising the combination of modifications can provide beneficial agronomic traits without any of the deleterious effects that can be associated with each genetic modification individually. For instance, plants comprising a constitutively active phyB photoreceptor when combined with a loss-of-function mutation in an *ELF3* gene is not etiolated (a phenotype of a loss-of-function mutation in an *ELF3* gene without a constitutively active phyB) and can flower earlier than plants comprising either mutation alone.

[00133] Plants of the instant disclosure comprise genetic modifications that modify expression of a component of the circadian clock and expression of an environmental signal sensing function. A genetic modification that modifies expression of a component of the circadian clock can results in a modification of a circadian function. A circadian function can be any developmental, physiological, and/or metabolic function that could be affected by the circadian clock. Non-limiting examples of circadian functions include transitions from shoot elongation, regulation of root gravitropism, altered flowering time, growth cessation of leaves, and timing of germination, the synthesis of chlorophyll, de-etiolation (when a seedling emerges into the light and starts its photo-autotrophic life style), stomata development, transition to flowering, senescence, shade avoidance, elongation of seedlings, size, shape, number, and movement of leaves, and the timing of flowering in adult plants.

[00134] Further the resulting plants exhibit agronomic traits beneficial for crop production using modern agricultural practices. Non-limiting examples of beneficial or desirable agronomic traits include accelerated or delayed flowering, consistent flowering, seed quality, seed protein content, seed protein composition, seed oil content, seed oil composition, yield, seed set, response to photoperiod, abiotic stress tolerance, biotic stress tolerance, flowering time and maturity, regulation of circadian clock light response-related flowering, high latitude adaptation, earlier flowering, reduced cellular elongation response to increasing temperature, a uniform time of flowering, consistent secondary metabolite production or any combination thereof. The genetic modifications can stabilize the production of valuable metabolites, compounds, and proteins by reducing fluctuations in metabolism and protein synthesis in plants that produce such molecules for chemistry and pharmaceutical uses. The genetic modifications can reduce temperature-induced architectural changes in plant height, petiole, internode, and organ elongation, allowing plants to maintain their ideotype under temperature changes. The genetic modifications can reduce responsiveness to reduced light quality and shade conditions, preventing unnecessary elongation and competition with neighboring plants.

[00135] In some aspects, modified plants of the instant disclosure comprise a genetic modification of a polynucleotide encoding a component of the circadian clock that modifies expression of the component of the circadian clock; and a genetic modification of a polynucleotide encoding an environmental signal sensor that modifies expression of the environmental signal sensor. The modified expression of the component of the circadian clock and the modified expression of the environmental signal sensor causes the plant to have reduced developmental plasticity in response to changes in environmental conditions during growth and modified circadian function. In some aspects, the component of the circadian clock comprising modified expression is an ELF3 protein and the environmental signal sensor is a PhyB photoreceptor. In some aspects, when the component of the circadian clock comprising modified expression is an ELF3 protein and the environmental signal sensor is a PhyB photoreceptor, the modified plant of the instant disclosure comprises a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation and a polynucleotide encoding a constitutively active PhyB photoreceptor. ELF3 proteins, PhyB photoreceptors, polynucleotides encoding the ELF3 proteins and PhyB photoreceptors, genetic modifications of polynucleotides encoding the ELF3 proteins and PhyB photoreceptors, and modified plants comprising the modified polynucleotides can be as described in **Sections I(a) and I(b)** herein above.

[00136] In some aspects, a modified plant of the instant disclosure is *A. thaliana*. When the modified plant is *A. thaliana*, the plant can comprise a polynucleotide comprising an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof. In some aspects, the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence

identity with an amino acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof. Further, when the modified plant is *A. thaliana*, the plant can comprise a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof. In some aspects, the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof. Additionally, when the modified plant is *A. thaliana*, the plant can comprise a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence SEQ ID NO: 7. In some aspects, the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7.

[00137] In some aspects, a modified plant of the instant disclosure is *T. arvensis*. When the modified plant is *T. arvensis*, the plant can comprise a polynucleotide comprising an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof. In some aspects, the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID

NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof. Further, when the modified plant is *T. arvensis*, the plant can comprise a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with an amino acid sequence SEQ ID NO: 25, SEQ ID NO: 27, or a combination thereof. In some aspects, the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25, SEQ ID NO: 27, or a combination thereof.

II. Engineered nucleic acid modification system

[00138] One aspect of the present disclosure encompasses a system for modifying an environmental signal sensor in a plant. Non-limiting examples of suitable systems for modifying an environmental signal sensor in a plant include programmable nucleic acid modification systems, an expression constructs comprising a promoter operably linked to a polynucleotide encoding a polypeptide or polynucleotide, or any combination thereof. In some aspects, the system comprises a nucleic acid construct comprising at least one or both of a programmable nucleic acid modification system comprising a targeting nucleic acid sequence targeting a nucleic acid sequence in a polynucleotide sequence encoding a component of the circadian clock; and an expression construct comprising a promoter operably linked to a polynucleotide encoding a polynucleotide encoding an environmental signal sensor. The programmable nucleic acid modification system introduces a loss of function mutation into the polynucleotide sequence encoding the component of the circadian clock, and the expression construct comprising a promoter operably linked to a polynucleotide encoding a polynucleotide encoding an environmental signal sensor increases expression of the environmental signal sensor, thereby causing the plant to exhibit

reduced developmental plasticity in response to changes in environmental conditions during growth, and modified circadian function.

[00139] In some aspects, the nucleic acid modification system is an expression construct comprising a promoter operably linked to a polynucleotide encoding a component of the circadian clock, an expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor, or a combination thereof. In some aspects, the nucleic acid modification system is an expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor. Environmental signal sensors, polynucleotides encoding the environmental signal sensors, genetic modifications of polynucleotides encoding the environmental signal sensors, and modified plants comprising the modified polynucleotides can be as described in **Section I(b)** herein above. Expression constructs can be as described in **Section III** herein below.

[00140] In other aspects, the nucleic acid modification system is a programmable nucleic acid modification system targeted to a nucleic acid sequence in a polynucleotide encoding a component of the circadian clock, encoding an environmental signal sensor, or a combination thereof. In some aspects, the expression construct comprising a promoter operably linked to a polynucleotide encoding a polynucleotide encoding an environmental signal sensor increases expression of the environmental signal sensor. Programmable nucleic acid modification systems are described in **Section II(a)** herein below.

(a) Programmable nucleic acid modification systems

[00141] As used herein, a “programmable nucleic acid modification system” is a system capable of targeting a nucleic acid sequence in a polynucleotide and modifying the nucleic acid sequence of the polynucleotide or modifying the expression of the polynucleotide. Accordingly, a programmable nucleic acid modification system can be used to alter a polynucleotide or to alter a protein encoded by the nucleic acid sequence. A programmable nucleic acid modification system can also be used to

modify the expression of a nucleic acid sequence encoded by the polynucleotide or modify the expression of a polypeptide encoded by the polynucleotide. In the context of a genetic modification of polynucleotides encoding components of the circadian clock, and environmental signal sensors, the programmable nucleic acid modification system specifically targets a nucleic acid sequence in a polynucleotide encoding the components of the circadian clock, environmental signal sensors, or any combination thereof. The programmable nucleic acid modification system can comprise an interfering nucleic acid molecule or a nucleic acid editing system.

A. RNAi

[00142] In some aspects, the programmable expression modification system comprises an interfering nucleic acid (RNAi) molecule having a nucleotide sequence complementary to a target sequence within a gene encoding the polypeptide or polynucleotide used to inhibit expression of the polypeptide or polynucleotide. RNAi molecules generally act by forming a heteroduplex with a target RNA molecule, which is selectively degraded or “knocked down,” hence inactivating the target RNA. Under some conditions, an interfering RNA molecule can also inactivate a target transcript by repressing transcript translation and/or inhibiting transcription. An interfering RNA is more generally said to be “targeted against” a biologically relevant target, such as a protein, when it is targeted against the nucleic acid encoding the target. For example, an interfering RNA molecule has a nucleotide (nt) sequence which is complementary to an endogenous mRNA of a target gene sequence. Thus, given a target gene sequence, an interfering RNA molecule can be prepared which has a nucleotide sequence at least a portion of which is complementary to a target gene sequence. When introduced into cells, the interfering RNA binds to the target mRNA, thereby functionally inactivating the target mRNA and/or leading to degradation of the target mRNA.

[00143] Interfering RNA molecules include, inter alia, small interfering RNA (siRNA), microRNA (miRNA), piwi-interacting RNA (piRNA), long non-coding RNAs

(long ncRNAs or lncRNAs), and small hairpin RNAs (shRNA). lncRNAs are widely expressed and have key roles in gene regulation. Depending on their localization and their specific interactions with DNA, RNA and proteins, lncRNAs can modulate chromatin function, regulate the assembly and function of membraneless nuclear bodies, alter the stability and translation of cytoplasmic mRNAs, and interfere with signaling pathways. Piwi-interacting RNA (piRNA) is the largest class of small non-coding RNA molecules expressed in animal cells. piRNAs regulate gene expression through interactions with piwi-subfamily Argonaute proteins. siRNA are double-stranded RNA molecules, preferably about 19-25 nucleotides in length. When transfected into cells, siRNA inhibit the target mRNA transiently until they are also degraded within the cell. miRNA and siRNA are biochemically and functionally indistinguishable. Both are about the same in nucleotide length with 5'-phosphate and 3'-hydroxyl ends, and assemble into an RNA-induced silencing complex (RISC) to silence specific gene expression. siRNA and miRNA are distinguished based on origin. siRNA is obtained from long double-stranded RNA (dsRNA), while miRNA is derived from the double-stranded region of a 60-70nt RNA hairpin precursor. Small hairpin RNAs (shRNA) are sequences of RNA, typically about 50-80 base pairs, or about 50, 55, 60, 65, 70, 75, or about 80 base pairs in length, that include a region of internal hybridization forming a stem loop structure consisting of a base-pair region of about 19-29 base pairs of double-strand RNA (the stem) bridged by a region of single-strand RNA (the loop) and a short 3' overhang. shRNA molecules are processed within the cell to form siRNA which in turn knock down target gene expression. shRNA can be incorporated into plasmid vectors and integrated into genomic DNA for longer-term or stable expression, and thus longer knockdown of the target mRNA.

[00144] Interfering nucleic acid molecules can contain RNA bases, non-RNA bases, or a mixture of RNA bases and non-RNA bases. For example, interfering nucleic acid molecules provided herein can be primarily composed of RNA bases but also contain DNA bases or non-naturally occurring nucleotides. The interfering nucleic acids can employ a variety of oligonucleotide chemistries. Examples of oligonucleotide

chemistries include, without limitation, peptide nucleic acid (PNA), linked nucleic acid (LNA), phosphorothioate, 2'O-Me-modified oligonucleotides, and morpholino chemistries, including combinations of any of the foregoing. In general, PNA and LNA chemistries can utilize shorter targeting sequences because of their relatively high target binding strength relative to 2'O-Me oligonucleotides. Phosphorothioate and 2'O-Me-modified chemistries are often combined to generate 2'O-Me-modified oligonucleotides having a phosphorothioate backbone.

B. Programmable nucleic acid editing systems

[00145] In some aspects, the programmable nucleic acid modification system is a programmable nucleic acid editing system. Editing systems generally comprise a programmable nucleic acid binding domain and a nuclease domain to generate a programmable nucleic acid nuclease system or a transcription factor domain to create a programmable transcription regulation system. A programmable nucleic acid binding domain of an editing system is capable of targeting a nucleic acid sequence in a polynucleotide, a nuclease is capable of facilitating modification of the nucleic acid sequence of the polynucleotide, and a transcription factor is capable of regulating transcription and thus expression of the polynucleotide.

[00146] Programmable nucleic acid binding domains rely for specificity on the delivery of exogenous protein(s), and/or a guide RNA (gRNA), deadRNA (dRNA), or single guide RNA (sgRNA) having a sequence which binds specifically to a gene sequence of interest. Non-limiting examples of programmable nucleic acid binding domains that can be used in a programmable nucleic acid editing system include, without limit, a programmable nucleic acid domain of RNA-guided clustered regularly interspersed short palindromic repeats (CRISPR)/CRISPR-associated (Cas) (CRISPR/Cas) nuclease systems, a CRISPR/Cpf1 nuclease system, a zinc finger nuclease (ZFN), a transcription activator-like effector (TALE), a meganuclease, and a ribozyme. Other suitable programmable nucleic acid binding domains will be recognized by individuals skilled in the art.

[00147] When the programmable nucleic acid modification system comprises more than one component, such as a binding protein, a nuclease, a transcription factor or a guide nucleic acid, the multi-component modification system can be modular, in that the different components can optionally be distributed among two or more nucleic acid constructs as described herein. The system components can be delivered by a plasmid or viral vector or as a synthetic oligonucleotide. More detailed descriptions of non-limiting examples of programmable nucleic acid editing systems can be as described further below. All the systems described herein below can be modified to comprise a transcription factor, a nuclease, or both.

i. CRISPR nuclease systems.

[00148] The programmable targeting nuclease can be an RNA-guided CRISPR endonuclease system. The CRISPR system comprises a guide RNA or sgRNA to a target sequence at which a protein of the system introduces a double-stranded break in a target nucleic acid sequence, and a CRISPR-associated endonuclease. The gRNA is a short synthetic RNA comprising a sequence necessary for endonuclease binding, and a preselected ~20 nucleotide spacer sequence targeting the sequence of interest in a genomic target. Non-limiting examples of endonucleases include Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas100, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cpf1 endonuclease, or a homolog thereof, a recombination of the naturally occurring molecule thereof, a codon-optimized version thereof, or a modified version thereof, or any combination thereof.

[00149] The CRISPR nuclease system can be derived from any type of CRISPR system, including a type I (i.e., IA, IB, IC, ID, IE, or IF), type II (i.e., IIA, IIB, or IIC), type III (i.e., IIIA or IIIB), or type V CRISPR system. The CRISPR/Cas system can be from *Streptococcus* sp. (e.g., *Streptococcus pyogenes*), *Campylobacter* sp. (e.g., *Campylobacter jejuni*), *Francisella* sp. (e.g., *Francisella novicida*), *Acaryochloris* sp., *Acetohalobium* sp., *Acidaminococcus* sp., *Acidithiobacillus* sp., *Alicyclobacillus* sp.,

Allochromatium sp., *Ammonifex* sp., *Anabaena* sp., *Arthrospira* sp., *Bacillus* sp., *Burkholderiales* sp., *Caldicelulosiruptor* sp., *Candidatus* sp., *Clostridium* sp., *Crocospaera* sp., *Cyanothece* sp., *Exiguobacterium* sp., *Finegoldia* sp., *Ktedonobacter* sp., *Lactobacillus* sp., *Lyngbya* sp., *Marinobacter* sp., *Methanohalobium* sp., *Microscilla* sp., *Microcoleus* sp., *Microcystis* sp., *Natranaerobius* sp., *Neisseria* sp., *Nitrosococcus* sp., *Nocardiopsis* sp., *Nodularia* sp., *Nostoc* sp., *Oscillatoria* sp., *Polaromonas* sp., *Pelotomaculum* sp., *Pseudoalteromonas* sp., *Petrotoga* sp., *Prevotella* sp., *Staphylococcus* sp., *Streptomyces* sp., *Streptosporangium* sp., *Synechococcus* sp., or *Thermosipho* sp.

[00150] Non-limiting examples of suitable CRISPR systems include CRISPR/Cas systems, CRISPR/Cpf systems, CRISPR/Cmr systems, CRISPR/Csa systems, CRISPR/Csb systems, CRISPR/Csc systems, CRISPR/Cse systems, CRISPR/Csf systems, CRISPR/Csm systems, CRISPR/Csn systems, CRISPR/Csx systems, CRISPR/Csy systems, CRISPR/Csz systems, and derivatives or variants thereof. Preferably, the CRISPR system can be a type II Cas9 protein, a type V Cpf1 protein, or a derivative thereof. In some aspects, the CRISPR/Cas nuclease is *Streptococcus pyogenes* Cas9 (SpCas9), *Streptococcus thermophilus* Cas9 (StCas9), *Campylobacter jejuni* Cas9 (CjCas9), *Francisella novicida* Cas9 (FnCas9), or *Francisella novicida* Cpf1 (FnCpf1).

[00151] In general, a protein of the CRISPR system comprises an RNA recognition and/or RNA binding domain, which interacts with the guide RNA. A protein of the CRISPR system also comprises at least one nuclease domain having endonuclease activity. For example, a Cas9 protein can comprise a RuvC-like nuclease domain and an HNH-like nuclease domain, and a Cpf1 protein can comprise a RuvC-like domain. A protein of the CRISPR system can also comprise DNA binding domains, helicase domains, RNase domains, protein-protein interaction domains, dimerization domains, as well as other domains.

[00152] A protein of the CRISPR system can be associated with guide RNAs (gRNA). The guide RNA can be a single guide RNA (i.e., sgRNA), or can comprise two

RNA molecules (i.e., crRNA and tracrRNA). The guide RNA interacts with a protein of the CRISPR system to guide it to a target site in the DNA. The target site has no sequence limitation except that the sequence is bordered by a protospacer adjacent motif (PAM). For example, PAM sequences for Cas9 include 3'-NGG, 3'-NGGNG, 3'-NNAGAAW, and 3'-ACAY, and PAM sequences for Cpf1 include 5'-TTN (wherein N is defined as any nucleotide, W is defined as either A or T, and Y is defined as either C or T). Each gRNA comprises a sequence that is complementary to the target sequence (e.g., a Cas9 gRNA can comprise GN17-20GG). The gRNA can also comprise a scaffold sequence that forms a stem loop structure and a single-stranded region. The scaffold region can be the same in every gRNA. In some aspects, the gRNA can be a single molecule (i.e., sgRNA). In other aspects, the gRNA can be two separate molecules. Those skilled in the art are familiar with gRNA design and construction, e.g., gRNA design tools are available on the internet or from commercial sources.

[00153] A CRISPR system can comprise one or more nucleic acid binding domains associated with one or more, or two or more selected guide RNAs used to direct the CRISPR system to one or more, or two or more selected target nucleic acid loci. For instance, a nucleic acid binding domain can be associated with one or more, or two or more selected guide RNAs, each selected guide RNA, when complexed with a nucleic acid binding domain, causing the CRISPR system to localize to the target of the guide RNA.

[00154] The programmable targeting nuclease can also be a CRISPR nickase system. CRISPR nickase systems are similar to the CRISPR nuclease systems described above except that a CRISPR nuclease of the system is modified to cleave only one strand of a double-stranded nucleic acid sequence. Thus, a CRISPR nickase, in combination with a guide RNA of the system, can create a single-stranded break or nick in the target nucleic acid sequence. Alternatively, a CRISPR nickase in combination with a pair of offset gRNAs can create a double-stranded break in the nucleic acid sequence.

[00155] A CRISPR nuclease of the system can be converted to a nickase by one or more mutations and/or deletions. For example, a Cas9 nickase can comprise one or more mutations in one of the nuclease domains, wherein the one or more mutations can be D10A, E762A, and/or D986A in the RuvC-like domain, or the one or more mutations can be H840A (or H839A), N854A and/or N863A in the HNH-like domain.

[00156] A nuclease of a CRISPR nuclease system can be inactivated to obtain a programmable targeting protein that can be associated with a transcription factor capable of regulating expression of a polynucleotide. For instance, a CRISPR/Cas system can comprise a nuclease-deficient CAS9 protein (dCAS9) fused to a transcriptional activator and a guide RNA (gRNA).

ii. *ssDNA-guided Argonaute systems.*

[00157] Alternatively, the programmable targeting nuclease can comprise a single-stranded DNA-guided Argonaute (Ago) protein. Ago proteins are ubiquitously expressed and bind to siRNAs or miRNAs to guide post-transcriptional gene silencing either by destabilization of the mRNA or by translational repression.

[00158] Some prokaryotic Agos use single-stranded guide DNAs and create double-stranded breaks in nucleic acid sequences. The ssDNA-guided Ago endonuclease can be associated with a single-stranded guide DNA.

[00159] The Ago programmable protein can be derived from *Alistipes* sp., *Aquifex* sp., *Archaeoglobus* sp., *Bacteriodes* sp., *Bradyrhizobium* sp., *Burkholderia* sp., *Cellvibrio* sp., *Chlorobium* sp., *Geobacter* sp., *Mariprofundus* sp., *Natronobacterium* sp., *Parabacteriodes* sp., *Parvularcula* sp., *Planctomyces* sp., *Pseudomonas* sp., *Pyrococcus* sp., *Thermus* sp., or *Xanthomonas* sp. For instance, the Ago protein can be *Natronobacterium gregoryi* Ago (NgAgo). Alternatively, the Ago protein can be *Thermus thermophilus* Ago (TtAgo). The Ago protein can also be *Pyrococcus furiosus* (PfAgo).

[00160] The single-stranded guide DNA (gDNA) of an ssDNA-guided Argonaute system is complementary to the target site in the nucleic acid sequence. The target site has no sequence limitations and does not require a PAM. The gDNA generally ranges

in length from about 15-30 nucleotides. The gDNA can comprise a 5' phosphate group. Those skilled in the art are familiar with ssDNA oligonucleotide design and construction.

iii. Zinc finger programmable targeting proteins.

[00161] A ZFN programmable nucleic acid binding protein comprises a DNA-binding zinc finger region that can comprise from about two to seven zinc fingers, for example, about four to six zinc fingers, wherein each zinc finger binds three nucleotides. The zinc finger region can be engineered to recognize and bind to any DNA sequence. Zinc finger design tools or algorithms are available on the internet or from commercial sources. The zinc fingers can be linked together using suitable linker sequences. ZFN programmable nucleic acid binding proteins can be linked to a nuclease or a transcription factor to generate a programmable nucleic acid modification system comprising targeting a specific nucleic acid sequence.

iv. Transcription activator-like effector nuclease systems.

[00162] The programmable targeting protein can also be a transcription activator-like effector (TALE) or the like. TALENs comprise a DNA-binding domain composed of highly conserved repeats derived from transcription activator-like effectors (TALEs) that are linked to a nuclease domain. TALEs are proteins secreted by plant pathogen *Xanthomonas* to alter transcription of genes in host plant cells. TALE repeat arrays can be engineered via modular protein design to target any DNA sequence of interest. Other transcription activator-like effector nuclease systems can comprise, but are not limited to, the repetitive sequence, transcription activator like effector (RipTAL) system from the bacterial plant pathogenic *Ralstonia solanacearum* species complex (Rssc). The nuclease domain of TALEs can be any nuclease domain as described above in **Section IV(a)(i)**.

v. Meganucleases or rare-cutting endonuclease systems.

[00163] The programmable targeting nuclease can also be a meganuclease or derivative thereof. Meganucleases are endodeoxyribonucleases characterized by long recognition sequences, i.e., the recognition sequence generally ranges from about 12 base pairs to about 45 base pairs. As a consequence of this requirement, the

recognition sequence generally occurs only once in any given genome. Among meganucleases, the family of homing endonucleases named LAGLIDADG has become a valuable tool for the study of genomes and genome engineering. Non-limiting examples of meganucleases that can be suitable for the instant disclosure include I-SceI, I-CreI, I-DmOI, or variants and combinations thereof. A meganuclease can be targeted to a specific nucleic acid sequence by modifying its recognition sequence using techniques well known to those skilled in the art.

[00164] The programmable targeting nuclease can be a rare-cutting endonuclease or derivative thereof. Rare-cutting endonucleases are site-specific endonucleases whose recognition sequence occurs rarely in a genome, such as only once in a genome. The rare-cutting endonuclease can recognize a 7-nucleotide sequence, an 8-nucleotide sequence, or longer recognition sequence. Non-limiting examples of rare-cutting endonucleases include NotI, Ascl, PacI, AsiSI, SbfI, and FseI.

vi. Endonuclease domains

[00165] Non-limiting examples of endonucleases include Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas100, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cpf1 endonuclease, or a homolog thereof, a recombination of the naturally occurring molecule thereof, a codon-optimized version thereof, or a modified version thereof, or any combination thereof.

vii. Transcription factor domains

[00166] Non-limiting examples of suitable transcription transcriptional activation domains include, without limit, herpes simplex virus VP16 domain, VP64 (which is a tetrameric derivative of VP16), VP160 (i.e., 10xVP16), VP128, p65 activation domain from NFkB, p53 activation domains 1 and 2, heat-shock factor 1 (HSF1) activation domain, MyoD1 activation domain, GCN4 peptide, 10xGCN4, viral R transactivator (Rta), VPR (a fusion of VP64-p65-Rta), p53 activation domains 1 and 2, CREB (cAMP response element binding protein) activation domains, E2A activation domains,

activation domains from human heat-shock factor 1 (HSF1), NFAT (nuclear factor of activated T-cells) activation domains, a histone acetyltransferase, activation domains from the *Arabidopsis thaliana* MYB46, HAM1, HAM2, MYB112, WRKY11, ERF6, or a combination thereof. Engineered transcription activation systems may comprise one transcription activation domain, two transcription activation domains, three transcription activation domains, or more than three transcription activation domains.

[00167] Non-limiting examples of transcription repressor domains include Kruppel-associated Box (KRAB), EAR-repression domain (SRDX), and BRD.

viii. Optional additional domains.

[00168] The programmable targeting nuclease can further comprise at least one nuclear localization signal (NLS), at least one cell-penetrating domain, at least one reporter domain, and/or at least one linker.

[00169] In general, an NLS comprises a stretch of basic amino acids. Nuclear localization signals are known in the art (see, e.g., Lange et al., J. Biol. Chem., 2007, 282:5101-5105). The NLS can be located at the N-terminus, the C-terminal, or in an internal location of the fusion protein.

[00170] A cell-penetrating domain can be a cell-penetrating peptide sequence derived from the HIV-1 TAT protein. The cell-penetrating domain can be located at the N-terminus, the C-terminal, or in an internal location of the fusion protein.

[00171] A programmable targeting nuclease can further comprise at least one linker. For example, the programmable targeting nuclease, the nuclease domain of the targeting nuclease, and other optional domains can be linked via one or more linkers. The linker can be flexible (e.g., comprising small, non-polar (e.g., Gly) or polar (e.g., Ser, Thr) amino acids). Examples of suitable linkers are well known in the art, and programs to design linkers are readily available (Crasto et al., Protein Eng., 2000, 13(5):3096-312). In alternate aspects, the programmable targeting nuclease, the cell cycle regulated protein, and other optional domains can be linked directly.

[00172] A programmable targeting nuclease can further comprise an organelle localization or targeting signal that directs a molecule to a specific organelle. A signal

can be a polynucleotide or polypeptide signal, or can be an organic or inorganic compound sufficient to direct an attached molecule to a desired organelle. Organelle localization signals can be as described in U.S. Patent Publication No. 20070196334, the disclosure of which is incorporated herein in its entirety.

(b) Aspects of engineered nucleic acid modification systems

[00173] In some aspects, the engineered nucleic acid modification system is a programmable nucleic acid editing system. Programmable nucleic acid editing systems can be as described in **Section II(a)** herein above. In some aspects, the programmable nucleic acid modification system comprises a CRISPR/Cas nuclease system comprising a CAS9 protein (dCAS9) and a guide RNA (gRNA). In some aspects, an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32. In some aspects, an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.

[00174] In some aspects, the programmable nucleic acid editing system is targeted to a nucleic acid sequence in a polynucleotide encoding a component of the circadian clock. In some aspects, the programmable nucleic acid modification system introduces a loss of function mutation into a polynucleotide encoding a component of the circadian clock. In some aspects, the component of the circadian clock is an ELF3 protein and the programmable nucleic acid editing system is targeted to a nucleic acid sequence in a polynucleotide encoding the ELF3 protein. In some aspects, the programmable nucleic acid editing system introduces a loss of function mutation into a polynucleotide encoding an ELF3 protein. In some aspects, the programmable nucleic

acid modification system is a CRISPR/Cas system comprising a Cas9 nuclease and a guide RNA (gRNA) comprising a sequence complementary to a target sequence within a nucleic acid sequence in a polynucleotide encoding an ELF3 protein.

[00175] In some aspects, the modified plant is *T. arvense*. When the modified plant is *T. arvense*, the programmable nucleic acid modification system can comprise a Cas9 protein encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and one or more gRNAs comprising a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof. In some aspects, when the modified plant is *T. arvense*, the programmable nucleic acid modification system comprises a Cas9 protein encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and one or more gRNAs comprising a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof.

[00176] In some aspects, the modified plant is basil. When the modified plant is basil, the programmable nucleic acid modification system can comprise a Cas9 protein encoded by a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and one or more gRNAs comprising a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof. In some aspects, when the modified plant is basil, the programmable nucleic acid modification system comprises a Cas9 protein encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and one or more gRNAs comprising a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.

III. Nucleic acid constructs

[00177] Another aspect of the present disclosure encompasses one or more nucleic acid constructs for genetically modifying a plant. In some aspects, the one or more constructs can modify a component of the circadian clock, modify an environmental signal sensor, or both in a plant.

[00178] Any of the multi-component systems described herein are to be considered modular, in that the different components can optionally be distributed among two or more nucleic acid constructs as described herein. The nucleic acid constructs can be DNA or RNA, linear or circular, single-stranded or double-stranded, or any combination thereof. The nucleic acid constructs can be codon-optimized for efficient translation into protein, and possibly for transcription into an RNA donor polynucleotide transcript in the cell of interest. Codon optimization programs are available as freeware or from commercial sources.

[00179] The nucleic acid constructs can be used to express one or more components of the system for later introduction into a cell to be modified. Alternatively, the nucleic acid constructs can be introduced into the cell to be modified for expression of the components of the system in the cell. In some aspects, the nucleic acid constructs transiently express the various components of the system. Transiently expressing the system in a plant overcomes the cumbersome regulatory hurdles required for traditionally modified crops. In some aspects, the engineered nucleic acid modification system is expressed in male reproductive tissues, modifies expression of various factors described herein above in male reproductive tissues, or both.

[00180] Expression constructs generally comprise DNA coding sequences operably linked to at least one promoter control sequence for expression in a cell of interest. Promoter control sequences can control expression of a system for modifying a component of the circadian clock, a system for modifying an environmental signal sensor, or both in bacterial (e.g., *E. coli*) cells or eukaryotic (e.g., yeast, insect, mammalian, or plant) cells. Suitable bacterial promoters include, without limit, T7

promoters, lac operon promoters, trp promoters, tac promoters (which are hybrids of trp and lac promoters), variations of any of the foregoing, and combinations of any of the foregoing. Non-limiting examples of suitable eukaryotic promoters include constitutive, regulated, or cell- or tissue-specific promoters.

[00181] Suitable eukaryotic constitutive promoter control sequences include, but are not limited to, pU10, cytomegalovirus immediate early promoter (CMV), simian virus (SV40) promoter, adenovirus major late promoter, Rous sarcoma virus (RSV) promoter, mouse mammary tumor virus (MMTV) promoter, phosphoglycerate kinase (PGK) promoter, elongation factor (ED1)-alpha promoter, ubiquitin promoters, actin promoters, tubulin promoters, immunoglobulin promoters, fragments thereof, or combinations of any of the foregoing. Examples of suitable eukaryotic regulated promoter control sequences include, without limit, those regulated by heat shock, metals, steroids, antibiotics, or alcohol. Non-limiting examples of tissue-specific promoters include B29 promoter, CD14 promoter, CD43 promoter, CD45 promoter, CD68 promoter, desmin promoter, elastase-1 promoter, endoglin promoter, fibronectin promoter, Flt-1 promoter, GFAP promoter, GPIIb promoter, ICAM-2 promoter, INF- β promoter, Mb promoter, Nphs1 promoter, OG-2 promoter, SP-B promoter, SYN1 promoter, and WASP promoter.

[00182] Promoters can also be plant-specific promoters, or promoters that can be used in plants. A wide variety of plant promoters are known to those of ordinary skill in the art, as are other regulatory elements that can be used alone or in combination with promoters.

[00183] Promoters can be divided into two types, namely, constitutive promoters and non-constitutive promoters. Constitutive promoters are classified as providing for a range of constitutive expression. Thus, some are weak constitutive promoters, and others are strong constitutive promoters. Non-constitutive promoters include tissue-preferred promoters, tissue-specific promoters, cell-type specific promoters, and inducible promoters. Suitable plant-specific constitutive promoter control sequences include, but are not limited to, a CaMV35S promoter, CaMV 19S, GOS2, *Arabidopsis* At6669 promoter, Rice cyclophilin, Maize H3 histone, Synthetic Super MAS, an opine

promoter, a plant ubiquitin (Ubi) promoter, an actin 1 (Act-1) promoter, pEMU, Cestrum yellow leaf curling virus promoter (CYMLV promoter), and an alcohol dehydrogenase 1 (Adh-1) promoter. Other constitutive promoters include those in U.S. Pat. Nos. 5,659,026; 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; and 5,608,142.

[00184] Regulated plant promoters respond to various forms of environmental stresses, or other stimuli, including, for example, mechanical shock, heat, cold, flooding, drought, salt, anoxia, pathogens such as bacteria, fungi, and viruses, and nutritional deprivation, including deprivation during times of flowering and/or fruiting, and other forms of plant stress. For example, the promoter can be a promoter which is induced by one or more, but not limited to one of the following: abiotic stresses such as wounding, cold, desiccation, ultraviolet-B, heat shock or other heat stress, drought stress or water stress. The promoter can further be one induced by biotic stresses including pathogen stress, such as stress induced by a virus or fungi, stresses induced as part of the plant defense pathway or by other environmental signals, such as light, carbon dioxide, hormones or other signaling molecules such as auxin, hydrogen peroxide and salicylic acid, sugars and gibberellin or abscisic acid and ethylene. Suitable regulated plant promoter control sequences include, but are not limited to, salt-inducible promoters such as RD29A; drought-inducible promoters such as maize rab17 gene promoter, maize rab28 gene promoter, and maize lvr2 gene promoter; heat-inducible promoters such as heat tomato hsp80-promoter from tomato.

[00185] Tissue-specific promoters can include, but are not limited to, fiber-specific, green tissue-specific, root-specific, stem-specific, flower-specific, callus-specific, pollen-specific, egg-specific, promoters specific to male or female reproductive tissues, and seed coat-specific. Suitable tissue-specific plant promoter control sequences include, but are not limited to, leaf-specific promoters [such as described, for example, by Yamamoto et al., Plant J. 12:255-265, 1997; Kwon et al., Plant Physiol. 105:357-67, 1994; Yamamoto et al., Plant Cell Physiol. 35:773-778, 1994; Gotor et al., Plant J. 3:509-18, 1993; Orozco et al., Plant Mol. Biol. 23:1129-1138, 1993; and Matsuoka et al.,

Proc. Natl. Acad. Sci. USA 90:9586-9590, 1993], seed-preferred promoters [e.g., from seed-specific genes (Simon et al., Plant Mol. Biol. 5: 191, 1985; Scofield et al., J. Biol. Chem. 262: 12202, 1987; Baszczynski et al., Plant Mol. Biol. 14: 633, 1990), Brazil Nut albumin (Pearson et al., Plant Mol. Biol. 18: 235-245, 1992), legumin (Ellis et al., Plant Mol. Biol. 10: 203-214, 1988), Glutelin (rice) (Takaiwa et al., Mol. Gen. Genet. 208: 15-22, 1986; Takaiwa et al., FEBS Letts. 221: 43-47, 1987), Zein (Matzke et al., Plant Mol Biol, 143: 323-32, 1990), napA (Stalberg et al., Planta 199: 515-519, 1996), Wheat SPA (Albanietal, Plant Cell, 9: 171-184, 1997), sunflower oleosin (Cummins et al., Plant Mol. Biol. 19: 873-876, 1992)], endosperm specific promoters [e.g., wheat LMW and HMW, glutenin-1 (Mol Gen Genet 216:81-90, 1989; NAR 17:461-2), wheat a, b, and g gliadins (EMBO3:1409-15, 1984), Barley ltrI promoter, barley B1, C, D hordein (Theor Appl Gen 98:1253-62, 1999; Plant J 4:343-55, 1993; Mol Gen Genet 250:750-60, 1996), Barley DOF (Mena et al., The Plant Journal, 116(1): 53-62, 1998), Biz2 (EP99106056.7), Synthetic promoter (Vicente-Carbajosa et al., Plant J. 13: 629-640, 1998), rice prolamin NRP33, rice-globulin G1b-1 (Wu et al., Plant Cell Physiology 39(8) 885-889, 1998), rice alpha-globulin REB/OHP-1 (Nakase et al., Plant Mol. Biol. 33: 513-S22, 1997), rice ADP-glucose PP (Trans Res 6:157-68, 1997), maize ESR gene family (Plant J 12:235-46, 1997), sorghum gamma-kafirin (PMB 32:1029-35, 1996)], embryo-specific promoters [e.g., rice OSH1 (Sato et al., Proc. Natl. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma et al., Plant Mol. Biol. 39:257-71, 1999), rice oleosin (Wu et al., J. Biochem., 123:386, 1998)], and flower-specific promoters [e.g., AtPRP4, chalcone synthase (chsA) (Van der Meer et al., Plant Mol. Biol. 15, 95-109, 1990), LAT52 (Twell et al., Mol. Gen Genet. 217:240-245; 1989), apetala-3].

[00186] Any of the promoter sequences can be wild type or can be modified for more efficient or efficacious expression. The DNA coding sequence also can be linked to a polyadenylation signal (e.g., SV40 polyA signal, bovine growth hormone (BGH) polyA signal, etc.) and/or at least one transcriptional termination sequence. In some situations, the complex or fusion protein can be purified from the bacterial or eukaryotic cells.

[00187] Nucleic acids encoding one or more components of an engineered DNA methylation system and/or transcription activation system can be present in a construct. Suitable constructs include plasmid constructs, viral constructs, and self-replicating RNA (Yoshioka et al., Cell Stem Cell, 2013, 13:246-254). For instance, the nucleic acid encoding one or more components of an engineered DNA methylation system and/or transcription activation system can be present in a plasmid construct.

[00188] Non-limiting examples of suitable plasmid constructs include pUC, pBR322, pET, pBluescript, and variants thereof. Alternatively, the nucleic acid encoding one or more components of an engineered DNA methylation system and/or transcription activation system can be part of a viral vector (e.g., lentiviral vectors, adeno-associated viral vectors, adenoviral vectors, and so forth).

[00189] The plasmid or viral vector can comprise additional expression control sequences (e.g., enhancer sequences, Kozak sequences, polyadenylation sequences, transcriptional termination sequences, etc.), selectable reporter sequences (e.g., antibiotic resistance genes), origins of replication, T-DNA border sequences, and the like. The plasmid or viral vector can further comprise RNA processing elements such as glycine tRNAs, or Csy4 recognition sites. Such RNA processing elements can, for instance, intersperse polynucleotide sequences encoding multiple gRNAs under the control of a single promoter to produce the multiple gRNAs from a transcript encoding the multiple gRNAs. When a *cys4* recognition site is used, a vector can further comprise sequences for expression of Csy4 RNase to process the gRNA transcript. Additional information about vectors and use thereof can be found in "Current Protocols in Molecular Biology", Ausubel et al., John Wiley & Sons, New York, 2003, or "Molecular Cloning: A Laboratory Manual", Sambrook & Russell, Cold Spring Harbor Press, Cold Spring Harbor, NY, 3rd edition, 2001.

[00190] The plasmid or viral vector can also comprise a transit peptide for targeting of a protein product, particularly to a chloroplast, leucoplast or other plastid organelle or vacuole or an extracellular location. For descriptions of the use of chloroplast transit peptides, see U.S. Pat. No. 5,188,642 and U.S. Pat. No. 5,728,925,

herein incorporated by reference in their entirety. Many chloroplast-localized proteins are expressed from nuclear genes as precursors and are targeted to the chloroplast by a chloroplast transit peptide (CTP). Examples of other such isolated chloroplast proteins include, but are not limited to those associated with the small subunit (SSU) of ribulose-1,5,-biphosphate carboxylase, ferredoxin, ferredoxin oxidoreductase, the light-harvesting complex protein I and protein II, thioredoxin F, enolpyruvyl shikimate phosphate synthase (EPSPS) and transit peptides described in U.S. Pat. No. 7,193,133, herein incorporated by reference. It has been demonstrated in vivo and in vitro that non-chloroplast proteins can be targeted to the chloroplast by use of protein fusions with a heterologous CTP and that the CTP is sufficient to target a protein to the chloroplast. Incorporation of a suitable chloroplast transit peptide, such as, the *Arabidopsis thaliana* EPSPS CTP (CTP2, Klee et al., Mol. Gen. Genet. 210:437-442), and the *Petunia hybrida* EPSPS CTP (CTP4, della-Cioppa et al., Proc. Natl. Acad. Sci. USA 83:6873-6877) has been shown to target heterologous EPSPS protein sequences to chloroplasts in transgenic plants. The production of glyphosate tolerant plants by expression of a fusion protein comprising an amino-terminal CTP with a glyphosate resistant EPSPS enzyme is well known by those skilled in the art, (U.S. Pat. No. 5,627,061, U.S. Pat. No. 5,633,435, U.S. Pat. No. 5,312,910, EP 0218571, EP 189707, EP 508909, and EP 924299).

[00191] In some aspects, the one or more constructs comprise one or more expression constructs encoding a system for modifying a component of the circadian clock, a system for modifying an environmental signal sensor, or both in a plant. The constructs can comprise a construct comprising an expression construct for modifying the expression of a component of the circadian clock; a construct comprising an expression construct for modifying the expression of an environmental signal sensor; or a construct comprising an expression construct for modifying the expression of a component of the circadian clock and an expression construct for modifying the expression of an environmental signal sensor.

[00192] In some aspects, an expression construct comprises a promoter operably linked to a polynucleotide encoding a component of the circadian clock, an environmental signal sensor, or both. In some aspects, the expression construct comprises a promoter operably linked to a polynucleotide encoding an environmental signal sensor. In some aspects, the environmental sensor is phyB. In one aspect, the phyB photoreceptor is a constitutively expressed phytochrome B photoreceptor. In some aspects, the expression construct comprises a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with SEQ ID NO: 24 or a nucleic acid sequence comprising a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19. In some aspects, the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 24 or a nucleic acid sequence comprising a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19.

[00193] In other aspects, an expression construct comprises a promoter operably linked to a nucleic acid sequence encoding a programmable nucleic acid modification system targeted to a nucleic acid sequence in a polynucleotide encoding a component of the circadian clock, an environmental signal sensor, or both. As used herein, a “programmable nucleic acid modification system” is a system capable of targeting and modifying the nucleic acid or modifying the expression or stability of a nucleic acid to alter a polynucleotide sequence or a protein or the expression of a polynucleotide sequence or protein encoded by the nucleic acid. Programmable nucleic acid modification systems can be as described in **Section II** herein above.

[00194] In some aspects, the programmable nucleic acid modification system is CRISPR/Cas system comprising a Cas9 nuclease and a guide RNA (gRNA) comprising a sequence complementary to a target sequence within the polynucleotide encoding a component of the circadian clock; a gRNA comprising a sequence complementary to a target sequence within the polynucleotide encoding a component of the circadian clock; or a gRNA comprising a sequence complementary to a target sequence within the polynucleotide encoding a component of the circadian clock and a gRNA comprising a sequence complementary to a target sequence within the polynucleotide encoding a component of the circadian clock. In some aspects, the Cas9 nuclease comprises a Cas9 nuclease comprising a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29. In some aspects, the Cas9 nuclease comprises a Cas9 nuclease comprising a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29.

[00195] In some aspects, the plant is *Thlaspi arvense*. When the plant is *Thlaspi arvense*, the programmable nucleic acid modification system can be a CRISPR/Cas system comprising a Cas9 nuclease and a gRNA comprising a sequence complementary to a target sequence within a polynucleotide encoding ELF3, and the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20. In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20. In some aspects, the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30 (gRNA1), SEQ ID NO: 31 (gRNA2), or a combination thereof.

[00196] When the plant is *Thlaspi arvense*, the programmable nucleic acid modification system can be a CRISPR/Cas system comprising a Cas9 nuclease and a gRNA comprising a sequence complementary to a target sequence within a polynucleotide encoding ELF3, and an expression construct encoding SEQ ID NO: 30 (gRNA1) and SEQ ID NO: 31 (gRNA2) comprises at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence starting at base 254 to base 1287 of SEQ ID NO: 32. In some aspects, the expression construct encoding SEQ ID NO: 30 (gRNA1) and SEQ ID NO: 31 (gRNA2) comprises at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with a nucleic acid sequence starting at base 254 to base 1287 of SEQ ID NO: 32.

[00197] In some aspects, the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20. In some aspects, the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30 (gRNA1), SEQ ID NO: 31 (gRNA2), or a combination thereof.

[00198] In some aspects, the plant is *Basil*. When the plant is *Basil*, the programmable nucleic acid modification system can be a CRISPR/Cas system comprising a Cas9 nuclease and a gRNA comprising a sequence complementary to a target sequence within a polynucleotide encoding ELF3, and the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13. In some aspects, the gRNA comprises a nucleic acid sequence of SEQ ID NO: 33 to SEQ ID NO: 36, or a combination thereof.

[00199] In some aspects, an expression construct expressing the gRNAs of SEQ ID NOs: 33-36 comprises about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with SEQ ID NO: 23 or a nucleic acid sequence comprising a nucleic acid sequence comprising about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% of a nucleic acid sequence starting at base 695 to base 2799 of SEQ ID NO: 37. In some aspects, an expression construct expressing the gRNAs of SEQ ID NOs: 33-36 comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 23 or a nucleic acid sequence comprising a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 695 to base 2799 of SEQ ID NO: 37.

IV. Methods

[00200] A further aspect of the present disclosure encompasses a method of improving performance of a plant grown under intensive, precision outdoor farming conditions and Total Controlled Environment Agriculture (TCEA), or vertical farming. The method comprises obtaining or having obtained a modified (modified plant) plant having reduced developmental plasticity; and cultivating the plant under intensive, precision outdoor farming conditions, TCEA, or vertical farming. Modified plants can be as described in **Section I** herein above.

[00201] As explained above, the inventors surprisingly discovered that ability of the plant to sense and respond to environmental cues, when combined with a modification of a circadian function of the plant, can reduce the plasticity of the plant in response to changes in environmental conditions during growth all while exhibiting improved agronomic traits regardless of changing environmental conditions. As the pathways and components of pathways for sensing and responding to environmental cues, and circadian functions can be conserved in plants, any plant can be modified using methods of the instant disclosure to generate comprising a modified ability to sense and respond to environmental cues, a modification of a circadian function of the

plant. In some aspects, plants of the instant disclosure are *A. thaliana*. In some aspects, plants of the instant disclosure are *T. arvense*. In some aspects, plants of the instant disclosure are basil.

[00202] In some aspects, methods of the instant disclosure comprise introducing one or more expression constructs for modifying a plant exhibiting reduced developmental plasticity. The one or more expression constructs can comprise at least one or both of an expression construct for expressing a programmable nucleic acid modification system comprising a targeting nucleic acid sequence targeting a nucleic acid sequence in a polynucleotide sequence encoding a component of the circadian clock; and an expression construct for expressing an environmental signal sensor. The plant or plant cell is then grown under conditions whereby the one or more nucleic acid expression constructs express at least one or both of the programmable nucleic acid modification system; and the environmental signal sensor. In some aspects, the method can further comprise introducing the expression constructs. Nucleic acid constructs can be as described in **Section III**. Programmable nucleic acid modification systems can be as described in **Section II** herein above.

[00203] The expression constructs can comprise an exogenous nucleic acid molecule such as a chimeric nucleic acid of the disclosure. The term "exogenous" as used herein refers to a nucleic acid molecule originating from outside the plant cell. An exogenous nucleic acid molecule can be, for example, the coding sequence of a sterility factor or a fertility restorer. An exogenous nucleic acid molecule can have a naturally occurring or non-naturally occurring nucleotide sequence and can be a heterologous nucleic acid molecule derived from a different organism or a different plant species than the plant cell into which the nucleic acid molecule is introduced or can be a nucleic acid molecule derived from the same plant species as the plant cell into which it is introduced. The exogenous nucleic acid can or cannot be integrated in the plant cell's genome. When said exogenous nucleic acid/gene is not integrated, transient expression of the nucleic acid/gene occurs in the plant cell.

[00204] The one or more nucleic acid constructs can be introduced into the cell by a variety of means. Suitable delivery means include microinjection, electroporation, sonoporation, biolistics, calcium phosphate-mediated transfection, cationic transfection, liposomes and other lipids, dendrimer transfection, heat shock transfection, nucleofection transfection, gene gun delivery, dip transformation, supercharged proteins, cell-penetrating peptides, viral vectors, magnetofection, lipofection, impalefection, optical transfection, *Agrobacterium tumefaciens* mediated foreign gene transformation, proprietary agent-enhanced uptake of nucleic acids, and delivery via liposomes, immunoliposomes, virosomes, or artificial virions. The choice of means of introducing the system into a cell can and will vary depending on the cell, or the system or nucleic acid constructs encoding the system, among other variables.

[00205] The method can further comprise culturing a cell under conditions suitable for expressing the components of the systems and nucleic acid constructs of the instant disclosure. Methods of culturing cells are known in the art. In some aspects, the cell is from an animal, fungi, oomycete or prokaryote. In some aspects, the cell is a plant cell, plant, or plant part. When the cell is in tissue *ex vivo*, or *in vivo* within a plant or within a plant part, the plant part and/or plant can also be maintained under appropriate conditions for insertion of the donor polynucleotide. In general, the plant, plant part, or plant cell is maintained under conditions appropriate for cell growth and/or maintenance. Those of skill in the art appreciate that methods for culturing plant cells are known in the art and can and will vary depending on the cell type. Routine optimization can be used, in all cases, to determine the best techniques for a particular cell type. See for example, in Santiago et al. (2008) PNAS 105:5809-5814; Moehle et al. (2007) PNAS 104:3055-3060; Urnov et al. (2005) Nature 435:646-651; Lombardo et al. (2007) Nat. Biotechnology 25:1298-1306; and Taylor et al. (2012) Tropical Plant Biology 5:127-139.

[00206] Another aspect of the instant disclosure encompasses a method of reducing developmental plasticity of a plant. The method comprises generating a modified plant having reduced developmental plasticity. In some aspects, the plant is resistant to changes in growth conditions, which comprises daylength and temperature.

Modified plants can be as described in **Section I** herein above. In some aspects, the plant is resistant to changes in growth conditions of the plant. In other aspects, the growth conditions comprise daylength and temperature.

[00207] Yet another aspect of the instant disclosure encompasses a method of reducing a plastic response to competition among a co-cultivated group of plants. The method comprising, co-cultivating a group of plants having reduced developmental plasticity. Modified plants can be as described in **Section I** herein above.

[00208] A yet additional aspect of the instant disclosure encompasses a method of stabilizing production of a metabolite, nucleic acid, or protein in a plant. The method comprising, generating or having generated a plant having reduced developmental plasticity; cultivating the plant for a time sufficient to generate the metabolite, nucleic acid, or protein; and harvesting the metabolite, nucleic acid, or protein from the plant. In some aspects, the plant is grown under intensive, precision outdoor farming conditions, TCEA, or vertical farming.

V. Kits

[00209] A further aspect of the present disclosure provides kits for generating a modified, plant tissue, part thereof, plant cell, or seed having reduced developmental plasticity and improved agronomic traits. The kit can comprise one or more constructs for genetically modifying a plant to generate having reduced developmental plasticity and improved agronomic traits. The one or more constructs can modify a component of the circadian clock, modify an environmental signal sensor, or both in a plant. The kit can further comprise one or more modified plants, plant cells, or parts thereof comprising the one or more constructs can modify a component of the circadian clock, modify an environmental signal sensor, or both in a plant. The modified plants can be as described in **Section I** and the constructs can be as described in **Sections III**.

[00210] The kits can further comprise transfection reagents, cell growth media, selection media, *in vitro* transcription reagents, nucleic acid purification reagents, protein purification reagents, buffers, and the like. The kits provided herein generally

include instructions for carrying out the methods detailed below. Instructions included in the kits can be affixed to packaging material or can be included as a package insert. While the instructions are typically written or printed materials, they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this disclosure. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. As used herein, the term "instructions" can include the address of an internet site that provides the instructions

DEFINITIONS

[00211] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton et al., Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

[00212] When introducing elements of the present disclosure or the preferred aspects(s) thereof, the articles "a", "an", "the" and "said" are intended to mean that there are one or more of the elements. The terms "comprising", "including" and "having" are intended to be inclusive and mean that there may be additional elements other than the listed elements.

[00213] The term "entrain" as used in the context of a circadian clock refers to the coupling of one rhythm to the same period as another cycle, for example, the resetting of a circadian rhythm from its free-running period to exactly the 24-h period of the day/night cycle.

[00214] A “genetically modified” or “modified” plant refers to a plant in which the nuclear, organellar or extrachromosomal nucleic acid sequences of a cell has been modified, i.e., the cell contains at least one nucleic acid sequence that has been engineered to contain an insertion of at least one nucleotide, a deletion of at least one nucleotide, and/or a substitution of at least one nucleotide.

[00215] As used herein, the term “gene” refers to a DNA region (including exons and introns) encoding a gene product, as well as all DNA regions which regulate the production of the gene product, whether or not such regulatory sequences are adjacent to coding and/or transcribed sequences. Accordingly, a gene includes, but is not necessarily limited to, promoter sequences, terminators, translational regulatory sequences such as ribosome binding sites and internal ribosome entry sites, enhancers, silencers, insulators, boundary elements, replication origins, matrix attachment sites, and locus control regions.

[00216] As used herein, the term “engineered” when applied to a targeting protein refers to targeting proteins modified to specifically recognize and bind to a nucleic acid sequence at or near a target nucleic acid locus.

[00217] The term “nucleic acid modification” refers to processes by which a specific nucleic acid sequence in a polynucleotide is changed such that the nucleic acid sequence is modified. The nucleic acid sequence may be modified to comprise an insertion of at least one nucleotide, a deletion of at least one nucleotide, and/or a substitution of at least one nucleotide. The modified nucleic acid sequence is inactivated such that no product is made. Alternatively, the nucleic acid sequence may be modified such that an altered product is made.

[00218] As used herein, “protein expression” includes but is not limited to one or more of the following: transcription of a gene into precursor mRNA; splicing and other processing of the precursor mRNA to produce mature mRNA; mRNA stability; translation of the mature mRNA into protein (including codon usage and tRNA availability); production of a mutant protein comprising a mutation that modifies the

activity of the protein; and glycosylation and/or other modifications of the translation product, if required for proper expression and function.

[00219] The term "heterologous" refers to an entity that is not native to the cell or species of interest.

[00220] The terms "nucleic acid" and "polynucleotide" refer to a deoxyribonucleotide or ribonucleotide polymer, in linear or circular conformation. For the purposes of the present disclosure, these terms are not to be construed as limiting with respect to the length of a polymer. The terms may encompass known analogs of natural nucleotides, as well as nucleotides that are modified in the base, sugar and/or phosphate moieties. In general, an analog of a particular nucleotide has the same base-pairing specificity, i.e., an analog of A will base-pair with T. The nucleotides of a nucleic acid or polynucleotide may be linked by phosphodiester, phosphothioate, phosphoramidite, phosphorodiamidate bonds, or combinations thereof.

[00221] The term "nucleotide" refers to deoxyribonucleotides or ribonucleotides. The nucleotides may be standard nucleotides (i.e., adenosine, guanosine, cytidine, thymidine, and uridine) or nucleotide analogs. A nucleotide analog refers to a nucleotide having a modified purine or pyrimidine base or a modified ribose moiety. A nucleotide analog may be a naturally occurring nucleotide (e.g., inosine) or a non-naturally occurring nucleotide. Non-limiting examples of modifications on the sugar or base moieties of a nucleotide include the addition (or removal) of acetyl groups, amino groups, carboxyl groups, carboxymethyl groups, hydroxyl groups, methyl groups, phosphoryl groups, and thiol groups, as well as the substitution of the carbon and nitrogen atoms of the bases with other atoms (e.g., 7-deaza purines). Nucleotide analogs also include dideoxy nucleotides, 2'-O-methyl nucleotides, locked nucleic acids (LNA), peptide nucleic acids (PNA), and morpholinos.

[00222] The terms "polypeptide" and "protein" are used interchangeably to refer to a polymer of amino acid residues.

[00223] The term "allele" as used herein refers to one of two or more different nucleotide sequences that occur at a specific locus.

[00224] The terms “phenotype”, or “phenotypic trait” or “trait” refer to one or more traits of an organism. The phenotype can be observable to the naked eye, or by any other means of evaluation known in the art, e.g., microscopy, biochemical analysis, or an electromechanical assay. In some cases, a phenotype is directly controlled by a single gene or genetic locus, i.e., a “single gene trait”. In other cases, a phenotype is the result of several genes.

[00225] The term “genotype” is the genetic constitution of an individual (or group of individuals) at one or more genetic loci, as contrasted with the observable trait (the phenotype). Genotype is defined by the allele(s) of one or more known loci that the individual has inherited from its parents. The term genotype can be used to refer to an individual's genetic constitution at a single locus, at multiple loci, or, more generally, the term genotype can be used to refer to an individual's genetic make-up for all the genes in its genome.

[00226] The term “heterozygous” means a genetic condition wherein different alleles reside at corresponding loci on homologous chromosomes.

[00227] The term “homozygous” means a genetic condition wherein identical alleles reside at corresponding loci on homologous chromosomes.

[00228] The term “hybrid” means a progeny of mating between at least two genetically dissimilar parents. Without limitation, examples of mating schemes include single crosses, modified single cross, double modified single cross, three-way cross, modified three-way cross, and double cross wherein at least one parent in a modified cross is the progeny of a cross between sister lines.

[00229] “Hybridization” or “nucleic acid hybridization” refers to the pairing of complementary RNA and DNA strands as well as the pairing of complementary DNA single strands.

[00230] The term “hybridize” means the formation of base pairs between complementary regions of nucleic acid strands.

[00231] The term “inbred” means a line that has been bred for genetic homogeneity.

[00232] A “plant” can be a whole plant, any part thereof, or a cell or tissue culture derived from a plant. Thus, the term “plant” can refer to any of: whole plants, plant components or organs (e.g., leaves, stems, roots, etc.), plant tissues, seeds, plant cells, and/or progeny of the same. A plant cell is a cell of a plant, taken from a plant, or derived through culture from a cell taken from a plant.

[00233] As various changes could be made in the above-described cells and methods without departing from the scope of the invention, it is intended that all matter contained in the above description and in the examples given below, shall be interpreted as illustrative and not in a limiting sense.

SEQUENCES

SEQ ID NO.	Sequence	Description
1	1 atgaagagag ggaagatga ggagaagata ttggaaccta tgtttcctcg gttcatgtg 61 aatgatgcag ataaaggagg gcctagagct cctcctagaa acaagatggc tctttatgag 121 cagcttagta ttcctttctca gaggtttggt gatcatggaa cgatgaattc tcgtagtaac 181 aacacaagca ctttggttca tcctggacca tctagtcagc cttgtggtgt ggaaagaaac 241 ttatctgtcc agcatcttga ttcttcagcc gcaaaccaag caactgagaa gtttgtctcc 301 caaatgtcct tcatggaaaa tgtgagatct tcggcacagc atgatcagag gaaaatggtg 361 agagaggaag aagatttttg agttccagta tataattaact caagaagatc tcagtctcat 421 ggcaagaacca agagtggat tgagaaggaa aaacacaccc caatggtggc acctagctct 481 catcactcca ttcgatttca agaagtgaat cagacaggct caaagcaaaa cgtatgtttg 541 gctacttggt caaaacctga agttagggt caggtcaagg cgaatgcaag gtcagggtggc 601 tttgtaatct ctttagatgt atcagtcaca gaggagattg atctcgaaaa atcagcatca 661 agtcatgata gagtaaatga ttataatgct tccttgagac aagagtctag aaatcggtta 721 taccgagatg gtggcaaaac tcgtctgaag gacactgata atggagctga atctcacttg 781 gcaacggaaa atcattcaca agagggtcat ggcagtcctg aagacattga taatgatcgt 841 gaatacagca aaagcagagc atgcgctct ctgcagcaga taaatgaaga ggcaagtgat 901 gacgtttctg atgattcgat ggtggattct atatccagca tagatgtctc tcccgatgat 961 gttgtgggta tattaggtca aaaacgtttc tggagagcaa ggaaagccat tgccaatcaa 1021 caaagagtat ttgctgttca actatttgag ttgcacagac tgattaaggt tcaaaaactt 1081 attgctgcat caccggatct cttgctcgat gagatcagtt ttcttggaag agtttctgct 1141 aaaagctatc cagtgaagaa gctccttcca tcagaatttc tggtaaagcc tcctctacca 1201 catgttgtcg tcaaacaaag gggtgactcg gagaagactg accaacataa aatggaaagc 1261 tcagctgaga acgtagttgg gaggttgta aatcaaggtc atcatcaaca atccaactac 1321 atgccttttg caaacaaccc accggcttca ccggtctcaa atggatattg ctttcctcct 1381 cagcctctc cttcaggaaa tcatacagaa tggttgatcc ctgtaatgtc tcctcggaa 1441 ggaactgat atcaagcctca ccaggtatg gcacacacgg ggcattatgg aggatattat 1501 ggtcattata tgectacacc aatggtaatg cctcaatata accccggcat gggattccca 1561 cctcctggta atggctactt ccctccatat ggaatgatgc ccaccataat gaaccatat 1621 tgttcaagcc aacaacaaca acaacaaca ccaatgagc aaatgaacca gtttggacat 1681 cctggaatc ttcagaacac ccaacaaca caacagagat ctgataatga acctgctcca 1741 acagcaacgc aacagccaac aaagtcttat ccgagagcaa gaaagagcag gcaaggagc 1801 acaggaagca gtccaagtgg gccacaggga atctctggta gcaagtcctt tcggccattc 1861 gcagccgttg atgaggacag caacatcaac aatgcacctg agcaaacgat gacaacaacc 1921 acaacgacga caagaacaac tgttactcag acaacaagag atgggggagg agtgacgaga 1981 gtgataaagg tggtaacct caacgcaaag ctgcgagtg agaatgctgc cagaattttc 2041 cagtcaatac aagaagaacg taaacgctat gactcctcta agccttaa	Wild type A. <i>thaliana</i> ELF3 cDNA sequence
2	MKRGKDEEKILEPMFPRHLVNDADKGGFRAPPRNKMALYEQLSIPSQRFGDHGTMNSRSNNTSTLVHPGPS SQPCGVERNLSVQHLDSANQATEKFVSQMSFMENVRSSAQHDQKRMVREEDFAVPVYINSRRSQSHGR TKSGIEKEKHTPMVAPSSHHSIRFQEVNQTGSKQNVCLATCSKPEVRDQVKANARSGGFVISLDVSVTEEI DLEKSASSHDRVNDYNASLRQESRNRLYRDGGKTRLKDTDNGAESHLATENHSQEGHGPSPEDIDNDREYSK SRACASLQQINEASDDVSDSDSVSISSIDVSPDDVVGILGQKRFRARKAIAQQQRFVAVQLFELHRLI KVQKLIASPDLLLDEISFLGKVSAKSYPVKKLLPSEFLVKPLPHVVVKQRGDSKTDQHKMESSAENVV GRLSNQGHQGSNYMPFANNPPASPAPNGYCFPPQPPPSGNHQWLIPVMSPEGLIYKPHPGMAHTGHYG GYYGHYMPFMVMPQYHPGMGFPPPGNGYFPYGYMMPTIMNPYCSSQQQQQQQPNQMNQFGHPGNLQNTQ QQQQRSNDEPAPQQQQQFTKSYPRARKSRQGSTGSSPSGPGQISGSKSFRPFAAVDEDSNINNAPEQMTT TTTTTRTTVTQTTRDGGGVTRVIKVVPHNAKLASENAARIQSIEERKRYDSSKP-	Wild type A. <i>thaliana</i> ELF3 protein

3	1 atgaagagag ggaagatga ggagaagata ttggaaccta tgtttcctcg gcttcatgtg 61 aatgatgcag ataaaggagg gcctagagct cctcctagaa acaagatggc tctttatgag 121 cagcttagta ttccttctca gaggtttggt gatcatggaa cgatgaattc tcgtagtaac 181 aacacaagca ctttggttca tcttggaacca tctagtcagc cttgtggtgt ggaaagaaac 241 ttatctgtcc agcatcttga ttcttcagcc gcaaaccaag caactgagaa gtttgtctcc 301 caaatgtcct tcatggaaaa tgtgagatct tcggcacagc atgatcagag gaaaatggtg 361 agagaggaag aagattttgc agttccagta tatattaact caagaagatc tcagtctcat 421 ggcagaacca agagtgggtat tgagaaggaa aaacacaccc caatggtggc acctagctct 481 catcactcca ttcgatttca agaagtgaat cagacaggct caaagcaaaa cgtatgtttg 541 gctacttggt caaaacctga agttagggat caggtaagg cgaatgcaag gtcagggtggc 601 tttgtaatct cttagatgt atcagtcaca gaggagattg atctcgaaaa atcagcatca 661 agtcatgata gagtaaatga ttataatgct tccttgagac aagagtctag aaatcggtta 721 taccgagatg gtggcaaaac tcgtctgaag gacactgata atggagctga atctcacttg 781 gcaacggaaa atcattcaca agagggtcat ggcagtcctg aagacattga taatgatcgt 841 gaatacagca aaagcagagc atgcgcctct ctgcagcaga taaatgaaga ggcaagtgat 901 gacgtttctg atgattcgat ggtggattct atatccagca tagatgtctc tcccgatgat 961 gttgtgggta tattaggtca aaaacgtttc tggagagcaa ggaagccat tgccaatcaa 1021 caaagagtat ttgctgttca actatttgag ttgcacagac tgattaaggt tcaaaaactt 1081 attgctgcat caccgatct ctgctcgat gagatcagtt ttcttgaaa agtttctgct 1141 aaaagctatc cagtgaagaa gtccttcca tcagaatttc tggtaaagcc tctctacca 1201 catgttgctg tcaaacaaaagg gggtagctcg gagaagactg accaacataa aatggaaaagc 1261 tcagctgaga acgtagtgtg gaggttgctc aatcaaggtc atcatcaata atccaactac 1321 atgccttttg caaacaaccc accggcttca ccggctccaa atggatattg ctttctcct 1381 cagcctctct cttcaggaat tcatcagcaa tgggtgatcc ctgtaatgtc tccctcgaa 1441 ggactgatat acaagcctca ccaggtatg gcacacacgg gccattatgg aggatattat 1501 ggtcattata tgectacacc aatggtaatg cctcaatatc acccggcat gggattccca 1561 cctcctggta atggctactt cctccatat ggaatgatgc ccaccataat gaaccatata 1621 tgttcaagcc aacaacaaca acaacaaca ccaatgagc aaatgaacca gtttggacat 1681 cctggaaatc ttcagaacac ccaacaaca caacagagat ctgataatga acctgctcca 1741 cagcaacagc aacagccaac aaagtcttat ccgagagcaa gaaagagcag gcaagggagc 1801 acaggaagca gtccaagtgg gccacaggga atctctggta gcaagtcctt tcggccattc 1861 gcagccgttg atgaggacag caacatcaac aatgcacctg agcaaacgat gacaacaacc 1921 acaacgacga caagaacaac tgttactcag acaacaagag atgggggag agtgacgaga 1981 gtgataaagg tggtaacctca caacgcaaag ctgcgagtg agaatgctgc cagaattttc 2041 cagtcaatac aagaagaacg taaacgctat gactcctcta agccttaa	Elf3-1 mutant allele of <i>A. thaliana</i> (converts nucleotide 1309C to T, converts Q 437 to stop)
4	1 atgaagagag ggaagatga ggagaagata ttggaaccta tgtttcctcg gcttcatgtg 61 aatgatgcag ataaaggagg gcctagagct cctcctagaa acaagatggc tctttatgag 121 cagcttagta ttccttctca gaggtttggt gatcatggaa cgatgaattc tcgtagtaac 181 aacacaagca ctttggttca tcttggaacca tctagtcagc cttgtggtgt ggaaagaaac 241 ttatctgtcc agcatcttga ttcttcagcc gcaaaccaag caactgagaa gtttgtctcc 301 caaatgtcct tcatggaaaa tgtgagatct tcggcacagc atgatcagag gaaaatggtg 361 agagaggaag aagattttgc agttccagta tatattaact caagaagatc tcagtctcat 421 ggcagaacca agagtgggtat tgagaaggaa aaacacaccc caatggtggc acctagctct 481 catcactcca ttcgatttca agaagtgaat cagacaggct caaagcaaaa cgtatgtttg 541 gctacttggt caaaacctga agttagggat caggtaagg cgaatgcaag gtcagggtggc 601 tttgtaatct cttagatgt atcagtcaca gaggagattg atctcgaaaa atcagcatca 661 agtcatgata gagtaaatga ttataatgct tccttgagac aagagtctag aaatcggtta 721 taccgagatg gtggcaaaac tcgtctgaag gacactgata atggagctga atctcacttg 781 gcaacggaaa atcattcaca agagggtcat ggcagtcctg aagacattga taatgatcgt 841 gaatacagca aaagcagagc atgcgcctct ctgcagcaga taaatgaaga ggcaagtgat 901 gacgtttctg atgattcgat ggtggattct atatccagca tagatgtctc tcccgatgat 961 gttgtgggta tattaggtca aaaacgtttc tggagagcaa ggaagccat tgccaagtaa	ELF3-2 mutant sequence of <i>A. thaliana</i> (nucleotide_1017 T to G converting N339 to K, and_Nucleotide 1018 C to T, converts Q340 to_stop, followed by

	1021 gttcactaga aatttacagt ttggttattt attctccgct ctttctattt atctccttct 1081 ttgataccaa cattttttgc ttgaaagaag ttaatatatta agcattgttc cgtagtctta 1141 ctgaagcttt ttctctgtt gttttttgct attttcattg aggactgttg tagggcatat 1201 ttactatca ccaaatttca aatttctaga acactctcct tcataatttt tttcatgat 1261 taatgctgca attgattgct gatatacata tatgactatt tgtttcagct cgagaagaaa 1321 caaatactca tggaacata tgagaaggtt tctgaatgac tttaccttaa tcagtctggt 1381 gcaactcaaa tagttgaaca gcaaaatact ctttggtgac tggtaatgga gaaacagagt 1441 c	insertion of unknown length)
5	1 atggtttccg gactcggggg tagtggcggg ggcctgtggc gtggcgtgg cgagaagaa 61 gaaccgtcgt caagtcacac tctaataaac cgaagaggag gagaacaagc tcaatcgtcg 121 ggaacgaaat ctctcagacc aagaagcaac actgaatcaa tgagcaaagc aattcaacag 181 tacaccgtcg acgcaagact ccacgccgtt ttcgaacaat ccggcgaatc agggaaatca 241 ttgactact cacaatcact caaacgacg acgtacgggt cctctgtacc tgagcaacag 301 atcacagctt atctctctcg aatccagcga ggtggttaca ttcagccttt cggatgtatg 361 atcgccgtcg atgaatccag tttccggatc atcggttaca gtgaaaacgc cagagaaatg 421 ttagggatta tgcctcaatc tgttcctact cttgagaaac ctgagattct agctatggga 481 actgatgtga gatctttgtt cacttcttcg agctcgatc tactcgagcg tgctttcgtt 541 gctcgagaga ttacctgtt aaatccgggt tggatccatt ccaagaatac tggtaaaccg 601 ttttacgcca ttcttcatag gattgatgtt ggtgttgta ttgatttaga gccagctaga 661 actgaagatc ctgcgcttct tattgctggt gctgttcaat cgcagaaact cgcggttcgt 721 gcgatttctc agttacaggc tcttcctggt ggagatatta agcttttctg tgacactgtc 781 gtggaagtgt tgagggactt gactggttat gatcgtgta ttggtttataa gtttcatgaa 841 gatgagcatg gagaagttgt agctgagagt aaacgagatg atttagagcc ttatatgga 901 ctgcattatc ctgctactga tttccctcaa gcgtcaagggt tcttggttaa gcagaaccgt 961 gtccgaatga tagtagattg caatgccaca cctgttcttg tggtcagga cgataggcta 1021 actcagtcta tgtgcttgggt tggttctact cttagggtc ctcatggttg tcaactctcag 1081 tatatggcta acatgggatc tattgctgtt ttagcaatgg cgtttataat caatggaat 1141 gaagatgatg ggagcaatgt agctagtgtg agaagctcga tgaggctttg gggtttggtt 1201 gtttgccatc acacttcttc tcgctgcata ccgtttccgc taaggatgct tttgtagttt 1261 ttgatgcagg ctttcgggtt acagttaaac atggaattgc agttagcttt gcaaatgtca 1321 gagaaacgcg ttttgagaac gcagacactg ttatgtgata tgcttctgct tgactcgcct 1381 gctggaattg ttacacagag tcccagtatc atggacttag tgaatgtga cgggtgcagca 1441 tttctttacc acgggaagta ttaccggttg ggtgttgctc ctagtgaagt tcagataaaa 1501 gatgttgttg agtggttgct tgccaatcat gcgattcaa ccggaattaag cactgatagt 1561 ttaggcgatg cggggtatcc cgggtgcagct gcgttagggg atgctgtgtg cggtatggca 1621 gttgcatata tcacaaaaag agactttctt ttttggtttc gatctcacac tgcgaaagaa 1681 atcaaatggg gaggcgctaa gcatcatccg gaggataaag atgatgggca acgaatgcat 1741 cctcgttcgt ctttccaggtc ttttcttgaa gttgttaaga gccggagtca gccatgggaa 1801 actgcggaaa tggatgcgat tcaactcgtc cagcttattc tgagagactc ttttaagaa 1861 tctgagggcg ctatgaactc taaagtgtg gatggtgtg ttccagccatg tagggatatg 1921 gcgggggaac aggggattga tgagttaggt gcagttgcaa gagagatggt taggctcatt 1981 gagactgcaa ctgttcctat attcgctgtg gatgcggag gctgcatcaa tggatggaa 2041 gctaagattg cagagttgac aggtctctca gttgaagaag ctatggggaa gtctctggtt 2101 tctgatttaa tatacaaaag gaatgaagca actgtcaata agcttctttc tctgctttg 2161 agaggggacg aggaaaagaa tgtggaggtt aagctgaaaa ctttcagccc cgaactacaa 2221 gggaaagcag tttttgtggt tgtgaatgct tgttcagca aggaactact gaacaacatt 2281 gtcggcggtt gttttgttgg acaagacgtt actagtcaga aaatcgtaat ggataagttc 2341 atcaacatac aaggagatta caaggctatt gtacatagcc caaacctct aatcccgcc 2401 atttttgctg ctgacgagaa cacgtgctgc ctggaatgga acatggcgat ggaaaagctt 2461 acgggttggt ctgcagtgat agtgattggg aaaatgattg tcggggaagt gtttgggagc 2521 tgttgcatgc taaagggtcc tgatgcttta accaagttca tgattgtatt gcataatgcg 2581 attggtggcc aagatacggg taagttccct ttccattct ttgaccgcaa tgggaagttt	<i>A. thaliana</i> PhyB wild type

	2641 gttcaggctc tattgactgc aaacaagcgg gttagcctcg agggaaaggt tattggggct 2701 ttctgtttct tgcaaatccc gagccctgag ctgcagcaag ctttagcagt ccaacggagg 2761 caggacacag agtggtttcac gaaggcaaaa gaggttggctt atatttgtca ggtgataaag 2821 aatccctttga gcggtatgcg ttctgcaaac tcattgttg aggccacaga cttgaacgag 2881 gaccagaagc agttacttga aacaagtgtt tcttgcgaga aacagatctc aaggatcgctc 2941 ggggacatgg atcttgaaag cattgaagac ggttcatttg tgctaaagag ggaagagttt 3001 ttcccttgga gtgtcataaa cgcgattgta agtcaagcga tgttcttatt aaggacaga 3061 ggtcttcagc tgatccgtga cattcccga gagatcaaat caatagaggt ttttgagac 3121 cagataagga ttcaacagct cctggctgag ttctctgctga gtataatccg gtatgcacca 3181 tctcaagagt ggggtggagat ccatttaagc caactttcaa agcaaatggc tgatggattc 3241 gccgccatcc gcacagaatt cagaatggcg tgtccagggt aaggtctgcc tccagagcta 3301 gtcgagaca tgttccatag cagcaggtgg acaagccctg aaggtttagg tctaagcgt 3361 tgtcgaaaga ttttaaagct aatgaacggg gaggttcaat acatccgaga atcagaacgg 3421 tcctatttcc tcatcattct ggaactccct gtacctcgaa agcgaccatt gtcaactgct 3481 agtgggaagt gtgacatgat gctgatgatg ccatattag	
6	MVSGVGGSGGGRRGGGEEEPSSSTFPNNRRGGEQAQSSGSKSLRPRSNTESMSKAIQQYTVDARLHAVF EQSGESGKSFYDSQSLKTTTYGSSVPEQQITAYLSRIQRGGYIQPFGCMIAVDESSFRIIGYSENAREMLG IMPQSVPTLEKPEILAMGTDVRSFLTSSSSILLERAFVAREITLLNPFVWHSKNTGKPFYAILHRIDVGVV IDLEPARTEDPALS IAGAVQS QKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTG YDRVMVYKFHEDEHG EVVAESKRDDLEPYIGLHYPATDI PQASRFLFKQNRVRMI VDCNATPVLVVQDDRLTQSMCLVGSTLRAPH GCHSQYMANMGS IASLAMAVI INGNEDDGSNVASGRSSMRWLGLVVCCHTS SRCPFFPLRYACEFLMQAFG LQLNMELQLALQMSEKRVLRQTLLCDMLLRDSFAGIVTQSPSIMDLVKCDGAFLYHGKYYPLGVAPSEV QIKDVVEWLLANHADSTGLSTDSLGDAGYPGAAALGDAVCGMAVAYITKRDFLFWFRSHTAKEIKWGGAKH HPEDKDDGQRMHPRSSFQAFLEVVKSRSQPWETAEMDAIHSLLQLILRDSFKES EAMNSKVVDGVVQPCRD MAGEQGIDELGAVAREMVRLETATVPIFAVDAGGCINGWNAKIAELTGLSVEEAMGKSLVSDLIYKENEA TVNKLSSRALRGDEEKNVEVKLTFSPELQKAVFVVVNACSSKDYLNIVGVCFVGQDVT SQKIVMDKFI NIQGDYKAI VHSNPLIPPIFAADENTCCLEWNMAAMEKLTGWSRSEVIGKMIVGEVFGSCCMLKGPDALTK FMIVLHNAI GGQDTDKFFPFFDRNGKFVQALLTANKRVSLEGKVI GAFCLQIPSPELQQALAVQRRQDT ECFTKAKELAYICQVIKNPLSGMRFANS LLEATDLNEDQKQLLET SVSCEKQISRIVGDMDESIEDGSFV LKREEFFLGSVINAIVSQAMFLLRDRGLQLIRDIPEEIKSIEVFGDQIRIQQLLAEFLLSIIRYAPSQEWV EIHLSQLSKQMDGFAAIRTEFRMACPGELPPELVDRDMFHSSRWTSPEGLGLSVCRKILKLMNGEVQYIR ESERSYFLIILELPVPRKRPLSTASGSGDMLMMPY-	<i>A. thaliana</i> PhyB wild type protein
7	1 atggtttccg gtagtcgggg tagtgccggt ggcctgtggc gtggccgtgg cggagaagaa 61 gaaccgtcgt caagtcacac tctaataaac cgaagaggag gagaacaagc tcaatcgtcg 121 ggaacgaaat ctctcagacc aagaagcaac actgaatcaa tgagcaaaagc aattcaacag 181 tacaccgtcg acgcaagact ccacgccgtt ttcgaacaat ccggcgaaac agggaaatca 241 ttcgactact cacaatcact caaaacgacg acgtacgggt cctctgtacc tgagcaacag 301 atcacagctt atctctctcg aatccagcga ggtggttaca ttcagccttt cggatgtatg 361 atcgccgtcg atgaatccag tttccggatc atcggttaca gtgaaaacgc cagagaaatg 421 ttagggatta tgcctcaatc tgttctact cttgagaaac ctgagattct agctatggga 481 actgatgtga gatctttgtt cacttctctg agctcgattc tactcgagcg tgctttcgtt 541 gctcgagaga ttaccttggt aaatccggtt tggatccatt ccaagaatac tggtaaaccg 601 ttttacgcca ttcttcatag gattgatgtt ggtgttggtt ttgatttaga gccagctaga 661 actgaagatc ctgcgctttc tattgctggt gctgttcaat cgcagaaact cgcggttcgt 721 gcgattttct agttacaggc tcttctggt ggagatatta agcttttggt tgacactgtc 781 gtggaaagtg tgagggactt gactggttat gatcgtgtta tggttcataa gtttcatgaa 841 gatgagcatg gagaagtgtt agctgagagt aaacgagatg atttagagcc ttatatggga 901 ctgcattatc ctgctactga tattcctcaa gcgtcaaggt tcttgtttaa gcagaaccgt 961 gtccgaatga tagtagattg caatgccaca cctgttcttg tggccagga cgataggcta 1021 actcagtcta tgtgcttggt tgggtctact cttagggtc ctcattggtt tcaactctcag 1081 tatatggcta acatgggatc tattgctgtt ttagcaatgg cgtttataat caatggaat	YHB allele of <i>A. thaliana</i> phyB. Comprises a Y2/6H mutation. Constitutively active

	1141 gaagatgatg ggagcaatgt agctagtggga agaagctcga tgaggccttg gggtttggtt 1201 gtttgccatc acacttcttc tcgctgcata ccgtttccgc taaggatgac ttgtgagttt 1261 ttgatgcagg ctttcggttt acagttaaac atggaattgc agttagcttt gcaaagtgtca 1321 gaaaaacgcg ttttgagaac gcagacactg ttatgtgata tgcttctgcg tgactcgctt 1381 gctggaattg ttacacagag tcccagtatc atggacttag tgaaatgtga cgggtgcagca 1441 tttctttacc acgggaagta ttaccggttg ggtgttgctc ctagtgaagt tcagataaaa 1501 gatgttggtg agtgggtgct tgcgaatcat gcggattcaa ccggattaag cactgatagt 1561 ttaggcgatg cggggtatcc cgggtgcagct gcgttagggg atgctgtgtg cggtatggca 1621 gttgcatata tcacaaaaag agactttctt ttttggtttc gatctcacac tgcgaaagaa 1681 atcaaatggg gaggcgctaa gcatcatccg gaggataaag atgatgggca acgaatgcat 1741 cctcgctcgt cctttcaggc ttttctgaa gttgttaaga gccggagtca gccatgggaa 1801 actgcggaaa tggatgcgat tcaactcgctc cagcttattc tgagagactc ttttaaagaa 1861 tctgaggcgg ctatgaactc taaagtgtg gatggtgtg ttcagccatg tagggatatg 1921 gcgggggaac aggggattga tgagttagggt gcagttgcaa gagagatggt taggctcatt 1981 gagactgcaa ctgttcctat attcgctgtg gatgccggag gctgcatcaa tggatggaac 2041 gctaagattg cagagttgac aggtctctca gttgaagaag ctatggggaa gtctctggtt 2101 tctgatttaa tatacaaaaga gaatgaagca actgtcaata agcttctttc tcgtgctttg 2161 agaggggacg aggaaaagaa tgtggaggtt aagctgaaaa ctttcagccc cgaactacaa 2221 gggaaagcag tttttgttgt tgtgaatgct tgttccagca aggactactt gaacaacatt 2281 gtcggcgctt gttttgttgt acaagacgtt actagtcaga aaatcgtaat ggataagttc 2341 atcaacatac aaggagatta caaggctatt gtacatagcc caaacctct aatcccgcca 2401 atttttgctg ctgacgagaa cacgtgctgc ctggaatgga acatggcgat ggaaaagctt 2461 acgggttggt ctgcagtgat agtgattggg aaaatgattg tcggggaagt gtttgaggac 2521 tgttgcatgc taaagggtcc tgatgcttta accaagttca tgattgtatt gcataatgcg 2581 attggtggcc aagatacgga taagttccct ttccattctt ttgaccgcaa tgggaagttt 2641 gttcaggctc tattgactgc aaacaagcgg gttagcctcg agggaaaggt tattggggct 2701 ttctgtttct tgcaaatccc gagccctgag ctgcagcaag ctttagcagt ccaacggagg 2761 caggacacag agtggtttcac gaaggcaaaa gagttggctt atatttgtca ggtgataaag 2821 aatcctttga gcggtatgcg tttcgcaaac tcattgttg aggccacaga cttgaacgag 2881 gaccagaagc agttacttga aacaagtgtt tcttgcgaga aacagatctc aaggatcgtc 2941 ggggacatgg atcttgaaag cattgaagac ggttcatttg tgctaaagag ggaagagttt 3001 ttcttgtaa gtgtcataaa cgcgattgta agtcaagcga tgttcttatt aaggacaga 3061 ggtcttcagc tgatccgtga cattcccgaa gagatcaaat caatagaggt ttttgagac 3121 cagataagga ttcaacagct cctggctgag tttctgctga gtataatccg gtatgcacca 3181 tctcaagagt ggttgagat ccatttaagc caactttcaa agcaaatggc tgatggattc 3241 gccgcatcc gcacagaatt cagaatggcg tgtccagggt aaggtctgcc tccagagcta 3301 gtccgagaca tgttccatag cagcaggtgg acaagccctg aaggtttagg tctaagcgta 3361 tgtcgaaaga ttttaaagct aatgaacggg gaggttcaat acatccgaga atcagaacgg 3421 tcctatttcc tcatcattct ggaactccct gtacctgaa agcgaccatt gtcaactgct 3481 agtgggaagt gtagcatgat gctgatgatg ccatattag	
8	MVSGVGSGGGRGGRGGGEEEPSSSHTPNRRGGEQAQSSGTKSLRPSNTESMSKAIQQYTVDARLHAVF EQSGESGKSFYDSQSLKTTTYGSSVPEQQITAYLSRIQRGGYIQPFGCMIAVDESSFRIGYSENAREMLG IMPQSVPTLEKPEILAMGTDVRSFLTSSSSILLERAFVAREITLLNPVWIHSHKNTGKPFYAILHRIDVG IDLEPARTEDPALS IAGAVQSQKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTG YDRVMVHKFHEDEHG EVVAESKRDDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCNATPVLVQDDRLTQSMCLVGSTLRAPH GCHSQYMANMGSIASLAMAVIINGNEDDGSNVASGRSSMRLWGLVVCCHHTSSRCIPFPLRYACEFLMQAFG LQLNMELQLALQMSEKRVLRQTLLCDMLLRDSPAGIVTQSPSIMDLVKCDGAFLYHGKYYPLGVAPSEV QIKDVVEWLLANHADSTGLSTD SLGDAGYPGAAALGDAVCGMAVAYITKRDFLFWFRSHTAKEIKWGGAKH HPEDKDDGQRMHPRSSQAFLEVVKSRSQPWETAEMDAIHSLQLILRDSFKESEAMNSKVVDGVVQPCRD MAGEQGI DELGAVAREMVR LIETATVPIFAVDAGGCINGWNAKIAELTGLSVEEAMGKSLVSDLIYKENEA TVNKLRSALRGDEEKVVEVKLKTFSPELQGKAVFVVVNACSKDYLNINIVGVCFVGQDVT SQKIVMDKFI NIQGDYKAIVHSPNFIPIPIFAADENTCCLEWNNAMEKLTGWSRSEVIGKMIVGEVFGSCCMLKGPDALTK	<i>A. thaliana</i> PHY-B protein encoded by YHB allele of phyB

	FMIVLHNAIGGQDTDKFFPPFFDRNGKFVQALLTANKRVSLEKVGAFCLQIPSPELQQALAVQRRQDT ECFTKAKELAYICQVIKNPLSGMRFANSLLEATDLNEDQKQLLETSSVSCEKQISRIVGMDLESIEDGSFV LKREEFFLGSVINAIVSQAMFLLRDRGLQLIRDIPEEIKSIEVFGDQIRIQQLLAEFLLSIIRYAPSQEWV EIHLSQLSKQMDAGFAAIRTEFRMACPGEGLPPELVDRDMFHSRWTSPPEGLGLSVCRKILKLMNGEVQYIR ESERSYFLIILELPVPRKRPLSTASGSGDMLMMPY-	
9	1 atggttttcg gagtcggggg tagtggcggg ggcggtggcg gtggccgtgg cggagaagaa 61 gaaccgtcgt caagtcacac tccataatac cgaagaggag gagaacaagc tcaatcgtcg 121 ggaacgaaat ctctcagacc aagaagcaac actgaatcaa tgagcaaagc aattcaacag 181 tacaccgtcg acgcaagact ccacgcggtt ttcgaacaat ccggcggaatc agggaaatca 241 ttcgactact cacaatcact caaaacgacg acgtacgggtt cctctgtacc tgagcaacag 301 atcacagctt atctctctcg aatccagcga ggtggttaca ttcagccttt cggatgtatg 361 atcgccgtcg atgaatccag tttccggatc atcggttata gtgaaaacgc cagagaaatg 421 ttagggatta tgcctcaatc tgttcctact cttgagaaac ctgagattct agctatggga 481 actgatgtga gatctttgtt cacttcttcg agctcgattc tactcgagcg tgctttcgtt 541 gctcgagaga ttaccttgtt aaatccggtt tggatccatt ccaagaatac tggtaaaccg 601 ttttacgcca ttcttcatag gattgatgtt ggtgttgta ttgatttaga gccagctaga 661 actgaagatc ctgcgctttc tattgctggt gctgttcaat cgcagaaact cgcgggttcgt 721 gcgattttct agttacaggc tcttctggt ggagatatta agcttttgtg tgacactgtc 781 gtggaaagtg tgagggactt gactggttat gatcgtgtta tggtttataa gtttcatgaa 841 gatgagcatg gagaagtgt agctgagagt aaacgagatg atttagagcc ttatatggga 901 ctgcattatc ctgctactga tattcctcaa gcgtcaaggt tcttgtttaa gcagaaccgt 961 gtccgaatga tagtagattg caatgccaca cctgttcttg tggtcaggga cgataggcta 1021 actcagtccta tgtgcttggg tggttctact cttagggctc ctcatggttg tcaactctcag 1081 tatatggcta acatgggac tattgcgtct ttagcaatgg cggttataat caatggaat 1141 gaagatgatg ggagcaatgt agctagtgtga agaagctcga tgaggctttg aggtttggtt 1201 gtttgcctac acacttcttc tcgctgcata ccgtttccgc taaggatgct ttgtgagttt 1261 ttgatgcagg ctttcgggtt acagttaaac atggaattgc agttagcttt gcaaatgtca 1321 gagaaacgcg ttttgagaac gcagacactg ttatgtgata tgcttctgcg tgactcgcct 1381 gctggaattg ttacacagag tcccagtatc atggacttag tgaaatgtga cgggtgcagca 1441 tttctttacc acgggaagta ttaccggttg ggtgttgctc ctagtgaagt tcagataaaa 1501 gatgttgttg agtggttgct tgcgaatcat gcggttcaa ccggtattaag cactgatagt 1561 ttaggcgatg cgggggatcc cgggtcagct gcgttagggg atgctgtgtg cggtatggca 1621 gttgcatata tcacaaaaag agacttctt ttttggtttc gatctcacac tgcgaaaaga 1681 atcaaatggg gaggcgctaa gcatcatccg gaggataaag atgatgggca acgaatgcat 1741 cctcgctcgt cttttcaggc ttttcttgaa gttgttaaga gccggagtca gccatgggaa 1801 actgcggaaa tggatgcgat tcaactcgtc cagcttattc tgagagactc ttttaaagaa 1861 tctgaggcgg ctatgaatc taaagtgtg gatggtgtgg ttcagccatg tagggatatg 1921 gcgggggaac aggggattga tgagttaggt gcagttgcaa gagagatggt taggctcatt 1981 gagactgcaa ctgttcttat attcgctgtg gatgccggag gctgcatcaa tggatggaac 2041 gctaagattg cagagttgac aggtctctca gttgaagaag ctatggggaa gtctctggtt 2101 tctgatttaa tatacaaa gaatgaagca actgtcaata agcttctttc tctgtcttg 2161 agaggggacg aggaaaagaa tgtggagggt aagctgaaaa ctttcagccc cgaactacaa 2221 gggaaagcag tttttgtggt tgtgaatgct tgttcagca aggactactt gaacaacatt 2281 gtcggcgctt gttttgttg acaagcgtt actagtcaga aaatcgtaat ggataagttc 2341 atcaacatac aaggagatta caaggctatt gtacatagcc caaacctct aatcccgcca 2401 atttttgctg ctgacgagaa cacgtgctgc ctggaatgga acatggcgat ggaaaagctt 2461 acgggttggt ctgcagtg agtgattggg aaaatgattg tcggggaagt gtttgggagc 2521 tgttgcatgc taaaggttcc tgatgcttta accaagttca tgattgtatt gcataatgcg 2581 attggtggcc aagatacgg taagttccct tcccattct ttgaccgcaa tgggaagttt 2641 gttcaggctc tattgactgc aaacaagcgg gttagcctcg agggaaaggt tattggggct 2701 ttctgtttct tgcaaatccc gagccctgag ctgcagcaag ctttagcagt ccaacggagg 2761 caggacacag agtggtttcac gaaggcaaaa gagtggctt atatttgtca ggtgataaag	A.t. loss of function phyB 9 mutant cDNA sequence has a G to A mutation at nucleotide 3489 that changes a tryptophan codon to a stop codon at amino acid position 398

	2821 aatcctttga gcggtatgcg tttcgcaaac tcattgttgg aggccacaga cttgaacgag 2881 gaccagaagc agttacttga aacaagtgtt tcttgcgaga aacagatctc aaggatcgtc 2941 ggggacatgg atcttgaaaag cattgaagac ggttcatttg tgctaaagag ggaagagttt 3001 ttctttggaa gtgtcataaa cgcgattgta agtcaagcga tgttcttatt aaggacaga 3061 ggtcttcagc tgatccgtga cattcccga gagatcaa ataatagaggt ttttgagac 3121 cagataagga ttcaacagct cctggtgag tttctgctga gtataatccg gtatgcacca 3181 tctcaagagt ggggtggagat ccatttaagc caactttcaa agcaa atggc tgatggattc 3241 gccgccatcc gcacagaatt cagaatggcg tgtccagggt aaggtctgcc tccagagcta 3301 gtccgagaca tgttccatag cagcagggtg acaagccctg aaggtttagg tctaagcgta 3361 tgtcgaaaga ttttaagct aatgaacggt gaggttcaat acatccgaga atcagaacgg 3421 tcctatttcc tcatcattct ggaactccct gtacctcgaa agcgaccatt gtcaactgct 3481 agtggaagtg gtgacatgat gctgatgatg ccatattag	
10	MVSGVGS GGGRGGGGGEEEPSSSHTPNRRRGGEQAQSSGTSKSLRPRSNTESMSKAIQQYTVDARLHAVF EQSGESGKSF DYSQSLKTTTYGSSVPEQQITAYLSRIQRGGYIQPF GCMIAVDESSFRIIGYSENAREMLG IMPQSVPTLEKPEILAMGTDVRS LFTSSSSILLERAFVAREITLLNPVWIHSKNTGKPFYAILHRIDVGVV IDLEPARTEDPALSIAGAVQSQKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHG EVVAESKRDDLEPYIGLHYPATDIPQASRFLFKQNRVMI VDCNATPVLVVDRLTQSMCLVGSTLRAPH GCHSQYMANMGSIASLAMAVIINGNEDDGSNVASGRSSMRL-	A. t. phyB protein fragment encoded by the phyB-9 loss-of- function allele of phyB (SEQ ID NO: 9).
11	1 ATGGTTTCG GAGTCGGGGG TAGTGGCGGT GGCCGTGGCG GTGGCCGTGG CGGAGAAGAA 61 GAACCGTCGT CAAGTCACAC TCCTAATAAC CGAAGAGGAG GAGAACAAGC TCAATCGTCG 121 GGAACGAAAT CTCTCAGACC AAGAAGCAAC ACTGAATCAA TGAGCAAAGC AATTCAACAG 181 TACACCGTCG ACGCAAGACT CCACGCCGTT TTCGAACAAT CCGGCGAATC AGGGAAATCA 241 TTCGACTACT CACAATCACT CAAAACGACG ACGTACGGTT CCTCTGTACC TGAGCAACAG 301 ATCACAGCTT ATCTCTCTCG AATCCAGCGA GGTGGTTACA TTCAGCCTTT CGGATGTATG 361 ATCGCCGTCG ATGAATCCAG TTTCCGGATC ATCGGTTACA GTGAAAACGC CAGAGAAATG 421 TTAGGGATTA TGCCTCAATC TGTTCTTACT CTTGAGAAAC CTGAGATTCT AGCTATGGGA 481 ACTGATGTGA GATCTTTGTT CACTTCTCG AGCTCGATT CACTCGAGCG TGCTTTCGTT 541 GCTCGAGAGA TTACCTTGTT AAATCCGGTT TGGATCCATT CCAAGAATAC TGGTAAACCG 601 TTTTACGCCA TTCTTCATAG GATTGATGTT GGTGTTGTTA TTGATTTAGA GCCAGCTAGA 661 ACTGAAGATC CTGCGCTTTC TATTGCTGGT GCTGTTCAAT CGCAGAACT CGCGGTTCTG 721 GCGATTTCTC AGTTACAGGC TCTTCTGGT GGAGATATTA AGCTTTTGTG TGACACTGTC 781 GTGGAAGTG TGAGGGACTT GACTGGTTAT GATCGTGTTA TGGTTTATAA GTTTCATGAA 841 GATGAGCATG GAGAAGTTGT AGCTGAGAGT AAACGAGATG ATTTAGAGCC TTATATTGGA 901 CTGCATGTTT CTGCTACTGA TATTCCTCAA GCGTCAAGGT TCTGTTTAA GCAGAACCGT 961 GTCCGAATGA TAGTAGATTG CAATGCCACA CCTGTCTTG TGGTCCAGGA CGATAGGCTA 1021 ACTCAGTCTA TGTGCTTGGT TGGTCTTACT CTTAGGGCTC CTCATGGTTG TCACTCTCAG 1081 TATATGGCTA ACATGGGATC TATTGCGTCT TTAGCAATGG CGGTTATAAT CAATGGAAT 1141 GAAGATGATG GGAGCAATGT AGCTAGTGGA AGAAGCTCGA TGAGGCTTTG GGGTTTGGTT 1201 GTTTGCCATC ACACTTCTTC TCGCTGCATA CCGTTTCCGC TAAGGTATGC TTGTGAGTTT 1261 TTGATGCAGG CTTTCGGTTT ACAGTTAAAC ATGGAATTGC AGTTAGCTTT GCAAATGTCA 1321 GAGAAACGCG TTTTGAGAAC GCAGACACTG TTATGTGATA TGCTTCTGCG TGA CTGCGCT 1381 GCTGGAATTG TTACACAGAG TCCCAGTATC ATGGACTTAG TGAAATGTGA CGGTGCAGCA 1441 TTTCTTTACC ACGGGAAGTA TTACCCGTTG GGTGTTGCTC CTAGTGAAGT TCAGATAAAA 1501 GATGTTGTGG AGTGGTTGCT TGCGAATCAT CGGATTCAA CCGGATTAAG CACTGATAGT 1561 TTAGGCGATG CCGGGTATCC CGGTGACGT GCGTTAGGGG ATGCTGTGTG CCGTATGGCA 1621 GTTGCAATATA TCACAAAAAG AGACTTTCTT TTTTGGTTTC GATCTCACAC TGCGAAAGAA 1681 ATCAAATGGG GAGGCGCTAA GCATCATCCG GAGGATAAAG ATGATGGGCA ACGAATGCAT	A. thaliana phyB Y303V cDNA (a different version of YHB)

	1741 CCTCGTTCGT CCTTTCAGGC TTTTCTTGAA GTTGTTAAGA GCCGGAGTCA GCCATGGGAA 1801 ACTGCGGAAA TGGATGCGAT TCACTCGCTC CAGCTTATTC TGAGAGACTC TTTTAAAGAA 1861 TCTGAGGCGG CTATGAACTC TAAAGTTGTG GATGGTGTGG TTCAGCCATG TAGGGATATG 1921 GCGGGGGAAC AGGGGATTGA TGAGTTAGGT GCAGTTGCAA GAGAGATGGT TAGGCTCATT 1981 GAGACTGCAA CTGTTCTAT ATTCTGCTGTG GATGCCGAG GCTGCATCAA TGGATGGAAC 2041 GCTAAGATTG CAGAGTTGAC AGGTCTCTCA GTTGAAGAAG CTATGGGGAA GTCTCTGGTT 2101 TCTGATTTAA TATACAAAGA GAATGAAGCA ACTGTCAATA AGCTTCTTTC TCGTGCCTTG 2161 AGAGGGGACG AGGAAAAGAA TGTGGAGGTT AAGCTGAAAA CTTTCAGCCC CGAACTACAA 2221 GGGAAAGCAG TTTTGTGGT TGTGAATGCT TGTTCCAGCA AGGACTACTT GAACAACATT 2281 GTCGGCGTTT GTTTTGTGGT ACAAGACGTT ACTAGTCAGA AAATCGTAAT GGATAAGTTC 2341 ATCAACATAC AAGGAGATTA CAAGGCTATT GTACATAGCC CAAACCCTCT AATCCCGCCA 2401 ATTTTGTCTG CTGACGAGAA CACGTGCTGC CTGGAATGGA ACATGGCGAT GGAAAAGCTT 2461 ACGGGTTGGT CTCGCAGTGA AGTGATTGGG AAAATGATTG TCGGGGAAGT GTTTGGGAGC 2521 TGTTGCATGC TAAAGGGTCC TGATGCTTTA ACCAAGTTCA TGATTGTATT GCATAATGCG 2581 ATTGGTGGCC AAGATACGGA TAAGTCCCT TTCCCATCTT TTGACCGCAA TGGGAAGTTT 2641 GTTCAGGCTC TATTGACTGC AAACAAGCGG GTTAGCCTCG AGGGAAAGGT TATTGGGGCT 2701 TTCTGTTTCT TGCAAATCCC GAGCCCTGAG CTGCAGCAAG CTTTAGCAGT CCAACGGAGG 2761 CAGGACACAG AGTGTTCAC GAAGGCAAAA GAGTTGGCTT ATATTTGTCA GGTGATAAAG 2821 AATCCTTTGA GCGGTATGCG TTTGCGAAAT TCATTGTTGG AGGCCACAGA CTTGAACGAG 2881 GACCAGAAGC AGTTACTTGA AACAAGTGT TCTTGCGAGA AACAGATCTC AAGGATCGTC 2941 GGGGACATGG ATCTTGAAAG CATTGAAGAC GGTTCAATTG TGCTAAAGAG GGAAGAGTTT 3001 TTCCTTGAA GTGTCATAAA CGCGATTGTA AGTCAAGCGA TGTTCCTATT AAGGGACAGA 3061 GGTCTTCAGC TGATCCGTGA CATTCCCGAA GAGATCAAAT CAATAGAGGT TTTTGGAGAC 3121 CAGATAAGGA TTCAACAGCT CCTGGCTGAG TTTCTGCTGA GTATAATCCG GTATGCACCA 3181 TCTCAAGAGT GGGTGGAGAT CCATTTAAGC CAACTTTCAA AGCAAATGGC TGATGGATTG 3241 GCCGCCATCC GCACAGAATT CAGAATGGCG TGTCAGGTG AAGGTCTGCC TCCAGAGCTA 3301 GTCCGAGACA GTTCCATAG CAGCAGGTG ACAAGCCCTG AAGGTTTAGG TCTAAGCGTA 3361 TGTCGAAAGA TTTTAAAGCT AATGAACGGT GAGGTTCAT ACATCCGAGA ATCAGAACGG 3421 TCCTATTTCC TCATCATTCT GGAACCTCCT GTACCTCGAA AGCGACCATT GTCAACTGCT 3481 AGTGAAGTG GTGACATGAT GCTGATGATG CCATATTAG	
12	MVSGVGGSGGGRRGGRRGGEEEPSSSHTPNRRRGGEQAQSSGTKSLRPRSNTESMSKAIQQYTVDARLHAVF EQSGESGKSFYDSQSLKTTTYGSSVPEQQITAYLSRIQRGGYIQPFGCMIADDESSFRIGYSENAREMLG IMPQSVPTLEKPEILAMGTDVRSFLTSSSSILLERAFVAREITLLNPVWIHSHKNTGKPFYAILHRIDVGVV IDLEPARTEDPALS IAGAVQSQKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHG EVVAESKRDDLEPYIGLHVPATDIPQASRFLFKQNRVRMIVDCNATPVLVQDDRLTQSMCLVGSTLRAPH GCHSQYMANMGSIASLAMAIIINGNEDDGSNVASGRSSMRLWGLVVCCHHTSSRCIPFPLRYACEFLMQAFG LQLNMELQLALQMSEKRVLRQTLLCDMLLRDSPAGIVTQSPSIMDLVKCDGAFLYHGKYYPLGVAPSEV QIKDVVWLLANHADSTGLSTDLSLDAGYPGAALGDAVCGMAVAYITKRDFLFWFRSHTAKEIKWGGAKH HPEDKDDGQRMHPRSSFOAFLEVVKSRSPWETAEMDAIHSLQLILRDSFKESSEAMNSKVVDGVVQPCRD MAGEQGIDELGAVAREMVRLEIATVPIFAVDAGGCIINGWNAKIAELTGLSVEEAMGKSLVSDLIYKENEA TVNKLRSRALRGDEEKNVEVKLTFSPELQKAVFVVVNACSSKDYLNINIVGVCFVGQDVTSQLIVMDKFI NIQGDYKAIHSPNPLIPPIFAADENTCCLEWNNAMEKLTGWSRSEVIGRMIVGEVFGSCCMLKGPDALTK FMIVLHNAIGQDQTDKFFPFFDRNGKFVQALLTANKRVSLEGKVI GAFCLQIPSPQLQALAVQRRQDT ECFTKAKELAYICQVIKNPLSGMRFANSLEATDLNEDQKQLLETSVSCEKQISRVGMDLESIEDGSFV LKREEFFLGSVINAIVSQAMFLLRDRGLQLIRDIPEEIKSIEVFGDQIRIQQLLAEFLLSIIRYAPSQEWV EIHLSQLSKQMDGFAAIRTEFRMACPGEGLPELVDRDMFHSSRWTSPEGLGLSVCRKILKLMNGEVQYIR ESERSYFLIILELPVPRKRPLSTASGSGDMMMLMPY-	Another A.t. YHB allele (phyB Y303V) protein (encoded by SEQ ID NO: 11)
13	ATGAAGAGGGGAAAAGATGAGGGAAAGATTATGGGGCCTATGTTTCCGAGGCTCCATGTGAATGATACCGA GAAAGGGGGGCCAAGAGCCCCCTCTAGAAACAAGATGGCTCTTTATGAGCAGCTCAGCATTCTTTCACAGA GACTCAGTAATTCTGTTAGACCCCGAATTCGGAGCACGCTTCGGATCAGGGGGCTGCAAACGAAAGGGGT GCGTTTTTCTCGTATCAGCTGCCTAACAGACATAAGTCAGATAAGATAAGCAGCCAATATTCCGATTTCAG	A basil elf3 isoform

	CGCTCCATTACGCCACTTGGCCGGAGAAAGAAATCCGATGAAGAGGAATTGAGAGTTCCCGTTTTCCACC ATTCCATCCAAAATCAAGAATGCGGTGATTATGTTAAGAAGGATAACCCCGTGCATGAAAAAGTCTCCGCT TCCAACCCCTCTAGTCTCAATCGTCCGTGAAATTCATAAATTCAAAAGCCAGACAGACAAGAATTCAAA AGAGTTCCCTCTGATCGAACAAAAGTTGTGTCAAATTCATCCATCATCGAGAAGCAAATGATTGAGCTT TTTGTCTGAGCCAACAGATTGTCAAGCTAGTAGTATTGGCAGATTACAGACCCGCGATATGAGTGAGCCA GAGCTACGTGCTGATTCTGAGCATGATGAAATTAGGCGTGCTAACTCTGTGGTAATGAAGAATTTTCCAAC CTTAGATGAAAGAAATTCATAAGAATTGGGAAATGATGAAGGATCTCAGAAAAGATTGGTACCAATGGGAG ACCTTGAGAGGGCTGACAGTGTGTCTGAGATTTGCGTTGTGAGTCCATTGCTGGGCTCGATATGACACCC GACGACGTGGTGGGAATAATTGGTCAGAAACATTTTTGGAAGGCCAGAAAGAATATTCTTAATCAACAAAG AGTTTTTGTCTGTTCAAGTATTTCGAGTTGCATCGATTGGTTAAGGTCCAGAGATTGATCGCTGCATTGCCAC AGTTCTTGTCTGACAACACGGCCTTCGTGACAAACCAAACGCTGCGCCCGGACCAAAAGTCCCATCGGTT AGTCCCCCTCAAAGCCCGCAATCCCGAAATTCCAAAGCGAAAAGGCGAACTCCAGAAGCCGAGCCATAACAA GGAAAGCTCCGCGGAAAACACTGCCGAGAAACCATCGTTCTCGTCCATTCAAACGGCGAGCTCCCGTCTG GCTACGGGCCGTTGACAGGCAACTCTCTGGGCCCTCCCGTTTCGAGCAATCCAAATACCGGGCCCGGGCCG TGGTGCTTCAACCAACCTCAAGGGCACCAATGGTTGATTCTGTGATGACACCTTCAGAAGGACTAGTTTA CAAGCCATATCCCGGGCCGGGCTTCGTGGGCCAGCCTGCGGCGGCTGTGGCCACCCGCGCCAATTCCAG CGTATGGAATCCCGGCCCCACATCCTCATTATCAGCTCCCATCGTTCCCGCACGGCTACTTCCCGACGTAC GGCATGCCGATGATGAACACGGCCGAGTGTGCGGCTCGTCCGTGAGCAGACGAACCTCAACCTGTTCC TAGCCAAGCTTCGGGAGGCGGAACCGGTGCCAGCTTTCACATCATCAGAACTTGCCTTCGACACCAAGCC GCAAGAAATCGAGCAGATCCTGACAGGACGAATGCGTCGAAGAACTACGAACCTGTTGAGACTAGCAGAGGA AGTAGCCCCGTTGAAAGATTGGTCGATAATGGAGGAGGAAGCGATGACGGGGAAAGAGGGAATATGCTCTC ACTTTTCCAATGGCCCCATCTTCCGATGAGCCTGGTTTCGAGCCAGCCTGTACGAAGCCGATCGGCCGA CTCAAGTGGTCAGGGTTGTGCCTCATAATGCAAGATCTGCCACTGAATCTGCTGCAAGGATTTTTAGATTT ATACAAGAAGGAAGAAAACAGTATGATTCTGTGTGA	
14	ATGAAGAGAGGGAGAGATGAGGGGAAGATTATGGGGCCAATGTTTCCAAGGCTACATGTGAATGACACTGA GAAAGGAGGGCCAAGAGCCCTCCAGAAACAAAATGGCTCTGTATGAGCAGCTCACCATCCCTTCCCACA GACTCACCATTCCGCCAGGGTGTTCAACTGATACTGGTGCAATTTTCCCATACAAGCCGTCTAACAGA CATCAGTCCGAGAATCTATGCGGTCAATATTCGATTTCAGTATACCGTCGACGCCAGTCAGCTGGAGAAA GAAATCGGACGAAGAGGATTTGAGAGTTCCATTTTCAACGATTCTGTCCGAAGTCAAGAACGTAGAAAAT GTGGTAATGACCCGTTGACGAGAAAAGGTCAATCACCCTGCGAAATTCATAAATTCAAAAGGACAGGCATG CTTGAAAGTAACATGAGGCAAGAAGGCAAAAAGCCAGACAGAAAAGAATTACAAGCGCTTGCATTGATCG AGCAAAAGCTTTATCAAACCTATCTAGCATCGAGAAGCAGAAATGGTTACCTATATTTCTGTAACGGAGAG ATTGTCTCTGCTAAAAGTGTGACAGATTACAGACCCGCGATGCCATTGAGCCGAAGCTCCGTCTCTGATTCA GAGCGTGTGGAACGGGTGCACTACCTCGCTGTTGGAGAAGGCTTCGGCAACCTTAGATGAAAGAACTC TTCTGCTCCATTGAGAGATCAGAGAAATTCTTGTGATTGGGAAACAATCGCAAAGGTGAGTGGCGGTGA CAAATCTTGATATGGCTGACAGTGTGTCGGAGATCTCGCTTGTGGAGTCCATCGCCGGACCGGATATGACG CCTGATGACGTGGTGGGAATAATCGGTCCGAAACATTTTGGAAAGCCAGAAAAGCCATTCTCAACCAACA AAGAGTTTTCGCGATCCAAGTATTCGAGTTGCATCGACTGATAAAGGTCCAGAGATCGATCGCCGAATCAC CCCAGATGTTGGCCGACAACCTCGGTTTTCTGTCGACAAACCAGACTTGGCTAGTCCCGTCAAACCTATTCCC AATGCTTCCAAGCGTACGGCCAGCCCCATCAAAGCATTTCCCGCCGTTTTCCAAGAAAAAACCCGAACCCAA AAAGGCGAGTCAGAACAGGAAAGCCCCGTGAAAAGGCCCTCTTTTTCGACGGGCCATGGCGGGCCGTGGT GCTTCAACCAGCCTCAAGGCCACCAATGGCTGATTCTGTGATGACTCCTTCGGAGGGACTCGTGTATAAG CCATATCCCGGGCCGGGCTTCGTTGGCCCGAATCCGACAATGGGCAGTTTCTTGCCTCCTCCGGGATATGG AATCCCACCACACTATCAGGGCTGCTACTTTTTCGCGGTATGCAATGTGCGCGGCTGCAGTGTGCGGCTCGT CTGTGAGCAGACGAACCTCCCAATCAAGCAGAGCAAGTAGCCCTGTTGAGAGATTGGTGGATAGTGGA GGAAGCAATGATATGGAAGAGGGAAATGTGCTGCCACTTTTCCCGTGGCGCCCGACTCAAGCCCGGCCG GTCCAAGCCCGAGTCCGAGCCCGATCGCCCTGCTCGGGTGATAAGAGTTGTGCCTCATAATGCAACTTCAG CAACTGAATCTGCTGCAAGAATTTTCAGGTCTATTCAAGAGGAAAGAAGACGGTATGATTCTGTGTAA	
15	ATGAAGAGAGGGAGAGATGAGGGGAAGATTATGGGGCCAATGTTTCCAAGGCTACATGTGAATGACACTGA GAAAGGAGGGCCAAGAGCCCTCCAGAAACAAAATGGCTCTGTATGAGCAGCTCACCATCCCTTCCCACA GACTCACCATTCCGCCAGACATCAGTCCGAGAATCTATGCGGTCAATATTCGATTTCAGTATACCGTC	

	GACGCCAGTCAGCTGGAGAAAGAAATCGGACGAAGAGGATTTGAGAGTTCCCATTTTTCAACGATTCTGTCCGAAGTCAAGAACGTAG	
16	ATGAAGAGAAATAATGAAGGGGAGAAGATAATGGGGGCCATGTTTCCTAGGCTTCATGTGAACGACACCGA AAAGGGGGGGGCCACGAGCACCCCCGAGAAACAAGATGGCTTTATACGAGCAGCTTAGCATACCTTCACACA GACTGAATCATGCTGTGATGCCCCGAAACCCGACTAACAACGCCACTAGCACGGCCCCCTTCATCGAGAATG GGCGGTGGAAATCATCGGGGTTCTGTCAGTGCTGTGTACGGCGTCGTGCATATCCATCTCAGGATCAATA TACCCAATATTGAGAATCGAGCACTTCACCACCACCACAAGTAGAGCCAAGAAAGAAAATCTACGACAATG ACAATAGGGTTCTTATTTTCATCCAGCCCATACTCAAGAATTTGATAAATACAGCAGTGGCTTTCTCTCC AATCCTCCATATTTGGACCCTCCATTGAAATTTTCATCAGACCAATGAAATGAGCACGCTTGAAGTTAGTAT TGGAGATGAGGGGCAAATCAAGAAGAGAGAAAATTCAAATGCAGTGAGCTCGGAGAAGGATGATACTGCCT CTGAACTTCGATTTTGGATACGGAATCAGCCCTCGAAATAACGCCCGATGATGTTGTGGGTGCAATGGGG CAAGAACATTTTTGGAAAGCCAGAAGAGCAATCATGAATCAGCAAAGAGTGTTCGAGTTCAGATATTCGA GTTGCATAGATTGATAAAGGTCCAGAGATCGATCGCTGCATCGCCACATCTTTTGACGACGAAGCTGCTT ATCTCGACGACCCCCACAAAACCATTACCGGCAAGAAACGGCCGCTCGATTGCACTGATAATGCGGTCTTG AACGCTGAGAACCCGAGACACAAGAAGGAGCGGTCCGCCAAAAACACGGTCGAGAAAGAGAAAACGCCTCT TTCTTCAGCTCGTCCGGCTTCGACCGTCGTGAGCACTGATTGGAGCAACGCTCGAACATCATATTTCAATG ATCCCCTGCCACACGGACACCAATGGTTGATTCCTATAATGTCTCCTTCAGAAGGATTAGTATACAAGCCG TGTTCCGGCCCCGGATTCTCGGCCCGATAGGGTTGAATCCGACAACGATCGGAACTTCGTAGCTCCCGT ATACGGCTCCCGCCACCGTCGCATCCGTTCCACCTTTTACGGGCCCTCATTACAGCATGCCGGTTATGA GCTCTGCAGCCTTCTCGGCCGTGAATCCACGTTGGATCGGCTGCCTTGAAAGCCGGACCGTGCCAACTG GCTCGGAGGAGATCAAAGTGGCCATAGTAGGGTTAGCAACGGCATTCTTCAACGTTTCCCGATATCGTC TCCGGCCACCACCGATGCCTCGGAATCGAGCTGTCGCGTTCTGTCGGCGGGGCCCGGCCCGGGCCGAGGGT GAT	
17	ATGAAGAGAGGGAATGATGGGGAGAAGATAATGGGCCCTATGTTCCCTAGGCTTCATGTAAATGATGCTGA TAAGGGCGGGGCCAGAGCTCCTCCAAGGAATAAGATGGCCTTGATGAGCAGCTCAGCATTCTTCTCAGA GATTGAGTCATGCCGTGCCGCCCATATAGGAATAATAACATGGCCACTTCAGTGCCCAAGTCGAGCCTG AGCGGTGGGAACGATAGGGGCGCGTTCAGTGCTCGGCAGGTGCATCGAGCATATCCATATGAGATTGAGAA GCAATACAGGGACTGCTCGGAATTGAGTGCTCCGCTGGCACAAGTAAAGCAAAGAAAGAAAATCGACGAAG ATGACTATGCAGTTCCTGTTTTTCATCCAGCCTAAACCTTCAGAATTCGAAAACACAGCAAGGAAAACTC TCACCCTCCAATCCTCCTTATTTGCACCCTTCGTTGAAATCTCAGCTCTCCAACGAAATAGACACGCTCGA AATTAGTATCGGACGAGAAGGGGGAAGCAAGAAGAGAGAAAAATTCAGACGAGTACGTGACTGGGAGTAAAG AACTGTTTCCTCAATTAGTCATGAATTTGGAGCAAATCTCGTCAACAGCGTCGACATATTAAGGAATGAT GACATGGCTGCGGAAAAAGAAATCCATCTAATTTAGGGGAAGTTCTACAATCGGAGGATCAGAATACAGT CCATGATCTTAGTTATGAGACGGGTCTGATGAAGATGGGTCTTTGCAAGAAGGGAATTTGGAAGGCGAG ATAGTGCCCTCGGAAACATCCGTTTTGGATACGGAATCTGCCATGGAAATAACGCCCGACGACGTTGTGGGT ACGATAGGCCAGAAGCATTTTTGGAAAGCCAGAAGAGCTATCATGAAAATATTAATTCCTCATAGTGAGGA AATTTATTTCTTCAGCCACCTTTGAT	
18	ATGAAGAGAGGGAATGATGGGGAGAAGATAATGGGCCCTATGTTCCCTAGGCTTCATGTAAATGATGCTGA TAAGGGCGGGGCCAGAGCTCCTCCAAGGAATAAGATGGCCTTGATGAGCAGCTCAGCATTCTTCTCAGA GATTCAGTCATGCCGTGCCGCCCATATAGGAATAATAACATGGCCACTTCAGTGCCCAAGTCGAGCCTG AGCGGTGGGAACGATAGGGGCGCGTTCAGTGCTCGGCAGGTGCATCGAGCATATCCATATGAGATTGAGAA GCAATACAGGGACTGCTCGGAATTGAGTGCTCCGCTGGCACAAGTAAAGCAAAGAAAGAAAATCGACGAAG ATGACTATGCAGTTCCTGTTTTTCATCCAGCCTAAACCTTCAGAATTCGAAAACACAGCAAGGAAAACTC TCACCCTCCAATCCTCCTTATTTGCACCCTTCGTTGAAATCTCAGCTCTCCAACGAAATAGACACGCTCGA AATTAGTATCGGACGAGAAGGGGGAAGCAAGAAGAGAGAAAAATTCAGACGAGTACGTGACTGGGAGTAAAG AACTGTTTCCTCAATTAGTCATGAATTTGGAGCAAATCTCGTCAACAGCGTCGACATATTAAGGAATGAT GACATGGCTGCGGAAAAAGAAATCCATCTAATTTAGGGGAAGTTCTACAATCGGAGGATCAGAATACAGT CCATGATCTTAGTTATGAGACGGGTCTGATGAAGATGGGTCTTTGCAAGAAGGGAATTTGGAAGGCGAG ATAGTGCCCTCGGAAACATCCGTTTTGGATACGGAATCTGCCATGGAAATAACGCCCGACGACGTTGTGGGT ACGATAGGCCAGAAGCATTTTTGGAAAGCCAGAAGAGCTATCATGAAAATATTAATTCCTCATAGTGAGGA AATTTATTTCTTCAGCCACCTTTGAT	

19	1 ggccctctag aggatccccg ggtaccctcg aattatcata catgagaatt aagggagtca 61 cgttatgacc cccgccgatg acgcgggaca agccgtttta cgtttggaac tgacagaacc 121 gcaacgttga aggagccact cagccgcggg tttctggagt ttaatgagct aagcacatac 181 gtcagaaacc attattgcgc gttcaaaagt cgcctaaggc cactatcagc tagcaaatat 241 ttcttgtaaa aaatgctcca ctgacgttcc ataaattccc ctcggtatcc aattagagtc 301 tcatattcac tctcaactcg atcgaggcat gattgaacaa gatggattgc acgcaggttc 361 tccggccgct tgggtggaga ggctattcgg ctatgactgg gcacaacaga caatcggctg 421 ctctgatgcc gccgtgttcc ggctgtcagc gcaggggcgc ccggttcttt ttgtcaagac 481 cgacctgtcc ggtgccctga atgaactcca agacgaggca gcgcggctat cgtggctggc 541 cagcaggggc gttccttgcg cagctgtgct cgacgttgct actgaagcgg gaagggactg 601 gctgctattg ggcgaagtgc cggggcagga tctcctgtca tctcaccttg ctctgcccga 661 gaaagtatcc atcatggctg atgcaatgcg gcgctgcgat acgcttgatc cggctacctg 721 cccattcgac caccaagcga aacatcgcat cgagcgagca cgtactcgga tggaagccgg 781 tcttgctgat caggatgatc tggacgaaga gcatcagggg ctgcgcgcag ccgaactggt 841 cgccaggctc aaggcgcgga tgcccgacgg cgaggatctc gtcgtgaccc acggcgatgc 901 ctgcttgccg aatatcatgg tggaaaatgg ccgcttttct ggattcatcg actgtggccg 961 gctgggtgtg gcggaccgct atcaggacat agcgttggct acccgtgata ttgctgaaga 1021 gcttgggcgc gaatgggctg accgcttccct cgtgctttac ggtatcgccg ctcccgatcc 1081 gcagcgcacg gccttctatc gccttcttga cgagttcttc tgagcgggac tctggggttc 1141 ggactctagc tagagtcagg cagatcgctc aaacatttgg caataaagtt tottaagatt 1201 gaatcctggt gcgggtcttg cgatgattat catataattt ctggtgaatt acggttaagca 1261 tgtaataaatt aacatgtaat gcatgacgtt atttatgaga tgggttttta tgattagagt 1321 cccgcaatta tacatttaat acgcgataga aaacaaaata tagcgcgcaa actaggataa 1381 attatcgcg cgggtgtcat ctatgttact agatcgaccg gcatgcaagc tgataattca 1441 attcggcggt aattcagtac attaaaaacg tccgcaatgt gttattaagt tgtctaagcg 1501 tcaatttggt tacaccacaa tatatcctgc caccagccag ccaacagctc cccgaccggc 1561 agctcggcac aaaatcacca ctcgatacag gcagcccatc agtcggggac ggcgtcagcg 1621 ggagagccgt tgtaaggcgg cagactttgc tcatgttacc gatgctattc ggaagaacgg 1681 caactaagct gccgggtttg aaacacggat gatctcgcg agggtagcat gttgattgta 1741 acgatgacag agcgttgctg cctgtgatca attcgggcac gaaccagtg gacataagcc 1801 tcgttcgggt cgtaagctgt aatgcaagta gcgtaactgc cgtcacgcaa ctgggtccaga 1861 accttgaccg aacgcagcgg tggtaacggc gcagtggcgg ttttcatggc ttcttgttat 1921 gacatgtttt tttgggttac agtctatgcc tcgggcaccc aagcagcaag cgcgttacgc 1981 cgtgggtcga tgtttgatgt tatggagcag caacgatggt acgcagcagg gcagtcgccc 2041 taaaacaaag taaacatca tgggggaagc ggtgatcgcc gaagtatcga ctcaactatc 2101 agaggtagtt ggcgtcatcg agcgccatct cgaaccgacg ttgctggccg tacatttgta 2161 cggctccgca gtggatggcg gcctgaagcc acacagtgat attgatttgc tggttacggt 2221 gaccgtaagg ctgatgaaa caacgcggcg agctttgatc aacgacctt tggaaacttc 2281 ggcttccctt ggagagagcg agattctccg cgctgtagaa gtcaccattg ttgtgcaaga 2341 cgacatcatt ccgtggcggt atccagctaa gcgcgaactg caatttggag aatggcagcg 2401 caatgacatt cttgcaggtg tcttcgagcc agccacgatc gacattgatc tggctatctt 2461 gctgacaaaa gcaagagaac atagcgttgc cttggtaggt ccagcggcgg aggaactctt 2521 tgatccggtt cctgaacagg atctatttga ggcgctaaat gaaaccttaa cgctatggaa 2581 ctgcgcgccc gactgggctg gcgatgagcg aaatgtagtg ctacgttgt cccgcatttg 2641 gtacagcgca gtaaccggca aaatcgcgcc gaaggatgtc gctgccgact gggcaatgga 2701 gcgcctgccg gccagtatc agcccgctcat acttgaagct agacaggctt atcttgga 2761 agaagaagat cgcttggcct cgcgcgcaga tcagttggaa gaatttgtcc actacgtgaa 2821 aggcgagatc accaaggtag tcggcaaaata atgtctagct agaaattcgt tcaagccgac 2881 gccgcttcgc cggcggttaac tcaagcgatt agatgcacta agcacataat tgctcacagc 2941 caaactatca ggtcaagtct gcttttatta tttttaagcg tgcataataa gccctacaca 3001 aattgggaga tatatcatgc atgacaaaaa tcccttaacg tgagttttcg tccactgag 3061 cgtcagaccc cgtagaaaaa atcaaaagat cttcttgaga tccttttttt ctgcgcgtaa	pK7-353::YHB- mCer-SHH. Plasmid comprising expression construct for A.t. YHB which has a sequence of SEQ ID NO: 24
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3121	tctgctgctt	gcaaacaaaa	aaaccaccgc	taccagcggg	ggtttgtttg	cggatcaag
3181	agctaccaac	tctttttccg	aaggttaactg	gcttcagcag	agcgcagata	ccaaatactg
3241	tcctttctagt	gtagccgtag	ttaggccacc	acttcaagaa	ctctgtagca	cgcctacat
3301	acctcgctct	gctaatactg	ttaccagtgg	ctgctgccag	tggcgataag	tcgtgtctta
3361	cggggttgga	ctcaagacga	tagttaccgg	ataaggcgca	gcggtcgggc	tgaacggggg
3421	gttcgtgcac	acagcccagc	ttggagcgaa	cgacctacac	cgaactgaga	tacctacagc
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3541	gcggcagggg	cggaacagga	gagcgacga	gggagcttcc	agggggaaac	gcctggtatc
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20	1 atgaagagag ggaatatga ggagaagata cttgagccga tgtttctctg acttcatgtg 61 aacgatgctg ataaaggagg gcctagagct cctccaagaa acaagatggc tctctatgag 121 caacttagca tcccttctca gaggtttagt agtgatcatg gatcggtgccc tcgtaacacc 181 agcactttgg ttcctctgt tggatcatct agtcagcctt gtagcgtgga aagaaactta 241 tctgcccagc atcttgatc ttcagctgca gtccatgcaa ctgagaagtt tgtctcccaa 301 atgtcgttca tggaaaatgt gagaattttg gcacagcatg atcagaaaaa attagtaaga 361 gaggaggatg atttcgcagt tccagtattt attaaactca gaagatttca gtctcatggc 421 agaaccaaga gaggtgttga gaaggaaaga cacaccacat tggtaaggg gagcgctaag 481 cgaggtggct ttgtaaaactc tgtggatgta tcagctacag aggaaatgga tcttgaaaaa 541 tcatcatcga gttgtgacag agttaatgat tgtaatgatt ccttgagaga ggagtctaga 601 aatagggttag gccgagatgg tgggtgaaact cgagcgatgg aactgataa tggagttaga 661 tctcacttgg gatcagaatg tcattcagaa gagggatcat acaatcctaa tgacgttgat 721 aatggctcgtg aatactgcac aagtagagga tatgtctctc tgcagcagat aaatgaagag 781 gcgagcgatg atgtttctga tgattcgatg gtggattcta tatccagcat agatgtctct 841 cctgatgacg ttgtgggagt attaggtcaa aaacgtttct ggagagcaag gaaagctatt 901 gccaatcaac aaagagtatt tgctgttcaa ctatttgagt tgcacagact gattaaggta 961 caaagactta ttgctgcac accggatgtc ttgctcgatg acatcagtta tcttgaaaaa 1021 gtctgtgtta aaagctttcc agtgaagaag ctcttccat cagagaagcc tctctacca 1081 caagttatca aacacagcgg ccgagactcc gcggagaaga ccgaccaaca taaaatggaa 1141 tgctcggtg agaacgtagt cgggaagatg tcaaaccaag ttcacatca acctccaac 1201 tacatgcctt tccgagcaa ccaagccact gctaattgat gttactttcc tcccagcct 1261 cctacttcag gaggaatca gcaatggta atccctgtaa tgtctcttc cgaaggtctg 1321 atatacaagc cgcattccag tccaggacac acaggacctc cggctctgtg agggattat 1381 ggtcattaca tgctgtctc tatggtaatg ggtaatttca tggcggtggt tggtaaacct 1441 ccgtttcacc cggggatgg ccttgcatct ctgggtaatg gctacttccc tcttatggt 1501 ataatgccac acaccatgat gaatacttat tgctccggcc aacaacaaca acaacaacc 1561 aatgagcata tgaatcagtt tgggcattca gtaaatcttc agaacgcac aggtttgaac	Thlaspi arvensi wt ELF3 cDNA

	1621 aaccaacaac agagctcggg taacgaagag gcggcgcaac aacagccggc gaaatcatat 1681 catcgggcta gaaagagcag gcaagggagc acaggaagca gcagttcaga gggaatctcc 1741 ggtaagaact cctttcggcc attctcagcg gttgatgagg acagcatcaa cgaccaacct 1801 gagcaaatga tgacgacaac gacgaccaca acaagaacaa ctgttactca gacgacaaga 1861 gatggagtag gaggagtgc gagagtgatc aaagtgggtc cacacaacgc gaagctggcg 1921 agtgagtatg ctgcaaggat tttccgggtca attcaagaag aacgtaaaca ctacgactcc 1981 ttctctaacc actcttaa	
21	MKRGKYEEKILEPMFPRHLVNDADKGGPRAPPRNKMALYEQLSIPSQRFSSDHGSLPRNTSTLVPPVGSSS QPCSVERNLSAQHLDSAAVHATEKFVSQMSFMENVRI LAQHDQKKLVREDDFAVPVFINSRRFQSHGRT KRGVEKERHTTLVKGSAKRGGFVNSVDVSATEEMDLEKSSSSCDRVNDCNDSLREESRNRLGRDGGETRAM DTDNGVESHLSGECHSEEGHDNPNDVDNGREYCTSRGYVSLQQINEEASDDVSDSMVDSISSIDVSPDDV VGVLGQKREWRARKAIANQQRVFAVQLFELHRLIKVQRLIAASPDVLLDDI SYLGKVAVKSPVKKLLPSE KPPLPQVIKHSGRDSAEKTDQHKMECSAENVVGMNSQVHHQPSNYMPFSPNQATANGCYFPPQPPSTSGGN QQWLIPVMSPEGLIYKPHPGPGHTGPPVCGGYGYHYMPAPMVMGNFMGGGGQPPFHPGMGLASLNGYFYP PYGIMPHMTMMNTYCSGQQQQQQPNEHMNQFGHSVNQLNASGLNNQQQS SVNEEAQQQPAKSYHRARKSRQ GSTGSSSSSEGISGKNSFRFPFSAVEDDSINDQPEQMMTTTTTTRTTVTQTTRDGVGGVTRVIKVVPHNAKL ASEYAARIFRSIQEERKHYDSFSNHS-	Thlaspi arvensi wt ELF3 protein
22	AGCGAGGTGGCTTTGTAACCTCTGTGGATGTATCAGCTACAGAGGAAATG GATCTTGAAAAATCATCATCGAGTTGTGACAGAGTTAATGATTGTAATGATTCCTTGA GAGAGGAGTCTAGAAATAGGTTAGGCCGAGATGGTGGTGAACCTCGAGCGATGGACAC TGATAATGGAGTTGAATCTCACTTGGGATCAGAATGTCATTGAGAAGAGGGTCATGAC AATCCTAATGACGTTGATAAATGGTGGTGAATACTGCACAAGTAGAGGATATGTCTCTC TGCAGCAGATAAAATGAAGAGCGGAGCGATGATGTTTCTGATGATTGATGGTGGATTC TATATCCAGCATAGATGTCTCTCTGATGACGTTGTGGGAGTATTAGGTCAAAACGT TTCTGGAGAGCAAGGAAAGCTATTGCCAATCAACAAAGAGTATTGCTGTTCAACTAT TTGAGTTGCACAGACTGATTAAGGTACAAAGACTATTGCTGCATCACCGGATGTCTT GCTCGATGACATCAGTTATCTTGAAAAAGTCGCTGTTAAAGCTTTCCAGTGAAGAAG CTCCTTCCATCAGAGAAGCCTCCTCTACCACAAGTTATCAAC	Large deletion in Thlaspi arvensi ELF3 (Taelf3-1). Shows sequence deleted from ELF3. See FIG. 13
23	ATTGTATGAAGAGAGGGAATGATGTTTTAGAGCTAGAAATAGCAAGTTAAATAAGGCTAGTCCGTTATCA ACTTGAAAAAGTGGCACCAGTGGTGTCTTTTTTTTGCAAAATTTTCCAGATCGATTTCTTCTCTCTGT TCTTCGGCGTTCAATTTCTGGGGTTTCTCTCTGTTTTCTGTAAGTAAACCTAAATTTGACCTAAAAA AATCTCAAATAATATGATTCAGTGGTTTTGTACTTTTTCAGTTAGTTGAGTTTTGCAGTTCCGATGAGATAA ACCAATATTAATCCAACTACTGCAGCCTGACAGACAAATGAGGATGCAACAATTTTAAAGTTTATCTAA CGCTAGCTGTTTTGTTTCTCTCTGTTGACCAACGACGGCGTTTTCTCAATCATAAAGAGGCTTGT TACTTAAGGCCAATAATGTTGATGGATCGAAAGAGAGGGCTTTTAATAAACGAGCCCGTTAAGCTGTAA ACGATGTCAAAACATCCCACATCGTTTCAGTTGAAATAGAGCTCTGTTTATATATTGGTAGAGTCGACT AAGAGATTGGCGTTGTTAGTCGGGTTTCTGTTTAGAGCTAGAAATAGCAAGTTAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCAGTGGTGTCTTTTTTTGGATAGAATTTCCAGCTTTTTTGCGTGT CAGCTCTCATGATCCTTGGCCAATGGGTGTAGTAAATTTCTGCACATTCATTGGATGGAAAATAATGGT TTAGCTTTAGGGAATAAGAAAAGTGTATAGGAAGGGGATTTTGTACAATCACATTTGAATTAGGTCTTTG AAATGACAGGGAATGAGGACATATGATGAGACGGTCATTGTTTAGTTCCACCACGATTATATTTGAAAT TACGTGAGTGTGAGTGAGACTTGCATAAGAAAAATAAATCTTTAGTTGGGAAAAAATCAATAATATAAT GGGCTTGAGAAGGAAGCGAGGGATAGGCCTTTTTCTAAATAGGCCATTAAAGCTATTAACAATCTTCAA AAGTACCACAGCGCTTAGGTAAAGAAAGCAGCTGAGTTTATATATGGTTAGAGACGAAGTAGTGATTGAAT CGGTGAGTCTGTGGGAGTTTATAGCTAGAAATAGCAAGTTAAATAAGGCTAGTCCGTTATCAACTGAA AAAGTGGCACCAGTGGTGTCTTTTTTTGGCAAAATTTTTCAGATTTTTCTTCATCTGTAGATTTCTGG GTTTTTTTTTCCGTTTCGTGAATCATAAGTGAAGTTTGGATGCAATCTGCGGAAAAAAGTTGGACCTG CAATGAGCTTATTTAGATAGCTAAGACAAAGTATTGGTCCGTTCCGACTTGCCTTCCGCACAATACATCAT TTCTTCTTAGCTTTTTTCTTCTTCTCGTTTCATACAGTTTTTTTTTTGTTTATCAGCTTACATTTTCTGA ACCGTAGCTTTCGTTTTCTTCTTTAACTTTCCATTCCGAGTTTTTGTATCTTGTTCATAGTTTGTCCC AGGATTAGAATGATTAGGCATCGAACCTTCAAGAATTTGATTGAATAAAACATCTTCATCTTAAGATATG	Expression construct for expressing gRNAs of phse401-basil- x4 CRISPR construct (SEQ ID NO: 37) to disrupt elf3 in basil

	AAGATAATCTTCAAAAGGCCCTGGGAATCTGAAAGAAGAGAAGCAGGCCCATTTATATGGGAAAGAACAA TAGTATTTCTTATATAGGCCCATTTAAGTTGAAAACAATCTTCAAAAGTCCACATCGCTTAGATAAGAAA ACGAAGCTGAGTTTATATACAGCTAGAGTCGAAGTAGTGATTGACGGACGATTGAGACTAGAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	
24	GACTAGAGCCAAGCTGATCTCCTTTGCCCGGAGATCACCATGGACGACTTCTCTATCTCTACGATCTAG GAAGAAAGTTCGACGGAGAAGGTGACGATACCATGTTACCACCGATAATGAGAAGATTAGCCTCTTCAAT TTCAGAAAGAATGCTGACCCACAGATGGTTAGAGAGGCCTACGCGGCAGGTCTCATCAAGACGATCTACCC GAGTAATAATCTCCAGGAGATCAAATACCTTCCCAAGAAGGTTAAAGATGCAGTCAAAAGATTGAGGACTA ACTGCATCAAGAACACAGAGAAAGATATATTTCTCAAGATCAGAAGTACTATTCCAGTATGGACGATTCAA GGCTTGCTTCATAAACCAAGGCAAGTAATAGAGATTGGAGTCTCTAAGAAAGTAGTTCCTACTGAATCAAA GGCCATGGAGTCAAAAATTGAGATCGAGGATCTAACAGAACTCGCCGTGAAGACTGGCGAACAGTTTCATAC AGAGTCTTTTACGACTCAATGACAGAAGAAAATCTTCGTCAACATGGTGGAGCACGACACTCTCGTCTAC TCCAAGAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCTATTGAGACTTTTCAACAAAGGGTAATATC GGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTG GCACCTACAAATGCCATCATTGCCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCC AAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAGACGTTCCAACCACGTCTTCAAAGCAAGT GGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCACTATCCTTCGCAAGACCCCTTCCT CTATATAAGGAAGTTCATTTCAATTTGGAGAGGACTCCGGTATTTTACAACAATACCACAACAAAACAAAC AACAAACAACATTACAATTTACTATTTCTAGTCGACCTGCAGGCGGCCGCACTAGTGATATCACAAGTTTGT ACAAAAAAGCAGGCTCCGCGGCCGCCCTTACCATGGTTTCCGGAGTCGGGGGTAGTGGCGGTGGCCGT GCCGCTGGCCGTGGCGGAGAAGAAGAACCGTCTCAAGTCACACTCCTAATAACCGAAGAGGAGGAGAACA AGCTCAATCGTCGGGAACGAAATCTCTCAGACCAAGAAGCAACACTGAATCAATGAGCAAAGCAATTCAAC AGTACACCGTCGACGCAAGACTCCACGCCGTTTTCGAACAATCCGGCGAATCAGGGAAATCATTGACTAC TCACAATCACTCAAAACGACGACGTACGTTCTCTGTACCTGAGCAACAGATCACAGCTTATCTCTCTCG AATCCAGCGAGGTGGTTACATTGACGCTTTCGGATGTATGATCGCCGTGATGAATCCAGTTTCCGGATCA TCGGTTACAGTGAAAACGCCAGAGAAATGTTAGGGATTATGCCTCAATCTGTTCTACTCTTGAGAAACCT GAGATTCTAGCTATGGAACTGATGTGAGATCTTTGTTCACTTCTTCGAGCTCGATTCTACTCGAGCGTGC TTTCGTTGCTCGAGAGATTACCTTGTAAATCCGGTTTGGATCCATTCCAAGAATACTGGTAAACCGTTTTT ACGCCATTCTTCATAGGATTGATGTTGGTGTGTTATTGATTAGAGCCAGCTAGAACTGAAGATCTCGCG CTTTCTATTGCTGGTGCTGTTCAATCGCAGAACTCGCGGTTCTGCGATTCTCAGTTACAGGCTCTTCC TGGTGGAGATATTAAGCTTTTGTGTGACACTGTCTGGAAAGTGTGAGGGACTTGACTGGTTATGATCGTG TTATGGTTCAATAAGTTTCATGAAGATGAGCATGGAGAAGTTGTAGCTGAGAGTAAACGAGATGATTTAGAG CCTTATATTGGACTGCATTATCCTGCTACTGATATTCTCAAGCGTCAAGGTTCTTGTTTAAAGCAGAACCG TGTCGGAATGATAGTAGATTGCAATGCCACACCTGTTCTTGTGGTCCAGGACGATAGGCTAACTCAGTCTA TGTGCTTGGTTGGTTCTACTCTTAGGGCTCCTCATGGTTGTCACTCTCAGTATATGGCTAACATGGGATCT ATTGCGTCTTTAGCAATGGCGGTTATAATCAATGGAAATGAAGATGATGGGAGCAATGTAGCTAGTGAAG AAGCTCGATGAGGCTTTGGGGTTTGGTTGTTTGCCATCACACTTCTTCTCGCTGCATACCGTTTCCGCTAA GGTATGCTTGTGAGTTTTTGTGTCAGGCTTTCGGTTTACAGTTAAACATGGAATTGCAGTTAGCTTTGCAA ATGTCAGAGAAACGCGTTTTGAGAACGCAGACACTGTTATGTGATATGCTTCTGCGTGAAGTCTGCGTGG AATTGTTACACAGAGTCCCAGTATCATGGACTTAGTGAAATGTGACGGTGCAGCATTCTTTTACCACGGGA AGTATTACCCGTTGGGTGTTGCTCCTAGTGAAGTTCAGATAAAAGATGTTGTGGAGTGGTTGCTTGCGAAT CATGCGGATTCAACCGGATTAAGCACTGATAGTTTAGGCGATGCGGGGTATCCCGGTGCAGCTGCGTTAGG GGATGCTGTGTGCGGTATGGCAGTTGCATATATCACAAAAGAGACTTTCTTTTTTGGTTTCGATCTCACA CTGCGAAAGAAATCAAATGGGGAGGCGCTAAGCATCATCCGGAGGATAAAGATGATGGGCAACGAATGCAT CCTCGTTCGTCCTTTTCAAGGCTTTTCTTGAAGTTGTTAAGAGCCGGAGTCAAGCATGGGAACTGCGGAAAT GGATGCGATTCACTCGCTCCAGCTTATTCTGAGAGACTCTTTTAAAGAATCTGAGGCGGCTATGAACTCTA AAGTTGTGGATGGTGTGGTTCAAGCATGTAGGGATATGGCGGGGGAACAGGGGATTGATGAGTTAGGTGCA GTTGCAAGAGAGATGGTTAGGCTCATTGAGACTGCAACTGTTCTATATTGCTGTGGATGCCGGAGGCTG CATCAATGGATGGAACGCTAAGATTGCAGAGTTGACAGGTCTCTCAGTTGAAGAAGCTATGGGGAAGTCTC TGGTTTCTGATTTAATATACAAAGAGAATGAAGCAACTGTCAATAAGCTTCTTCTCGTCTTTGAGAGGG GACGAGGAAAAGAATGTGGAGGTTAAGCTGAAACTTTTCAAGCCCGAATACAAGGGAAGCAGTTTTTGT GGTTGTGAATGCTTGTTCAGCAAGGACTACTTGAACAACATTGTGCGCGTTTGTGTTTGTGGACAAGACG	A.t. YHB expression construct from SEQ ID NO 19

	TTACTAGTCAGAAAATCGTAATGGATAAGTTTCATCAACATACAAGGAGATTACAAGGCTATTGTACATAGC CCAAACCTCTAATCCCGCCAATTTTGGCTGCTGACGAGAACACGTGCTGCCTGGAATGGAACATGGCGAT GGAAAAGCTTACGGGTGGTCTCGCAGTGAAGTGATTGGGAAAATGATTGTCGGGGAAGTGTGGGAGCT GTTGCATGCTAAAGGGTCTGATGCTTTAACCAAGTTCATGATTGTATTGCATAATGCGATTGGTGGCCAA GATACGGATAAGTTCCTTTCCCATCTTTGACCGCAATGGGAAGTTTGTTCAGGCTCTATTGACTGCAAA CAAGCGGGTTAGCCTCGAGGGAAAGGTTATTGGGGCTTTCTGTTTCTTGCAAATCCCAGCCCTGAGCTGC AGCAAGCTTTAGCAGTCCAACGGAGGCAGGACACAGAGTGTTCACGAAGGCAAAAGAGTTGGCTTATATT TGTCAGGTGATAAAGAATCCTTTGAGCGGTATGCGTTTCGCAAACCTCATTGTTGGAGGCCACAGACTTGAA CGAGGACCAGAAGCAGTTACTTGAACAAGTGTTCCTTGCAGAAACAGATCTCAAGGATCGTCGGGGACA TGGATCTTGAAAGCATTGAAGACGGTTCATTTGTGCTAAAGAGGGAAGAGTTTTTCTTGAAGTGTGATA AACCGGATTGTAAGTCAAGCGATGTTCTTATTAAGGGACAGAGGTCTTCAGCTGATCCGTGACATTCCTCGA AGAGATCAAAATCAATAGAGGTTTTTGGAGACCAGATAAGGATTCAACAGCTCCTGGCTGAGTTTCTGCTGA GTATAATCCGGTATGCACCATCTCAAGAGTGGGTGGAGATCCATTTAAGCCAACTTTCAAAGCAAATGGCT GATGGATTTCGCCGCCATCCGCACAGAATTCAGAATGGCGTGTCCAGGTGAAGGTCTGCCTCCAGAGCTAGT CCGAGACATGTTCCATAGCAGCAGGTGGACAAGCCCTGAAGGTTTAGGTCTAAGCGTATGTGAAAGATTT TAAAGCTAATGAACGGTGAGGTTCAATACATCCGAGAATCAGAACGGTCTATTTCTCATCATTCTGGAA CTCCCTGTACCTCGAAAGCGACCATTTGTCAACTGCTAGTGGAAGTGGTGACATGATGCTGATGATGCCATA TAAGGGTGGGCGCGCCGACCCAGCTTTCTTGTACAAAGTGGTGCGAATGGTGAACAAGGGCGAGGAGCTGT TCACCGGGGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGT GCCCTGGCCCAACCTCGTGACCACCTGACCTGGGGCGTGAGTGCTTCGCCCGCTACCCCGACCACATGA AGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAA GGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAGCTGGAGTACAACGCCATCAGCGACAACG TCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGC TGGAGTTCGTGACCGCCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAAGTCTAGGGGTGGAAGCTGG AGCCACCTCAATTTGAAAAGGGAGGAGGATCTGGAGGTGGTCTGGTGGTGGTCTTGGTCTCACCCACA ATTCGAAAAGGGTCTTACCCATACGATGTTCCAGATTACGTCATCACCATCACCATCACTAG	
25	1 atggtttccg gaggtaacgg cggtagtggc cgcggacgtg gtgaagaagc agcgtcgtca 61 agtcaccgtg ccgaacgcag tctccacacc acaacttacc accggagaga acaagctcaa 121 tcttctggga cgaaatcgct taggcgcgaa aatcagccgc agagccacac tgaatcagt 181 agcaaaagca ttcaacagta caccgtcgac gcgaggtccc acgcggtcct cgaacagtct 241 ggcgagtccg gcaagtcggt tgattactca cagtccctca aaacgacgac gtacgggtcc 301 tctgtaccgg agcagcagat caccggcgtat ctctctagga tccagcgagg aggtacatc 361 cagcccttcg gatgtatgat cgcgctcgat gaatccacct tcagaatcat cggctacagc 421 gaaaacgcgc gggaaatggt aggccttact cctcagtcgg ttcctagcct cgagaaaccg 481 gagattctag cgatgggaac agatgtgcgc tctctcttca cgcgctcgag ctcaattctc 541 ctcgagcgtg ctttctgtggc tcgagaaatc acactgctga atccggtttg gatccactcc 601 aagaacaccg gtaagccctt ttacgcaatt ctccatagga tcgacggttg agtcgctatc 661 gatttagagc cagctagaac cgaagatccg gcgctttcga tcgcccggagc agtccaatcg 721 cagaagctcg cggttcgcgc gatttcacag ttacagtcgc ttcccgggtg ggacatcaag 781 cttctctgcg acactgttgt ggaaagcgtg agagacctca ctggacacga ccgtgtaatg 841 gtctacaagt ttcacgaaga cgagcacgga gaagttgtcg ccgagagccg gcgagaagat 901 ttagaacctt acatcgggtc acattatccg gcaactgata ttccctcaagc gtcacgggtc 961 ttattcaagc agaaccgtgt ccgtatgac gtagattgcc acgcccacac ggttcttgtg 1021 gtccaggacg ataggctcac tcagtctatg tgcttggttg gttctactct aagggctcct 1081 caccgatgtc actctcagta tatggctaac atgggatcta ttgcatcttt agctatggca 1141 gttataataa acggcaacga agaagacggg ggcaatgtcg gtggtgggag aaactcaatg 1201 aggctttggg gtttagtcgt ttgccatcac acctcttctc gctgcatacc gtttctctc 1261 aggtatgctt gcgagtttct aatgcaggca tttggtttac agttaaacat ggaactgcag	Thlaspi arvensi version of YHB allele of phyB. cDNA TaPHYB_YHB_cDNA

	1321 ttagcattgc aaatgtcaga gaaacgcgtt ttgagaacgc agacactgtt atgcatatg 1381 cttctgcgtg attctcctgc tgggattggt acacagagtc ctagtatcat ggacttagtg 1441 aaatgtgacg gtgcagcgtt tctttaccat gggaagtact acccggtggg tgttgctcgg 1501 acggaagtcc aaataaaaaga cgttgctcag tgggtgcttg cgagtcagtc ggattcgaca 1561 gggtaagca cggatagttt aggcgatgca ggatatcccg gtgcagctgc gttaggggat 1621 gctgtgtgcg gtatggcggt tgcgtatata aaaaaagag actttctttt ctggttccgt 1681 tctcatactg ccaagaaat caaatgggga ggcgctaagc atcatccaga ggacaaagat 1741 gatgggcaac ggatgcatcc tcttctgctc ttcaaggctt ttcttgaagt tgttaagagc 1801 aggagccagc catgggaaac tgcagaaatg gatgcgattc actcgctcca gcttattcta 1861 agagactctt ttaaagaatc agaggcagct atgaactcta aaaatgcaga ggggtgcggt 1921 cagccttgta gggatattgc gggatgcag gggattgatg agttaggggc agttgcaaga 1981 gagatgggta ggctcattga aaccgctact gttctatat ttgctgtgga cgtggaggc 2041 tgcattaatg gatggaacgc taagatggcg gaactgacag gtctctcggg tgaagaagct 2101 atgggggaagt ctctggttct tgatctaata tacaagaga acgaagaaac tgttgataag 2161 ctcatctctc gtgctctgag aggggacgag gacaagaatg tggaggtgaa gctgaaaact 2221 ttcatccccg aacttgaagg gaatgcagtt tttgtggttg tgaatgcgtg ttcgagcaag 2281 gactacttga acaacattgt cggcgtctgt tttgtcggac aggatgtcac tggtcagaaa 2341 atcgtaatgg ataagttcat caacatacaa ggagactaca aggcattgt ccatagccca 2401 aacgcgctga ttccgcgaat ctttgcggcg gacgagaaca cgtgctgcct tgagtggaa 2461 atcgcgatgg aaaagctcac gggttggtcc cgcagtgaag ttattgggaa aatgcttgtt 2521 ggggaagtgt ttggtagctg ttgcaggcta aagggtcatg atgctttaac caagttcatg 2581 attgcattgc ataacgcgat ggggtgcca gaaacggata agttcccttt cccgttcttt 2641 gaccgcaacg ggaagtttgt tcaggctcta ttgactgcaa acaagcgggt tagcctcgac 2701 ggaaagggta ttggggcttt ctgcttcttg cagatcccga gtccggaact gcagcaagct 2761 ttagcagtc aacggaggca ggacacagag tgtttcacga aggcgaaaga gctagcttac 2821 atttgtcagg tgataaagaa ccttttgagt ggtttgcgtt tcacaaactc actgctggaa 2881 gctacagact tgaaagaa tcagaaagag ttcttgaaa cgagtgtttc ttgagagaaa 2941 cagatctcga ggatcgtcag tgacatggat cttgaaagaa ttgaagacgg ttcatttgag 3001 ctgagagagag cagagttttt cctcggaagt gtcataaacg cgatagtaag ccaggcgatg 3061 ttcttattaa gggagagggc tcttcagctg atccgtgaca tcccgaaga gataaaatct 3121 atagctgttt atggagacca gacaaggatt caacagatcc tggctgagtt tcttctgagt 3181 ataatccggt atgcaccgtc tcaagagtgg gtggagatcc atctaagcca agttccgaag 3241 caaatggctg acggattctc cgtatccgc acagagttca gaatggcgtg cccaggtgaa 3301 ggtctgcctc cagagctggt ccgagacatg ttccatagca gcaggtggac gagtccgaa 3361 gggtaggtc taagcgtgtg tcgaaagatt ctgaagctaa tgaacgggtga ggttcaatac 3421 atccgagagt cggaaacggt ctatttctc atcattctcg aactccctgt tctctgaaa 3481 cgcccttttt caaccgctag cggcagcggc gacatgatgt tgatgatgcc atag	
26	MVSGGNGSGRGRGEEAASSSHRAERSLHTTTYHREQAQSSGKSLRPQNQPQSHTESVSKAIQYTVDA RLHAVFEQSGESGKSFYDSQSLKTTYGSSVPEQQITAYLSRIQRGGYIQPFGCMIAVDESTFRIIGYSEN AREMLGLTPQSVPSLEKPEILAMGTDVRSFLTASSILLERAFVAREITLLNPFVWHSKNTGKPFYAILHR IDVGVVIDLEPARTEDPALS IAGAVQSQKLAVRAISQLQSLPGGDIKLLCDTVVESVRDLTGHDRVMYKF HEDEHGEVVAESRRDLEPYIGLHYPATDI PQASRFLFKQNRVRMIVDCHATPVLVVQDDRLTQSMCLVGS TLRAPHGCHSQYMANMGSIASLAMAVIINGNEEDGGNVGGGRNSMRLWGLVCHHTSSRCIPFPLRYACEF LMQAFGLQLNMELQLALQMSEKRVLRQTLLCDMLLRDSPAGIVTQSPSIMDLVKCDGAAFLYHGKYYPLG VAPTEVQIKDVVEWLLASHADSTGLSTDGLDAGYPGAAALGDAVCGMAVAYITKRDFLFWFRSHTAKEIK WGGAKHHHPEDKDDGQRMHPRSSFKAFLEVVKSRSPFWETAEMDAIHSLQLILRDSFKESAEAMNSKNAEGA VQPCRDIAGMQGIDELGAVAREMVRLETATVPIFAVDAGGCINGWNAKMAELTGLSVEEAMGKSLVSDLI YKENEETVDKLI SRALRGDEDKNVEVKLKTFIPELEGNVAVVVNACSSKDYLNINIVGCVFGQDVTGQKI VMDKFINIQDYKAIHSPNALIPPIFAADENTCCLEWNIAMEKLTGWSRSEVIGKMLVGEVFGSCRLKG HDALTKFMIALHNAMGGQETDKFPFFFDNRNGKFVQALLTANKRVS LDGKVIGAFCFQLIPSPELQALAV QRRQDTECFTHAKELAYICQVIKNPLSGLRFTNSLLEATDLNEDQKEFLET SVSCEKQISRIVSDMDLERI EDGSFELERAFFLGSVINAIVSQAMFLLRERALLQIRDIPEEIKS IAVYGDQTRIQQILAEFLLSIIRYA	Thlaspi arvensi version of YHB allele of phyB. Protein translated from TaPHYB_YHB_cDNA

	PSQEWVEIHL SQVPRQMDGFSAIRTEFRMACPGEGLPPELVRDMFHSSRWTSPEGLGLSVCRKILKLMNG EVQYIRESERSYFLIIILELPVPLKRFSTASGSGDMLMMP-	
27	1 atggtttccg gaggtaacgg cggtagtggc cgcggacgtg gtgaagaagc agcgtcgta 61 agtcaccgtg ccgaacgcag tctccacacc acaacttata accggagaga acaagctcaa 121 tcttctggga cgaaatcgct taggcgcgaa aatcagccgc agagccacac tgaatcagt 181 agcaaaagcca ttcaacagta caccgtcgac gcgaggetcc acgcgcgtctt cgaacagtct 241 ggcgagtcgg gcaagtcgtt tgattactca cagtcctcca aaacgacgac gtacgggtcc 301 tctgtaccgg agcagcagat caccggcgtat ctctctagga tccagcgagg aggtacatc 361 cagcccttcg gatgtatgat cgcgcgtgat gaatccacct tcagaatcat cggctacagc 421 gaaaacgcgc gggaaatggt aggccttact cctcagtcgg ttcttagcct cgagaaaccg 481 gagattctag cgatgggaac agatgtgcgc tctctcttca cgcgcgtcag ctcaattctc 541 ctgcagcgtg ctttcgtggc tcgagaaatc aactcgtga atccggtttg gatccactcc 601 aagaacaccg gtaagccctt ttacgcaatt ctccatagga tcgacgttgg agtcgttatac 661 gatttagagc cagctagaac cgaagatccg gcgctttcga tcgcgggagc agtccaatcg 721 cagaagctcg cggttcgcgc gatttcacag ttacagtcgc ttcccgggtg ggacatcaag 781 cttctctgcg aactggtgt ggaaagcgtg agagacctca ctggatacga ccgtgtaatg 841 gtctacaagt ttcacgaaga cagcacgga gaagtgtcg ccgagagccg gcgagaagat 901 ttagaacctt acatcgggtc acattatccg gcaactgata ttctcaagc gtcacgggtc 961 ttattcaagc agaaccgtgt ccgtatgatc gtatattgcc acgccacacc ggttcttgtg 1021 gtccaggacg ataggctcac tcagtctatg tgcttggttg gttctactct aagggtcctc 1081 caccgatgtc actctcagta tatggctaac atgggatcta ttgcatcttt agctatggca 1141 gttataataa acggcaacga agaagacggg ggcaatgtcg gtggtgggag aaactcaatg 1201 aggttttggg gtttagtcgt ttgccatcac acctcttctc gctgcatacc gtttctctc 1261 aggtatgctt gcgagtttct aatgcaggca tttggtttac agttaaacat ggaactgcag 1321 ttagcattgc aaatgtcaga gaaacgcgtt ttgagaacgc agacactgtt atgcgatatg 1381 cttctgcgtg attctctcgc tgggattgtt acacagagtc ctagtatcat ggacttagtg 1441 aaatgtgacg gtgcagcgtt tctttaccat gggaagtact accegttggg tgttgctccg 1501 acggaagtgc aaataaaaaga cgttgctcag tgggtgcttg cgagtcatgc ggattcgaca 1561 ggggttaagc cgatagttt aggcgatgca ggatatcccg gtgcagctgc gttaggggat 1621 gctgtgtgcg gtatggcgtt tgcgtatata aaaaaagag actttctttt ctgggtccgt 1681 tctcactactg ccaagaaat caaatgggga ggcgctaagc atcatccaga ggacaaagat 1741 gatgggcaac ggatgcattc tcgttcgtcc ttcaaggctt ttcttgaagt tgttaagagc 1801 aggagccagc catgggaaac tgcagaaatg gatgcgattc actcgtccca gcttattcta 1861 agagactctt ttaagaatc agaggcagct atgaactcta aaaatgcaga ggggtgcggtt 1921 cagccttgta gggatattgc gggaatgcag gggattgatg agttaggggc agttgcaaga 1981 gagatgggta ggtcattga aaccgctact gttcctatat ttgctgtgga cgctggaggc 2041 tgcattaatg gatggaacgc taagatggcg gaactgacag gtctctcggg tgaagaagct 2101 atggggaagt ctctggtttc tgatctaata tacaaagaga acgaagaaac tgttgataag 2161 ctcatctctc gtgctctgag aggggacgag gacaagaatg tggaggtgaa gctgaaaact 2221 ttcattcccg aacttgaagg gaatgcagtt tttgtggttg tgaatgcgtg ttcgagcaag 2281 gactacttga acaacattgt cggcgtctgt tttgtcggac aggatgtcac tggtcagaaa 2341 atcgtaatgg ataagttcat caacatacaa ggagactaca aggccattgt ccatagccca 2401 aacgcgctga ttccgccaat ctttgcggcg gacgagaaca cgtgctgcct tgagtggaa 2461 atcgcgatgg aaaagctcac gggttggtcc cgcagtgaag ttattgggaa aatgcttgtt 2521 ggggaagtgt ttggtagctg ttgcaggcta aagggtcatg atgctttaac caagttcatg 2581 attgcattgc ataacgcgat ggggtggcaa gaaacggata agttcccttt ccggttcttt 2641 gaccgcaacg ggaagtgtt tccaggtcta ttgactgcaa acaagcgggt tagcctcgac 2701 ggaaggttga ttggggcttt ctgcttcttg cagatcccg gtccggaaact gcagcaagct 2761 ttagcagtc aacggaggca ggacacagag tgtttcacga aggcgaaaga gctagcttac 2821 atttgtcagg tgataaagaa ccctttgagt ggtttgcgtt tcacaaactc actgctggaa 2881 gctacagact tgaacgaaga tcagaaagag ttcttgaaa cgagtgtttc ttgcgagaaa 2941 cagatctcga ggatcgtcag tgacatggat cttgaaagaa ttgaagacg ttcatttgag	WT TaPHYB_cDNA. Thlaspi arvensi phyB wt cDNA

	3001 cttagagagag cagagttttt cctcggaggt gtcataaacg cgatagtaag ccaggcgatg 3061 ttcttatttaa gggagagggc tcttcagctg atccgtgaca ttcccgaaga gataaaatct 3121 atagctgttt atggagacca gacaaggatt caacagatcc tggctgagtt tcttctgagt 3181 ataatccggt atgcaccgtc tcaagagtgg gtggagatcc atctaagcca agttccgaag 3241 caaatggctg acggattctc cgctatccgc acagagttca gaatggcgtg cccaggtgaa 3301 ggtctgcctc cagagctggt ccgagacatg ttccatagca gcagggtggac gagtccgtgaa 3361 gggtaggtc taagcgtgtg tcgaaagatt ctgaagctaa tgaacgggtga ggttcaatac 3421 atccgagagt cggaacggtc ctatttcctc atcattctcg aactccctgt tcctctgaaa 3481 cgcccttttt caaccgctag cggcagcggc gacatgatgt tgatgatgcc atag	
28	MVSGGNGSGRGRGEEAASSSHRAERSLHTTTYHRREQAQSSTKSLRPQNQPQSHTESVSKAIQQYTVDA RLHAVFEQSGESGKSFYDYSQSLKTTYGSSVPEQQITAYLSRIQRGGYIQPFGCMIAVDESTFRIIGYSEN AREMLGLTPQSVPSLEKPEILAMGTDVRSFLTASSILLERAFVAREITLLNPVWIHSKNTGKPFYAILHR IDVGVVIDLEPARTEDPALS IAGAVQSQKLAVRAISQLQSLPGGDIKLLCDTVVESVRDLTGYDRVMVYKF HEDEHGEVVAESRREDLEPYIGLHYPATDI PQASRFLFKQNRVRMIVDCHATPVLVVQDDRLTQSMCLVGS TLRAPHGCHSQYMANMGSIASLAMAVIINGNEEDGGNVGGGRNSMRLWGLVVCCHTSSRCIPFPLRYACEF LMQAFGLQLNMLQLALQMSEKRVLRQTLLCDMLLRDSPAGIVTQSPSIMDLVKCDGAAFLYHGKYYPLG VAPTEVQIKDVVEWLLASHADSTGLSTDLSLDGAGYPGAAALGDVCGMAVAYITKRDFLWFVRSHTAKEIK WGGAKHHPEDKDDGQRMHPRSSFKAFLEVVKSRSPFWETAEMDAIHSLQLI LRDSFKESEAMNSKNAEGA VQPCRDIAQMGIDELGAAREMVRLETATVPIFAVDAGGICINGWNAKMAELTGLSVEEAMGKSLVSDLI YKENEETVDKLI SRALRGDEDKNVEVKLKTFIPELEGNVAVVVNACSSKDYLNINIVGCVFVGQDVTGQKI VMDKFINIQGDYKAI VHSNALIPPIFAADENTCCLEWNIAMEKLTGWSRSEVIGKMLVGEVFGSCRLKG HDALTKEFMIALHNAMGGQETDKFPFFFFDRNGKFVQALLTANKRVS LDGKVI GAFCFLQIPSPELQQALAV QRRQDTECFTKAKELAYICQVIKNPLSGLRFTNSLLEATDLNEDQKEFLETSSVCEKQISRIVSDMDLERI EDGSFELERAFFLGSVINAIVSQAMFLLRERLQILIRDIPEEIKS IAVYGDQTRIQQILAEFLLSIIRYA PSQEWVEIHLSQVPMQADGFSAIRTEFRMACPGEGLPPELVDRMFHSSRWTSPEGLGLSVCRKILKLMNG EVQYIRESERSYFLIIILELPVPLKRPFSTASGSGDMMMLMP	TaPHYB_protein_ sequence. Encoded by SEQ ID NO: 27
29	ATGGATTACAAGGACCACGACGGGGATTACAAGGACCACGACATTGATTACAAGGATGATGATGACAAGAT GGCTCCGAAGAAGAAGAGGAAGGTTGGCATCCACGGGGTGCCAGCTGCTGACAAGAAGTACTCGATCGGCC TCGATATTGGGACTAACTCTGTTGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCTCAAAGAAGTTC AAGGTCCTGGGCAACACCGATCGGCATTCCATCAAGAAGAATCTCATTGGCGCTCTCCTGTTGACAGCGG CGAGACGGCTGAGGCTACGCGGCTCAAGCGCACCGCCCGCAGCGGTACACGCGCAGGAAGAATCGCATCT GCTACCTGCAGGAGATTTTCTCCAACGAGATGGCGAAGGTTGACGATTCTTCTTCCACAGGCTGGAGGAG TCATTCTCTCGTGGAGGAGGATAAGAAGCACGAGCGGCATCCATCTTCGGCAACATTGTCGACGAGGTTGC CTACCACGAGAAGTACCCTACGATCTACCATCTGCGGAAGAAGCTCGTGGACTCCACAGATAAGGCGGACC TCCGCCTGATCTACCTCGCTCTGGCCACATGATTAAGTTCAAGGGGCCATTTCTGATCGAGGGGGATCTC AACC CGGACAATAGCGATGTTGACAAGCTGTT CATCCAGCTCGTGCAGACGTACAACCAGCTCTTCGAGGA GAACCCCATTAATGCGTCAGGCGTCGACGCGAAGGCTATCCTGTCCGCTAGGCTCTCGAAGTCTCGGCGCC TCGAGAACCTGATCGCCAGCTGCCGGGCGAGAAGAAGACGGCCTGTTCCGGGAATCTCATTGCGCTCAGC CTGGGGCTCACGCCCACTTCAAGTCGAATTTGATCTCGCTGAGGACGCCAAGCTGCAGCTCTCCAAGGA CACATACGACGATGACCTGGATAACCTCCTGGCCAGATCGGCGATCAGTACGCGGACCTGTTCTCTCGCTG CCAAGAATCTGTGCGACGCCATCCTCCTGTCTGATATTCTCAGGGTGAACACCGAGATTACGAAGGTCGG CTCTCAGCTCCATGATCAAGCGCTACGACGAGCACCATCAGGATCTGACCTCCTGAAGGCGCTGGTCAG GCAGCAGCTCCCCGAGAAGTACAAGGAGATCTTCTTCGATCAGTCAAGAACGGCTACGCTGGGTACATTG ACGGCGGGGCTCTCAGGAGGAGTCTACAAGTTCATCAAGCCGATTCTGGAGAAGATGGACGGCACGGAG GAGCTGCTGGTGAAGCTCAATCGCGAGGACCTCCTGAGGAAGCAGCGGACATTGATAACGGCAGCATCCC ACACCAGATTCTCTCGGGGAGCTGCACGCTATCCTGAGGAGGCAGGAGGACTTCTACCTTTCTCTCAAGG ATAACCGCGAGAAGATCGAGAAGATTCTGACTTTCAAGATCCCGTACTACGTCGGCCCACTCGCTAGGGGC AACTCCCGCTTCGTTGGATGACCCGCAAGTCAGAGGAGACGATCACGCCGTGGAATTCGAGGAGGTGGT CGACAAGGGCGCTAGCGCTCAGTCGTTTCATCGAGAGGATGACGAATTTGACAAGAACCTGCCAATGAGA AGGTGCTCCCTAAGCACTCGCTCCTGTACGAGTACTTCACAGTCTACAACGAGCTGACTAAGGTGAAGTAT GTGACCGAGGGCATGAGGAAGCCGGCTTTCTGTCTGGGAGCAGAAGAAGCCATCGTGGACCTCTGTT	Cas9 DNA sequence

	CAAGACCAACCGGAAGGTCACGGTTAAGCAGCTCAAGGAGGACTACTTCAAGAAGATTGAGTGCTTCGATT CGGTTCGAGATCTCTGGCGTTGAGGACCGCTTCAACGCCTCCCTGGGGACCTACCACGATCTCCTGAAGATC ATTAAGGATAAGGACTTCTCGACAAACGAGGAGAATGAGGATATCCTCGAGGACATTGTGCTGACACTCAC TCTGTTTCGAGGACCGGGAGATGATCGAGGAGCGCTGAAGACTTACGCCCATCTCTTCGATGACAAGGTCA TGAAGCAGCTCAAGAGGAGGAGGTACACCGGCTGGGGGAGGCTGAGCAGGAAGCTCATCAACGGCATTTCGG GACAAGCAGTCCGGGAAGACGATCCTCGACTTCTGAAGAGCGATGGCTTCGCGAACCACAATTTTCATGCA GCTGATTACGATGACAGCCTCACATTCAAGGAGGATATCCAGAAGGCTCAGGTGAGCGGCCAGGGGGACT CGCTGCACGAGCATATCGCAACCTCGCTGGCTCGCCAGCTATCAAGAAGGGGATTCTGCAGACCGTGAAG GTTGTGGACGAGCTGGTGAAGGTCATGGGCAGGCACAAGCCTGAGAACATCGTCATTGAGATGGCCCGGA GAATCAGACCACGCAGAAGGGCCAGAAGAACTCACGCGAGAGGATGAAGAGGATCGAGGAGGGCATTAAAG AGCTGGGTCCCAGATCCTCAAGGAGCACCCGTTGGAGAACACGCAGCTGCAGAATGAGAAGCTCTACCTG TACTACCTCCAGAATGGCCGCGATATGTATGTGGACCAGGAGCTGGATATTAACAGGCTCAGCGATTACGA CGTCGATCATATCGTTCCACAGTCATTCTGAAGGATGACTCCATTGACAACAAGGTCCTCACCAGGTCCG ACAAGAACCGGGGCAAGTCTGATAATGTTCTTCAGAGGAGGTCGTTAAGAAGATGAAGAACTACTGGCGC CAGCTCCTGAATGCCAAGCTGATCACGCAGCGGAAGTTCGATAACCTCACAAAGGCTGAGAGGGGCGGGCT CTCTGAGCTGGACAAGGCGGGCTTCATCAAGAGGCAGCTGGTCGAGACACGGCAGATCACTAAGCACGTTG CGCAGATTCTCGACTCACGGATGAACACTAAGTACGATGAGAATGACAAGCTGATCCGCGAGGTGAAGGTC ATCACCTGAAGTCAAAGCTCGTCTCCGACTTCAGGAAGGATTTCCAGTTCTACAAGGTTCCGGGAGATCAA CAATTACCACCATGCCATGACGCGTACCTGAACGCGGTGGTCGGCACAGCTCTGATCAAGAAGTACCCAA AGCTCGAGAGCGAGTTTCGTGTACGGGGACTACAAGGTTTACGATGTGAGGAAGATGATCGCCAAGTCGGAG CAGGAGATTGGCAAGGCTACCGCCAAGTACTTCTCTACTCTAACATTATGAATTTCTTCAAGACAGAGAT CACTCTGGCCAATGGCGAGATCCGGAAGCGCCCTCATCGAGACGAACGCGAGACGGGGGAGATCGTGT GGGACAAGGGCAGGGATTTCGCGACCGTCAGGAAGGTTCTCTCCATGCCACAAGTGAATATCGTCAAGAAG ACAGAGGTCCAGACTGGCGGGTTCCTAAGGAGTCAATTCTGCCTAAGCGGAACAGCGACAAGCTCATCGC CCGCAAGAAGGACTGGGATCCGAAGAAGTACGGCGGGTTCGACAGCCCCACTGTGGCCTACTCGTCTCGG TTGTGGCGAAGGTTGAGAAGGGCAAGTCCAAGAAGCTCAAGAGCGTGAAGGAGCTGCTGGGGATCACGATT ATGGAGCGCTCCAGCTTCGAGAAGAACCCGATCGATTTCTGGAGGCGAAGGGCTACAAGGAGGTGAAGAA GGACCTGATCATTAAGTCCCCAAGTACTCACTCTTCGAGCTGGAGAACGGCAGGAAGCGGATGCTGGCTT CCGCTGGCGAGCTGCAGAAGGGGAACGAGCTGGCTCTGCCGTCCAAGTATGTGAATTCCTCTACCTGGCC TCCCCTACGAGAAGCTCAAGGGCAGCCCCGAGGACAACGAGCAGAAGCAGCTGTTCTGTCGAGCAGACAA GCATTACCTCGACGAGATCATTGAGCAGATTTCCGAGTTCTCCAAGCGCGTGATCCTGGCCGACGCGAATC TGGATAAGGTCTCTCCGCGTACAACAAGCACCGCGACAAGCCAATCAGGGAGCAGGCTGAGAATATCATT CATCTCTTCAACCCTGACGAACCTCGGCGCCCCCTGCTGCTTTCAGTACTTCGACACAACCTATCGATCGCAA GAGGTACACAAGCACTAAGGAGGTCTGACGCGACCCCTCATCCACCAGTCGATTACCGGCCTCTACGAGA CGCGCATCGACCTGTCTCAGCTCGGGGGCGACAAGCGGCCAGCGGCGACGAAGAAGGCGGGGCGAGCGAAG AAGAAGAAGTGA	
30	GTCAAGGGGAGCGCTAAGCG	gRNA1 from TaELF3 genomic sequence
31	CCACAAGTTATCAAACACAG	gRNA2 from TaELF3 genomic sequence
32	1 gtttaccgc caatatatcc tgtcaaacac tgatagttta aactgaaggc gggaaacgac 61 aatctgatcc aagctcaagc tgctctagca ttccgcatte aggtgcgca actgttgga 121 agggcgatcg gtgcgggcct ctctgctatt acgccagctg gcgaaaggg gatgtgctgc 181 aaggcgatta agttgggtaa cgccagggtt ttccagtcga cgacgttgta aaacgacgac 241 cagtgcgaag ctctgacttg ccttcgcgac aatacatcat ttcttcttag cttttttct 301 tcttcttctg tcatcacagt tttttttgtt tatcagctta cattttcttg aaccgtagct 361 ttctgtttct tctttttaac ttccattcg gagttttgt atctgtttc atagttgtc	pHEE401_TaELF3g RNA CRISPR construct.

421	ccaggattag	aatgattagg	catcgaacct	tcaagaatth	gattgaataa	aacatcttca	Base 254 to base 1287 contains the U6 promoter gRNA1 gRNA scaffold- U6 terminator, U6 promoter- gRNA2 gRNA scaffold U6 terminator. From 1552-7881 is the EC1 promoter zCAS9 rbcS E9 terminator
481	ttcttaagat	atgaagataa	tcttcaaaag	gccccctggga	atctgaaaga	agagaagcag	
541	gccccatttat	atgggaaaga	acaatagtat	ttcttatata	ggccccattta	agttgaaaac	
601	aatcttcaaaa	agtcccacat	cgcttagata	agaaaaacgaa	gctgagttta	tatacagcta	
661	gagtcgaagt	agtgattggg	caaggggagc	gctaagcggg	tttagagcta	gaaatagcaa	
721	gttaaaataa	ggctagtcgg	ttatcaactt	gaaaaagtgg	caccgagtcg	gtgctttttt	
781	ttgcaaaatt	ttccagatcg	atttcttctt	cctctgttct	tcggcggttc	atttctgggg	
841	ttttctcttc	gttttctgta	actgaaacct	aaaatttgac	ctaaaaaaa	tctcaataa	
901	tatgattcag	tggttttgta	cttttcagtt	agttgagttt	tgcagttccg	atgagataaa	
961	ccaatattaa	tccaaactac	tgcagcctga	cagacaaatg	aggatgcaaa	caatttttaa	
1021	gtttatctaa	cgctagctgt	tttgtttctt	ctctctgggtg	caccaacgac	ggcgttttct	
1081	caatcataaa	gaggettggt	ttacttaagg	ccaataatgt	tgatggatcg	aaagaagagg	
1141	gcttttaata	aacgagcccg	tttaagctgt	aaacgatgtc	aaaaacatcc	cacatcggtc	
1201	agttgaaaat	agaagctctg	tttatatatt	ggtagagtcg	actaagagat	tgccacaagt	
1261	tatcaaacac	aggtttttaga	gctagaaata	gcaagttaaa	ataaggctag	tccgttatca	
1321	acttgaaaaa	gtggcaccga	gtcgggtgct	ttttttgcaa	aattttccag	atcgatttct	
1381	tcttcctctg	ttcttcggcg	ttcaatttct	ggggttttct	cttcggtttc	tgtaactgaa	
1441	acctaaaatt	tgacctaaaa	aaaatctcaa	ataatatgat	tcagtgggtt	tgtacttttc	
1501	agttagttga	gttttgcagt	tccgatgaga	taaaccaata	ccatgggtat	actagtgaat	
1561	aaaagcattt	gcggttggtt	tatcattgcg	tttatacaag	gacagagatc	cactgagctg	
1621	gaatagctta	aaaccattat	cagaacaaaa	taaaccattt	ttgtttaaga	atcagagcat	
1681	agtaaacaac	agaaacaacc	taagagaggt	aacttgcca	agaagatagc	taatttatc	
1741	tattttataa	aagttatcat	agtttgaag	tcacaaaaga	tgcaataaac	agagaaacta	
1801	ggagacttga	gaatatacat	tcttgtatat	ttgtattcga	gattgtgaaa	atttgaccat	
1861	aagtttaaat	tcttaaaaag	atatactctga	tctaggtgat	ggttatagac	tgtaatttta	
1921	ccacatgttt	aatgatggat	agtgcacac	atgcacatc	gacaacacta	tagcatctta	
1981	tttagattac	aacatgaaat	ttttctgtaa	tacatgtctt	tgtaacataat	ttaaaagtaa	
2041	ttcctaagaa	atataatttat	acaaggagtt	taaagaaaac	atagcataaa	gttcaatgag	
2101	tagtaaaaac	catatacagt	atatagcata	aagttcaatg	agttttattac	aaaagcattg	
2161	gttcactttc	tgtaaacacga	cgttaaaacct	tcgtctccaa	taggagcgct	actgattcaa	
2221	catgccaaata	tataactaaat	acgtttctac	agtcaaatgc	tttaacgttt	catgattaag	
2281	tgactatttta	ccgtcaatcc	tttcccatc	ctcccaactaa	tccaactttt	taattactct	
2341	taaatcacca	ctaagctagt	aacgcctatc	atgaattagc	tctactaaat	ctagcaacct	
2401	ttcaaatttg	cagtattgca	gggtgtctctg	tgtctttaaa	atagttgcct	tatgatttct	
2461	tcgggtttcaa	gatgatcaaa	tagttataga	tttcatgctc	acacatgctc	attagatgtg	
2521	tacatacttt	acttaeccaa	atctattttc	tcgcaaagat	tttgatggta	aagctgattt	
2581	ggttctattg	aactaaatca	aacgagtttc	agactgagtg	attctaattc	ggcccattag	
2641	cccctaaaca	gaccactaa	ttacgcagct	tttaatagag	taattacacc	tagtttacc	
2701	actaaaccac	taagcactaa	ttatctcaca	atctaattgag	cttcctcgt	aattacttgg	
2761	gctttcactc	taccatttat	ttgtaacagt	caagtctcta	ctgtctctat	ataaactctc	
2821	taaagttaac	acacaattct	catcacaaac	aatcaacca	aagcaacttc	tactcttct	
2881	tctttcgacc	ttatcaatct	gttgagaaat	ctagatggat	tacaaggacc	acgacgggga	
2941	ttacaaggac	cacgacattg	attacaagga	tgatgatgac	aagatggctc	cgaagaagaa	
3001	gaggaagggt	ggcatccacg	gggtgccagc	tgctgacaag	aagtactcga	tcggcctcga	
3061	tattgggact	aactctgttg	gctgggcccgt	gatcacccgac	gagtacaagg	tgccctcaaa	
3121	gaagttcaag	gtcctgggca	acaccgatcg	gcattccatc	aagaagaatc	tcattggcgc	
3181	tctcctgttc	gacagcggcg	agacggctga	ggctacggcg	ctcaagcgca	ccgcccgcag	
3241	gcggtacacg	cgcaggaaga	atcgcatctg	ctacctgcag	gagattttct	ccaacgagat	
3301	ggcgaagggt	gacgattctt	tcttccacag	gctggaggag	tcattcctcg	tggaggagga	
3361	taagaagcac	gagcggcatc	caatcttcgg	caacattgtc	gacgagggtg	cctaccacga	
3421	gaagtaccct	acgatctacc	atctgcggaa	gaagctcgtg	gactccacag	ataaggcgga	
3481	cctccgcctg	atctacctcg	ctctggccca	catgattaag	ttcaggggcc	atttctctgat	

3541	cgaggggggat	ctcaaccggg	acaatagcga	tgttgacaag	ctgttcatcc	agctcgtgca
3601	gacgtacaac	cagctcttcg	aggagaaccc	cattaatgcg	tcaggcgctcg	acgcgaaggc
3661	tatcctgtcc	gctaggctct	cgaagtctcg	gcgcctcgag	aacctgatcg	cccagctgcc
3721	ggcgagagaag	aagaacggcc	tgttcgggaa	tctcattgcg	ctcagcctgg	ggctcacgcc
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15601	tgcgctcaag	tgccgggtac	agggctcagc	gatgcacgcc	aagcagtgca	gccgcctctt
15661	tcacgggtgc	gccttccctg	tcgatcagct	cgcgggcgtg	cgcgatctgt	gccgggggtga
15721	gggtagggcg	ggggccaaac	ttcacgcctc	gggccttggc	ggcctcgcgc	ccgctccggg
15781	tgcggtcgat	gattagggaa	cgctcgaact	cggcaatgcc	ggcgaacacg	gtcaacacca
15841	tgccggccggc	cggcggtggtg	gtgtcggccc	acggctctgc	caggctacgc	aggcccgcg
15901	cggcctcctg	gatgcgctcg	gcaatgtcca	gtaggctcgc	gggtgctgcg	gccaggcggt
15961	ctagcctgggt	cactgtcaca	acgtcgccag	ggcgtaggtg	gtcaagcatc	ctggccagct

	16021 ccgggcggtc ggcctggtg ccggtgatct tctcgaaaa cagcttggtg cagccggcgc 16081 cgtgcagttc ggcccggttg ttggtcaagt cctggtcgtc ggtgctgacg cgggcatagc 16141 ccagcaggcc agcggcggtg ctcttggtca tggcgtaatg tctccggttc tagtcgcaag 16201 tattctactt tatgcgacta aaacacgcga caagaaaacg ccaggaaaag ggcaggcg 16261 cagcctgtcg cgtaacttag gacttggtgcg acatgtcggt ttcagaagac ggctgcactg 16321 aacgtcagaa gccgactgca ctatagcagc ggaggggttg gatcaaagta ctttgatccc 16381 gaggggaacc ctgtggttg catgcacata caaatggacg aacggataaa ctttttcacg 16441 ccctttttaa tatccgttat tctaataaac gctcttttct cttag	
33	GTATGAAGAGAGGGAATGAT	A gRNA of phse401-basil- x4 CRISPR construct (SEQ ID NO: 37) to disrupt elf3 in basil.
34	GGCGTTGTTAGTCGGGTTTC	A gRNA of phse401-basil- x4 CRISPR construct (SEQ ID NO: 37) to disrupt elf3 in basil.
35	GAATCGGTGAGTCTGTGGGA	A gRNA of phse401-basil- x4 CRISPR construct (SEQ ID NO: 37) to disrupt elf3 in basil.
36	GACGGACGATTGAGACTAGA	A gRNA of phse401-basil- x4 CRISPR construct (SEQ ID NO: 37) to disrupt elf3 in basil.
37	1 TAAACGCTCT TTTCTCTTAG GTTACCCGC CAATATATCC TGTCAAACAC TGATAGTTTA 61 AACTGAAGGC GGGAAACGAC AATCTGATCC AAGCTCAAGC TGCTCTAGCA TTCGCCATTC 121 AGGCTGCGCA ACTGTTGGGA AGGGCGATCG GTGCGGGCCT CTTCGCTATT ACGCCAGCTG 181 GCGAAAGGGG GATGTGCTGC AAGGCGATTA AGTTGGGTAA CGCCAGGGTT TTCCAGTCA 241 CGACGTTGTA AAACGACGGC CAGTGCCAAG CTTCGACTTG CCTCCGCAC AATACATCAT 301 TTCTTCTTAG CTTTTTTTCT TCTTCTTCGT TCATACAGTT TTTTTTTGTT TATCAGCTTA 361 CATTTTCTTG AACCGTAGCT TTCGTTTCT TCTTTTAAAC TTTCCATTCT GAGTTTTTGT	pHSE401_basil_x 4 Plasmid comprising CRISPR system

421	ATCTTGTTTC	ATAGTTTGTC	CCAGGATTAG	AATGATTAGG	CATCGAACCT	TCAAGAATTT	to disrupt elf3 in basil.
481	GATTGAATAA	AACATCTTCA	TTCTTAAGAT	ATGAAGATAA	TCTTCAAAAG	GCCCCTGGGA	
541	ATCTGAAAGA	AGAGAAGCAG	GCCCATTAT	ATGGGAAAGA	ACAATAGTAT	TTCTTATATA	
601	GGCCCATTTA	AGTTGAAAAC	AATCTTCAAA	AGTCCCACAT	CGCTTAGATA	AGAAAACGAA	
661	GCTGAGTTTA	TATACAGCTA	GAGTCGAAGT	AGTGATTGTA	TGAAGAGAGG	GAATGATGTT	
721	TTAGAGCTAG	AAATAGCAAG	TTAAAATAAG	GCTAGTCCGT	TATCAACTTG	AAAAAGTGGC	
781	ACCGAGTCGG	TGCTTTTTTT	TGCAAAATTT	TCCAGATCGA	TTTCTTCTTC	CTCTGTTCTT	
841	CGGCGTTCAA	TTTCTGGGGT	TTTCTCTTCG	TTTTCTGTAA	CTGAAACCTA	AAATTTGACC	
901	TAAAAAAAT	CTCAAATAAT	ATGATTCAGT	GGTTTTGTAC	TTTTCAGTTA	GTTGAGTTTT	
961	GCAGTTCCGA	TGAGATAAAC	CAATATTAAT	CCAACTACT	GCAGCCTGAC	AGACAAATGA	
1021	GGATGCAAAC	AATTTTAAAG	TTTATCTAAC	GCTAGCTGTT	TTGTTTCTTC	TCTCTGTTGC	
1081	ACCAACGACG	GCGTTTTCTC	AATCATAAAG	AGGCTTGTTT	TACTTAAGGC	CAATAATGTT	
1141	GATGGATCGA	AAGAAGAGGG	CTTTTAATAA	ACGAGCCCGT	TTAAGCTGTA	AACGATGTCA	
1201	AAAACATCCC	ACATCGTTCA	GTTGAAAATA	GAAGCTCTGT	TTATATATTG	GTAGAGTCGA	
1261	CTAAGAGATT	GGCGTTGTTA	GTGCGGTTTC	GTTTTAGAGC	TAGAAATAGC	AAGTTAAAAAT	
1321	AAGGCTAGTC	CGTTATCAAC	TTGAAAAAGT	GGCACCGAGT	CGGTGCTTTT	TTTGGATAGA	
1381	ATTTCCCAGC	TTTTTTCGCT	GTTTCAGCTC	TCATGATCCT	TGGCCAATGG	GTGTAGTAAA	
1441	TTTTCTGCAC	ATTCATTGGA	TGGAAAATAA	TGGTTTTAGC	TTTAGGGAAT	AAGAAAAGTG	
1501	TATAGGAAGG	GGATTTTTGT	ACAATCACAT	TTGAATTAGG	TCTTTGAAAT	GACAGGGAAT	
1561	GAGGACATAT	GATGAGACGG	TCATTGTTTT	AGTTCACCA	CGATTATATT	TGAAATTTAC	
1621	GTGAGTGTGA	GTGAGACTTG	CATAAGAAAA	TAAAATCTTT	AGTTGGGAAA	AAATTCATAA	
1681	ATATAAATGG	GCTTGAGAAG	GAAGCGAGGG	ATAGGCCTTT	TTCTAAAATA	GGCCCATTTA	
1741	AGCTATTAAC	AATCTTCAAA	AGTACCACAG	CGCTTAGGTA	AAGAAAGCAG	CTGAGTTTAT	
1801	ATATGGTTAG	AGACGAAGTA	GTGATTGAAT	CGGTGAGTCT	GTGGGAGTTT	TAGAGCTAGA	
1861	AATAGCAAGT	TAAAATAAGG	CTAGTCCGTT	ATCAACTTGA	AAAAGTGGCA	CCGAGTCGGT	
1921	GCTTTTTTTT	GGCAAAAATT	TTCAGATTTT	TTCTTCATCT	GTAGATTTCT	GGGTTTTTTT	
1981	TTCCGTTTCG	TGAATCATAA	GTGAAGTTTT	GGATGCAAAT	CTGCGCGAAA	AAAGTTGGAC	
2041	CTGCAATGAG	CTTATTTAGA	TAGCTAAGAC	AAAGTGATTG	GTCCGTTTCA	CTTGCCTTCC	
2101	GCACAATACA	TCATTTCTTC	TTAGCTTTTT	TTCTTCTTCT	TCGTTCATAC	AGTTTTTTTT	
2161	TGTTTATCAG	CTTACATTTT	CTTGAACCGT	AGCTTTCGTT	TTCTTCTTTT	TAACTTTCCA	
2221	TTGCGAGTTT	TTGTATCTTG	TTTCATAGTT	TGTTCCAGGA	TTAGAATGAT	TAGGCATCGA	
2281	ACCTTCAAGA	ATTTGATTGA	ATAAAACATC	TTCAATCTTA	AGATATGAAG	ATAATCTTCA	
2341	AAAGGCCCCT	GGGAATCTGA	AAGAAGAGAA	GCAGGCCCAT	TTATATGGGA	AAGAACAATA	
2401	GTATTTCTTA	TATAGGCCCA	TTTAAGTTGA	AAACAATCTT	CAAAAGTCCC	ACATCGCTTA	
2461	GATAAGAAAA	CGAAGCTGAG	TTTATATACA	GCTAGAGTCG	AAGTAGTGAT	TGACGGACGA	
2521	TTGAGACTAG	AGTTTTAGAG	CTAGAAATAG	CAAGTTAAAA	TAAGGCTAGT	CCGTTATCAA	
2581	CTTGAAAAAG	TGGCACCGAG	TCGGTGCTTT	TTTTTGCAAA	ATTTTCCAGA	TCGATTTCTT	
2641	CTTCCTCTGT	TCTTCGGCGT	TCAATTTCTG	GGGTTTTCTC	TTGTTTTTCT	GTAACGAAA	
2701	CCTAAAATTT	GACCTAAAAA	AAATCTCAAA	TAATATGATT	CAGTGGTTTT	GTAATTTTCA	
2761	GTTAGTTGAG	TTTTGCAGTT	CCGATGAGAT	AAACCAATAA	GCTTGCATGC	CTGCAGGTCA	
2821	ACATGGTGGA	GCACGACACA	CTTGTCTACT	CCAAAAATAT	CAAAGATACA	GTCTCAGAAG	
2881	ACCAAAGGGC	AATTGAGACT	TTTCAACAAA	GGGTAATATC	CGGAAACCTC	CTCGGATTCC	
2941	ATTGCCCAGC	TATCTGTAC	TTTATTGTGA	AGATAGTGGA	AAAGGAAGGT	GGCTCCTACA	
3001	AATGCCATCA	TTGCGATAAA	GGAAAGGCCA	TCGTTGAAGA	TGCCTCTGCC	GACAGTGGTC	
3061	CCAAAGATGG	ACCCCCACCC	ACGAGGAGCA	TCGTGGAAAA	AGAAGACGTT	CCAACCACGT	
3121	CTTCAAAGCA	AGTGGATTGA	TGTGATAACA	TGGTGGAGCA	CGACACACTT	GTCTACTCCA	
3181	AAAATATCAA	AGATACAGTC	TCAGAAGACC	AAAGGGCAAT	TGAGACTTTT	CAACAAAGGG	
3241	TAATATCCGG	AAACCTCCTC	GGATTCCATT	GCCCAGCTAT	CTGTCACTTT	ATTGTGAAGA	
3301	TAGTGGAAAA	GGAAGGTGGC	TCCTACAAAT	GCCATCATTG	CGATAAAGGA	AAGGCCATCG	
3361	TTGAAGATGC	CTCTGCCGAC	AGTGGTCCCA	AAGATGGACC	CCCACCCACG	AGGAGCATCG	
3421	TGGAAAAAGA	AGACGTTCCA	ACCACGTCTT	CAAAGCAAGT	GGATTGATGT	GATATCTCCA	
3481	CTGACGTAAG	GGATGACGCA	CAATCCCACT	ATCCTTCGCA	AGACCCTTCC	TCTATATAAG	

3541	GAAGTTCATT	TCATTTGGAG	AGGACCTCGA	CCTCAACACA	ACATATACAA	AACAAACGAA
3601	TCTCAAGCAA	TCAAGCATTC	TACTTCTATT	GCAGCAATTT	AAATCATTTT	TTTTAAAGCA
3661	AAAGCAATTT	TCTGAAAAAT	TTCACCATTT	ACGAACGATA	CTCGAGTAAT	CTAGATGGAT
3721	TACAAGGACC	ACGACGGGGA	TTACAAGGAC	CACGACATTG	ATTACAAGGA	TGATGATGAC
3781	AAGATGGCTC	CGAAGAAGAA	GAGGAAGGTT	GGCATCCACG	GGGTGCCAGC	TGCTGACAAAG
3841	AAGTACTCGA	TCGGCCTCGA	TATTGGGACT	AACTCTGTTG	GCTGGGCCGT	GATCACCGAC
3901	GAGTACAAGG	TGCCCTCAAA	GAAGTTCAAG	GTCTGGGCA	ACACCGATCG	GCATTCCATC
3961	AAGAAGAATC	TCATTGGCGC	TCTCTGTTC	GACAGCGGCG	AGACGGCTGA	GGCTACGCGG
4021	CTCAAGCGCA	CCGCCCAGCAG	GCGGTACACG	CGCAGGAAGA	ATCGCATCTG	CTACCTGCAG
4081	GAGATTTTCT	CCAACGAGAT	GGCGAAGGTT	GACGATTCTT	TCTTCCACAG	GCTGGAGGAG
4141	TCATTCTCTG	TGGAGGAGGA	TAAGAAGCAC	GAGCGGCATC	CAATCTTCGG	CAACATTGTC
4201	GACGAGGTTG	CCTACCACGA	GAAGTACCCT	ACGATCTACC	ATCTGCGGAA	GAAGCTCGTG
4261	GACTCCACAG	ATAAGGCGGA	CCTCCGCCCTG	ATCTACCTCG	CTCTGGCCCA	CATGATTAAG
4321	TTCAGGGGCC	ATTTCTTGAT	CGAGGGGGAT	CTCAACCCGG	ACAATAGCGA	TGTTGACAAAG
4381	CTGTTTCATC	AGCTCGTGCA	GACGTACAAC	CAGCTCTTCG	AGGAGAACCC	CATTAATGCG
4441	TCAGGCGTCG	ACGCGAAGGC	TATCCTGTCC	GCTAGGCTCT	CGAAGTCTCG	GCGCCTCGAG
4501	AACCTGATCG	CCCAGCTGCC	GGGCGAGAAG	AAGAACGGCC	TGTTGCGGAA	TCTCATTGCG
4561	CTCAGCCTGG	GGCTCACGCC	CAACTTCAAG	TCGAATTTTCG	ATCTCGCTGA	GGACGCCAAG
4621	CTGCAGCTCT	CCAAGGACAC	ATACGACGAT	GACCTGGATA	ACCTCCTGGC	CCAGATCGGC
4681	GATCAGTACG	CGGACCTGTT	CCTCGCTGCC	AAGAATCTGT	CGGACGCCAT	CCTCCTGTCT
4741	GATATTCTCA	GGGTGAACAC	CGAGATTACG	AAGGCTCCGC	TCTCAGCCTC	CATGATCAAG
4801	CGTACGACG	AGCACCATCA	GGATCTGACC	CTCCTGAAGG	CGCTGGTCAG	GCAGCAGCTC
4861	CCCGAGAAGT	ACAAGGAGAT	CTTCTTCGAT	CAGTCGAAGA	ACGGCTACGC	TGGGTACATT
4921	GACGGCGGGG	CCTCTCAGGA	GGAGTTCTAC	AAGTTCATCA	AGCCGATTCT	GGAGAAGATG
4981	GACGGCACGG	AGGAGCTGCT	GGTGAAGCTC	AATCGCGAGG	ACCTCCTGAG	GAAGCAGCGG
5041	ACATTCGATA	ACGGCAGCAT	CCCACACCAG	ATTATCTCTG	GGGAGCTGCA	CGCTATCCTG
5101	AGGAGGCAGG	AGGACTTCTA	CCCTTTCTCT	AAGGATAACC	GCGAGAAGAT	CGAGAAGATT
5161	CTGACTTTCA	GGATCCCGTA	CTACGTCGGC	CCACTCGCTA	GGGGCAACTC	CCGCTTCGCT
5221	TGGATGACCC	GCAAGTCAGA	GGAGACGATC	ACGCCGTGGA	ACTTCGAGGA	GGTGGTCGAC
5281	AAGGGCGCTA	GCGCTCAGTC	GTTTCATCGAG	AGGATGACGA	ATTTGACAA	GAACCTGCCA
5341	AATGAGAAGG	TGCTCCCTAA	GCACTCGCTC	CTGTACGAGT	ACTTCACAGT	CTACAACGAG
5401	CTGACTAAGG	TGAAGTATGT	GACCGAGGGC	ATGAGGAAGC	CGGCTTTCCT	GTCTGGGGAG
5461	CAGAAGAAGG	CCATCGTGGA	CCTCCTGTTC	AAGACCAACC	GGAAGGTCAC	GGTTAAGCAG
5521	CTCAAGGAGG	ACTACTTCAA	GAAGATTGAG	TGCTTCGATT	CGGTGAGAT	CTCTGGCGTT
5581	GAGGACCGCT	TCAACGCCCTC	CCTGGGGACC	TACCACGATC	TCCTGAAGAT	CATTAAGGAT
5641	AAGGACTTCC	TGGACAACGA	GGAGATGAG	GATATCCTCG	AGGACATTGT	GCTGACACTC
5701	ACTCTGTTCC	AGGACCGGGA	GATGATCGAG	GAGCGCCTGA	AGACTTACGC	CCATCTCTTC
5761	GATGACAAGG	TCATGAAGCA	GCTCAAGAGG	AGGAGGTACA	CCGGCTGGGG	GAGGCTGAGC
5821	AGGAAGCTCA	TCAACGGCAT	TCGGGACAAG	CAGTCCGGGA	AGACGATCCT	CGACTTCCTG
5881	AAGAGCGATG	GCTTCGCGAA	CCGCAATTTT	ATGCAGCTGA	TTCACGATGA	CAGCCTCACA
5941	TTCAAGGAGG	ATATCCAGAA	GGCTCAGGTG	AGCGGCCAGG	GGGACTCGCT	GCACGAGCAT
6001	ATCGCGAACC	TCGCTGGCTC	GCCAGCTATC	AAGAAGGGGA	TTCTGCAGAC	CGTGAAGGTT
6061	GTGGACGAGC	TGGTGAAGGT	CATGGGCAGG	CACAAGCCTG	AGAACATCGT	CATTGAGATG
6121	GCCCGGGAGA	ATCAGACCAC	GCAGAAGGGC	CAGAAGAACT	CACGCGAGAG	GATGAAGAGG
6181	ATCGAGGAGG	GCATTAAGGA	GCTGGGGTCC	CAGATCCTCA	AGGAGCACCC	GGTGGAGAAC
6241	ACGCGAGCTG	AGAATGAGAA	GCTCTACCTG	TACTACCTCC	AGAATGGCCG	CGATATGTAT
6301	GTGGACCAGG	AGCTGGATAT	TAACAGGCTC	AGCGATTACG	ACGTCGATCA	TATCGTTCCA
6361	CAGTCATTCC	TGAAGGATGA	CTCCATTGAC	AACAAGGTCC	TCACCAGGTC	GGACAAGAAC
6421	CGGGGCAAGT	CTGATAATGT	TCCTTCAGAG	GAGGTGCTTA	AGAAGATGAA	GAAGTACTGG
6481	CGCCAGCTCC	TGAATGCCAA	GCTGATCACG	CAGCGGAAGT	TCGATAACCT	CACAAAGGCT
6541	GAGAGGGGCG	GGCTCTCTGA	GCTGGACAAG	GCGGGCTTCA	TCAAGAGGCA	GCTGGTCGAG
6601	ACACGGCAGA	TCACTAAGCA	CGTTGCGCAG	ATTCTCGACT	CACGGATGAA	CACTAAGTAC

6661	GATGAGAATG	ACAAGCTGAT	CCGCGAGGTG	AAGGTCATCA	CCCTGAAGTC	AAAGCTCGTC
6721	TCCGACTTCA	GGAAGGATTT	CCAGTTCTAC	AAGGTTCTGGG	AGATCAACAA	TTACCACCAT
6781	GCCCATGACG	CGTACCTGAA	CGCGGTGGTC	GGCACAGCTC	TGATCAAGAA	GTACCCAAAG
6841	CTCGAGAGCG	AGTTTCGTGTA	CGGGGACTAC	AAGGTTTACG	ATGTGAGGAA	GATGATCGCC
6901	AAGTCGAGC	AGGAGATTGG	CAAGGCTACC	GCCAAGTACT	TCTTCTACTC	TAACATTATG
6961	AATTTCTTCA	AGACAGAGAT	CACTCTGGCC	AATGGCGAGA	TCCGGAAGCG	CCCCCTCATC
7021	GAGACGAACG	GCGAGACGGG	GGAGATCGTG	TGGGACAAGG	GCAGGGATTT	CGCGACCGTC
7081	AGGAAGGTTT	TCTCCATGCC	ACAAGTGAAT	ATCGTCAAGA	AGACAGAGGT	CCAGACTGGC
7141	GGGTTCTCTA	AGGAGTCAAT	TCTGCCTAAG	CGGAACAGCG	ACAAGCTCAT	CGCCCGCAAG
7201	AAGGACTGGG	ATCCGAAGAA	GTACGGCGGG	TTGACAGGCC	CCACTGTGGC	CTACTCGGTC
7261	CTGGTTGTGG	CGAAGGTTGA	GAAGGGCAAG	TCCAAGAAGC	TCAAGAGCGT	GAAGGAGCTG
7321	CTGGGGATCA	CGATTATGGA	GCGCTCCAGC	TTGAGAAGA	ACCCGATCGA	TTTCCTGGAG
7381	GCGAAGGGCT	ACAAGGAGGT	GAAGAAGGAC	CTGATCATT	AGCTCCCCAA	GTACTCACTC
7441	TTGAGCTGG	AGAACGGCAG	GAAGCGGATG	CTGGCTTCCG	CTGGCGAGCT	GCAGAAGGGG
7501	AACGAGCTGG	CTCTGCCGTC	CAAGTATGTG	AACTTCCTCT	ACCTGGCCTC	CCACTACGAG
7561	AAGCTCAAGG	GCAGCCCCGA	GGACAACGAG	CAGAAGCAGC	TGTTTCGTCGA	GCAGCACAA
7621	CATTACCTCG	ACGAGATCAT	TGAGCAGATT	TCCGAGTTCT	CCAAGCGCGT	GATCCTGGCC
7681	GACGCGAATC	TGGATAAGGT	CCTCTCCGCG	TACAACAAGC	ACCGCGACAA	GCCAAATCAGG
7741	GAGCAGGCTG	AGAATATCAT	TCATCTCTTC	ACCCTGACGA	ACCTCGGCGC	CCCTGCTGCT
7801	TTCAAGTACT	TCGACACAAC	TATCGATCGC	AAGAGGTACA	CAAGCACTAA	GGAGGTCCTG
7861	GACGCGACCC	TCATCCACCA	GTGATTAC	GGCTCTACG	AGACGCGCAT	CGACCTGTCT
7921	CAGCTCGGGG	GCGACAAGCG	GCCAGCGGCG	ACGAAGAAGG	CGGGGCAGGC	GAAGAAGAAG
7981	AAGTGAGCTC	AGAGCTTTTCG	TTGCTATCAT	CGGTTTCGAC	AACGTTTCGTC	AAGTTCAATG
8041	CATCAGTTTC	ATTGCGCACA	CACCAGAATC	CTACTGAGTT	TGAGTATTAT	GGCATTTGGGA
8101	AAACTGTTTT	TCTTGTACCA	TTTGTGTGTC	TTGTAATTTA	CTGTGTTTTT	TATTCGGTTT
8161	TCGCTATCGA	ACTGTGAAAT	GGAAATGGAT	GGAGAAGAGT	TAATGAATGA	TATGGTCCTT
8221	TTGTTTCATT	TCAAATTAAT	ATTATTTGTT	TTTTCTCTTA	TTTGTGTGTG	GTTGAATTTG
8281	AAATTATAAG	AGATATGCAA	ACATTTTGTT	TTGAGTAAAA	ATGTGTCAA	TCGTGGCCTC
8341	TAATGACCGA	AGTTAATATG	AGGAGTAAAA	CACTGTAGT	TGTACCATTA	TGCTTATTCA
8401	CTAGGCAACA	AATATATTTT	CAGACCTAGA	AAAGCTGCAA	ATGTTACTGA	ATACAAGTAT
8461	GTCTCTTGT	GTTTTAGACA	TTTATGAAC	TTCTTTTATG	TAATTTTCCA	GAATCCTGT
8521	CAGATTCTAA	TCATTGCTTT	ATAATTATAG	TTATACTCAT	GGATTTGTAG	TTGAGTATGA
8581	AAATATTTTT	TAATGCATTT	TATGACTTGC	CAATTGATTG	ACAACGAATT	CGTAATCATG
8641	TCATAGCTGT	TTCTGTGTG	AAATTTGTTAT	CCGCTCACAA	TTCCACACAA	CATACGAGCC
8701	GGAAGCATAA	AGTGTAAGC	CTGGGGTGCC	TAATGAGTGA	GCTAACTCAC	ATTAATTGCG
8761	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCTG	GCCAGCTGCA	TTAATGAATC
8821	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT	ATTGGCTAGA	GCAGCTTGCC	AACATGGTGG
8881	AGCACGACAC	TCTCGTCTAC	TCCAAGAATA	TCAAAGATAC	AGTCTCAGAA	GACCAAAGGG
8941	CTATTGAGAC	TTTTCAACAA	AGGGTAATAT	CGGGAAACCT	CCTCGGATTC	CATTGCCCAG
9001	CTATCTGTCA	CTTCATCAA	AGGACAGTAG	AAAAGGAAGG	TGGCACCTAC	AAATGCCATC
9061	ATTGCGATAA	AGGAAAGGCT	ATCGTTCAAG	ATGCCTCTGC	CGACAGTGGT	CCCAAAGATG
9121	GACCCCCACC	CACGAGGAGC	ATCGTGGA	AAGAAGACGT	TCCAACCACG	TCTTCAAAGC
9181	AAGTGATTG	ATGTGAACAT	GGTGGAGCAC	GACACTCTCG	TCTACTCCAA	GAATATCAAA
9241	GATACAGTCT	CAGAAGACCA	AAGGGCTATT	GAGACTTTTC	AACAAAGGGT	AATATCGGGA
9301	AACCTCCTCG	GATTCCATTG	CCCAGCTATC	TGTCACTTCA	TCAAAAGGAC	AGTAGAAAAG
9361	GAAGGTGGCA	CCTACAAATG	CCATCATTGC	GATAAAGGAA	AGGCTATCGT	TCAAGATGCC
9421	TCTGCCGACA	GTGGTCCCAA	AGATGGACCC	CCACCCACGA	GGAGCATCGT	GGAAAAAGAA
9481	GACGTTCCAA	CCACGTCTTC	AAAGCAAGTG	GATTGATGTG	ATATCTCCAC	TGACGTAAGG
9541	GATGACGCAC	AATCCCAC	TCCTTCGCAA	GACCCTTCCT	CTATATAAGG	AAGTTTCATT
9601	CATTTGGAGA	GGACACGCTG	AAATCACCAG	TCTCTCTCTA	CAAATCTATC	TCTCTCGAGC
9661	TTTCGCAGAT	CCGGGGGGCA	ATGAGATATG	AAAAGCCTG	AACTCACC	GACGTCGTG
9721	GAGAAGTTTC	TGATCGAAAA	GTTGACAGC	GTCTCCGACC	TGATGCAGCT	CTCGGAGGGC

9781	GAAGAATCTC	GTGCTTTTCAG	CTTCGATGTA	GGAGGGCGTG	GATATGTCCT	GCGGGTAAAT
9841	AGCTGCGCCG	ATGGTTTCTA	CAAAGATCGT	TATGTTTATC	GGCACTTTGC	ATCGGCCGCG
9901	CTCCCGATTG	CGGAAGTGCT	TGACATTGGG	GAGTTTAGCG	AGAGCCTGAC	CTATTGCATC
9961	TCCCGCCGTT	CACAGGGTGT	CACGTTGCAA	GACCTGCCTG	AAACCGAACT	GCCCGCTGTT
10021	CTACAACCGG	TCGCGGAGGC	TATGGATGCG	ATCGCTGCGG	CCGATCTTAG	CCAGACGAGC
10081	GGGTTTCGCC	CATTTCGGACC	GCAAGGAATC	GGTCAATACA	CTACATGGCG	TGATTTTCATA
10141	TGCGCGATTG	CTGATCCCCA	TGTGTATCAC	TGGCAAACCTG	TGATGGACGA	CACCGTCAGT
10201	GCGTCCGTCG	CGCAGGCTCT	CGATGAGCTG	ATGCTTTGGG	CCGAGGACTG	CCCCGAAGTC
10261	CGGCACCTCG	TGCACGCGGA	TTTCGGCTCC	AACAATGTCC	TGACGGACAA	TGGCCGCATA
10321	ACAGCGGTCA	TTGACTGGAG	CGAGGCGATG	TTCGGGGATT	CCCAATACGA	GGTCGCCAAC
10381	ATCTTCTTCT	GGAGGCCGTG	GTTGGCTTGT	ATGGAGCAGC	AGACGCGCTA	CTTCGAGCGG
10441	AGGCATCCGG	AGCTTGACAG	ATCGCCACGA	CTCCGGGCGT	ATATGCTCCG	CATTGGTCTT
10501	GACCAACTCT	ATCAGAGCTT	GGTTGACGGC	AATTTTCGATG	ATGCAGCTTG	GGCGCAGGGT
10561	CGATGCGACG	CAATCGTCCG	ATCCGGAGCC	GGGACTGTGCG	GGCGTACACA	AATCGCCCCG
10621	AGAAGCGCGG	CCGTCTGGAC	CGATGGCTGT	GTAAGAAGTAC	TCGCCGATAG	TGGAACCCGA
10681	CGCCCCAGCA	CTCGTCCGAG	GGCAAAGAAA	TAGAGTAGAT	GCCGACCGGG	ATCTGTGCGAT
10741	CGACAAGCTC	GAGTTTCTCC	ATAATAATGT	GTGAGTAGTT	CCCAGATAAG	GGAATTAGGG
10801	TTCCTATAGG	GTTTCGCTCA	TGTGTTGAGC	ATATAAGAAA	CCCTTAGTAT	GTATTTGTAT
10861	TTGTAAAATA	CTTCTATCAA	TAAAAATTTCT	AATTCCTAAA	ACCAAAATCC	AGTACTAAAA
10921	TCCAGATCCC	CCGAATTAAT	TCGGCGTTAA	TTCACTACAT	TAAAAACGTC	CGCAATGTGT
10981	TATTAAGTTG	TCTAAGCGTC	AATTTGTTTA	CACCACAATA	TATCCTGCCA	CCAGCCAGCC
11041	AACAGCTCCC	CGACCGGCAG	CTCGGCACAA	AATCACCCT	CGATACAGGC	AGCCCCATCAG
11101	TCCGGGACGG	CGTCAGCGGG	AGAGCCGTTG	TAAGGCGGCA	GACTTTGCTC	ATGTTACCGA
11161	TGCTATTTCG	AAGAACGGCA	ACTAAGCTGC	CGGGTTTGAA	ACACGGATGA	TCTCGCGGAG
11221	GGTAGCATGT	TGATTGTAAC	GATGACAGAG	CGTTGCTGCC	TGTGATCACC	GCGGTTTCAA
11281	AATCGGCTCC	GTCGATACTA	TGTTATACGC	CAACTTTGAA	AACAACCTTG	AAAAAGCTGT
11341	TTTCTGGTAT	TTAAGGTTTT	AGAATGCAAG	GAACAGTGAA	TTGGAGTTTCG	TCTTGTATATA
11401	ATTAGCTTCT	TGGGGTATCT	TTAAATACTG	TAGAAAAGAG	GAAGGAAATA	ATAAATGGCT
11461	AAAATGAGAA	TATCACCAGG	ATTGAAAAAA	CTGATCGAAA	AATACCGCTG	CGTAAAAGAT
11521	ACGGAAGGAA	TGTCTCCTGC	TAAGGTATAT	AAGCTGGTGG	GAGAAAATGA	AAACCTATAT
11581	TTAAAAATGA	CGGACAGCCG	GTATAAAGGG	ACCACCTATG	ATGTGGAACG	GGAAAAGGAC
11641	ATGATGCTAT	GGCTGGAAGG	AAAGCTGCCT	GTCCAAAGG	TCCTGCACTT	TGAACGGCAT
11701	GATGGCTGGA	GCAATCTGCT	CATGAGTGAG	GCCGATGGCG	TCCTTTGCTC	GGAAGAGTAT
11761	GAAGATGAAC	AAAGCCCTGA	AAAGATTATC	GAGCTGTATG	CGGAGTGCAT	CAGGCTCTTT
11821	CACTCCATCG	ACATATCGGA	TTGTCCCTAT	ACGAATAGCT	TAGACAGCCG	CTTAGCCGAA
11881	TTGGATTACT	TACTGAATAA	CGATCTGGCC	GATGTGGATT	GCGAAAACCTG	GGAAGAAGAC
11941	ACTCCATTTA	AAGATCCGCG	CGAGCTGTAT	GATTTTTTAA	AGACGGAAAA	GCCCGAAGAG
12001	GAAGTTGTCT	TTTCCCACGG	CGACCTGGGA	GACAGCAACA	TCTTTGTGAA	AGATGGCAAA
12061	GTAAGTGGCT	TTATTGATCT	TGGGAGAAGC	GGCAGGGCGG	ACAAGTGGTA	TGACATTGCC
12121	TTCTGCGTCC	GGTCGATCAG	GGAGGATATC	GGGGAAGAAC	AGTATGTCGA	GCTATTTTTT
12181	GACTTACTGG	GGATCAAGCC	TGATTGGGAG	AAAATAAAAT	ATTATATTTT	ACTGGATGAA
12241	TTGTTTTAGT	ACCTAGAATG	CATGACCAAA	ATCCCTTAAC	GTGAGTTTTT	GTTCCACTGA
12301	GCGTCAGACC	CCGTAGAAAA	GATCAAAGGA	TCTTCTTGAG	ATCCTTTTTT	TCTGCGCGTA
12361	ATCTGCTGCT	TGCAAACAAA	AAAACCACCG	CTACCAGCGG	TGGTTTGTGT	GCCGGATCAA
12421	GAGCTACCAA	CTCTTTTTCC	GAAGGTAAC	GGCTTCAGCA	GAGCGCAGAT	ACCAAATACT
12481	GTCCTTCTAG	TGTAGCCGTA	GTTAGGCCAC	CACTTCAAGA	ACTCTGTAGC	ACCGCCTACA
12541	TACCTCGCTC	TGCTAATCCT	GTTACCAGTG	GCTGCTGCCA	GTGGCGATAA	GTCGTGTCTT
12601	ACCGGGTTGG	ACTCAAGACG	ATAGTTACCG	GATAAGGCGC	AGCGGTCGGG	CTGAACGGGG
12661	GGTTCGTGCA	CACAGCCCAG	CTTGGAGCGA	ACGACCTACA	CCGAAGTGA	ATACCTACAG
12721	CGTGAGCTAT	GAGAAAGCGC	CACGCTTCCC	GAAGGGAGAA	AGGCGGACAG	GTATCCGGTA
12781	AGCGGCAGGG	TCGGAACAGG	AGAGCGCACG	AGGGAGCTTC	CAGGGGAAAA	CGCCTGGTAT
12841	CTTTATAGTC	CTGTGCGGTT	TCGCCACCTC	TGACTTGAGC	GTGATTTTTT	GTGATGCTCG

12901	TCAGGGGGGC	GGAGCCTATG	GAAAAACGCC	AGCAACGCGG	CCTTTTTACG	GTTCTTGCC
12961	TTTTGCTGGC	CTTTTGCTCA	CATGTCTTTT	CCTGCGTTAT	CCCCTGATTC	TGTGGATAAC
13021	CGTATTACCG	CCTTTGAGTG	AGCTGATACC	GCTCGCCGCA	GCCGAACGAC	CGAGCGCAGC
13081	GAGTCAGTGA	GCGAGGAAGC	GGAAGAGCGC	CTGATGCGGT	ATTTTCTCCT	TACGCATCTG
13141	TGCGGTATTT	CACACCGCAT	ATGGTGCAC	CTCAGTACAA	TCTGCTCTGA	TGCCGCATAG
13201	TTAAGCCAGT	ATACACTCCG	CTATCGCTAC	GTGACTGGGT	CATGGCTGCG	CCCCGACACC
13261	CGCCAACACC	CGCTGACGCG	CCCTGACGGG	CTTGTCTGCT	CCCGGCATCC	GCTTACAGAC
13321	AAGCTGTGAC	CGTCTCCGGG	AGCTGCATGT	GTCAGAGGTT	TTCACCGTCA	TCACCGAAAC
13381	GCGCGAGGCA	GGGTGCCTTG	ATGTGGGCGC	CGGCGGTCGA	GTGGCGACGG	CGCGGCTTGT
13441	CGCGCCCTG	GTAGATTGCC	TGGCCGTAGG	CCAGCCATTT	TTGAGCGGCC	AGCGGCCGCG
13501	ATAGGCCGAC	GCGAAGCGGC	GGGGCGTAGG	GAGCGCAGCG	ACCGAAGGGT	AGGCGCTTTT
13561	TGCAGCTCTT	CGGCTGTGCG	CTGGCCAGAC	AGTTATGCAC	AGGCCAGGCG	GGTTTTAAGA
13621	GTTTTAATAA	GTTTTAAAGA	GTTTTAGGCG	GAAAAATCGC	CTTTTTTCTC	TTTTATATCA
13681	GTCACTTACA	TGTGTGACCG	GTTCCCAATG	TACGGCTTTG	GGTTCCCAAT	GTACGGGTTC
13741	CGGTTCCCAA	TGTACGGCTT	TGGGTTCCTA	ATGTACGTGC	TATCCACAGG	AAACAGACCT
13801	TTTCGACCTT	TTTCCCCTGC	TAGGGCAATT	TGCCCTAGCA	TCTGCTCCGT	ACATTAGGAA
13861	CCGGCGGATG	CTTCGCCCTC	GATCAGGTTG	CGGTAGCGCA	TGACTAGGAT	CGGGCCAGCC
13921	TGCCCCGCCT	CCTCCTTCAA	ATCGTACTCC	GGCAGGTCAT	TTGACCCGAT	CAGCTTGCGC
13981	ACGGTGAAAC	AGAACTTCTT	GAACCTCTCC	GCGCTGCCAC	TGCGTTCGTA	GATCGTCTTG
14041	AACAACCATC	TGGCTTCTGC	CTTGCTGCG	GCGCGGCGTG	CCAGGCGGTA	GAGAAAACGG
14101	CCGATGCCGG	GATCGATCAA	AAAGTAATCG	GGGTGAACCG	TCAGCACGTC	CGGGTCTTTC
14161	CCTTCTGTGA	TCTCGCGGTA	CATCCAATCA	GCTAGCTCGA	TCTCGATGTA	CTCCGGCCGC
14221	CCGGTTTTCG	TCTTTACGAT	CTTGTAGCGG	CTAATCAAGG	CTTACCCTC	GGATACCGTC
14281	ACCAGGCGGC	CGTTCTTGGC	CTTCTTCGTA	CGCTGCATGG	CAACGTGCGT	GGTGTTTAAC
14341	CGAATGCAGG	TTTCTACCAG	GTCGTCTTTC	TGCTTTCCGC	CATCGGCTCG	CCGGCAGAAC
14401	TTGAGTACGT	CCGCAACGTG	TGGACGGAAC	ACGCGGCCGG	GCTTGTCTCC	CTTCCCTTCC
14461	CGGTATCGGT	TCATGGATTC	GGTTAGATGG	GAAACCGCCA	TCAGTACCAG	GTCTGAATCC
14521	CACACACTGG	CCATGCCGGC	CGGCCCTGCG	GAAACCTCTA	CGTGCCCGTC	TGGAAGCTCG
14581	TAGCGGATCA	CCTCGCCAGC	TCGTGCGTCA	CGCTTCGACA	GACGGAAAAC	GGCCACGTCC
14641	ATGATGCTGC	GACTATCGCG	GGTGCCACG	TCATAGAGCA	TCGGAACGAA	AAAATCTGGT
14701	TGCTCGTCGC	CCTTGGGCGG	CTTCTAATC	GACGGCGCAC	CGGCTGCCGG	CGGTTGCCGG
14761	GATTCTTTGC	GGATTGATC	AGCGGCCGCT	TGCCACGATT	CACCGGGGCG	TGCTTCTGCC
14821	TCGATGCGTT	GCCGCTGGGC	GGCCTGCGCG	GCCTTCAACT	TCTCCACCAG	GTATCACCCC
14881	AGCGCCGCGC	CGATTGTGAC	CGGGCCGGAT	GGTTTGCGAC	CGCTCACGCC	GATTCTTCGG
14941	GCTTGGGGGT	TCCAGTGCCA	TTGCAGGGCC	GGCAGGCAAC	CCAGCCGCTT	ACGCCCTGGC
15001	AACCGCCCGT	TCCTCCACAC	ATGGGGCATT	CCACGGCGTC	GGTGCCTGGT	TGTTCTTGAT
15061	TTTCCATGCC	GCCTCCTTTA	GCCGCTAAAA	TTTATCTACT	CATTTATTCA	TTTGCTCATT
15121	TACTCTGGTA	GCTGCGCGAT	GTATTCAGAT	AGCAGCTCGG	TAATGGTCTT	GCCTTGCGGT
15181	ACCGCGTACA	TCTTCAGCTT	GGTGTGATCC	TCCGCCGGCA	ACTGAAAGTT	GACCCGCTTC
15241	ATGGCTGGCG	TGTCTGCCAG	GCTGGCCAAC	GTTCAGCCTT	TGCTGCTGCG	TGCGCTCGGA
15301	CGGCCGGCAC	TTAGCGTGTT	TGTGCTTTTG	CTCATTTTCT	CTTTACCTCA	TTAACTCAAA
15361	TGAGTTTTGA	TTTAATTTCA	GCGGCCAGCG	CCTGGACCTC	GCGGGCAGCG	TCGCCCTCGG
15421	GTTCTGATTC	AAGAACGGTT	GTGCCGGCGG	CGGCAGTGCC	TGGGTAGCTC	ACGCGCTGCG
15481	TGATACGGGA	CTCAAGAATG	GGCAGCTCGT	ACCCGGCCAG	CGCCTCGGCA	ACCTCACCGC
15541	CGATGCGCGT	GCCTTTGATC	GCCCCGACAC	CGACAAAGGC	CGCTTGATAG	CTTCCATCCG
15601	TGACCTCAAT	GCGCTGCTTA	ACCAGCTCCA	CCAGGTGCGC	GGTGGCCCAT	ATGTCGTAAG
15661	GGCTTGCGTG	CACCGGAATC	AGCACGAAGT	CGGCTGCCTT	GATCGCGGAC	ACAGCCAAGT
15721	CCGCCGCCCTG	GGGCGCTCCG	TCGATCACTA	CGAAGTCGCG	CCGGCCGATG	GCCTTCACGT
15781	CGCGGTCAAT	CGTCGGGCGG	TCGATGCCGA	CAACGGTTAG	CGGTTGATCT	TCCCGCACGG
15841	CCGCCCAATC	GCGGGCACTG	CCCTGGGGAT	CGGAATCGAC	TAACAGAAAC	TCGGCCCCGG
15901	CGAGTTGCAG	GGCGCGGGCT	AGATGGGTTG	CGATGGTCGT	CTTGCCTGAC	CCGCCCTTCT
15961	GGTTAAGTAC	AGCGATAACC	TTTATGCGTT	CCCCTTGCGT	ATTTGTTTAT	TTACTCATCG

16021	CATCATATAC	GCAGCGACCG	CATGACGCAA	GCTGTTTTAC	TCAAATACAC	ATCACCTTTT
16081	TAGACGGCGG	CGCTCGGTTT	CTTCAGCGGC	CAAGCTGGCC	GGCCAGGCCG	CCAGCTTGGC
16141	ATCAGACAAA	CCGGCCAGGA	TTTCATGCAG	CCGCACGGTT	GAGACGTGCG	CGGGCGGCTC
16201	GAACACGTAC	CCGGCCGCGA	TCATCTCCGC	CTCGATCTCT	TCGGTAATGA	AAAACGGTTC
16261	GTCCTGGCCG	TCCTGGTGCG	GTTTCATGCT	TGTTCTCTTT	GGCGTTCATT	CTCGGCGGCC
16321	GCCAGGGCGT	CGGCCTCGGT	CAATGCGTCC	TCACGGAAGG	CACCGCGCCG	CCTGGCCTCG
16381	GTGGGCGTCA	CTTCCTCGCT	GCGCTCAAGT	GCGCGGTACA	GGGTCGAGCG	ATGCACGCCA
16441	AGCAGTGCAG	CCGCCTCTTT	CACGGTGCGG	CCTTCCTGGT	CGATCAGCTC	GCGGGCGTGC
16501	GCGATCTGTG	CCGGGGTGAG	GGTAGGGCGG	GGGCCAAACT	TCACGCCTCG	GGCCTTGGCG
16561	GCCTCGCGCC	CGCTCCGGGT	GCGGTCGATG	ATTAGGGAAC	GCTCGAACTC	GGCAATGCCG
16621	GCGAACACGG	TCAACACCAT	GCGGCCGGCC	GGCGTGGTGG	TGTCGGCCCA	CGGCTCTGCC
16681	AGGCTACGCA	GGCCCGCGCC	GGCCTCCTGG	ATGCGCTCGG	CAATGTCCAG	TAGGTGCGGG
16741	GTGCTGCGGG	CCAGGCGGTC	TAGCCTGGTC	ACTGTCACAA	CGTCGCCAGG	GCGTAGGTGG
16801	TCAAGCATCC	TGGCCAGCTC	CGGGCGGTGC	CGCCTGGTGC	CGGTGATCTT	CTCGGAAAAC
16861	AGCTTGGTGC	AGCCGGCCGC	GTGCAGTTTC	GCCCGTTGGT	TGGTCAAGTC	CTGGTCGTGC
16921	GTGCTGACGC	GGGCATAGCC	CAGCAGGCCA	GCGGCGGCGC	TCTTGTTTCAT	GGCGTAATGT
16981	CTCCGGTTCT	AGTCGCAAGT	ATTCTACTTT	ATGCGACTAA	AACACGCGAC	AAGAAAACGC
17041	CAGGAAAAGG	GCAGGGCGGC	AGCCTGTGCG	GTAACCTTAGG	ACTTGTGCGA	CATGTCGTTT
17101	TCAGAAGACG	GCTGCACTGA	ACGTCAGAAG	CCGACTGCAC	TATAGCAGCG	GAGGGGTTGG
17161	ATCAAAGTAC	TTTGATCCCG	AGGGGAACCC	TGTGGTTGGC	ATGCACATAC	AAATGGACGA
17221	ACGGATAAAC	CTTTTCACGC	CCTTTTAAAT	ATCCGATTAT	TCTAA	

EXAMPLES

[00234] All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the present disclosure pertains. All patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference.

[00235] The publications discussed throughout are provided solely for their disclosure before the filing date of the present application. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

[00236] The following examples are included to demonstrate the disclosure. It should be appreciated by those of skill in the art that the techniques disclosed in the following examples represent techniques discovered by the inventors to function well in the practice of the disclosure. Those of skill in the art should, however, in light of the present disclosure, appreciate that many changes could be made in the disclosure and still obtain a like or similar result without departing from the spirit and scope of the

disclosure, therefore all matter set forth is to be interpreted as illustrative and not in a limiting sense.

Example 1. Combination of YHB and elf3 alleles restricts photomorphogenesis and flowering variation in response to environmental cues

[00237] Plants are very sensitive to their environment and respond to changes in light and temperature to optimize their growth unlike animals, they demonstrate developmental plasticity. Developmental plasticity is advantageous in natural conditions (where resources and environmental stresses vary across seasons and location) but is disadvantageous in modern crop monoculture where fertilizers, pesticides, irrigation, etc., can be provided. Climate change offers additional challenges, with more varied weather and increasing temperatures disrupting plant development. Importantly, flowering in many crops is dependent on day length and highly influenced by ambient temperatures. This is disruptive to farmers who can only harvest at defined times of the year.

[00238] One goal of modern breeding programs is to increase the uniformity of crops so that harvesting time is more predictable and quality is consistent. This is true for intensive, precision outdoor farming and Total Controlled Environment Agriculture (TCEA, or vertical farming). Candidate targets include genes encoding for photoreceptors and thermoreceptors (proteins responsive to light and/or temperature) and genes that disrupt the circadian clock (an endogenous molecular timekeeper that governs responses to environmental signals at different times of day). As the circadian system allows measurement of daylength, disruption of the clock should produce day-neutral plants that flower regardless of season.

[00239] Using the model plant *Arabidopsis thaliana*, two genetic traits were combined to limit plants' response to environmental signals; disruption of EARLY FLOWERING3 (ELF3) and the addition of the constitutively-active Y276H allele of the photoreceptor phytochromeB (which is referred to herein as YHB). Loss of ELF3 accelerates flowering, disrupts circadian rhythms and potentially impairs temperature

signaling, but induces an etiolated phenotype (that produces poor yield). YHB also induces earlier flowering and provides a consistent light signal regardless of irradiance, reducing etiolation. However, the combination of these two alleles has yet to be exploited.

[00240] Crucially, the inventors show that the combination of these two alleles [YHB(*elf3*)] has advantages over each allele individually. YHB(*elf3*) plants are not etiolated and flower earlier (so are good candidates for vegetative crops in TCEA). YHB(*elf3*) plants have reduced cellular elongation response to increasing temperature, which will reduce listing in the field. YHB(*elf3*) plants also flower at the same time regardless of day length- suggesting that crops can be developed that will flower consistently regardless of differences in day length at varied latitudes or in the face of climate change increasing temperatures and disrupting weather patterns. Similar traits can be exploited in TCEA to limit energy costs incurred when growing plants under artificial lighting, for example, shifted lighting regimes can be used to avoid peak energy supply rates or grow multiple species under a single lighting condition. Many secondary metabolite pathways are regulated by the clock, therefore valuable product production could be increased by “locking” the oscillator into an “on” position.

[00241] *Results.* Loss-of-function and over-expression analysis suggest that phytochrome- and ELF3-signaling pathways are genetically separable, although multiple lines of evidence demonstrate a functional interaction between these signaling pathways. To further characterize this relationship, the *YHB* allele was transformed into an *elf3-2* background (**FIG. 3A**). Importantly, *YHB* was sufficient to induce photomorphogenesis in *PHYB::YHB(elf3)* seedlings grown in constant darkness, with the degree of photomorphogenesis observed correlating with the expression level of *YHB* (**FIGs. 3B and 7A**). Similar data were obtained using independently transformed 35S::*YHB (phyb-9 elf3-1)* seedlings (*phyb-9*; loss of function allele of *PHYB*; SEQ ID NO: 9. Produces truncated protein comprising SEQ ID NO: 10). These data agree with previous work suggesting that ELF3 and phyB make additive contributions to photomorphogenesis.

[00242] Seedling hypocotyl growth is exquisitely sensitive to light and temperature. As *YHB (elf3-2)* seedlings retained a constitutively photomorphogenetic (cop) phenotype when grown in constant darkness (**FIGs. 3B-C**) it was tested whether these seedlings were able to regulate their development in response to environmental factors, including daylength and temperature. Hypocotyl growth is negatively correlated with photoperiod in wild-type seedlings (**FIG. 3C**). Consistent with data gathered from etiolated seedlings (**FIGs. 3B-3C**), *YHB (elf3)* hypocotyls were not significantly extended in either long-day or short-day conditions (**FIG. 3C**). These data suggest that *YHB (elf3)* seedlings are not able to adjust their development in response to varied light conditions.

[00243] Phytochromes and ELF3 have both been reported to serve as integrators of temperature signals, and therefore, how *YHB (elf3)* seedling growth was affected by growth in different ambient temperatures was examined (**FIG. 3D**). *elf3-2* responded in a similar fashion to wild type in the conditions used herein, while *YHB* seedlings failed to demonstrate hypocotyl extension when grown at 27°C, in line with previous reports (**FIG. 3D**). However, it was noted that the hypocotyls of *YHB (elf3)* seedlings were unresponsive to temperature (**FIG. 3D**). These data demonstrate that constitutively active phyB is sufficient to limit heat-induced hypocotyl elongation even in the absence of ELF3.

[00244] Next, the adult phenotypes of the *YHB (elf3)* plants (**FIGs. 3E and 3F**) were assessed. Following growth in short day conditions *YHB (elf3)* lines had a compact rosette comparable to *YHB* (**FIG. 3E**), demonstrating that ELF3 is not necessary for phyB-mediated changes in adult morphology (as in seedlings; **FIGs. 3B-3D**). In addition, the developmental time to flowering in short days was greatly accelerated in *YHB*, *elf3-2*, and *YHB (elf3)* plants despite the differences in rosette morphology observed (**FIGs 3E-3F**). In long days (16:8), flowering time was accelerated in *elf3-2* seedlings compared to wild type, although no differences in flowering time were observed between *elf3-2* and *YHB(elf3)* plants (**FIG. 3F**).

[00245] Importantly, constitutively expressed *YHB (elf3)* plants also showed strongly reduced plant elongation responses to daylength (**FIG. 4A**) and temperature (**FIG. 4B**). Further, *YHB (elf3)* plants lacked circadian rhythms, flattening internal metabolic cycles under constant conditions either when expressed from its own promoter (**FIG. 5A**) or when constitutively expressed (**FIG. 5B**).

[00246] *Discussion.* Plants are remarkably sensitive to environmental signals, adapting their growth and development to optimize survival and fecundity in the prevailing conditions. The flexibility of plant development greatly promotes survival in natural conditions but is sub-optimal for commercial farming where growth and harvesting schedules must be adjusted to match crop progression. It was sought to limit plants' inherent developmental plasticity by manipulating the *PHYTOCHROME B* (*PHYB*) and *EARLY FLOWERING3* (*ELF3*) loci within the *Arabidopsis* genome. It was demonstrated that these plants are unresponsive to environmental stimuli yet retain beneficial agronomic phenotypes that are lost in other manipulations.

Example 2. Combination of YHB and elf3 alleles restricts photomorphogenesis and flowering variation in response to environmental cues

[00247] A pennycress *YHB (elf3)* double mutant was also generated. The response of the double mutant plants to light and temperature and presence or absence of circadian rhythms is investigated. Pennycress *YHB (elf3)* double mutants show strongly reduced plant elongation responses to daylength and temperature. Further, *YHB (elf3)* pennycress lack circadian rhythms, flattening internal metabolic cycles.

Example 3. Characterization of plasticity of YHBelf3 plants

[00248] Plants demonstrate developmental plasticity which enables adaptation to prevailing environmental cues. Although valuable to maximize survival in nature, developmental plasticity restricts modern agricultural practices since economically important traits including vegetative growth and flowering time vary dependent upon local environmental conditions, preventing accurate prediction of harvesting times. In

this study, it was sought to restrict developmental plasticity through manipulation of two signaling systems that govern these responses. Constitutive activation of the plant photoreceptor phyB, along with disruption of the circadian system created plants that are less responsive to environmental signals, enabling the creation of crops with uniform flowering time and productivity. This has significant implications for future agriculture in both open fields and controlled environments.

[00249] It was first hypothesized that developmental plasticity in plants could be restricted by disrupting signaling pathways that modulate plant development in response to environmental signals. Plants respond to light and temperature signals differentially dependent upon time of day, utilizing photo- and thermo-sensors in combination with the circadian system which provides an internal timing reference to relative to dawn and dusk. A suite of photoreceptors including phytochromes, cryptochromes, zeitlupe (ZTL), and UVR8 each integrate light signals into the circadian clock. Photoreceptors integrate with the circadian system at multiple levels, with phytochromes physically interacting with EARLY FLOWERING3 (ELF3), a gene which is essential to maintain circadian rhythms in constant light. Both phyB and ELF3 have been shown to be responsive to temperature in addition to their roles in photoperception and the circadian system. Accordingly, an aim of this study was to determine whether manipulation of these two proteins could and would be sufficient to restrict developmental plasticity.

Phytochrome drives circadian rhythms via EARLY FLOWERING3

[00250] Loss-of-function and over-expression analysis suggest that phytochrome- and ELF3-signaling pathways are genetically separable, although multiple lines of evidence demonstrate a functional interaction between these signaling pathways. To further characterize this relationship a *PHYB* promoter driven *YHB* allele of *PhyB* was transformed into an *elf3-2* background or a constitutively expressed YHB (35S::YHB) was transformed into an *elf3-1 phyb-9* mutant background (**FIG. 3-5**) Since phyB and ELF3 physically interact, it was tested whether ELF3 is necessary for phyB signaling

into the circadian system (**FIG. 5A-5B**). Neither *PHYB::YHB* (*elf3-2*) nor *35S::YHB* (*elf3-1 phyb-9*) lines were able to maintain circadian rhythms of *CCA1*-driven bioluminescence in constant darkness, with only 15% of *YHB elf3-2* lines being assessed as rhythmic (**FIG. 5A-5B**). Subsequent qRT-PCR analysis was consistent with the bioluminescence data, with both *CCA1* and its orthologue *LATE ELONGATED HYPOCOTYL* (*LHY*) being damped in *YHBelf3* seedlings compared to *YHB* plants (**FIGs. 6G-6H**). By contrast, it was noted that clock genes expressed later in the day, including *GIGANTEA* and *PRR9*, were elevated in *elf3* and *YHBelf3* lines compared to wild-type and *YHB* controls (**FIGs. 6E-6F**). Despite the interaction between *phyB* and *ELF3*, not all genomic regions occupied by *phyB* are also bound by *ELF3* (**FIG. 8A-B and Table 1**). In contrast to *CCA1* and *LHY* (which are bound by *phyB* only), *GIGANTEA* and *PRR9* are bound by both *phyB* and *ELF3* (**FIG. 8B**). This data suggest that the role of *ELF3* as a transcriptional repressor is epistatic to *phyB* function in these cases (**FIGs. 6E-F and FIGs. 8A-B and Table 1**).

Table 1

Genes bound by;		
PHYB	ELF3	PHYB and ELF3
CCA1	ELF3	PRR9
LHY		PRR7
RVE6		GI
PRR5		LNK1
TOC1		
TCP21		
LUX		
ELF4		
LNK2		
TIC		

[00251] The luciferase and bioluminescence data suggest that the clock becomes arrhythmic in constant darkness in *YHBelf3* lines (**FIGs. 5A-B, 6E-H and FIGs 7C-D**). This observed difference in expression after loss of rhythmicity was further assessed in all 29 core circadian clock genes using RNA sequencing (RNAseq; **FIGs. 6A-B**). To this end, plants were sampled after 48 hours of dark exposure at respective dusk (ZT60), a point at which wild type seedlings were assumed to have become arrhythmic and would therefore have relatively stable levels of circadian-controlled transcript abundance. Transcript abundance in wild type seedlings was used as a baseline to assess differential expression of core circadian clock genes in *YHB*, *YHB(elf3-2)* and *elf3-2* seedlings. Fold change abundance of each gene was presented as a heat map (**FIG. 6A**) showing that more circadian genes are differentially expressed in *YHB(elf3-2)* seedlings than in *YHB* or *elf3-2* seedlings, relative to wild type. The most highly differentially expressed genes ($\log_2FC > 1.0$ or < -1.0) are highlighted in **FIG. 6A-B**, showing that 11 of the 29 core clock genes are highly differentially expressed in *YHB(elf3-2)* relative to wild type, while only 7 genes are highly differentially expressed in *elf3-2* and 5 in *YHB*. Of these highly differentially expressed genes, only *ELF4* is highly differentially expressed in all three mutants. Additionally, the overexpression of *ELF4* is stronger in *YHB(elf3-2)* than in *YHB* or *elf3-2* (**FIG. 6A**). *RVE4* and *PRR5* are upregulated to a similar degree in both *YHB* and *YHB(elf3-2)* but not highly differentially expressed in *elf3-2*. *GI*, *PRR9* and *BOA* are all highly upregulated and *CCA1* and *LHY* are highly downregulated in both *YHB(elf3-2)* and *elf3-2* but are not highly differentially expressed in *YHB* seedlings at ZT60 in the dark. Notably, *RVE8* is highly upregulated in *YHB* and highly downregulated in *elf3-2* but not highly differentially expressed in *YHB(elf3-2)* seedlings, suggesting that regulation of *RVE8* by phyB and ELF3 acts via distinct, opposing mechanisms.

ELF3 is not required for *YHB* plants to initiate photomorphogenesis in the dark.

[00252] After observing that *YHB* seedlings require ELF3 to maintain circadian function under constant darkness, it was examined whether *YHBelf3* seedlings retained

the constitutively photomorphogenic phenotype of *YHB* seedlings. In 5 day old seedlings grown under constant darkness (**FIG. 3B-C, 10A**), *YHB* and *YHB(elf3-2)* plants exhibited significantly shorter hypocotyls ($p < 0.0005$) and more uniform growth compared to wild type, whereas *elf3-2* seedlings are significantly longer ($p < 0.0001$). The average hypocotyl length of *YHB(elf3-2)* plants was comparable to *YHB* plants ($p = 0.2864$), while the average hypocotyl length of *elf3-2* mutants was significantly longer than all other genotypes ($p < 0.0001$).

[00253] To further address how the effects of *YHB* and *ELF3* influence photomorphogenesis, differential expression of photomorphogenesis associated genes was analyzed (list of 115 photomorphogenesis or photomorphogenesis associated genes was taken from TAIR a arabidopsis.org) in the RNAseq dataset obtained as described herein above of seedlings sampled at dusk after 48 hours of constant darkness. The fold change expression of the 36 photomorphogenesis associated genes which were highly differentially expressed ($\log_2FC > 1.0$ or < -1.0) in at least one mutant genotype relative to wild type is shown as a heatmap in **FIG. 6C**. The frequency of these genes being highly differentially expressed in *YHB*, *YHB(elf3-2)* and/or *elf3-2* respectively is presented as a venn diagram in **FIG. 6D**, which showed that 4 genes in *elf3-2* mutants experienced at least ± 1.0 $\log_2$ fold change in transcript abundance relative to wild type, while *YHB* and *YHB(elf3-2)* mutants had a respective total of 22 or 25 highly differentially expressed genes. Of these genes, *ASG4* and *ATH1* are both highly upregulated in all three mutants, while *HYH* and *STH* are both highly upregulated in *YHB* and *YHB(elf3-2)* but highly downregulated in *elf3-2*. No other photomorphogenesis associated genes are highly differentially expressed in either *YHB* and *elf3-2* or *YHBelf3-2* and *elf3-2*, but 19 genes are co-differentially expressed in *YHB* and *YHB(elf3-2)*. These data suggest that disruption of *ELF3* has comparatively little effect upon *YHB*-regulated photomorphogenesis genes in contrast to the essential role for *ELF3* in clock function.

***YHBelf3* seedlings are less responsive to varied light and temperature conditions**

[00254] Since the *YHBelf3* seedlings lack circadian rhythms yet demonstrate constitutive photomorphogenesis, how these plants responded to daily patterns of environmental change was of interest (**FIGs. 9, 10,11**). Each of the genotypes retained daily patterns of *CCA1::LUC2* bioluminescence in driven light:dark cycles, with this rhythmicity lost in *elf3-2* and *YHBelf3* seedlings within 24 hours of transfer to constant white light (**FIG. 9A**). It was interesting to note that in contrast to previous reports under monochromatic red light, *YHB* seedlings had an extended circadian period under these conditions (**FIG. 9A**). A phase response curve was next completed to establish whether *YHBelf3* lines were truly arrhythmic in constant light (like *elf3*) or whether the lack of bioluminescence rhythms was masking an underlying oscillation (**FIG. 11A**). Seedlings were held in constant light for different periods of time and then released into constant darkness to assess the new phase imposed upon circadian the circadian system. In contrast to wild type and *YHB* seedlings, which demonstrated circadian control of *CCA1::LUC* phasing following the transfer into constant darkness, both *elf3* and *YHBelf3* seedlings displayed a linear response to the release into constant darkness (**FIG. 11A**). These data reiterate that *ELF3* is essential for maintaining circadian rhythms in constant light, although daily rhythms are maintained in *elf3* and *YHBelf3* seedlings in driven conditions.

[00255] Next, how *YHBelf3* seedlings responded to varied light intensity during the photoperiod was examined (**FIGs. 9B and 9C**). In 'square wave' conditions, with lights either on or off, each of the genotypes was able to accurately anticipate dawn, with *CCA1::LUC* activity peaking at dawn in each case (**FIG. 9B**). In variable light conditions (**FIG. 9C**), all lines displayed a much weaker anticipation of dawn with peak *CCA1*-driven bioluminescence not being reached until hours after the onset of light. Under more varied lighting conditions, with low light at dawn being followed by an increase in fluence rate later in the day, it was found that *elf3-2* and *YHBelf3-2* seedlings demonstrated a peak in bioluminescence shortly after dawn, whereas wild-type and *YHB* seedlings peaked later in the morning (**FIG. 9C**). *elf3-2* and *YHB(elf3-2)* mutants displayed peak *CCA1*-driven luciferase expression on the examined day at around 3

hours after dawn (27 hours after the start of imaging), before wild type and *YHB* lines which peaked at around 4 hours after dawn (28 hours after the start of imaging). These differences between 'square wave' and 'varied' light conditions likely represent the contribution of metabolic dawn to circadian timing.

[00256] Since phyB signaling is responsive to temperature it was next assessed whether the plant circadian system was differentially sensitive to light at different ambient temperatures (**FIGs. 11B-11E, 12A-D**). It was found that the circadian system was unresponsive to light at 12°C, although responses to fluence rate were retained at 17°C, 22°C, and 27°C. It was also interesting to note that the *YHB* circadian phenotype under constant white light was dependent upon both light and temperature; the extension of circadian period in *YHB* lines was only observed at higher fluence rates and temperatures (**FIGs. 11B-11E, 12A-D**). These data are consistent with *YHB* seedlings being less responsive to light and temperature.

***YHBelf3* flower early regardless of daylength**

[00257] The combination of *YHB* and *elf3* alleles decouples the circadian system from photomorphogenesis, although *YHBelf3* plants retain reduced daily patterns of gene expression when grown in light:dark cycles (**FIGs 3B-F, 4A-B, 5A-b, 6A-H, 7C-D**). It was therefore of interest how the genetic manipulations described herein affected developmental traits in varied environmental conditions (**FIGs. 9A-C, 10A-H, 11B-E, 12A-D**). As anticipated, *YHBelf3* seedlings retained a short hypocotyl phenotype regardless of the light condition utilized for growth (**FIG. 3B-D, 4A-B, 10A**). Similarly, *YHBelf3* hypocotyl growth was unaffected by temperature, with no significant difference in hypocotyl growth between 12 and 27°C (**FIG. 3D**).

[00258] It was next examined how *YHB* and *elf3* manipulations affected flowering time. *YHB* and *elf3* plants flowered earlier than wild type in all conditions tested (under either long days or short days, as well as under elevated temperatures, **FIGs. 3F, 10D, 10E**). Differences in flowering time were especially apparent under short day conditions, where flowering was substantially delayed in wild-type plants. *YHB* plants

flowered slightly later at 27°C compared to 22°C (**FIG. 10E**). *YHBelf3* seedlings retained the early flowering phenotype of *YHB* and *elf3* lines regardless of condition (**FIGs. 3F, 10D, 10E**). Despite these differences in flowering time, it was interesting to note that there was no difference in growth rate between genotypes in long-day conditions (**FIG. 10G**). In short-day conditions, *YHBelf3* rosettes expand at a slower rate than the other genotypes ($p < 0.01$, **FIG. 10H**), although wild type plants are not significantly bigger than the other genotypes until later in their lifecycle as they continue to grow due to the absence of flowering.

Conclusions

[00259] The combination of *YHB* and *elf3* alleles decouples the circadian system from plant photoperception and produces plants less responsive to environmental signals. *YHBelf3* plants retain some molecular and developmental responses to light and temperature, although *YHBelf3* plants retain consistently earlier flowering times without inhibiting vegetative growth.

Example 4. Comparison of plant growth responses

[00260] Wild-type pennycress is compared with *elf3* gene mutant, *YHB*-transgene containing, and *elf3 YHB* transgenic pennycress lines for their growth in response to a variety of photoperiod conditions [e.g., short days (8 hours light/ 16 hours darkness), day-neutral (12 hours light/ 12 hours darkness), or long days (16 hours light/ 8 hours darkness) during juvenile and adult stages. The *YHB* and *elf3 YHB* transgenic pennycress lines show a reduced response to changing photoperiod conditions compared to the wild type, as it was demonstrated in *Arabidopsis thaliana* in the Examples herein above.

[00261] The above lines' growth responses to increased ambient temperature conditions (between 20-30 degrees Celsius) are also measured. The *YHB* and *elf3 YHB* transgenic pennycress lines also show a reduced elongation response to increases in temperature compared to wild type, as it was shown in *Arabidopsis thaliana* in the

examples herein above. Combining the *elf3* mutation with YHB shows reduced plasticity in growth to changing environment (light or temperature) conditions, producing a more uniform growth pattern regardless of day length or temperature.

Example 5. Comparison of plant flowering responses

[00262] Wild-type pennycress with *elf3* gene mutant, YHB-transgene containing, and *elf3* YHB transgenic pennycress lines are compared for their flowering in response to a variety of photoperiod conditions [e.g., short days (8 hours light/ 16 hours darkness), day-neutral (12 hours light/ 12 hours darkness), or long days (16 hours light/ 8 hours darkness)]. The *elf3* mutant and *elf3* YHB transgenic pennycress lines show a shorter time to flowering when compared to wild type or YHB transgenic lines, as it was shown in *Arabidopsis thaliana* in the examples herein above.

[00263] Time to flowering under increased ambient temperature (20-30 degrees Celsius) is also measured. As with above, the *elf3* mutant and *elf3* YHB transgenic pennycress lines show a reduced response to increasing temperature and flower at similar times regardless of temperature when compared to wild type, as it was shown in *Arabidopsis thaliana* in the examples herein above. Specifically combining the *elf3* mutation with YHB shows reduced plasticity in flowering to changing environment (light or temperature) conditions, flowering at similar days after planting regardless of day length or temperature.

Example 6. Comparison of diurnal metabolome

[00264] The clock arrhythmia produced by the *elf3* mutation, combined with constant light signaling from the constitutive YHB transgene, reduces the daily oscillations in gene expression and the resulting proteins, decreasing the variation in the daily production of metabolites. The metabolomes of wild-type and *elf3* YHB transgenic pennycress lines are measured over a 48-hour time course using mass spectrometry-based metabolome profiling. Daily rhythms of hundreds of metabolites in the *elf3* YHB transgenic lines are flattened, with metabolites now clamped at constitutively high,

intermediate, or low levels. The reduced dynamics of protein and metabolite production in the *elf3 YHB* transgenic lines makes it easier to predict and manipulate the production of high-value proteins or metabolites in plants.

CLAIMS

What is claimed is:

1. A modified plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity, comprising:
 - a. a modification of an endogenous polynucleotide sequence encoding a component of the circadian clock; and
 - b. an exogenous polynucleotide sequence encoding an environmental signal sensor;wherein the modification of the endogenous polynucleotide sequence encoding the component of the circadian clock modifies expression of the component of the circadian clock; and
wherein the modification of the endogenous polynucleotide encoding the environmental signal sensor modifies expression of the environmental signal sensor;
and
wherein the modified expression of the component of the circadian clock and of the environmental signal sensor causes the plant to exhibit (i) reduced developmental plasticity in response to changes in environmental conditions during growth and (ii) modified circadian function.
2. The modified plant or part thereof, plant cell, or seed of claim 1, wherein the component of the circadian clock is a component of the evening complex (EC).
3. The modified plant or part thereof, plant cell, or seed of claim 1 or claim 2, wherein the component of the circadian clock is selected from EARLY FLOWERING 3 (ELF3), EARLY FLOWERING 4 (ELF4), LUX ARRHYTHMO (LUX), or any combination thereof.
4. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the component of the circadian clock is an ELF3 protein.

5. The modified plant or part thereof, plant cell, or seed of claim 4, wherein the modification of a polynucleotide encoding the ELF3 protein is a loss-of-function mutation.
6. The modified plant or part thereof, plant cell, or seed of claim 5, wherein the plant is *Arabidopsis thaliana* (*A. thaliana*).
7. The modified plant or part thereof, plant cell, or seed of claim 6, wherein the ELF3 protein comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 2.
8. The modified plant or part thereof, plant cell, or seed of claim 6, wherein the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 1 and an ELF3 loss-of-function mutation comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof.
9. The modified plant or part thereof, plant cell, or seed of claim 5, wherein the modified plant is *Thlaspi arvense* (*T. arvense*).
10. The modified plant or part thereof, plant cell, or seed of claim 9, wherein the ELF3 protein comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 21.
11. The modified plant or part thereof, plant cell, or seed of claim 10, wherein the polynucleotide encoding the ELF3 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20.
12. The modified plant or part thereof, plant cell, or seed of claim 10, wherein the modification of the polynucleotide encoding the ELF3 protein comprises a deletion of

a nucleic acid segment in the polynucleotide encoding the ELF3 protein, wherein the nucleic acid segment comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof.

13. The modified plant or part thereof, plant cell, or seed of claim 10, wherein the modification of the polynucleotide encoding the ELF3 protein comprises a modification introduced by a programmable nucleic acid modification system comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA).
14. The modified plant or part thereof, plant cell, or seed of claim 13, wherein the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or a combination thereof.
15. The modified plant or part thereof, plant cell, or seed of claim 13, wherein an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.
16. The modified plant or part thereof, plant cell, or seed of claim 5, wherein the plant is *Basil*.
17. The modified plant or part thereof, plant cell, or seed of claim 16, wherein the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13.
18. The modified plant or part thereof, plant cell, or seed of claim 17, wherein the modification of the polynucleotide encoding the ELF3 protein comprises a modification introduced by a programmable nucleic acid modification system

comprising a CRISPR/Cas nuclease system, wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA).

19. The modified plant or part thereof, plant cell, or seed of claim 18, wherein the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.
20. The modified plant or part thereof, plant cell, or seed of claim 19, wherein an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.
21. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the environmental signal comprises photoperiod, light intensity and quality, temperature, chemicals, gravity, moisture, biotic or abiotic stress, oxygen and carbon dioxide concentrations, carbohydrate availability, or any combination thereof.
22. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the environmental signal sensor is a photoreceptor, temperature sensor, CO₂ sensor, O₂ sensor, ethylene sensor, gravitropic sensor, or any combination thereof.
23. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the environmental signal sensor is a photoreceptor.
24. The modified plant or part thereof, plant cell, or seed of claim 23, wherein the photoreceptor is a phytochrome; a cryptochrome, a phototropin, an F-box containing Flavin binding proteins; UVR8, or any combination thereof.
25. The modified plant or part thereof, plant cell, or seed of claim 23 or 24, wherein the photoreceptor is a phytochrome photoreceptor.

26. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the polynucleotide encoding an environmental signal sensor encodes a phytochrome B photoreceptor.
27. The modified plant or part thereof, plant cell, or seed of claim 26, wherein the phytochrome B photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 6 or SEQ ID NO: 28.
28. The modified plant or part thereof, plant cell, or seed of claim 27, wherein the polynucleotide encoding the phytochrome B photoreceptor comprises least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 5 or SEQ ID NO: 28.
29. The modified plant or part thereof, plant cell, or seed of claim 26, wherein the phytochrome B photoreceptor is overexpressed, constitutively expressed, or constitutively active.
30. The modified plant or part thereof, plant cell, or seed of claim 29, wherein the modification of a polynucleotide encoding a phyB photoreceptor encodes a constitutively active phyB photoreceptor.
31. The modified plant or part thereof, plant cell, or seed of claim 30, wherein the phytochrome B photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.
32. The modified plant or part thereof, plant cell, or seed of claim 30, wherein the polynucleotide encoding the phytochrome B photoreceptor comprises least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof.

33. The modified plant or part thereof, plant cell, or seed of claim 30, wherein the modified plant is *Arabidopsis thaliana* (*A. thaliana*).
34. The modified plant or part thereof, plant cell, or seed of claim 33, wherein the modified *A. thaliana* plant comprises a genetic modification of a polynucleotide encoding PhyB, wherein the polynucleotide comprising the genetic modification encodes a constitutively active PhyB photoreceptor.
35. The modified plant or part thereof, plant cell, or seed of claim 34, wherein constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.
36. The modified plant or part thereof, plant cell, or seed of claim 34, wherein constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or any combination thereof.
37. The modified plant or part thereof, plant cell, or seed of claim 34, wherein constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 12, or both.
38. The modified plant or part thereof, plant cell, or seed of claim 34, wherein the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or both.
39. The modified plant or part thereof, plant cell, or seed of claim 30, wherein the modified plant is *Thlaspi arvensis* (*T. arvensis*).

40. The modified plant or part thereof, plant cell, or seed of claim 39, wherein the modified *T. arvensis* plant comprises a genetic modification of a polynucleotide encoding PhyB, wherein the polynucleotide comprising the genetic modification encodes a constitutively active PhyB photoreceptor.
41. The modified plant or part thereof, plant cell, or seed of claim 40, wherein the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 8 SEQ ID NO: 12, SEQ ID NO: 26, or any combination thereof.
42. The modified plant or part thereof, plant cell, or seed of claim 40, wherein the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 25, or SEQ ID NO: 27.
43. The modified plant or part thereof, plant cell, or seed of claim 40, wherein the constitutively active PhyB photoreceptor comprises an amino acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 26.
44. The modified plant or part thereof, plant cell, or seed of claim 40, wherein the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25.
45. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, comprising:
- a. a modification of a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation; and

- b. a modification of a polynucleotide encoding a phyB photoreceptor wherein the polynucleotide encodes a constitutively active PhyB photoreceptor.
46. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the modified plant comprises constitutively inactivated temperature input to the circadian clock and a constitutively activated light input to the circadian clock.
47. The modified plant or part thereof, plant cell, or seed of any of the preceding claims, wherein the modified plant is not etiolated, flowers earlier and consistently regardless of changes in day length and has a reduced cellular elongation response to increasing temperature thereby reducing listing in the field, and any combination thereof.
48. The modified plant or part thereof, plant cell, or seed of claim 1, wherein the modified plant is plant is *A. thaliana* comprising:
- a. a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 3 (*elf3-1*), SEQ ID NO: 4 (*elf3-2*), or a combination thereof; and
 - b. a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or a combination thereof.
49. The modified plant or part thereof, plant cell, or seed of claim 1, wherein the modified plant is plant is *T. arvensis* comprising:
- a. a polynucleotide encoding an ELF3 protein wherein the polynucleotide encoding the ELF3 protein comprises an ELF3 loss-of-function mutation, wherein the polynucleotide comprises a nucleic acid sequence comprising

at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 22, a sequence comprising the AGCGCTA nucleic acid sequence, or a combination thereof; and

- b. a polynucleotide encoding a constitutively active PhyB photoreceptor, wherein the polynucleotide comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with an amino acid sequence of SEQ ID NO: 25.

50. A system for modifying a component of the circadian clock, an environmental signal sensor, or both in a plant or part thereof, plant cell, or seed, the system comprising a nucleic acid construct comprising at least one or both of:

- a. a programmable nucleic acid modification system comprising a targeting nucleic acid sequence targeting a nucleic acid sequence in a polynucleotide sequence encoding a component of the circadian clock; and
- b. an expression construct comprising a promoter operably linked to a polynucleotide encoding a polynucleotide encoding an environmental signal sensor;

wherein (a) introduces a loss of function mutation into the polynucleotide sequence encoding the component of the circadian clock, and

wherein (b) increases expression of the environmental signal sensor, thereby causing the plant to exhibit reduced developmental plasticity in response to changes in environmental conditions during growth and modified circadian function.

51. The system of claim 50, wherein the programmable nucleic acid modification system introduces a loss of function mutation into a polynucleotide encoding an ELF3 protein.

52. The system of claim 51, wherein the programmable nucleic acid modification system comprises a CRISPR/Cas nuclease system comprising a CAS9 protein (dCAS9) and a guide RNA (gRNA).
53. The system of claim 52, wherein the plant is *Thlaspi arvense*.
54. The system of claim 53, wherein the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or both.
55. The system of claim 52, wherein the plant is *Basil*.
56. The system of claim 55, wherein the Cas9 protein is encoded by a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 29 and the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.
57. The system of claim 50, wherein the expression construct comprises a promoter operably linked to a polynucleotide encoding a polynucleotide encoding a PhyB photoreceptor, wherein the expression construct increases expression of PhyB.
58. The system of claim 57, wherein the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a 35S promoter operably linked to a polynucleotide encoding the PhyB photoreceptor and wherein the construct constitutively expresses the PhyB photoreceptor.
59. The system of claim 57, wherein the PhyB photoreceptor is constitutively active.
60. The system of claim 59, wherein the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 24.
61. The system of claim 60, wherein the expression construct comprises a nucleic acid sequence comprising a nucleic acid sequence comprising about 75% or more, at

least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19.

62. One or more expression constructs for modifying a plant or part thereof, plant cell, or seed to exhibit reduced developmental plasticity, the one or more expression constructs comprising at least one or both of:
- a. an expression construct for modifying the expression of a component of the circadian clock; and
 - b. an expression construct for modifying the expression of an environmental signal sensor.
63. The one or more expression constructs of claim 62, wherein (a) comprises a promoter operably linked to a polynucleotide encoding a programmable nucleic acid modification system targeted to a nucleic acid sequence in a polynucleotide encoding a component of the circadian clock.
64. The one or more expression constructs of claim 63, wherein the programmable nucleic acid modification system comprises a CRISPR/Cas nuclease system and wherein the CRISPR/Cas nuclease system comprises a CAS9 protein (dCAS9) and a guide RNA (gRNA).
65. The one or more expression constructs of claim 64, wherein an expression construct expressing the Cas9 protein comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base number 1552 to base number 7881 of SEQ ID NO: 32.
66. The one or more expression constructs of claim 64, wherein the plant is *Thlaspi arvense*.
67. The one or more expression constructs of claim 66, wherein the polynucleotide encoding a component of the circadian clock encodes ELF3 and wherein the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or

- 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 20 and wherein the gRNA comprises a nucleic acid sequence of SEQ ID NO: 30, SEQ ID NO: 31, or both.
68. The one or more expression constructs of claim 66, wherein the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence starting at base 254 to base 1287 of SEQ ID NO: 32.
69. The one or more expression constructs of claim 64, wherein the plant is Basil.
70. The one or more expression constructs of claim 69, wherein the polynucleotide encoding a component of the circadian clock encodes ELF3 and wherein the polynucleotide encoding ELF3 comprises a nucleic acid sequence comprising at least about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 13 and wherein the gRNA comprises a nucleic acid sequence of SEQ ID NOs: 33-36, or any combination thereof.
71. The one or more expression constructs of claim 70, wherein the expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with the gRNA expression construct of SEQ ID NO: 37.
72. The one or more expression constructs of claim 70, wherein an expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 23.
73. The one or more expression constructs of claim 70, wherein an expression construct expressing the gRNA of SEQ ID NOs: 33-36 comprises about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 695 to base 2799 of SEQ ID NO: 37.

74. The one or more expression constructs of claim 62, wherein the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a constitutive expression promoter operably linked to a polynucleotide encoding a PhyB photoreceptor.
75. The one or more expression constructs of claim 74, wherein the expression construct comprising a promoter operably linked to a polynucleotide encoding an environmental signal sensor comprises a 35S promoter operably linked to a polynucleotide encoding a constitutively active PhyB photoreceptor.
76. The one or more expression constructs of claim 75, wherein the constitutively active PhyB photoreceptor is encoded by a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with a nucleic acid sequence of SEQ ID NO: 7, SEQ ID NO: 11, or both.
77. The one or more expression constructs of claim 75, wherein the expression construct comprises a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% sequence identity with SEQ ID NO: 24.
78. The one or more expression constructs of claim 75, wherein the expression construct comprising a nucleic acid sequence comprising about 75% or more, at least about 85% or more, at least about 95% or more, or 100% of a nucleic acid sequence starting at base 8148 to base 12020 of SEQ ID NO: 19.
79. A modified plant or part thereof, plant cell, or seed thereof comprising one or more expression constructs of claims 62-78.
80. A method of improving performance of a plant or part thereof, plant cell, or seed grown under intensive, precision outdoor farming conditions, Total Controlled Environment Agriculture (TCEA), or vertical farming, the method comprising:
- a. obtaining or having obtained a modified plant of any one of claims 1-49;
 - and

- b. cultivating the plant under intensive, precision outdoor farming conditions, TCEA, or vertical farming.

81. A method of reducing developmental plasticity of a plant or part thereof, plant cell, or seed, the method comprising generating a modified plant of any one of claims 1-49.

82. The method of claim 81, wherein the plant is resistant to changes in growth conditions of the plant.

83. The method of claim 82, wherein the growth conditions comprise daylength and temperature.

84. A method of reducing a plastic response to competition among a co-cultivated group of modified plants or parts thereof, plant cells, or seeds, the method comprising, co-cultivating a group of plants of any of claims 1-49.

85. A method of stabilizing production of a metabolite, nucleic acid, or protein in a plant or part thereof, plant cell, or seed, the method comprising:

- a. obtaining or having obtained a modified plant or part thereof, plant cell, or seed of any of claims 1-49;
- b. cultivating the plant for a time sufficient to generate the metabolite, nucleic acid, or protein; and
- c. harvesting the metabolite, nucleic acid, or protein from the plant or part thereof, plant cell, or seed.

86. The method of claim 85, wherein the plant or part thereof, plant cell, or seed is grown under intensive, precision outdoor farming conditions, TCEA, or vertical farming.

87. The method of claim 85, wherein stabilizing production of a metabolite, nucleic acid, or protein comprises equal production of the metabolite, nucleic acid, or protein irrespective of light period, temperature variation or both.

88. A kit for modifying a plant or part thereof, plant cell, or seed exhibiting reduced developmental plasticity, the kit comprising:
- a. one or more modified plants or parts thereof, plant cells, or seeds of any one of claims 1-49;
 - b. one or more expression constructs of any one of claims 62-78;
 - c. one or more modified plants, plant cells, or parts thereof of claim 79; or
 - d. any combination of (a) to (c).

FIG. 1

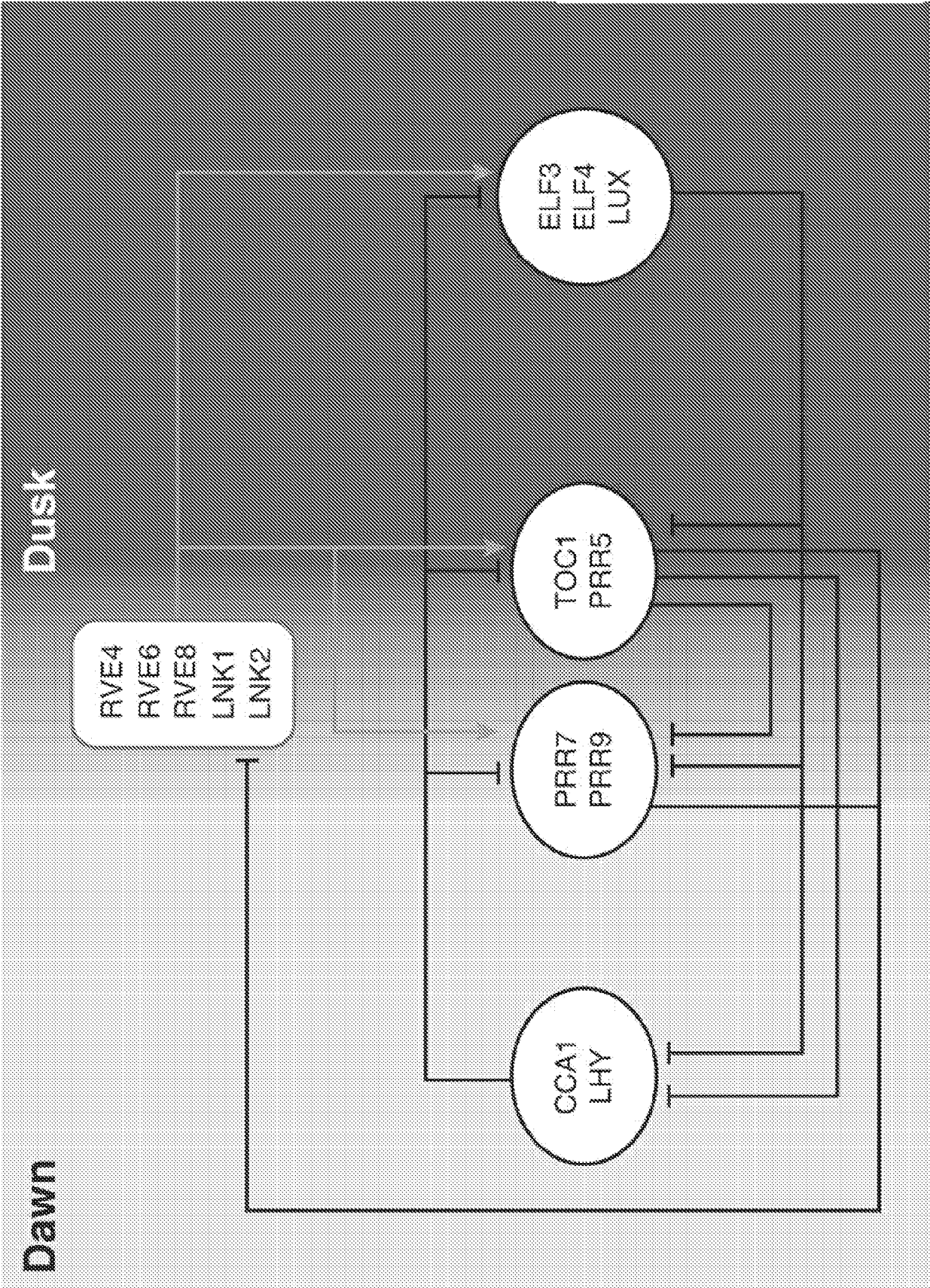


FIG. 2A

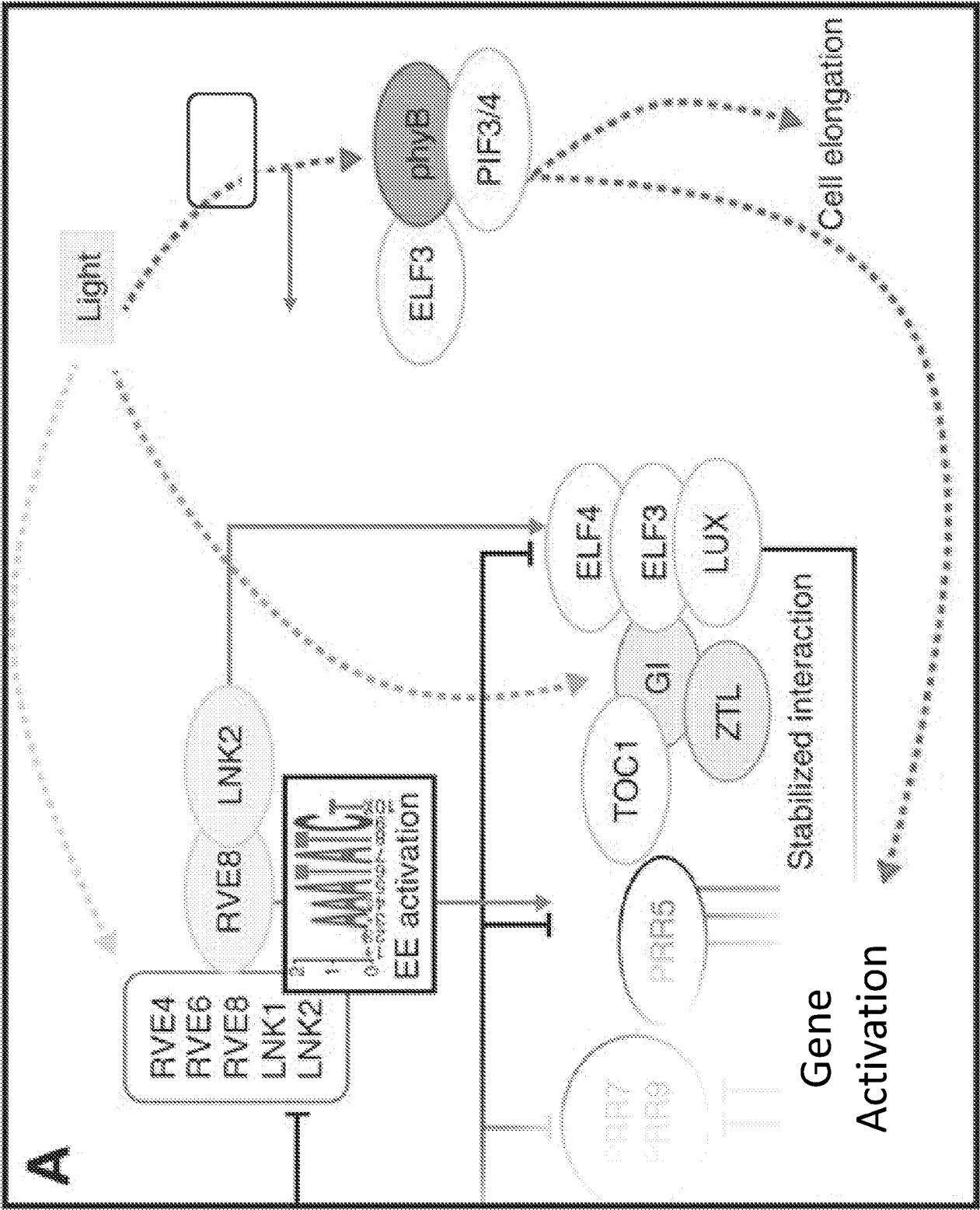


FIG. 2B

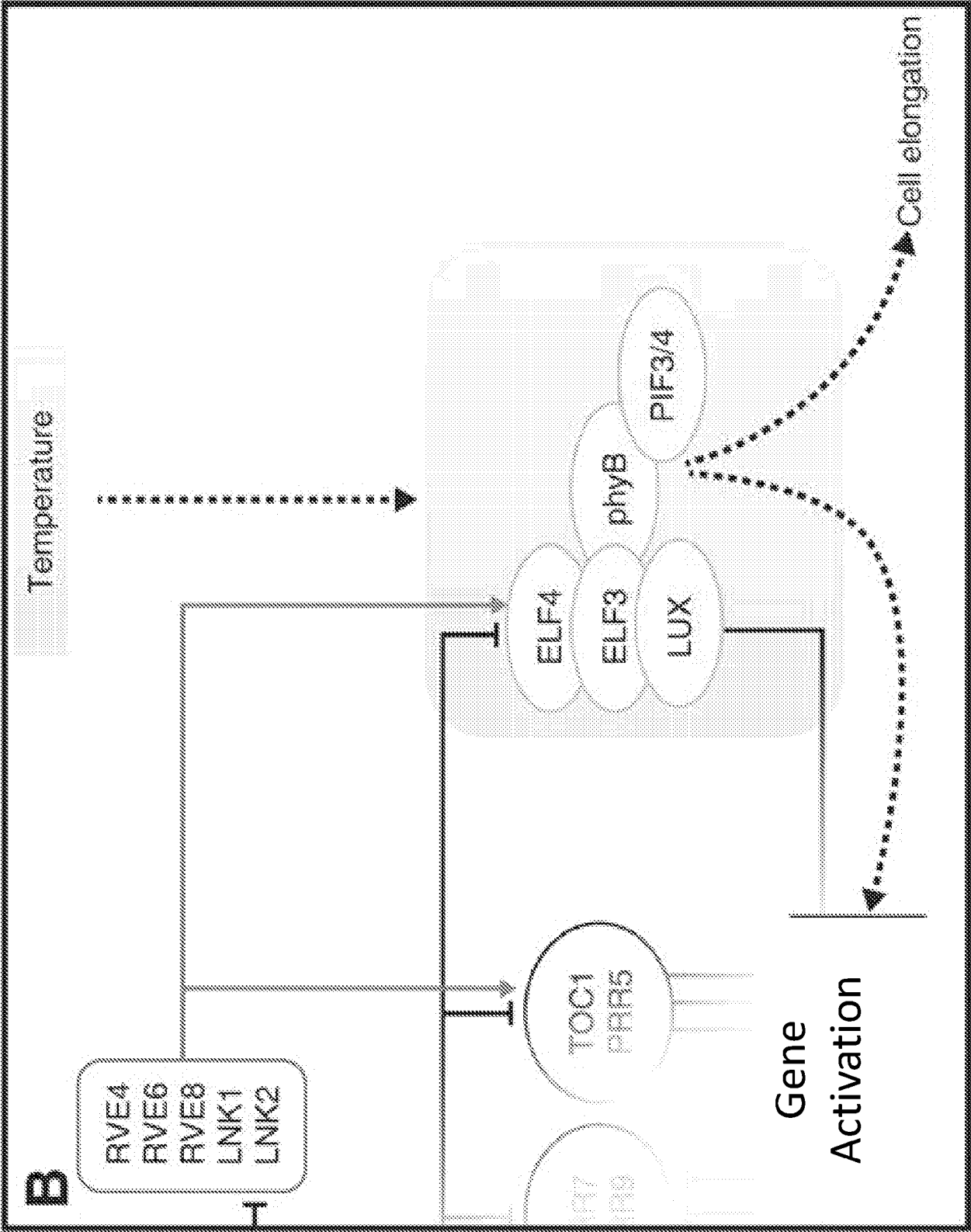


FIG. 3A

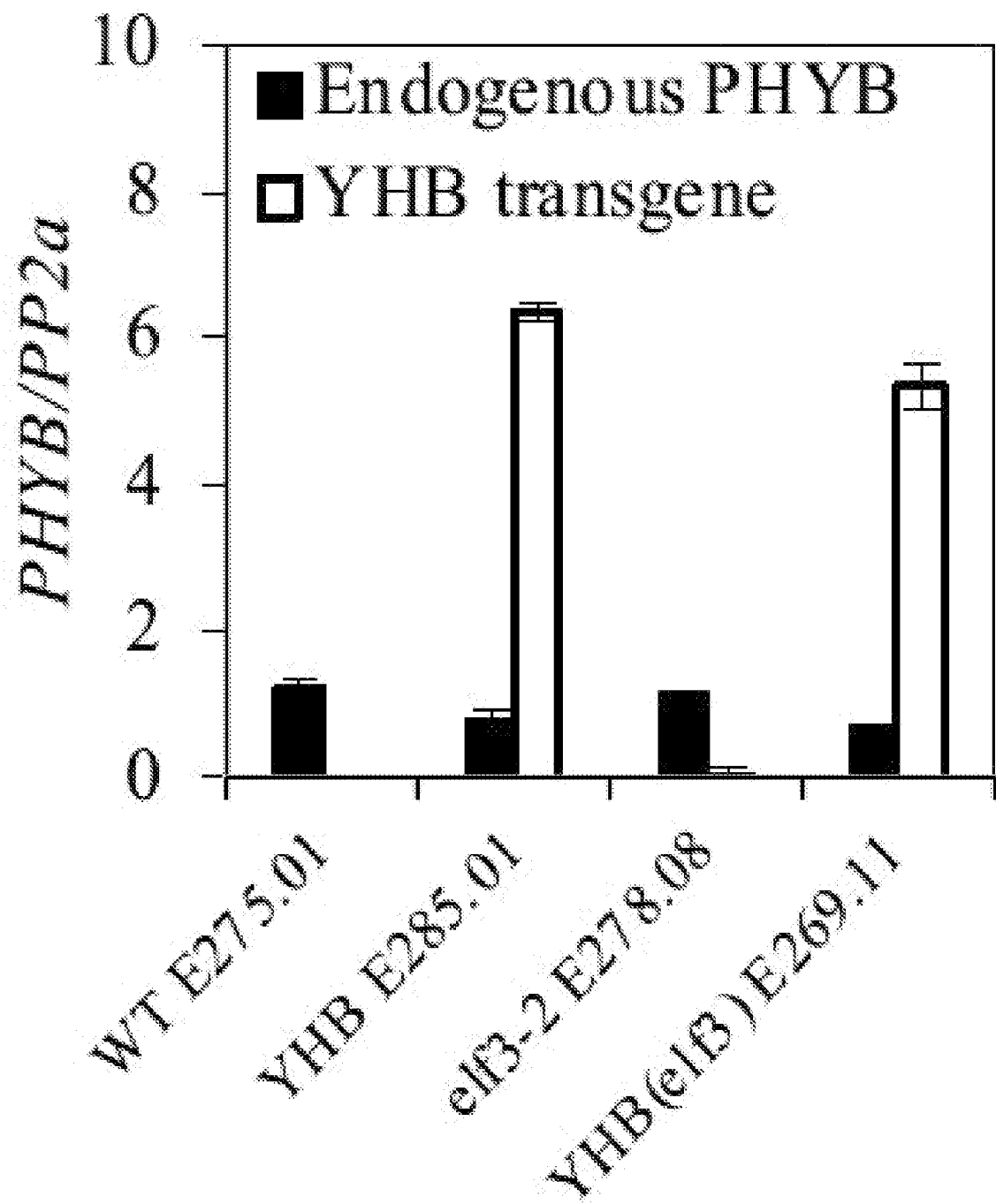


FIG. 3B

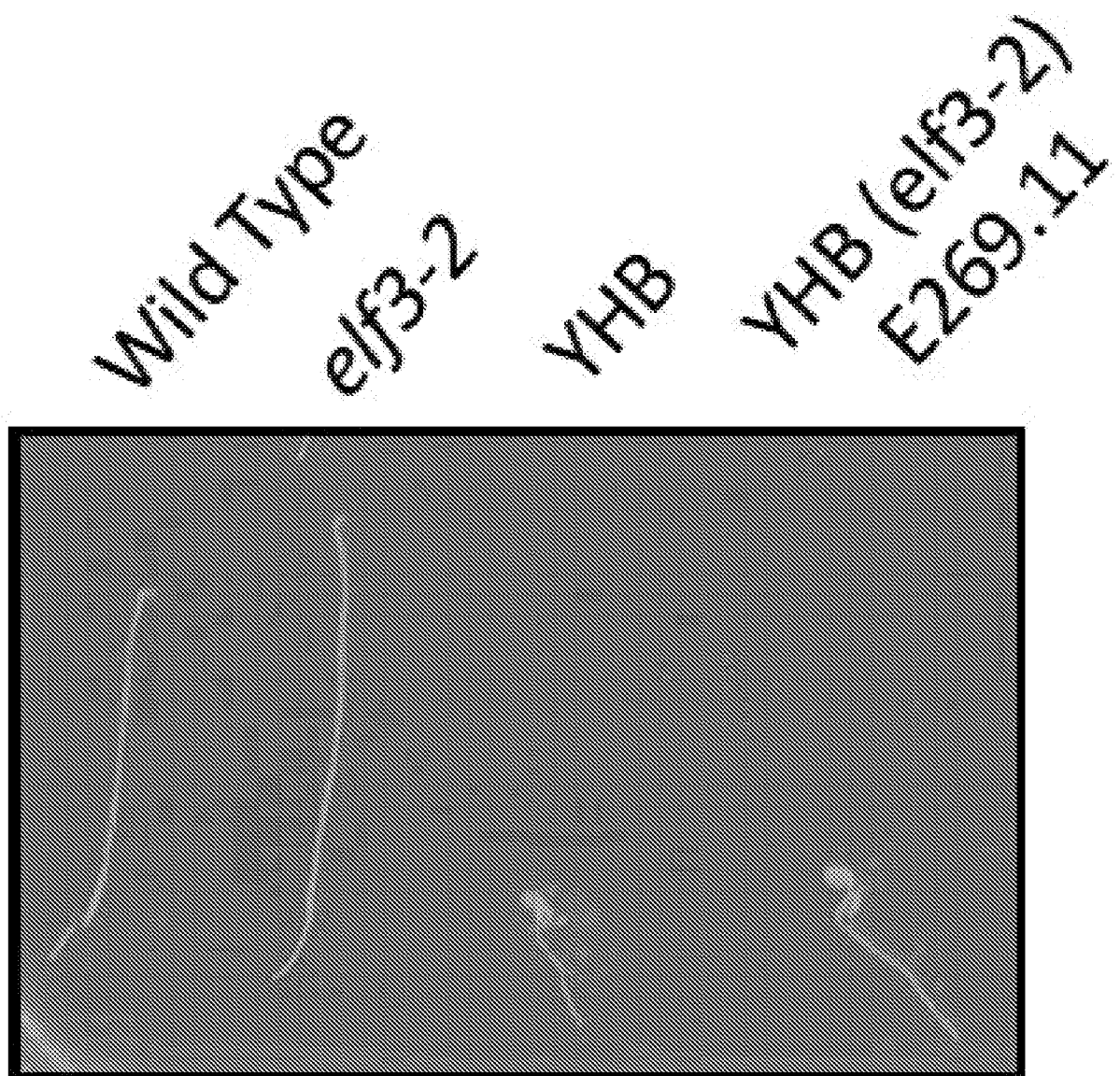


FIG. 3C

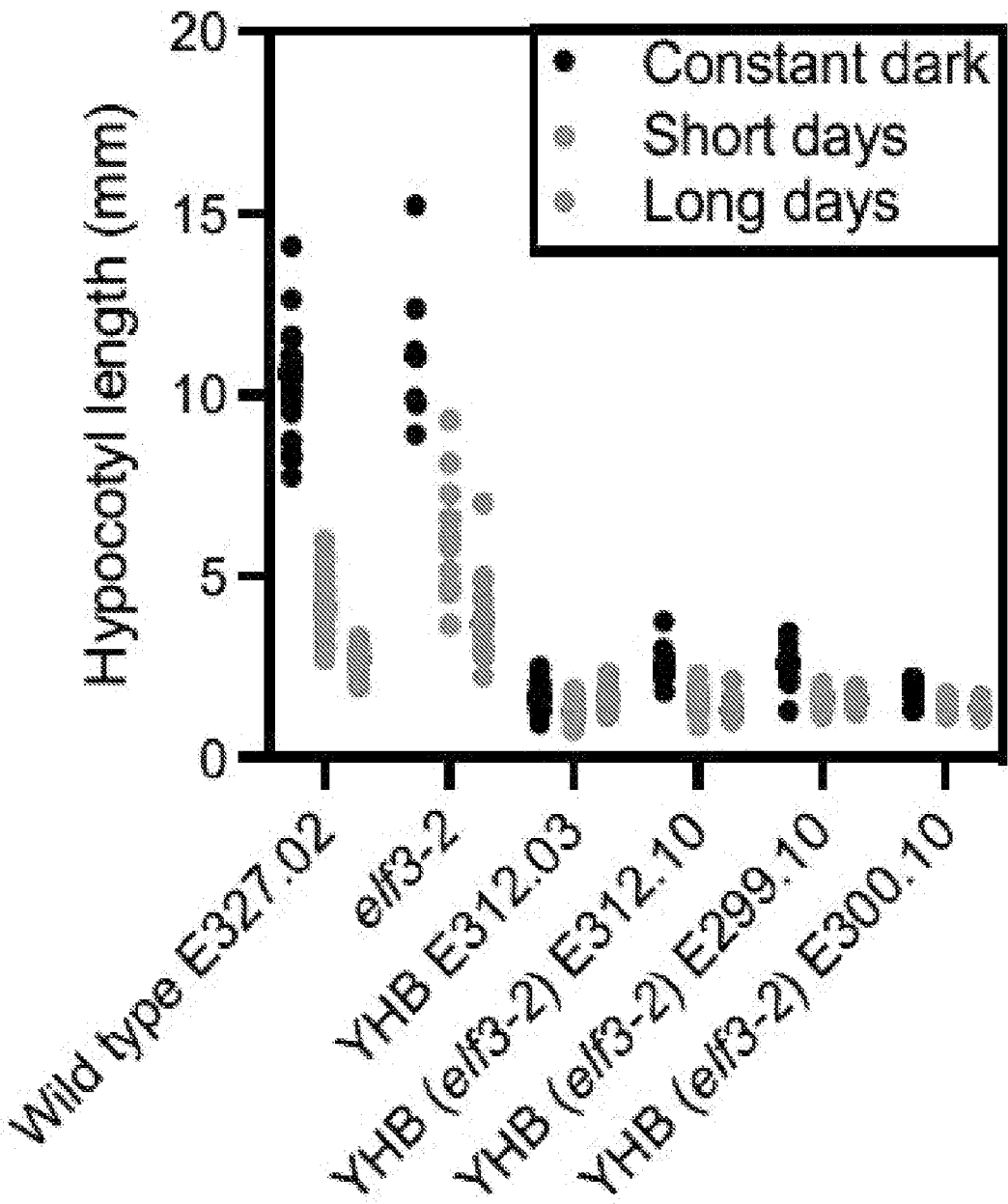


FIG. 3D

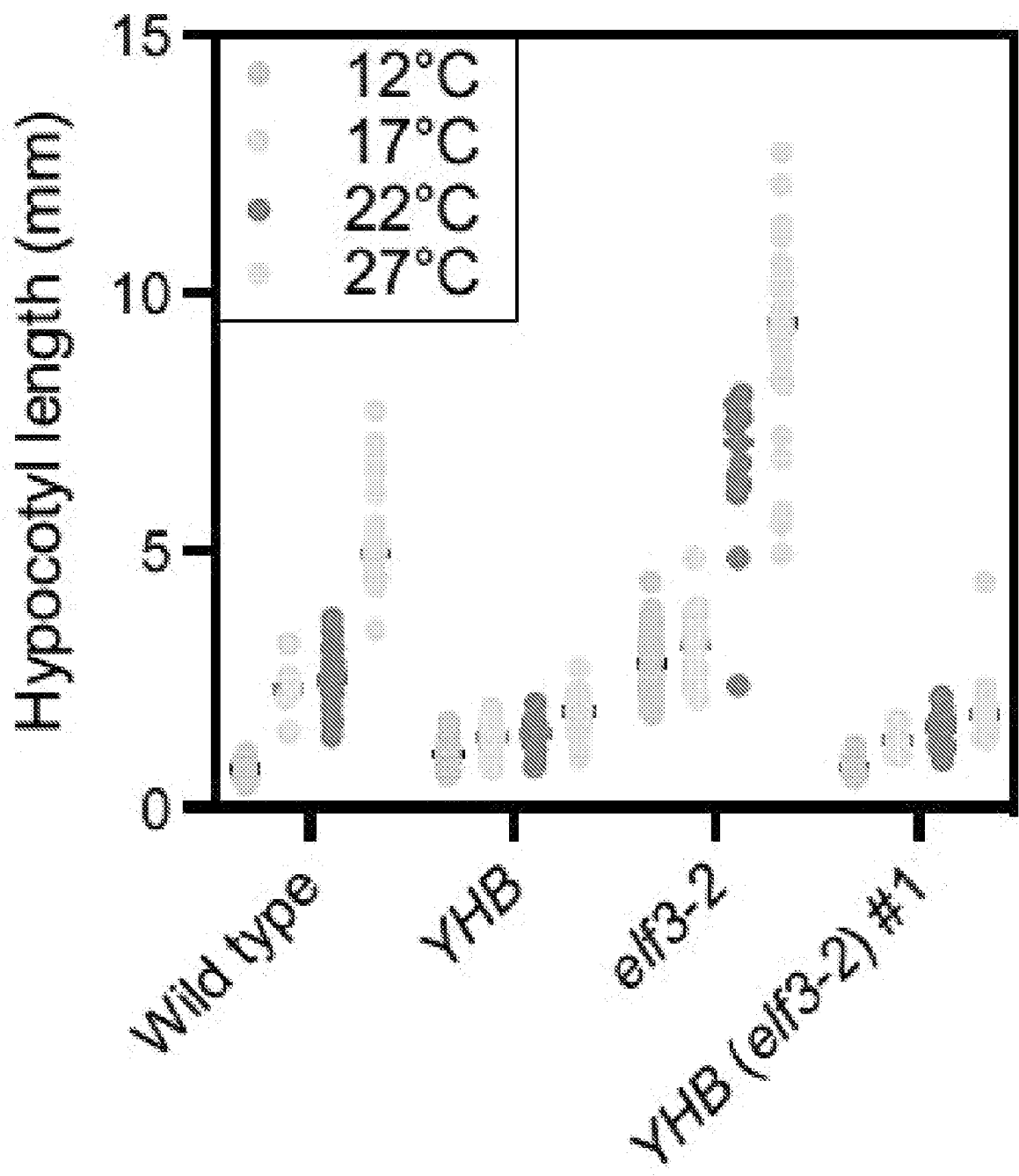
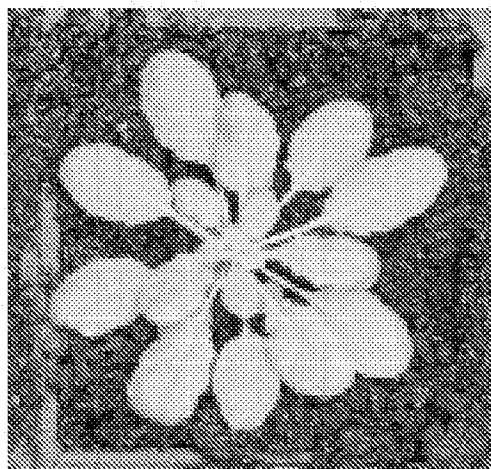
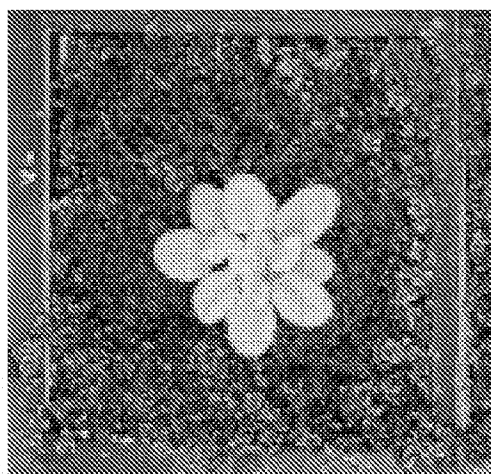
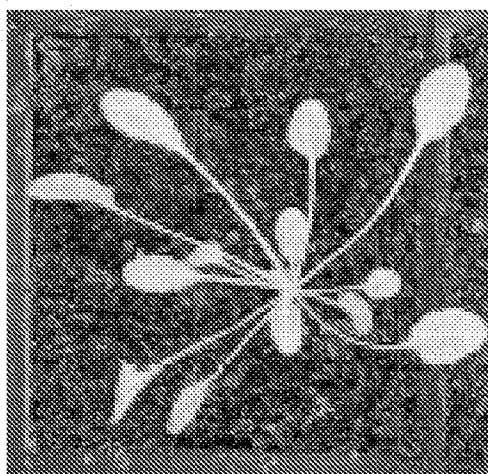


FIG. 3E

WT

*elf3-2*

YHB

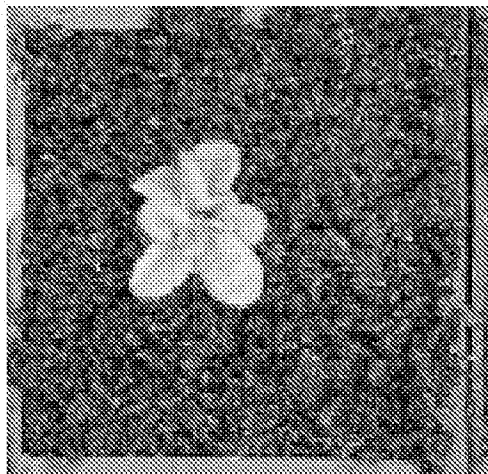
YHB
(*elf3*)

FIG. 3F

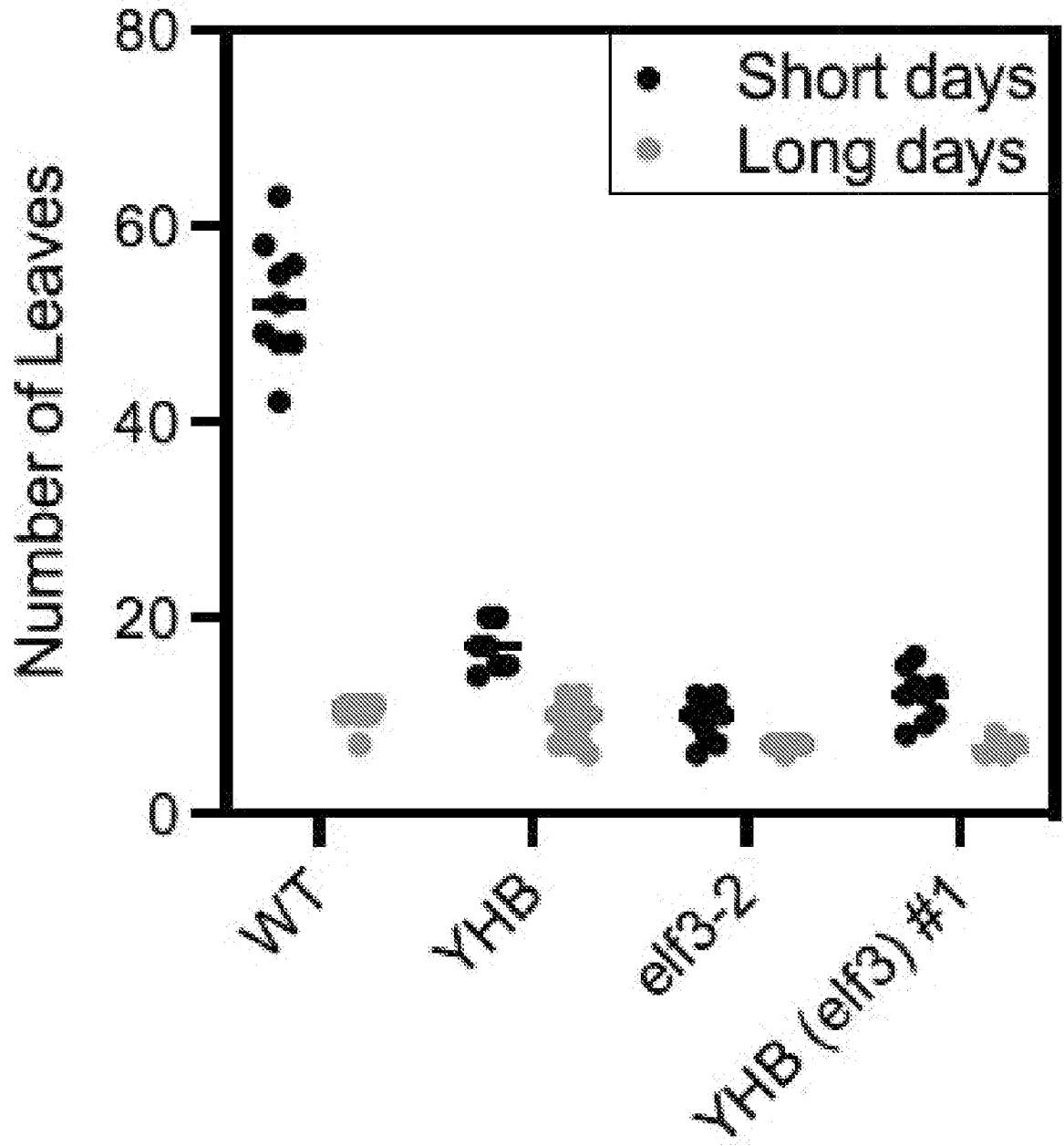


FIG. 4A

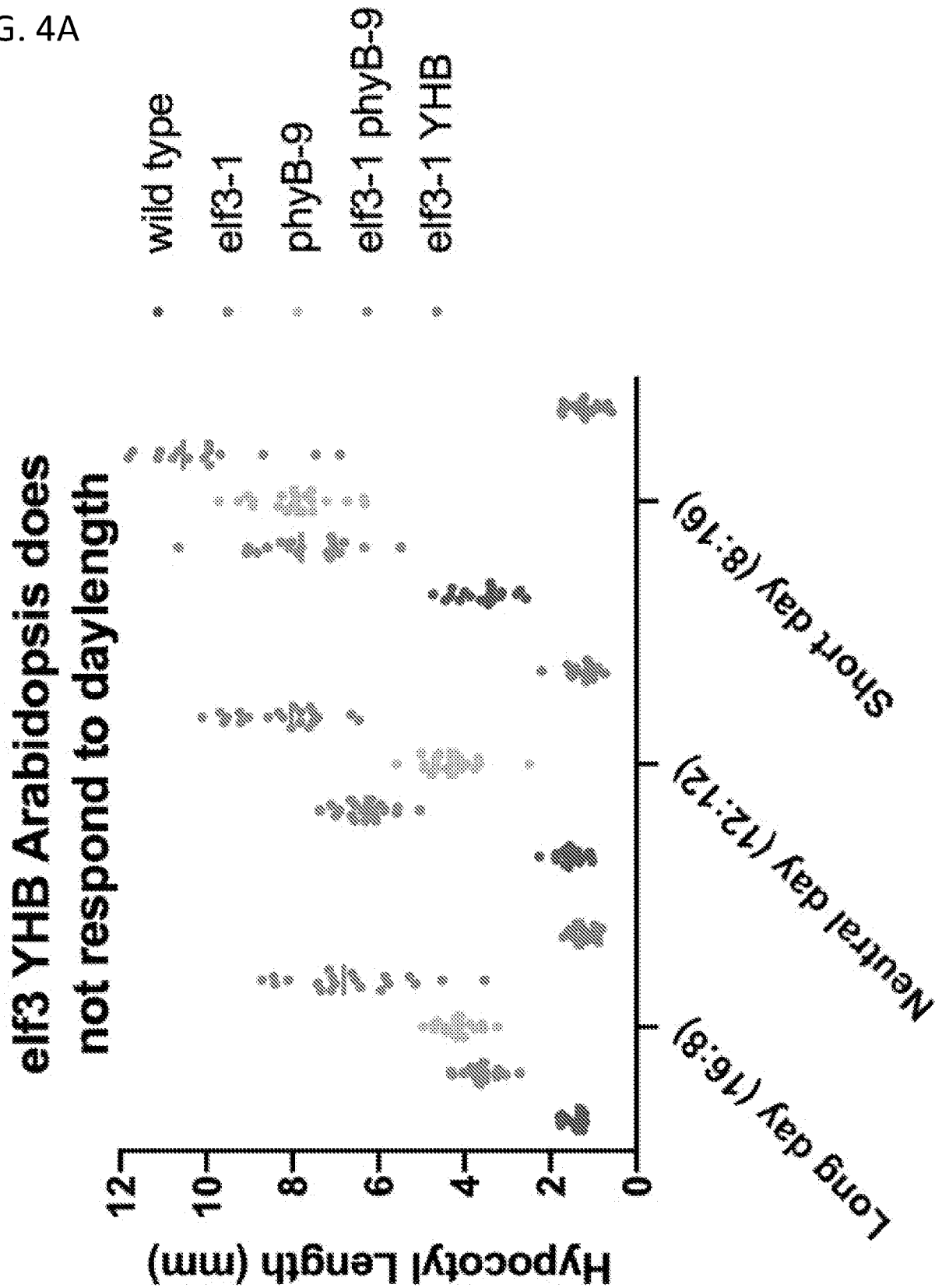


FIG. 4B

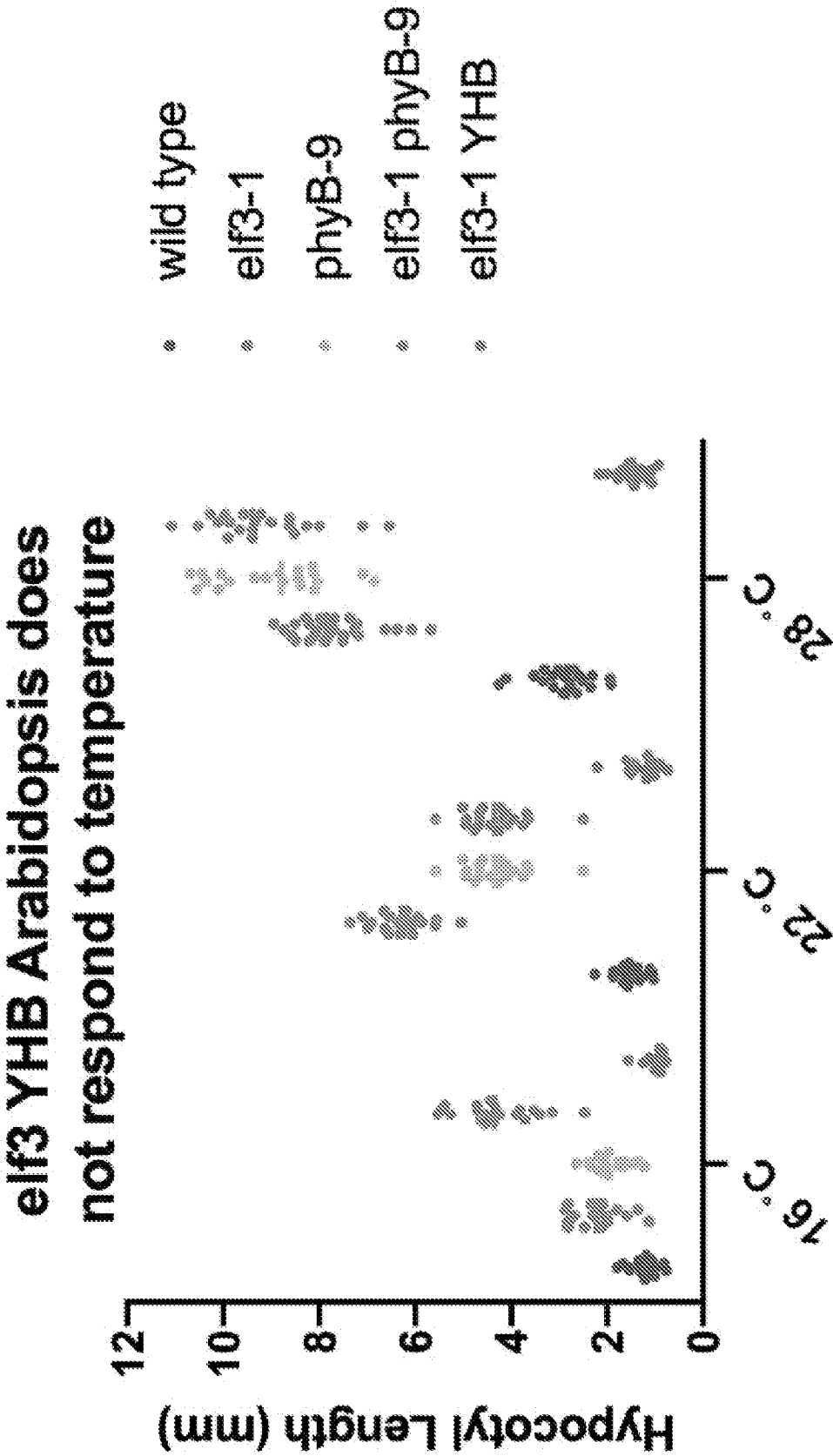


FIG. 5A

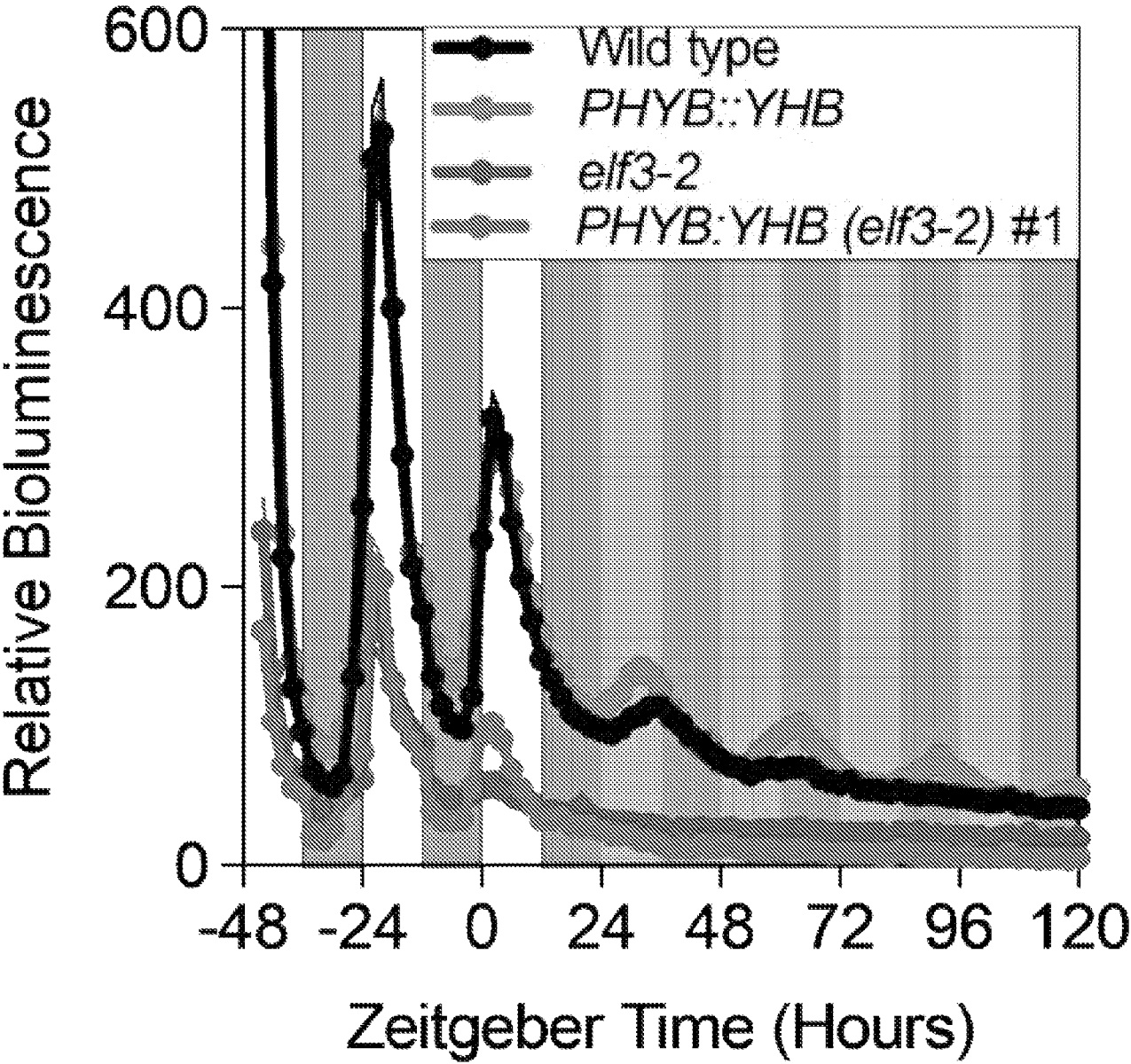


FIG. 5B

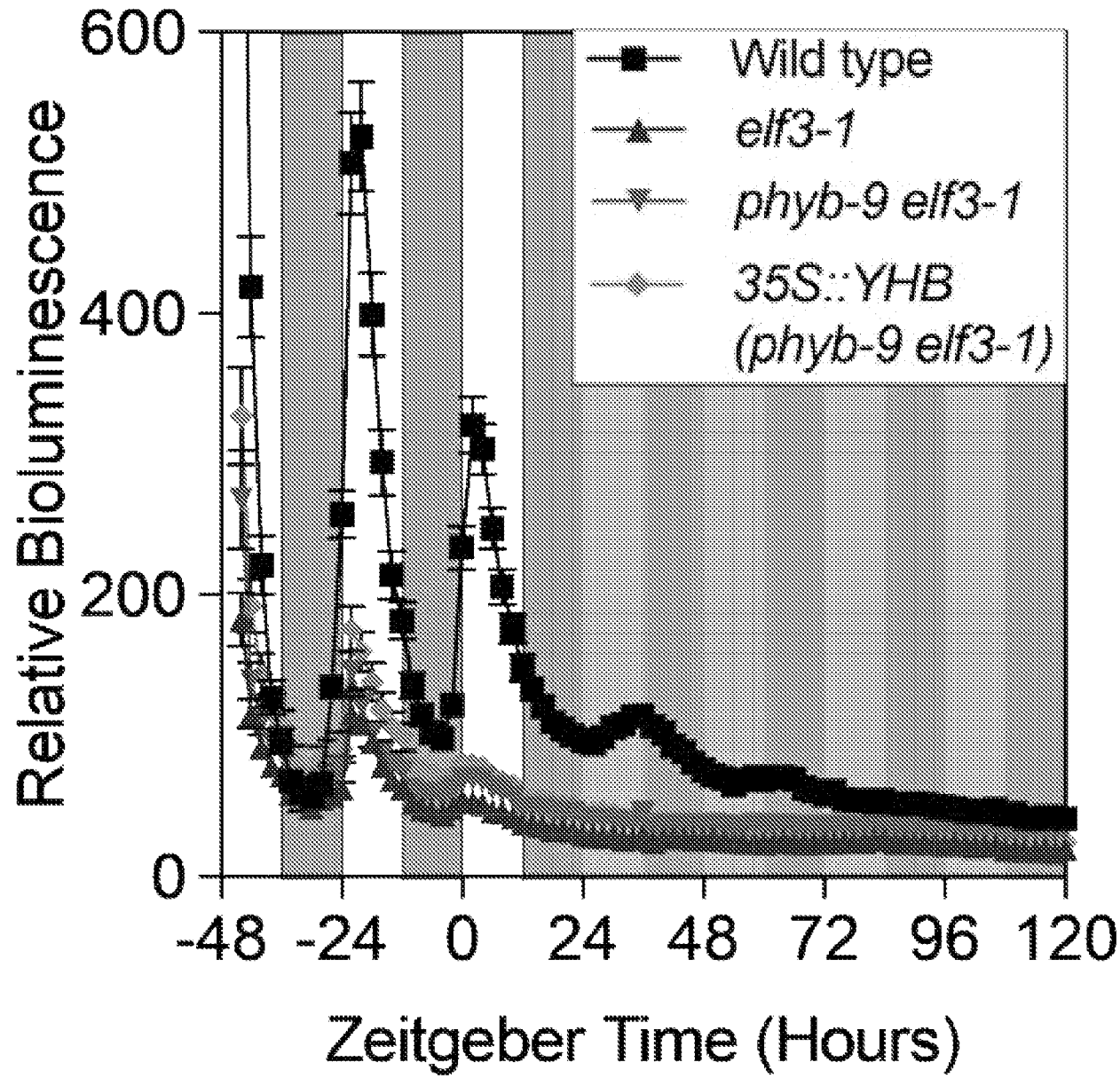


FIG. 6A

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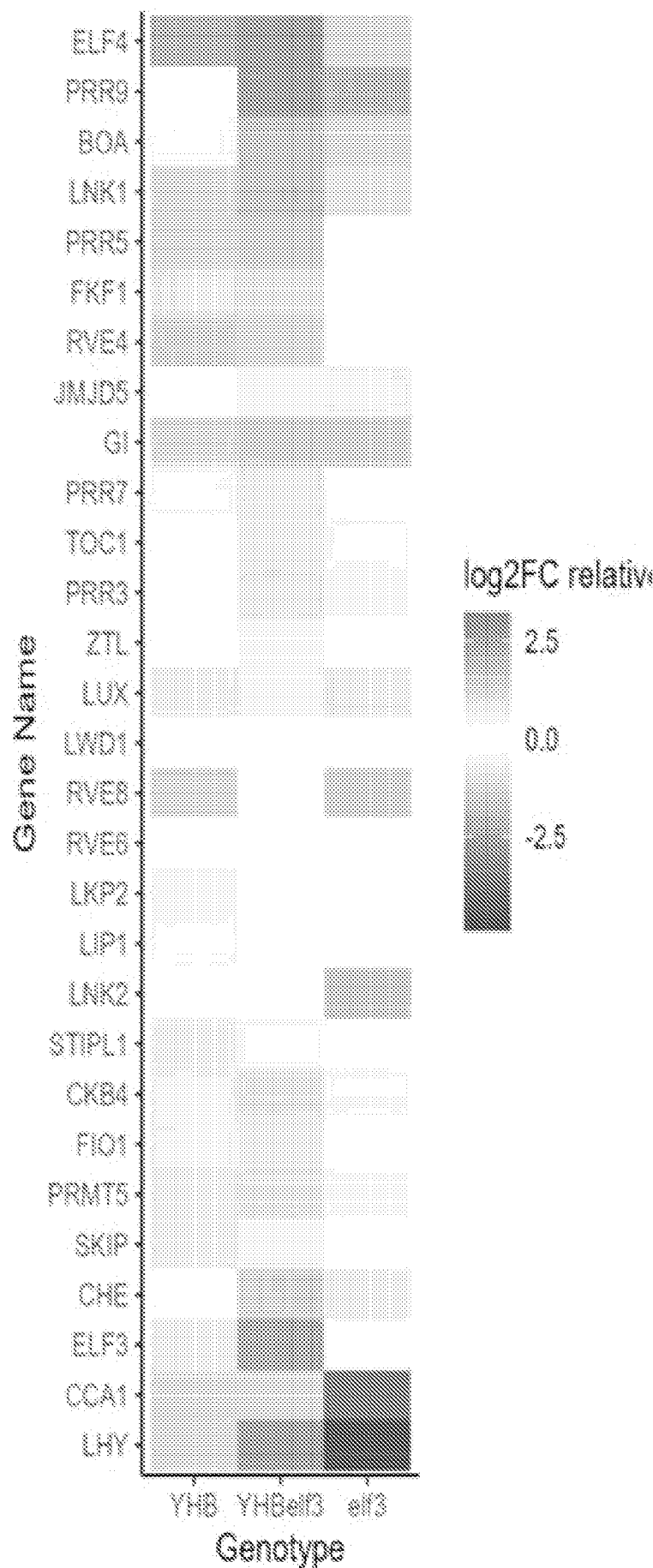


FIG. 6B

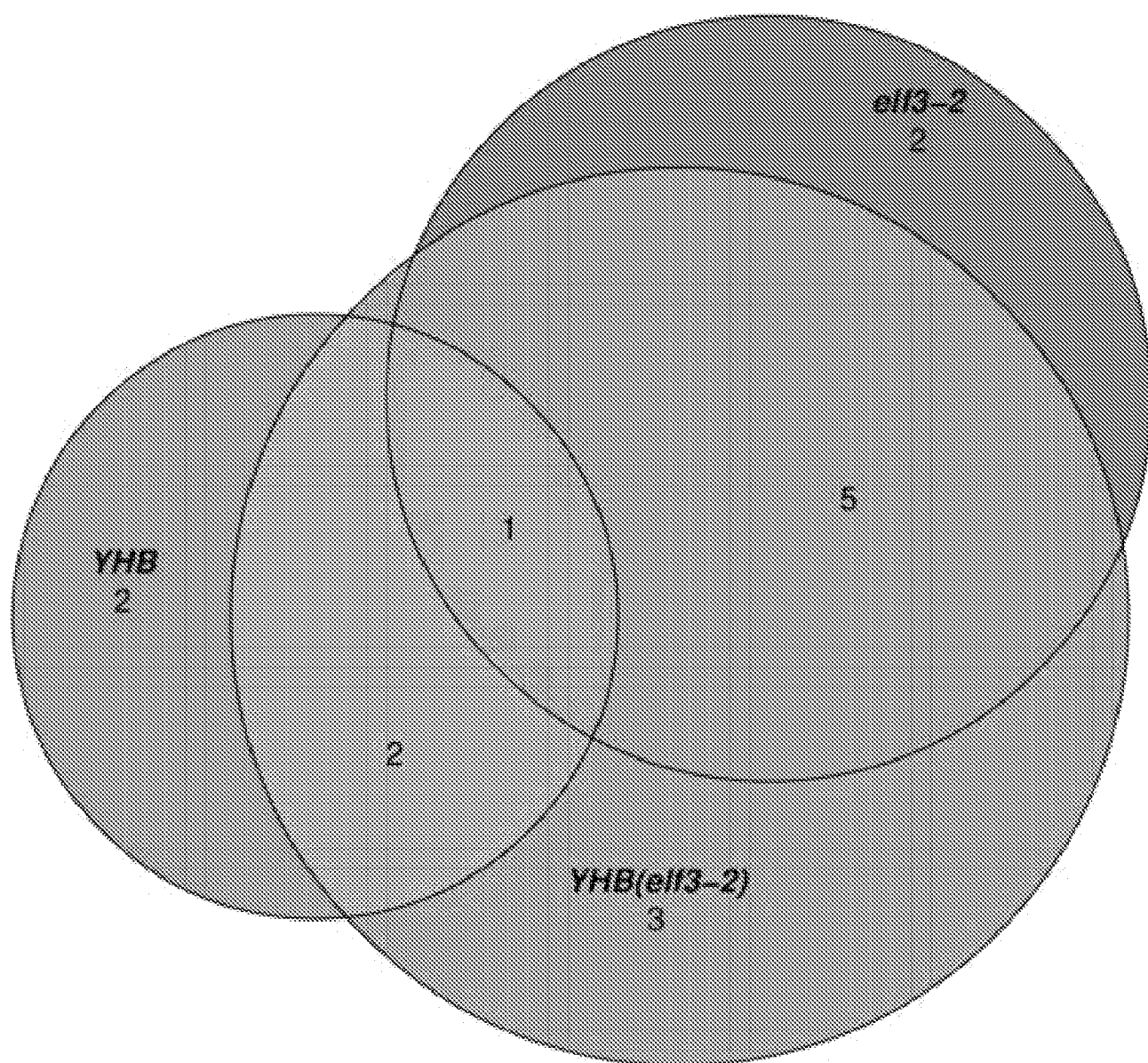


FIG. 6C

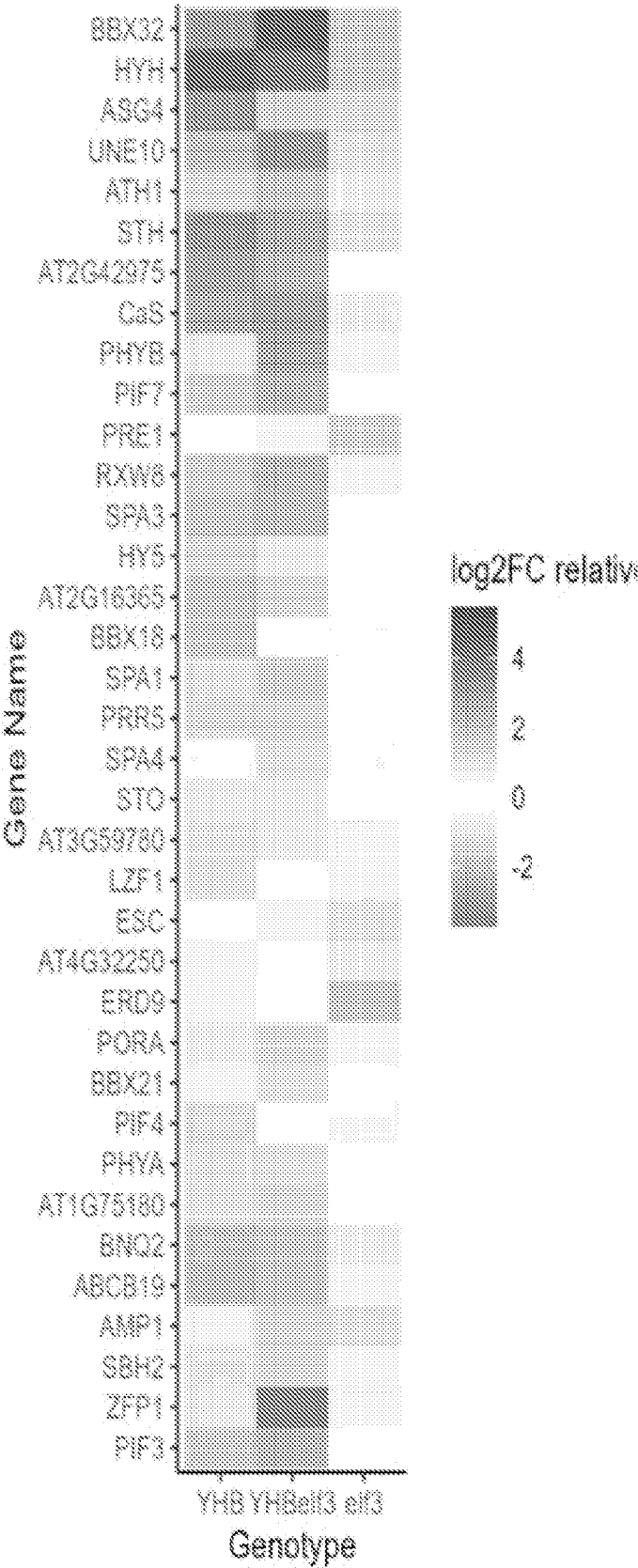


FIG. 6D

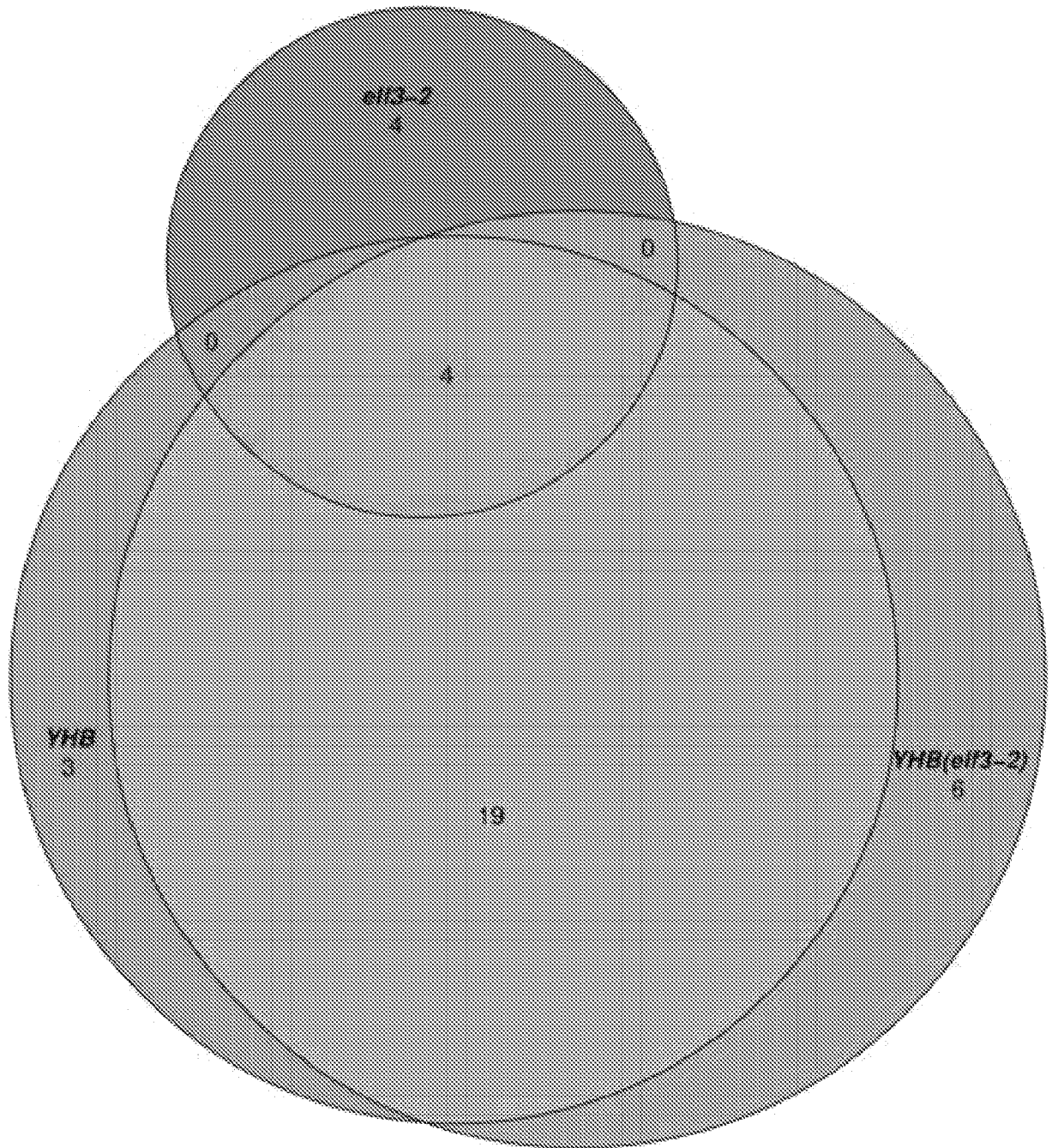


FIG. 6E

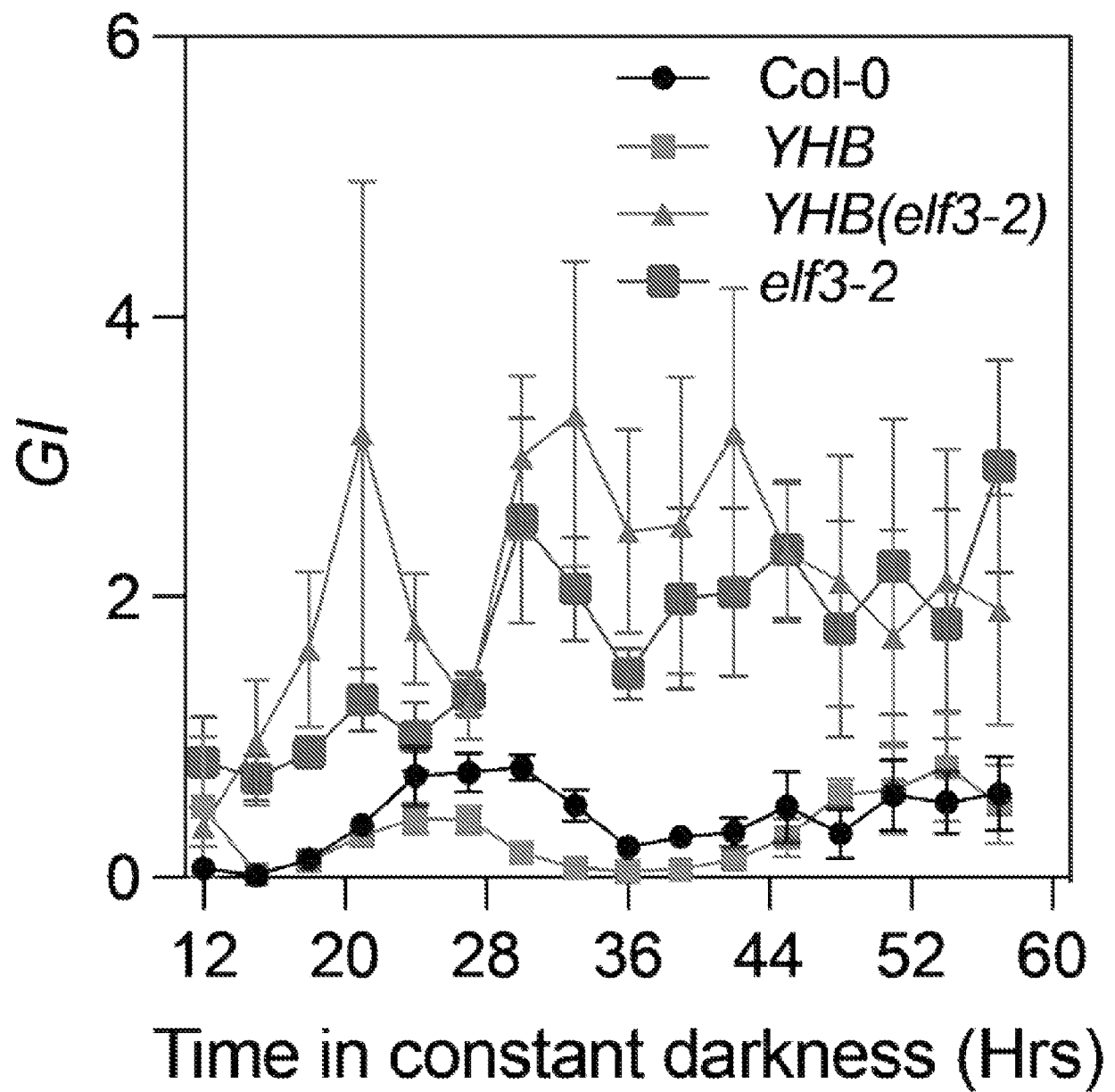


FIG. 6F

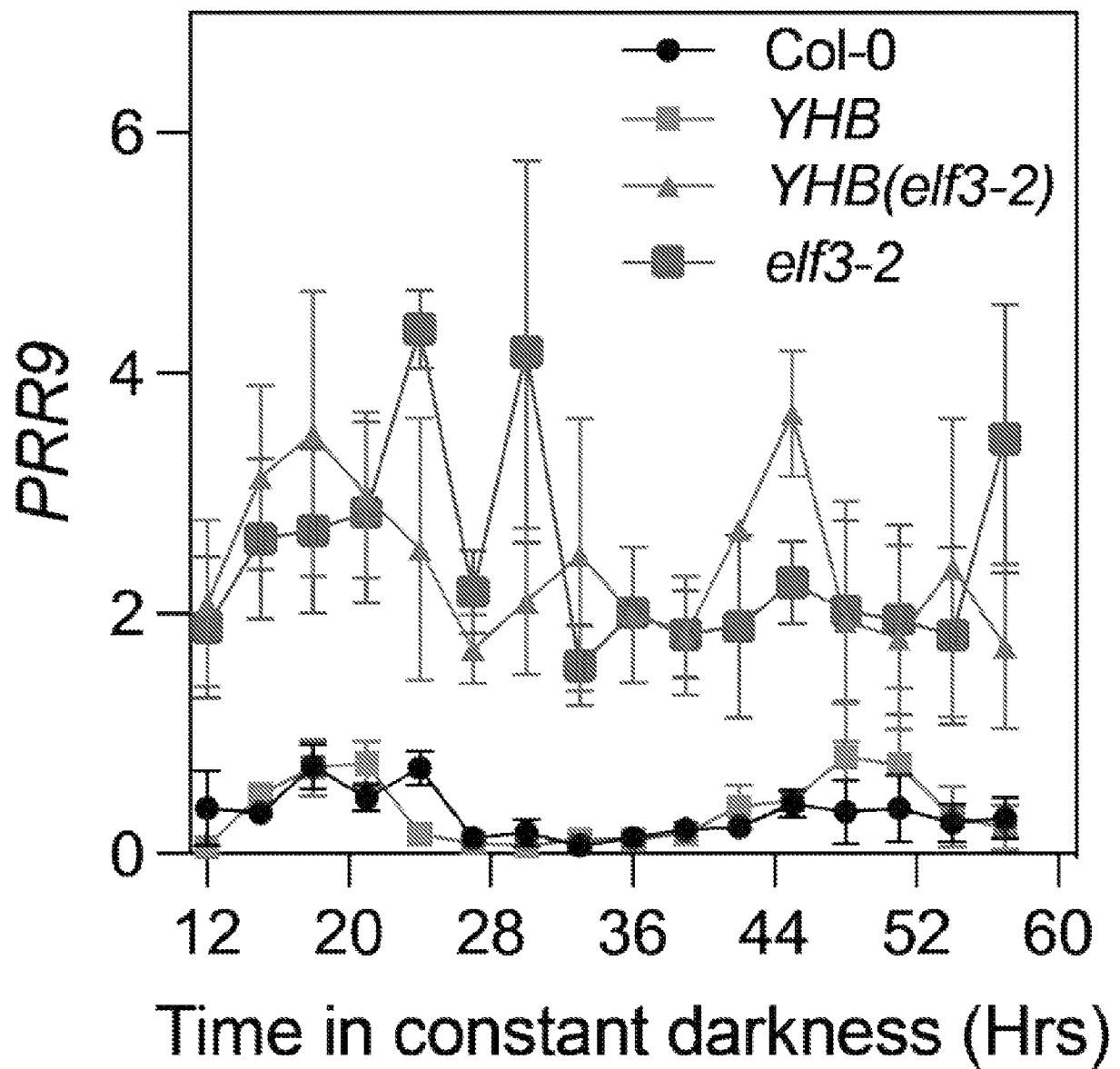


FIG. 6G

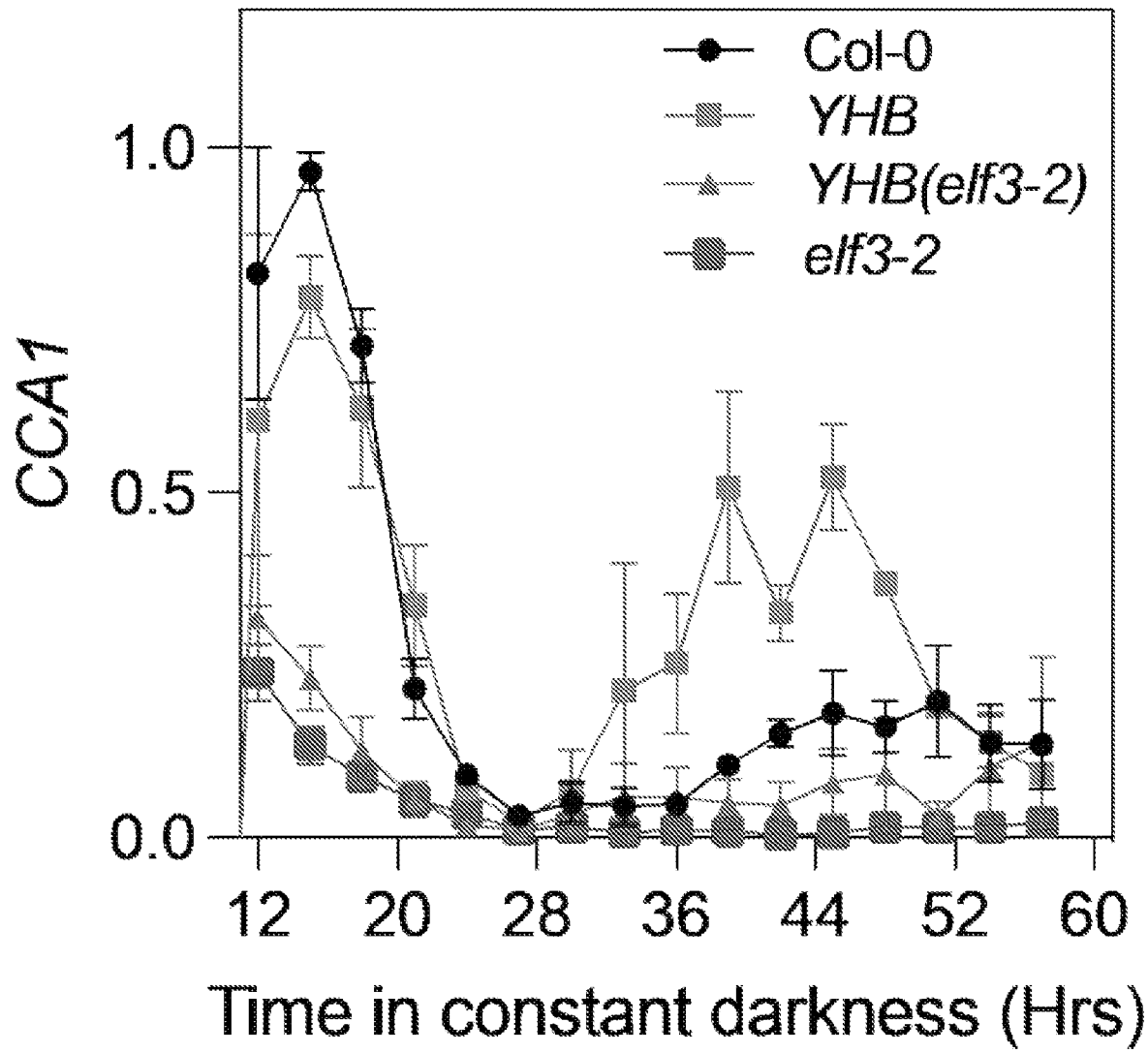


FIG. 6H

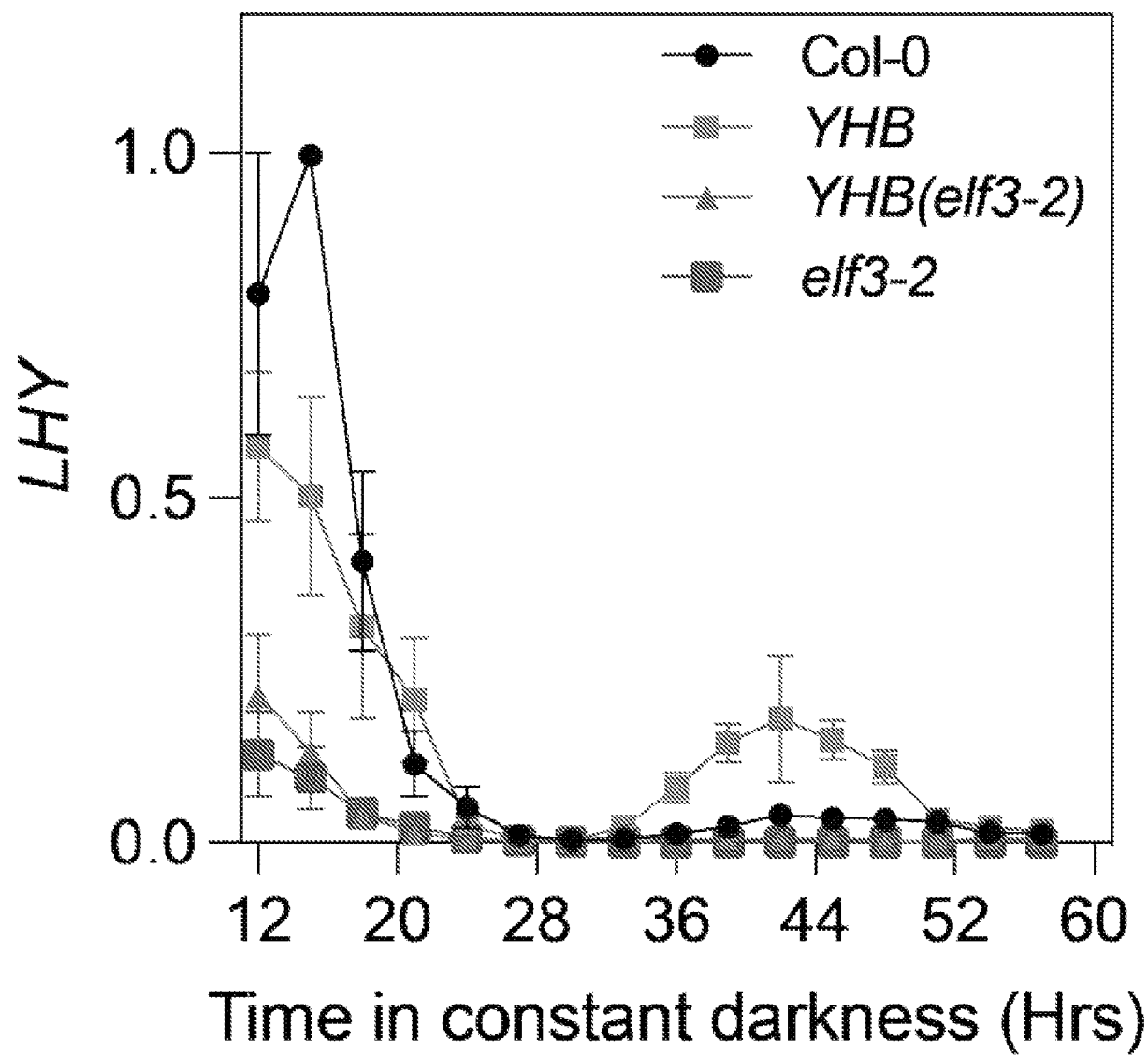
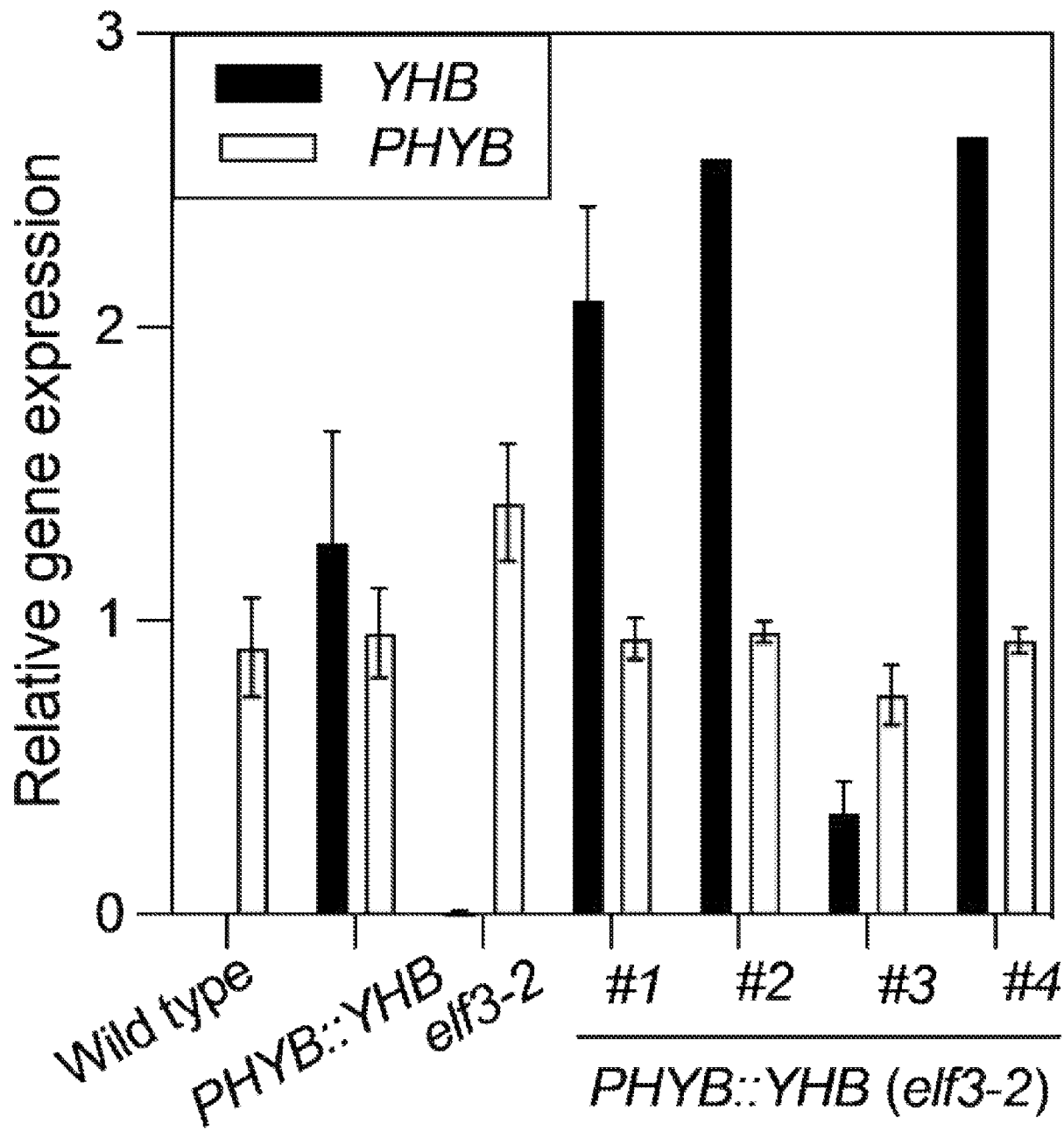


FIG. 7A



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FIG. 7B

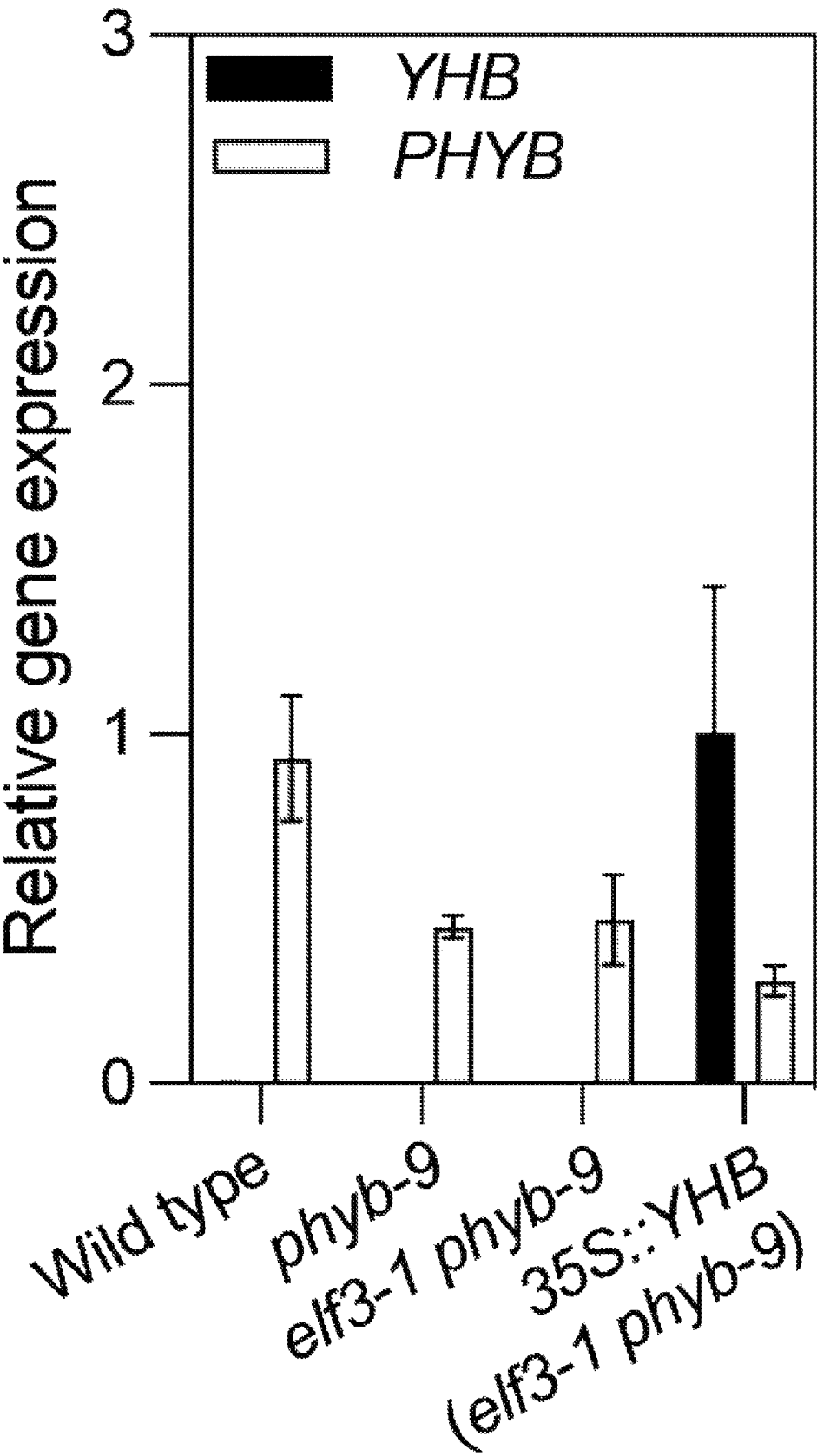


FIG. 7C

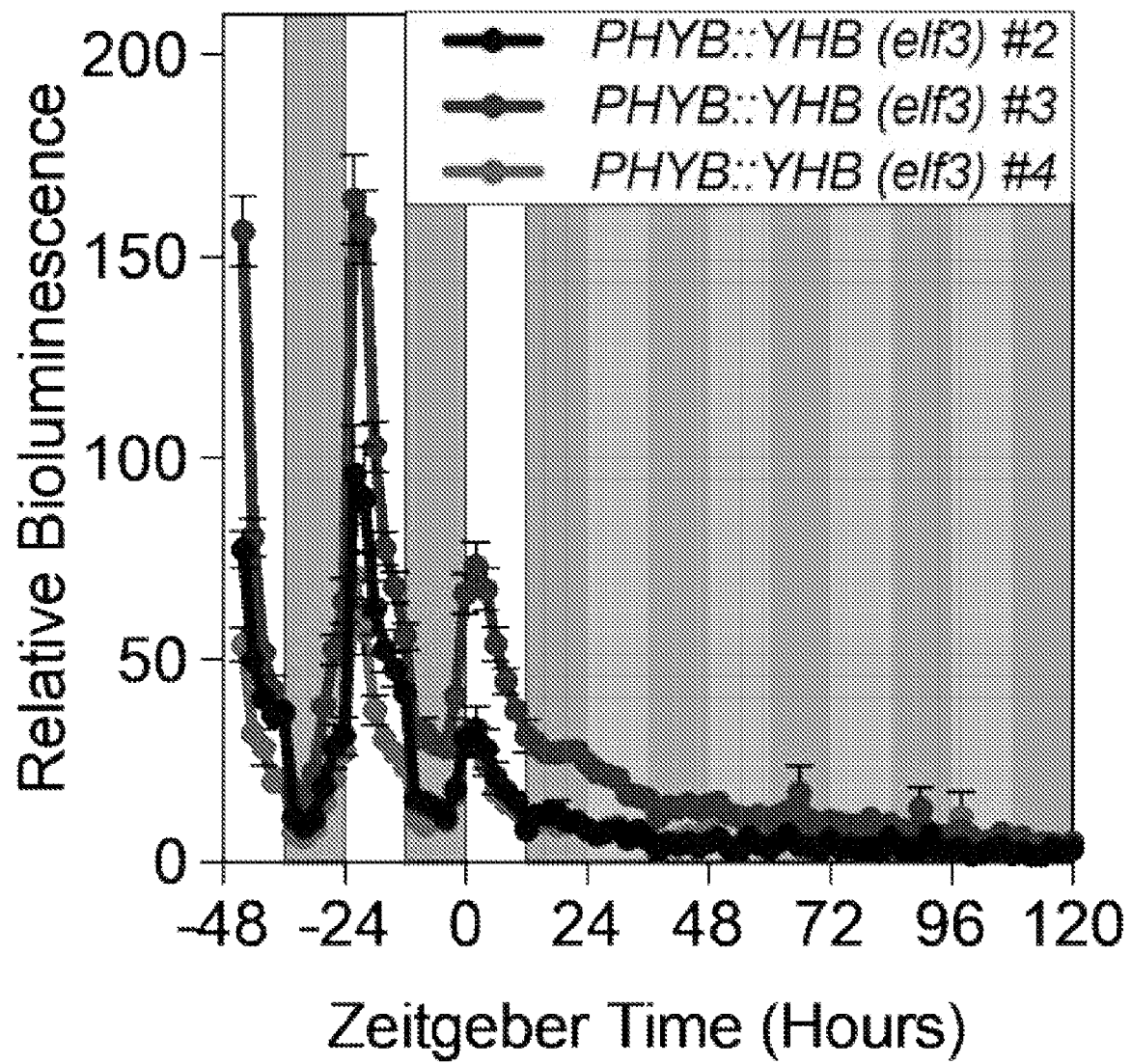


FIG. 7D

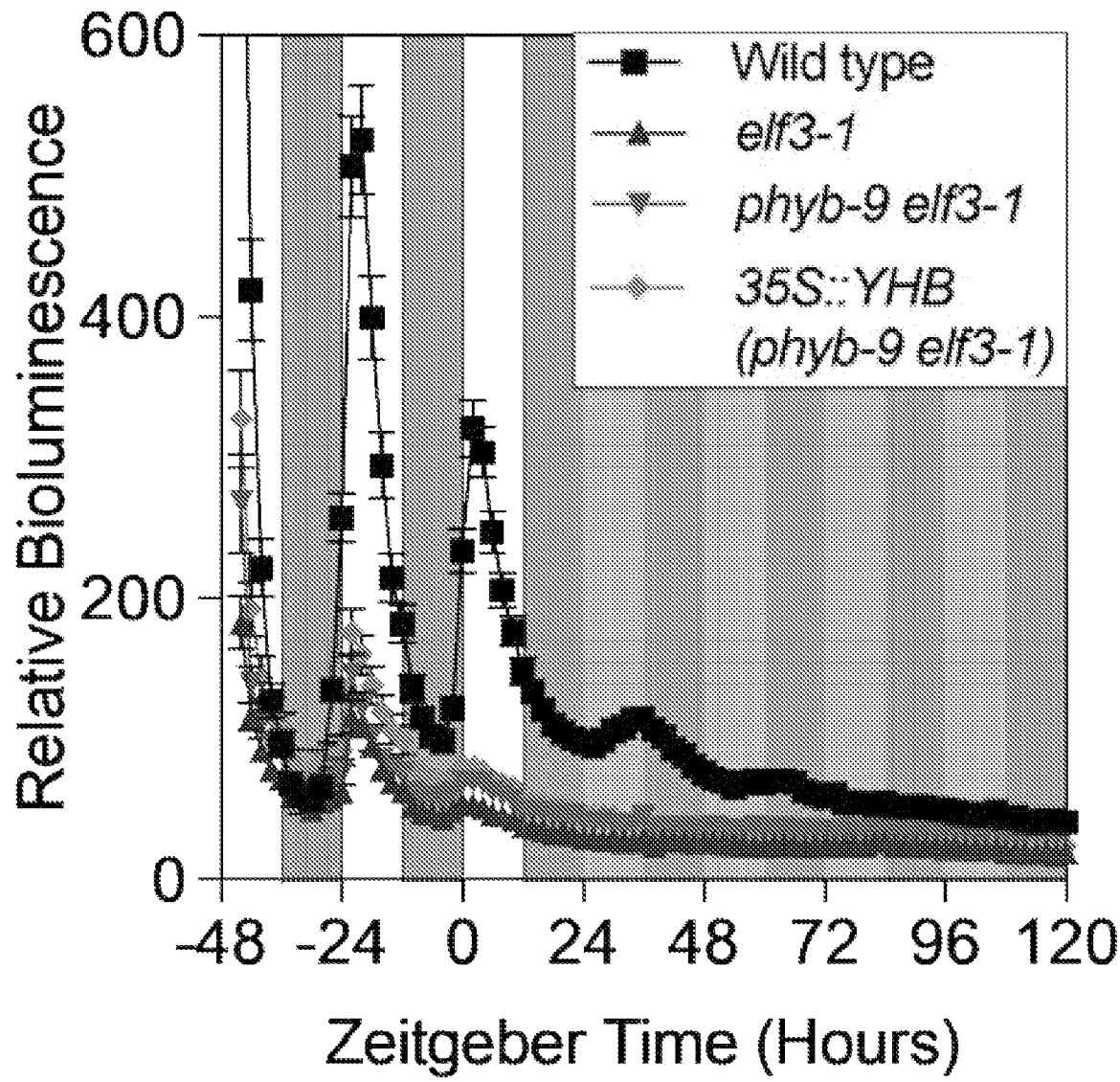


FIG. 8A

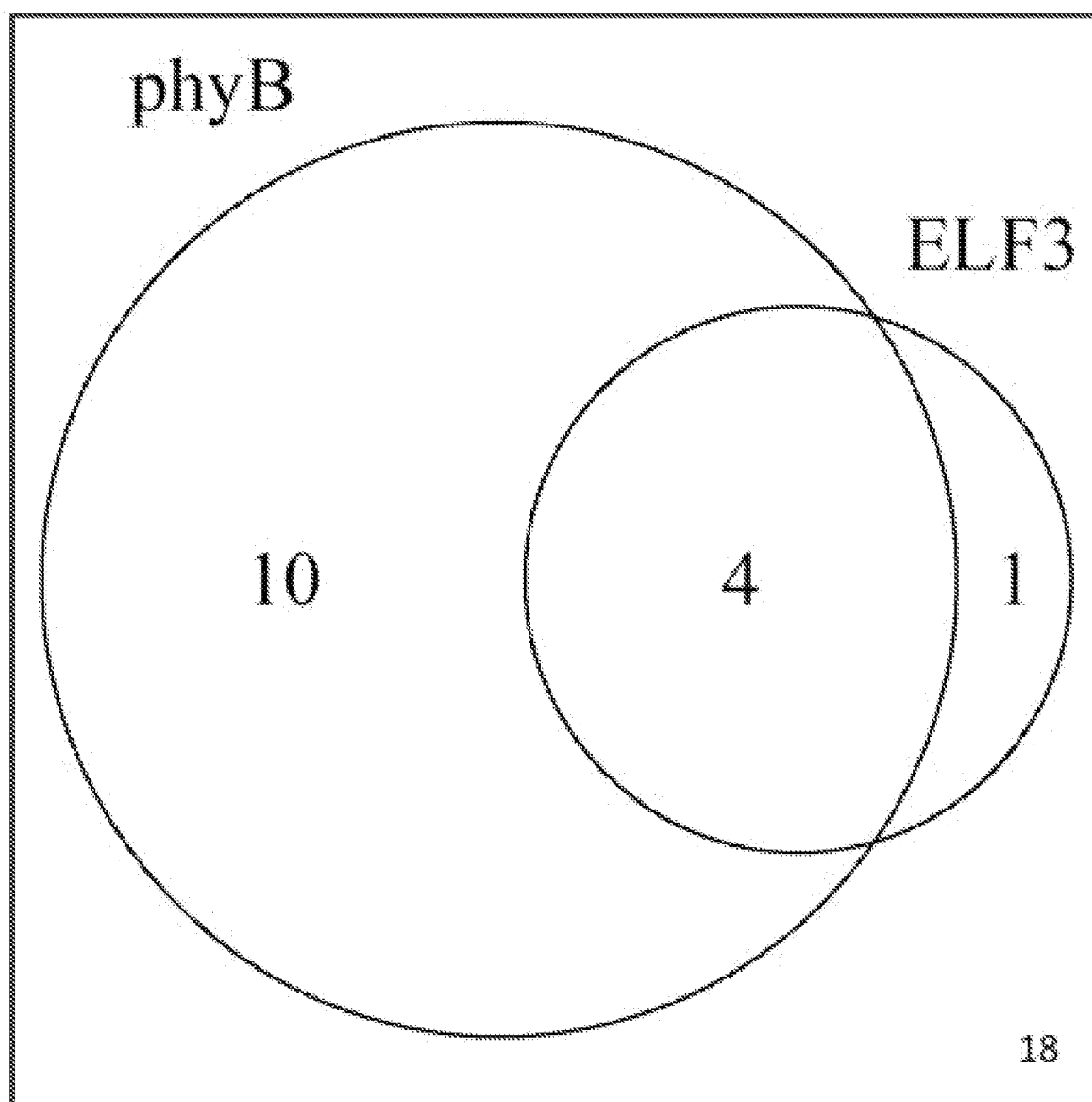


FIG. 8B

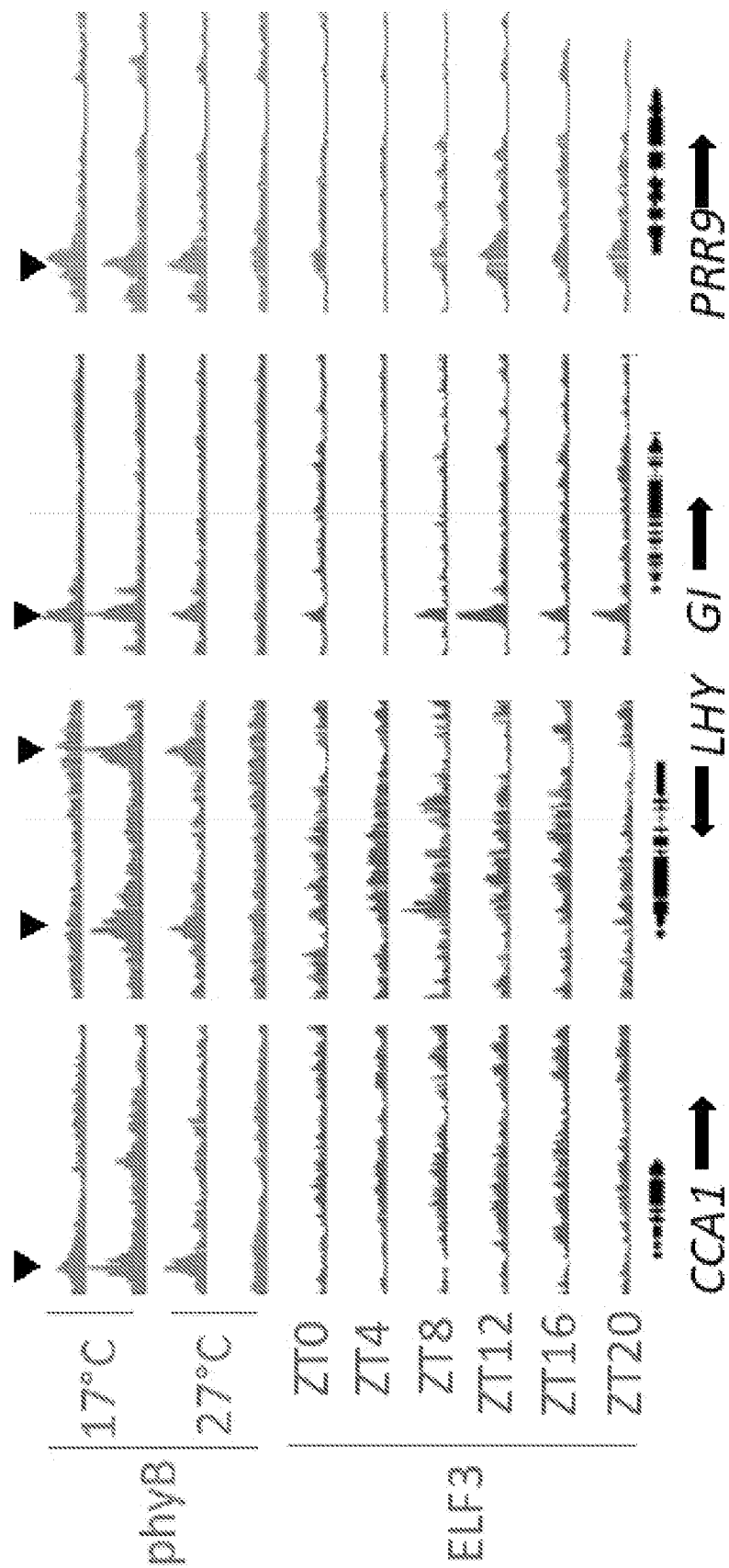


FIG. 9A

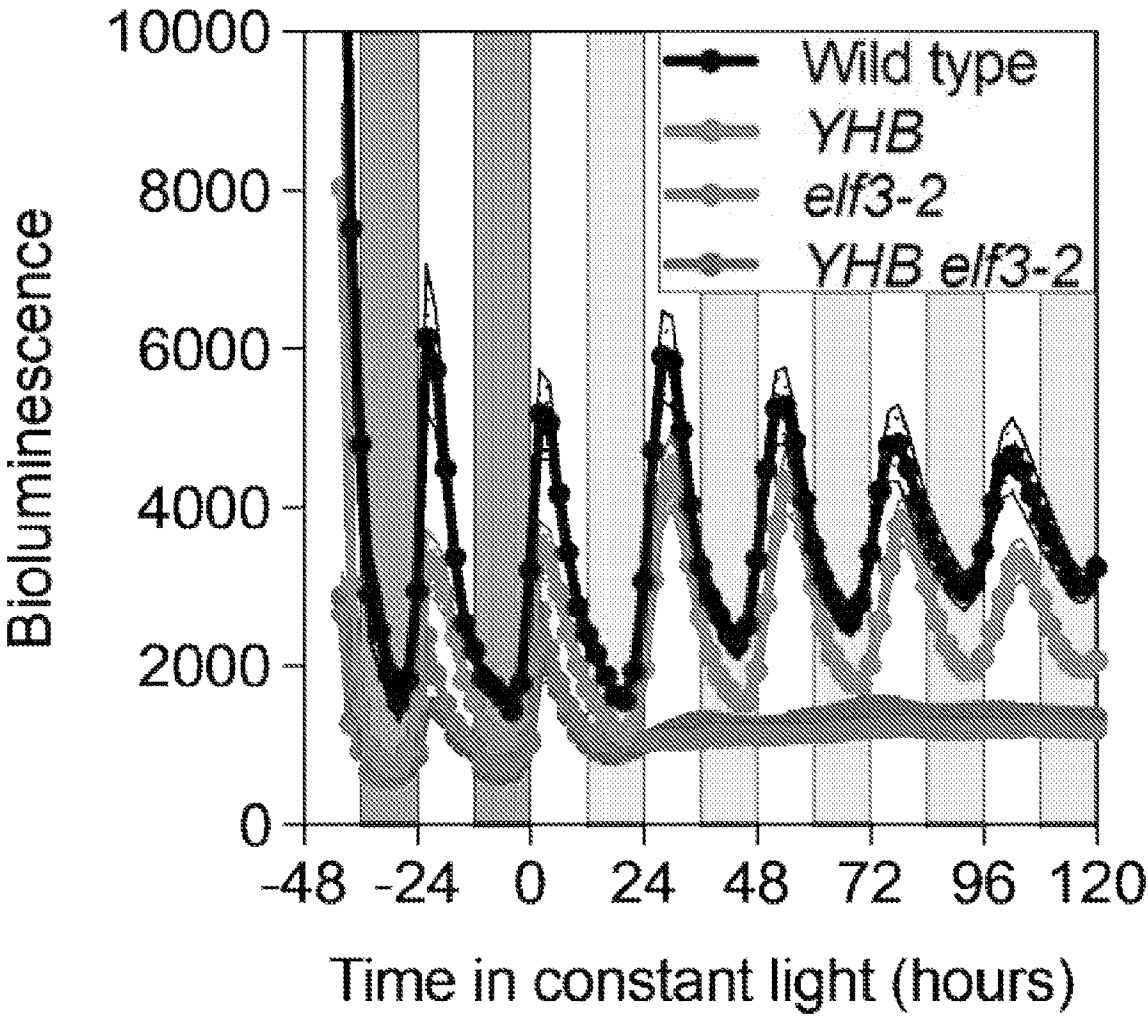


FIG. 9B

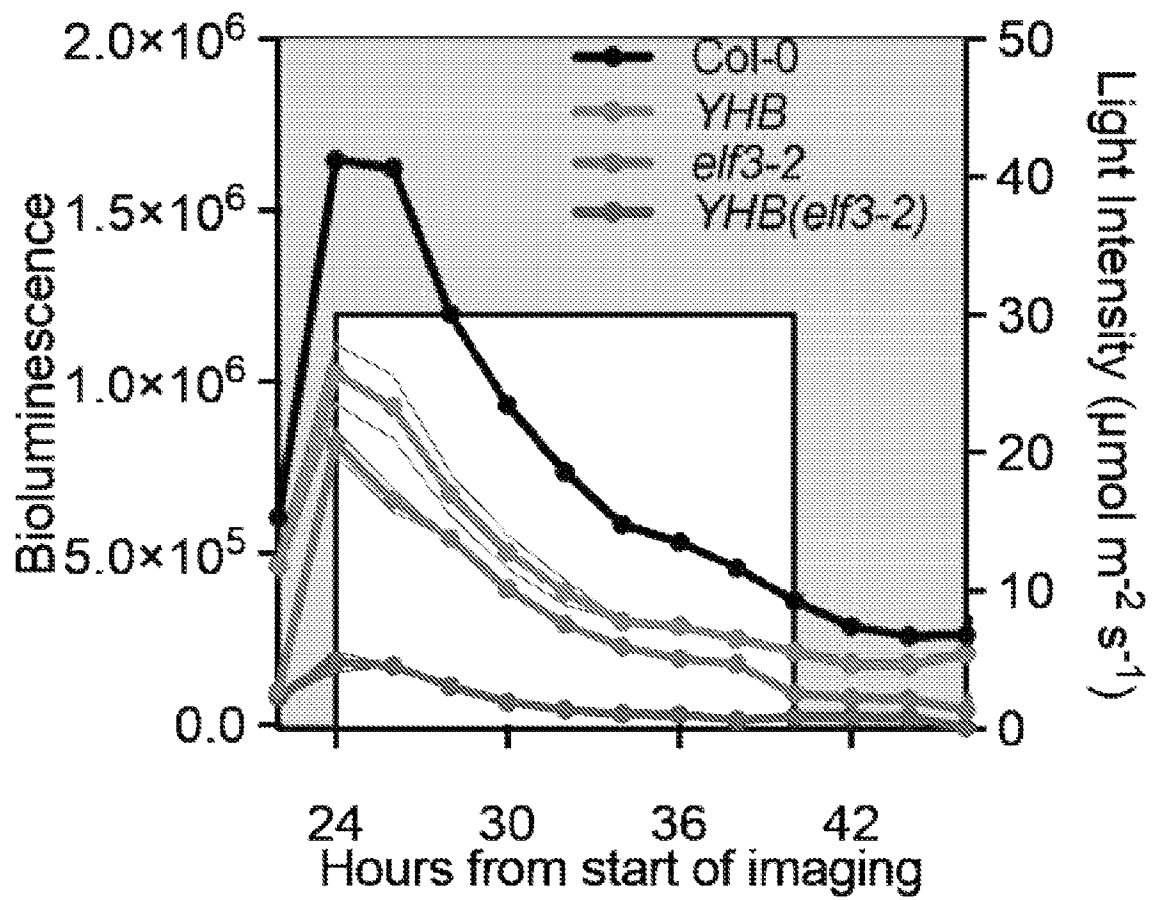


FIG. 9C

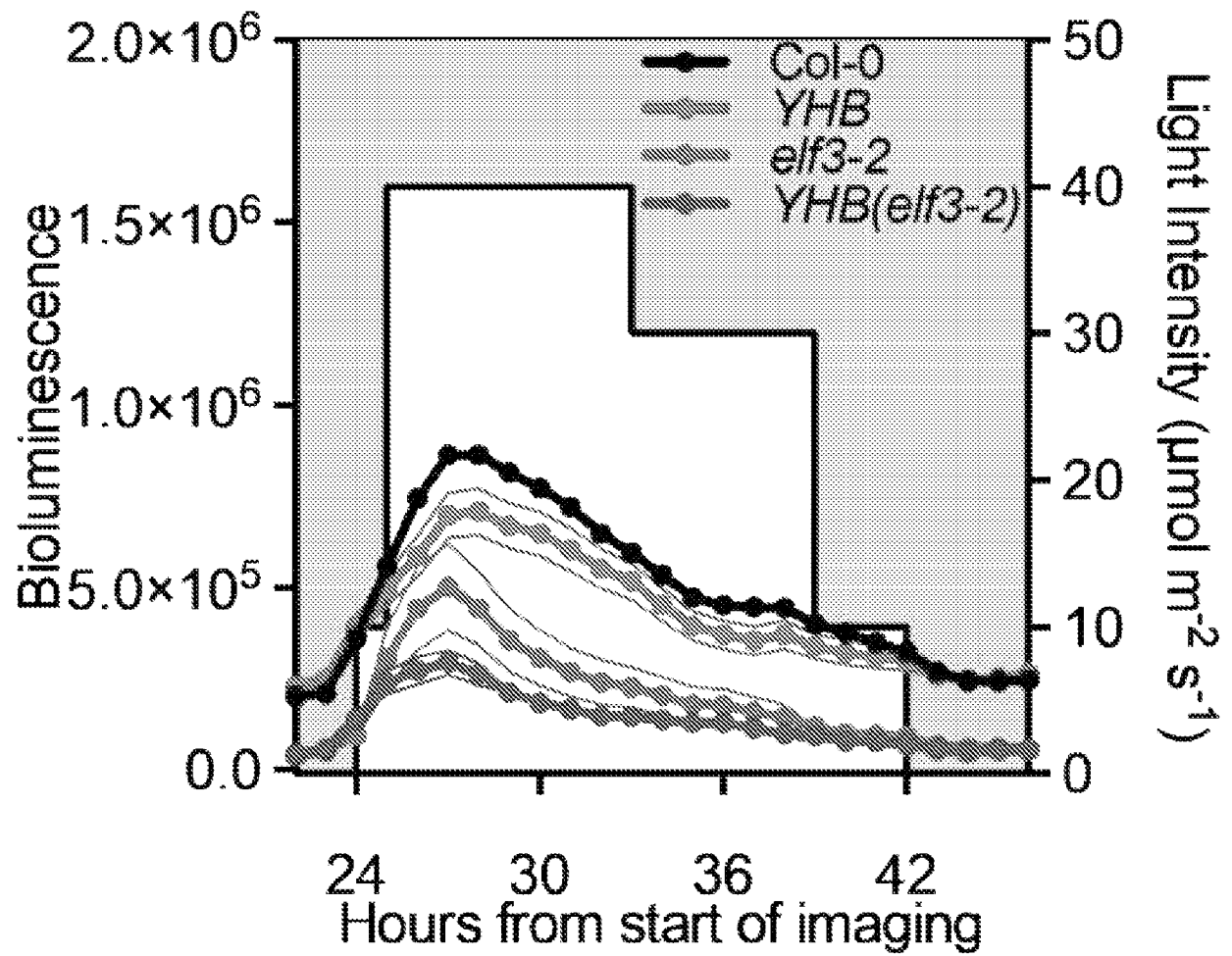


FIG. 10A

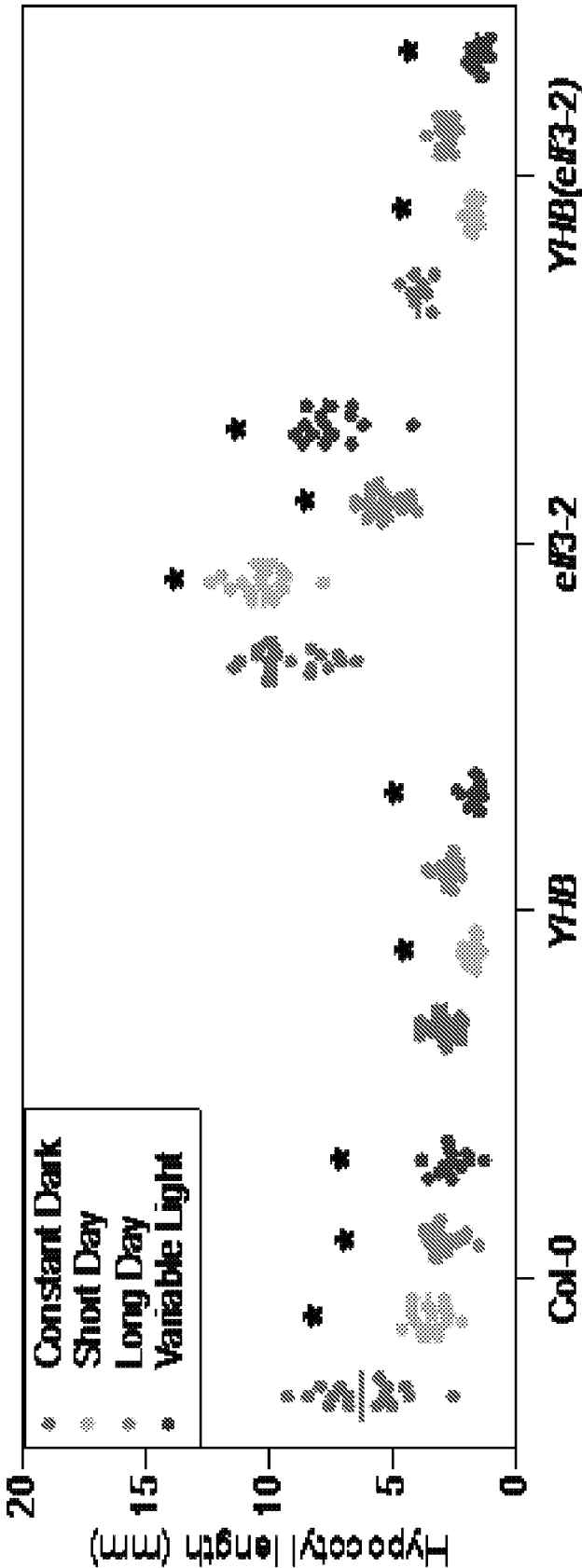


FIG. 10B

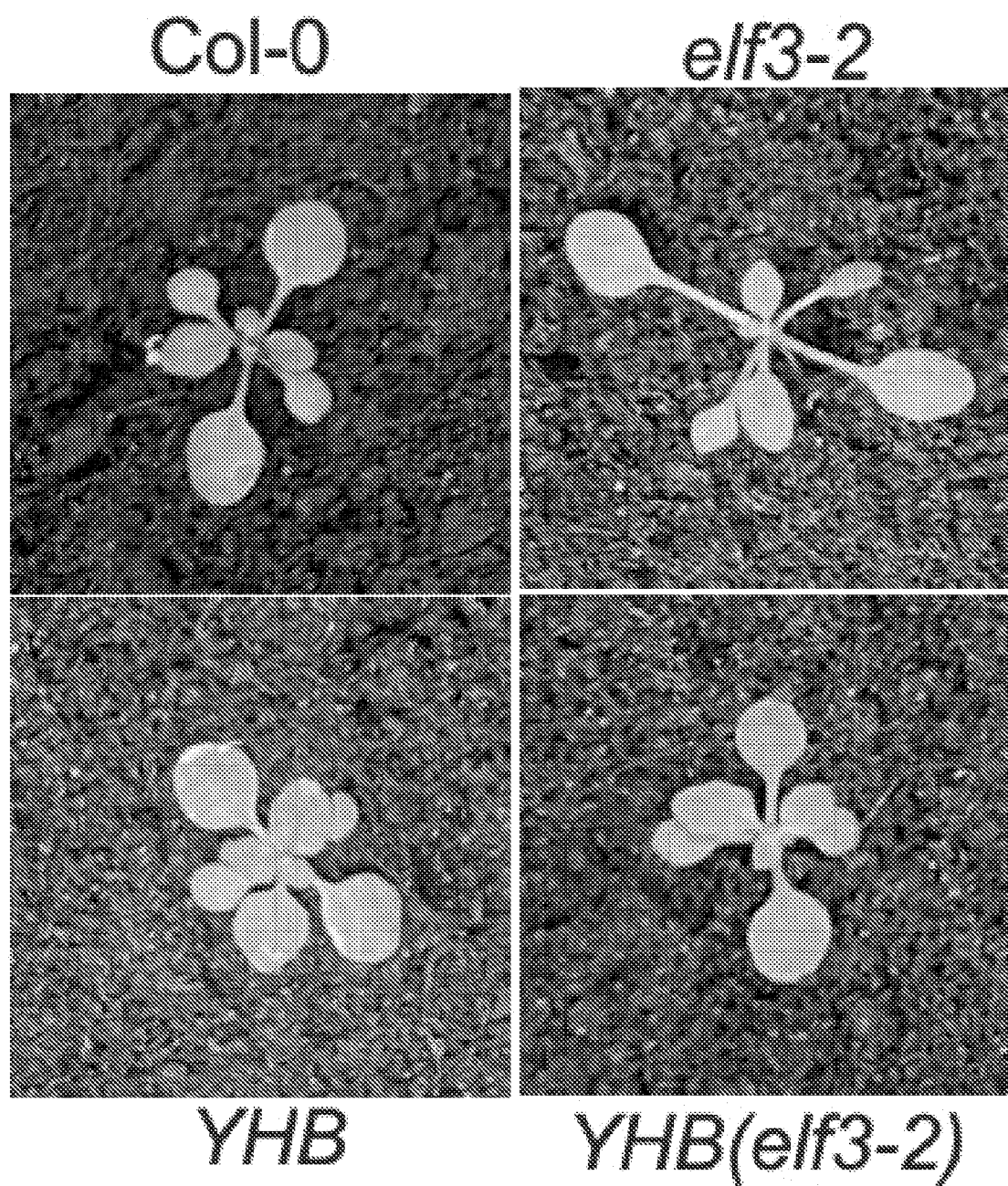


FIG. 10C

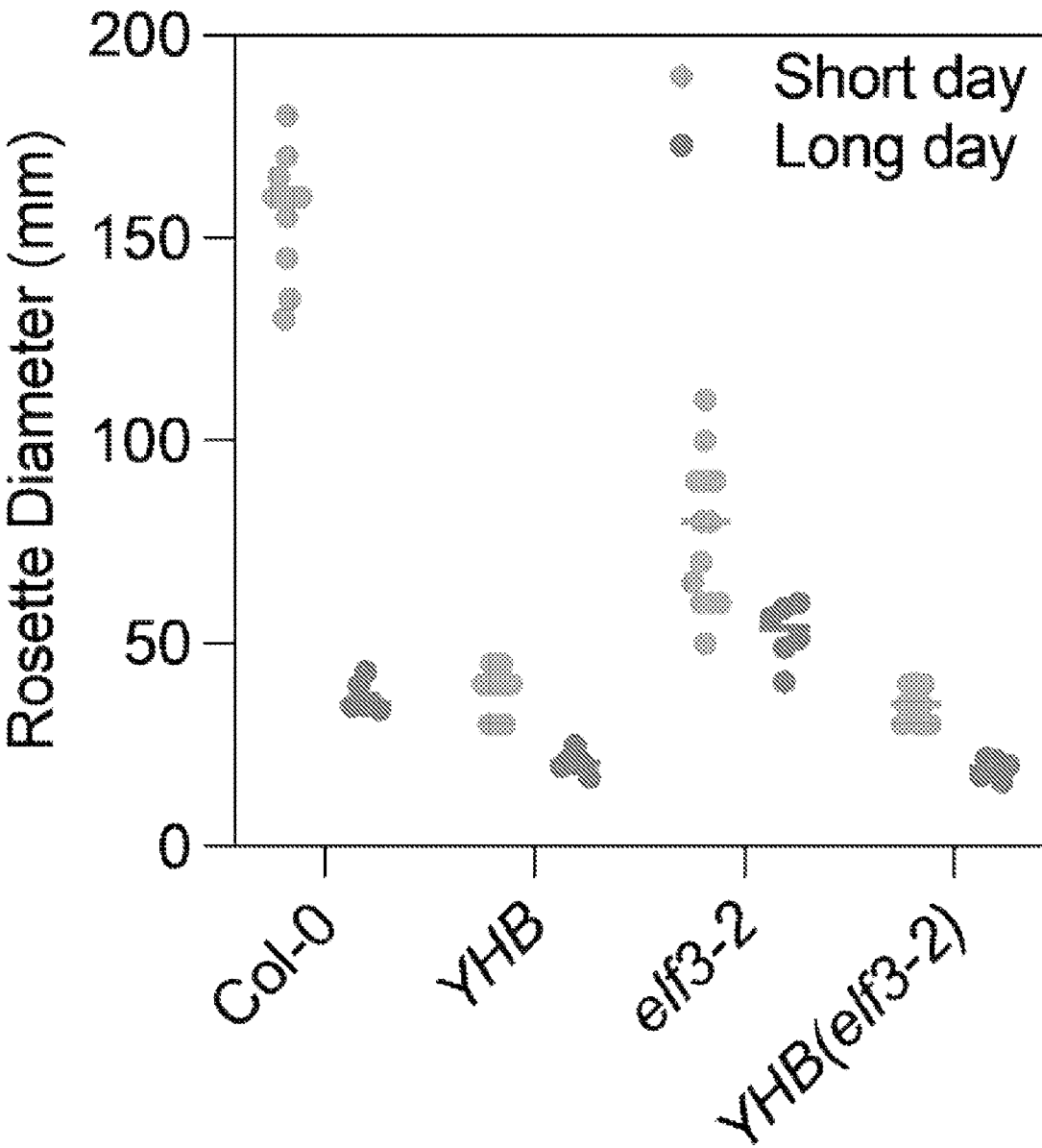


FIG. 10D

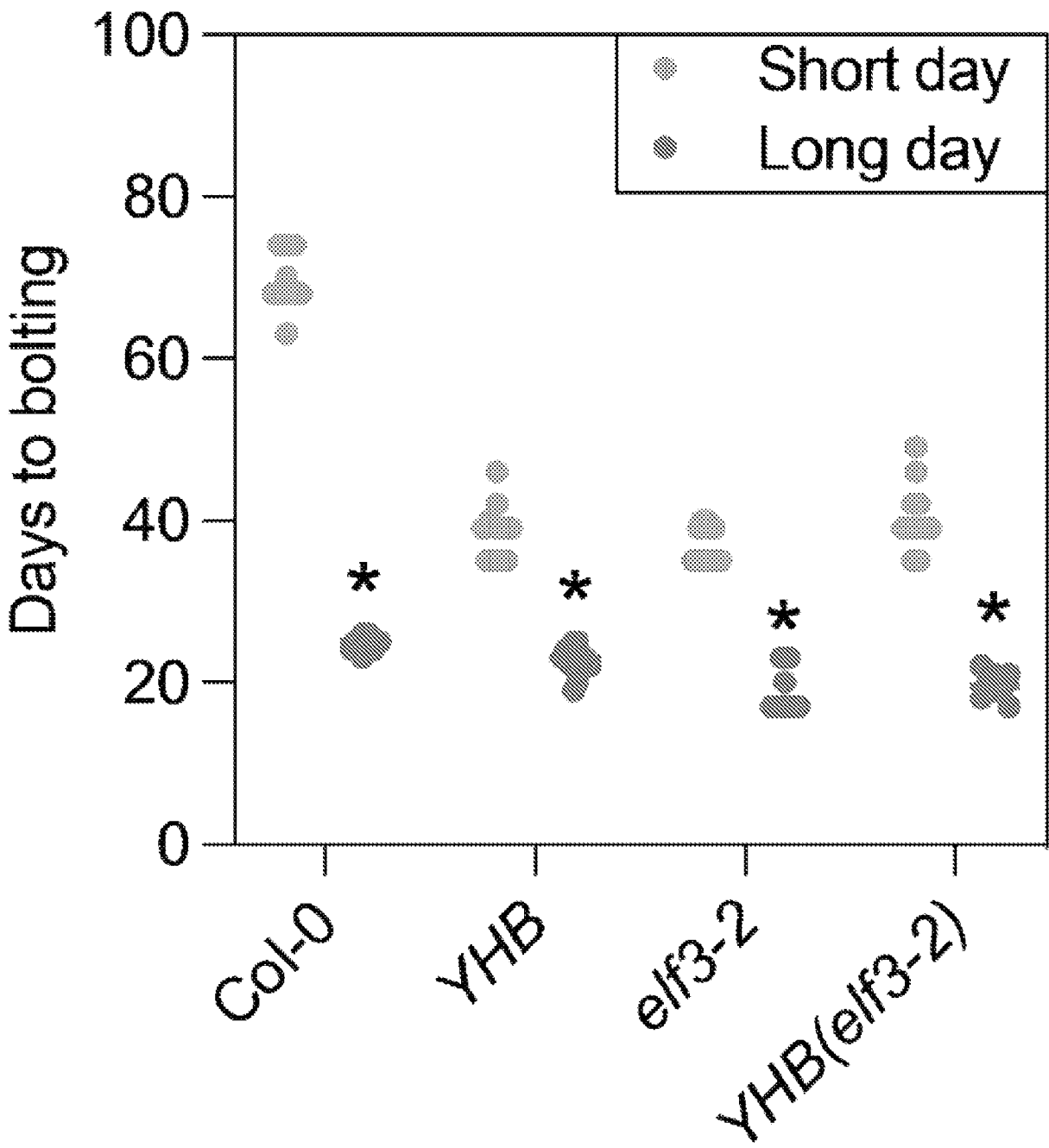


FIG. 10E

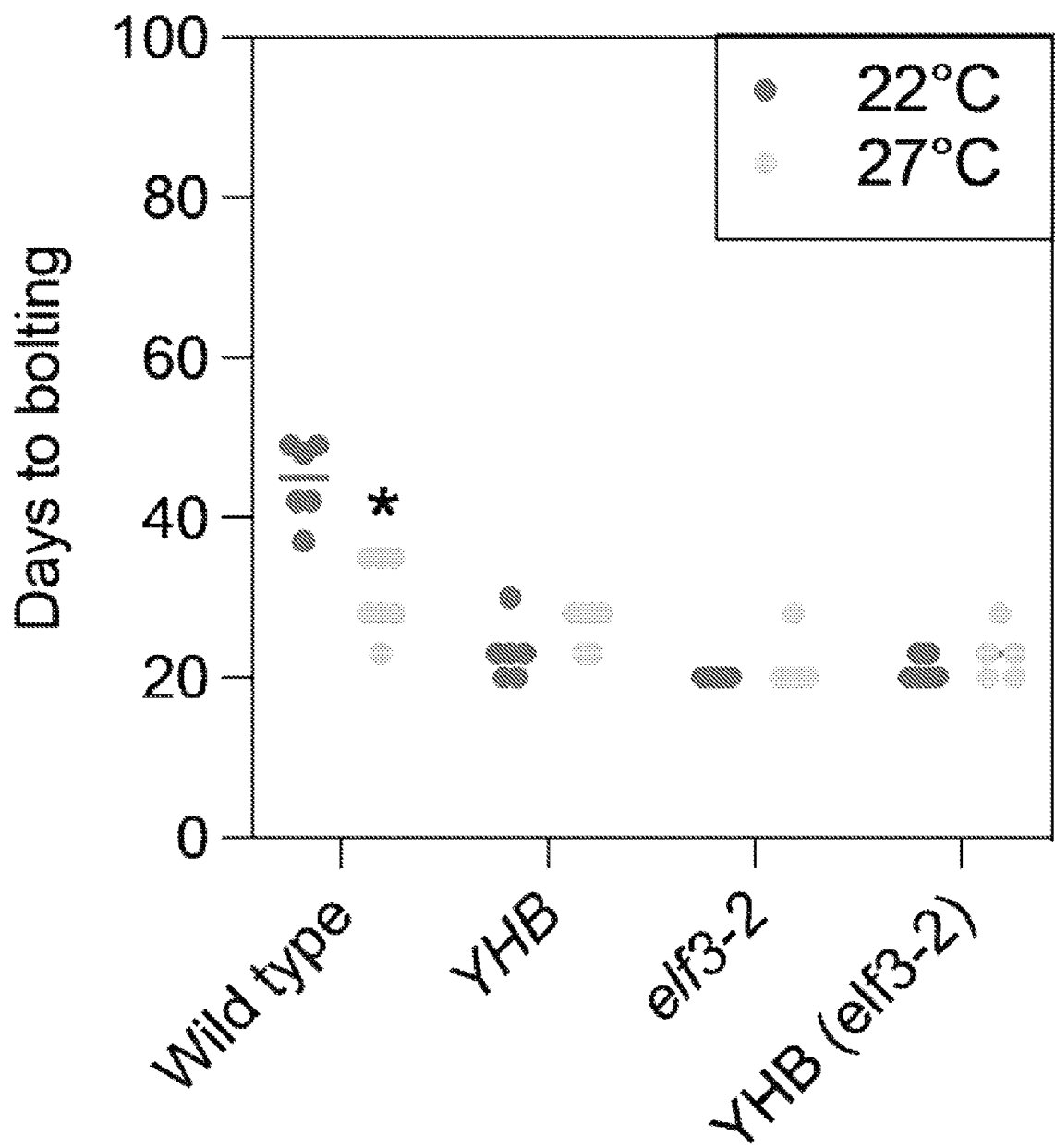


FIG. 10F

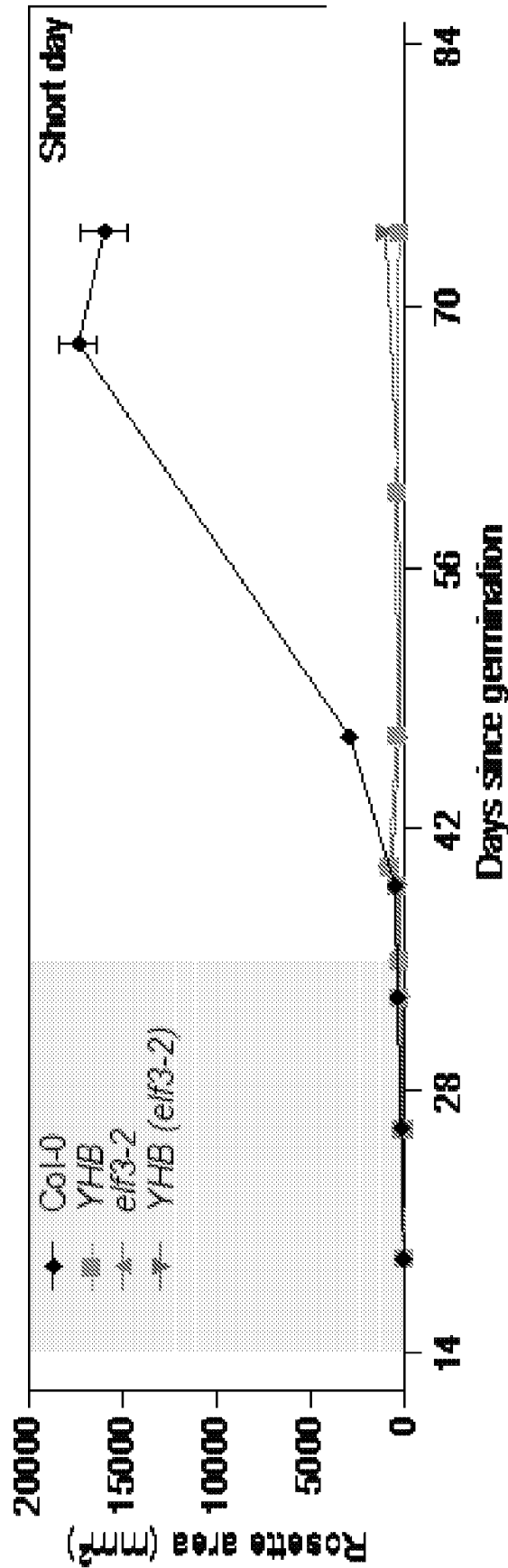


FIG. 10G

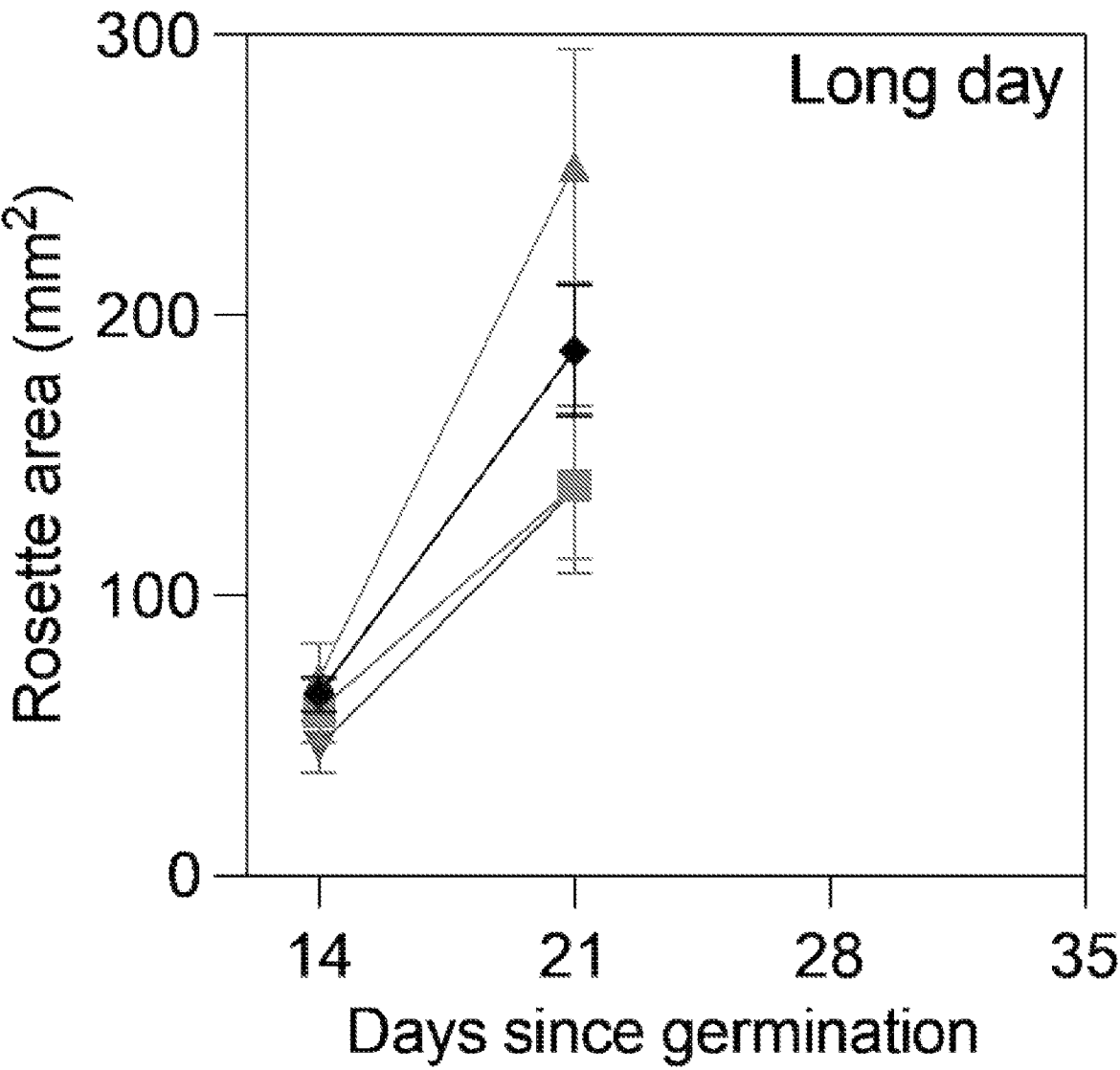


FIG. 10H

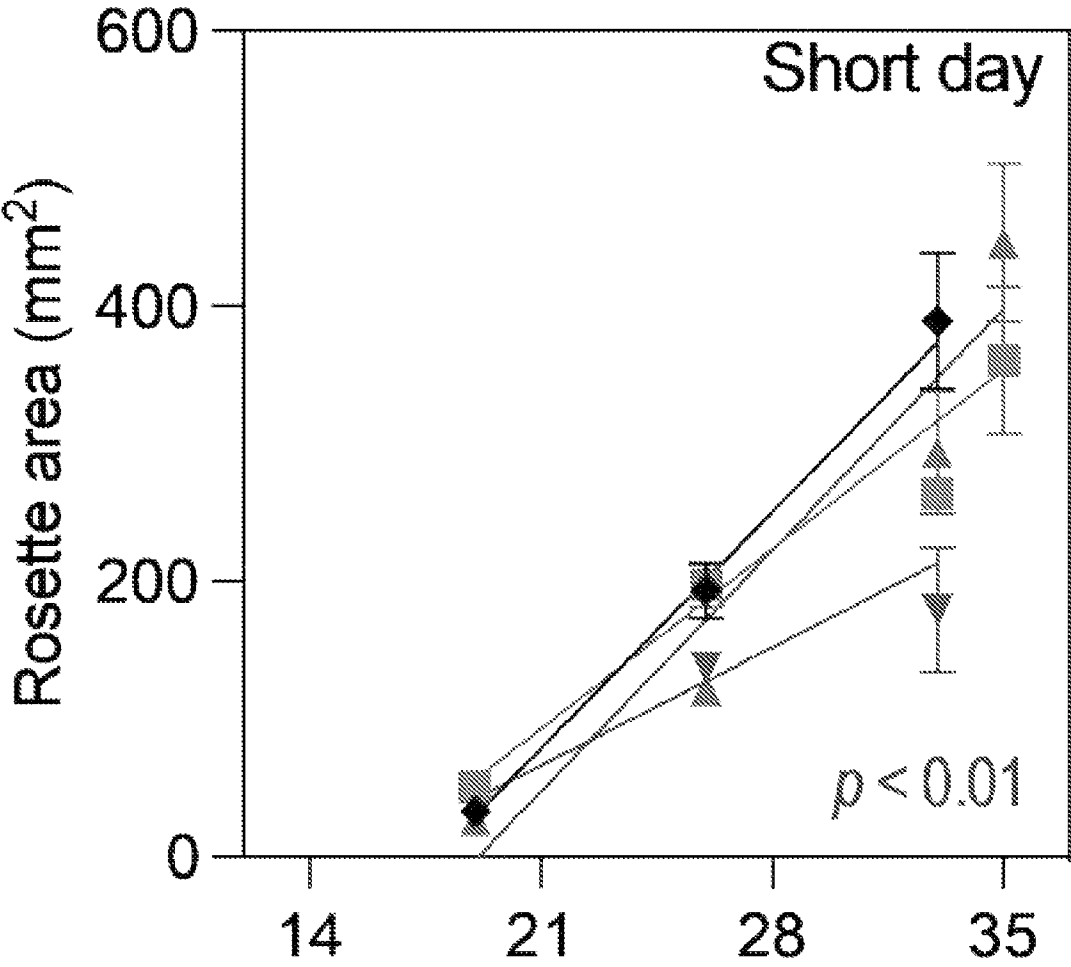


FIG. 11A

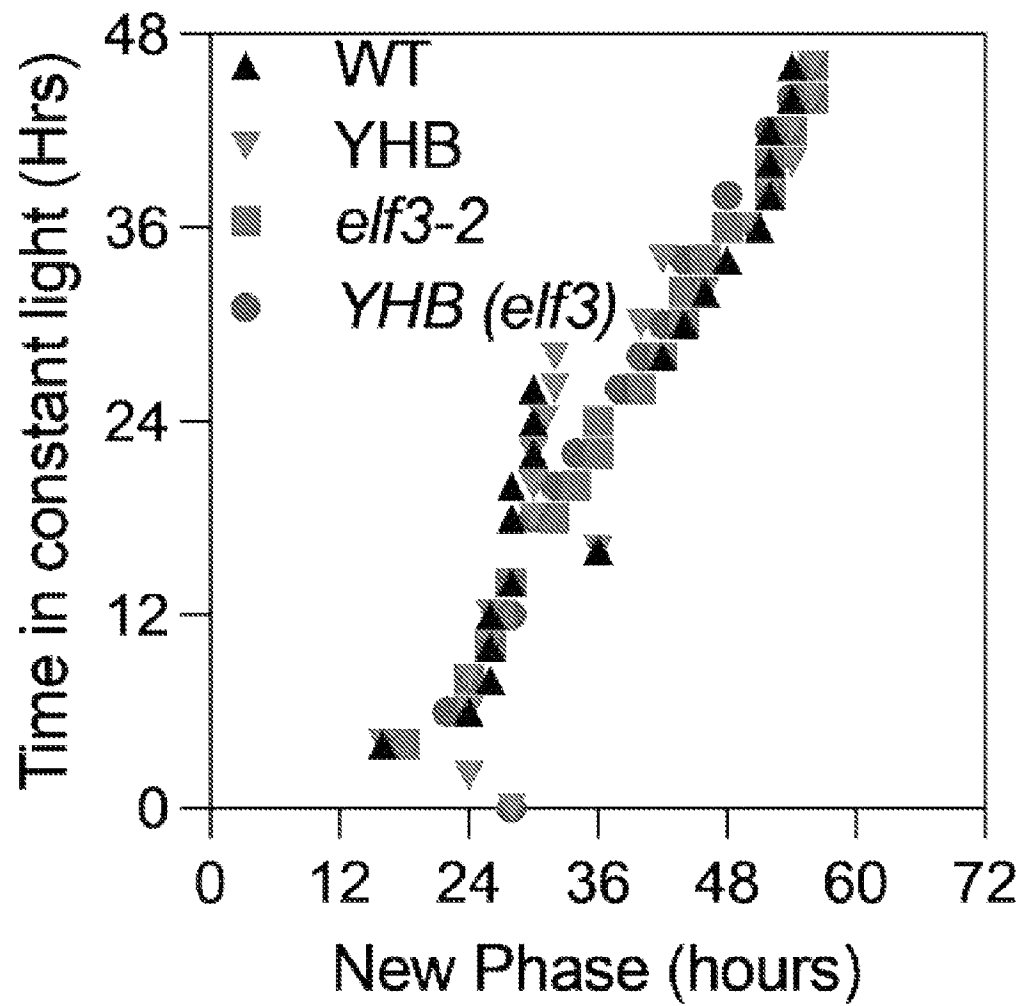


FIG. 11B

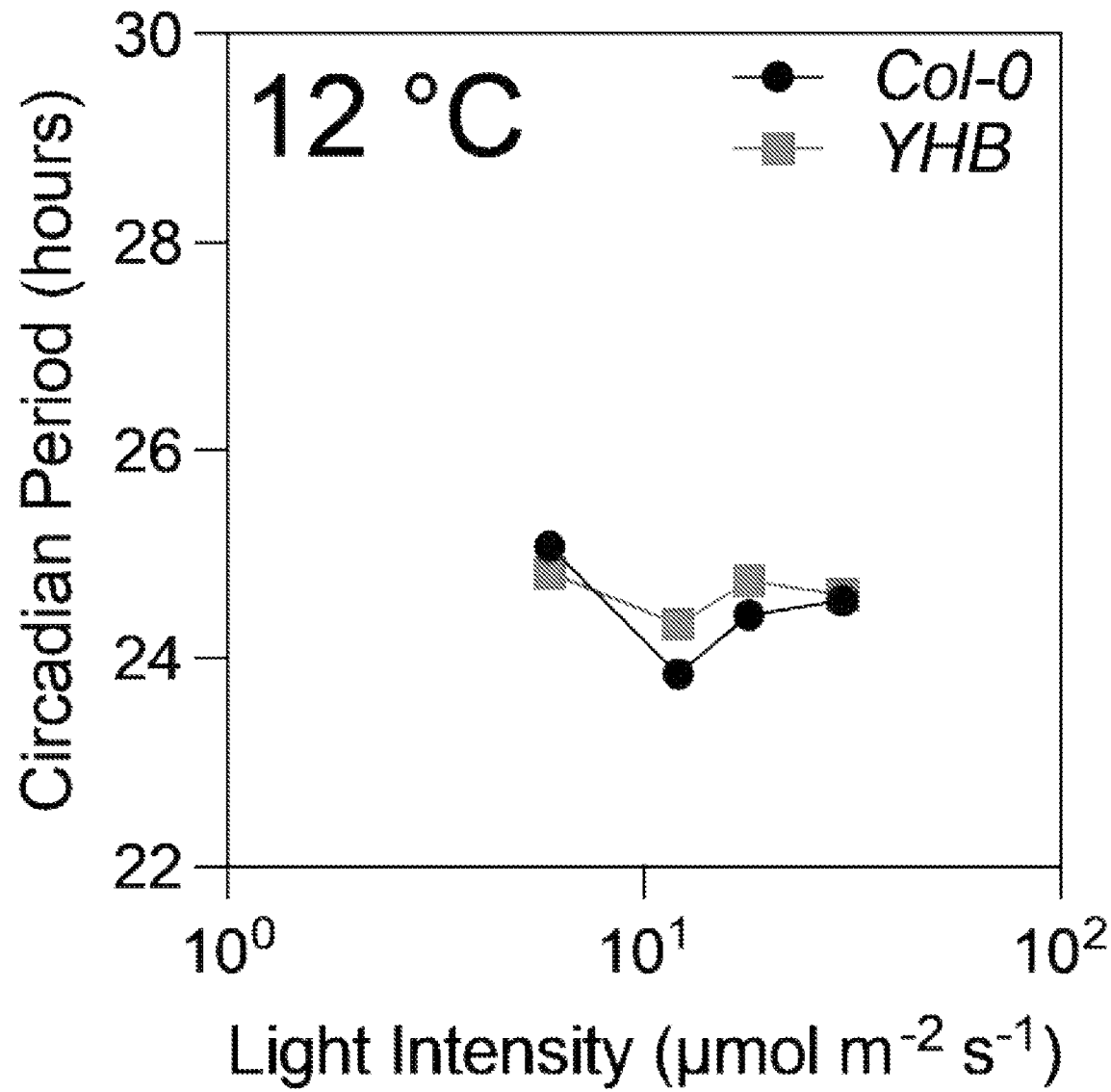


FIG.11C

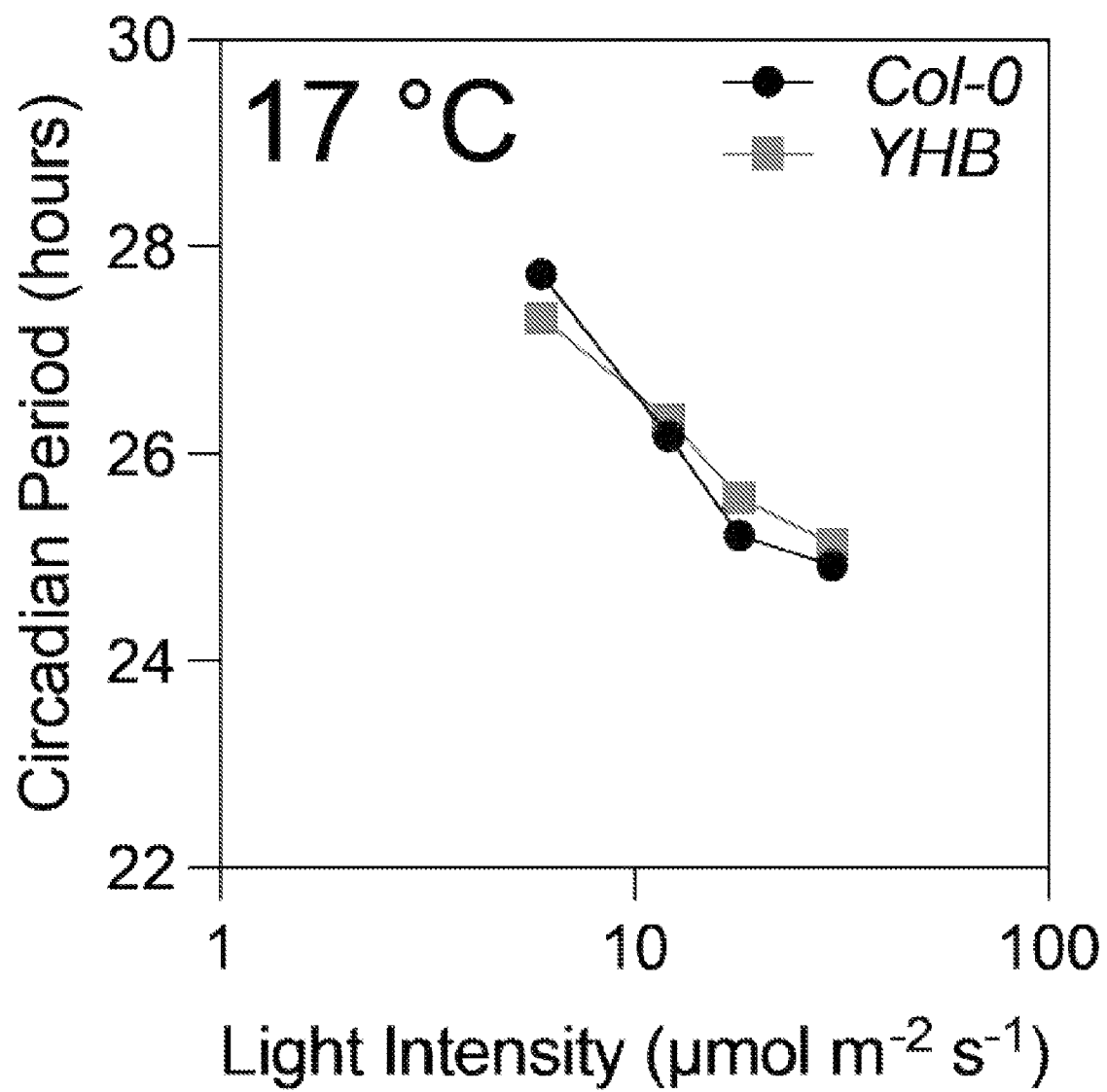


FIG. 11D

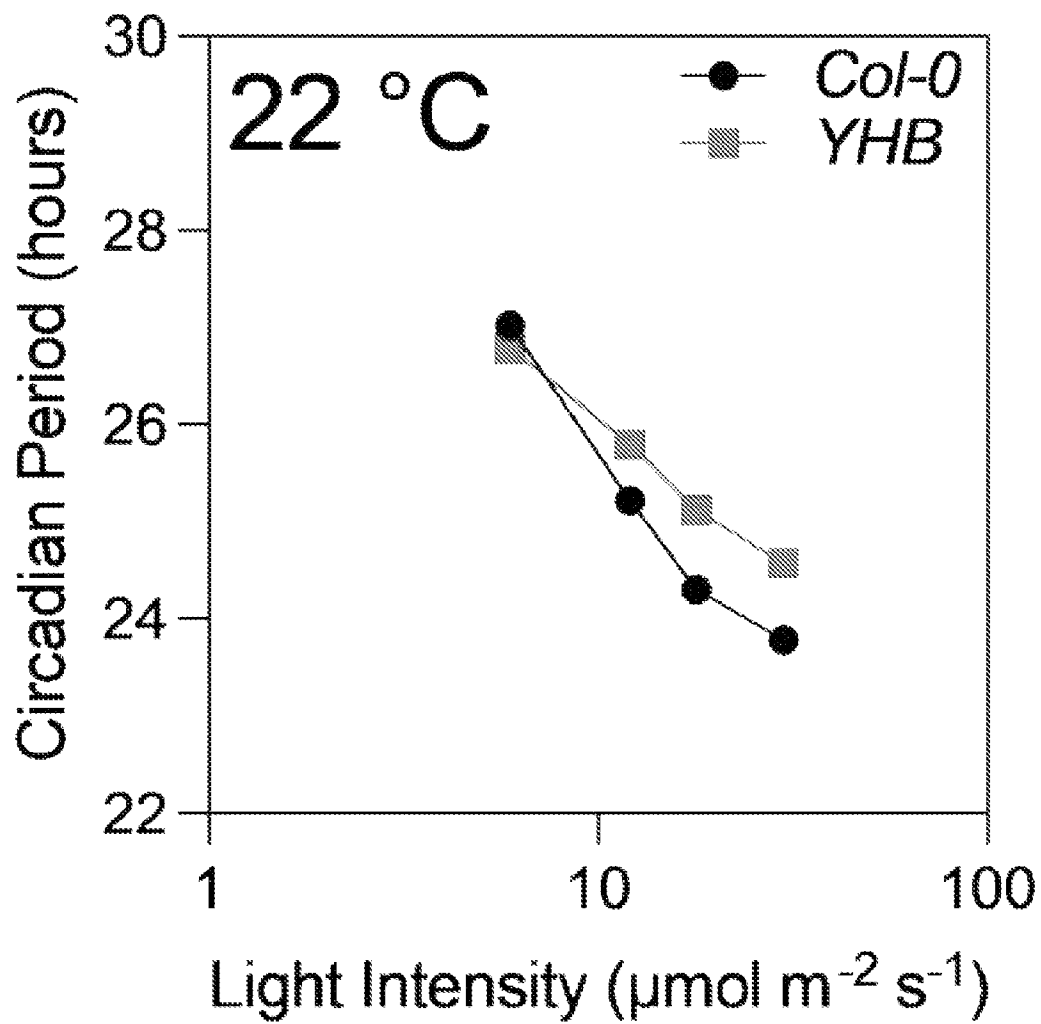


FIG. 11E

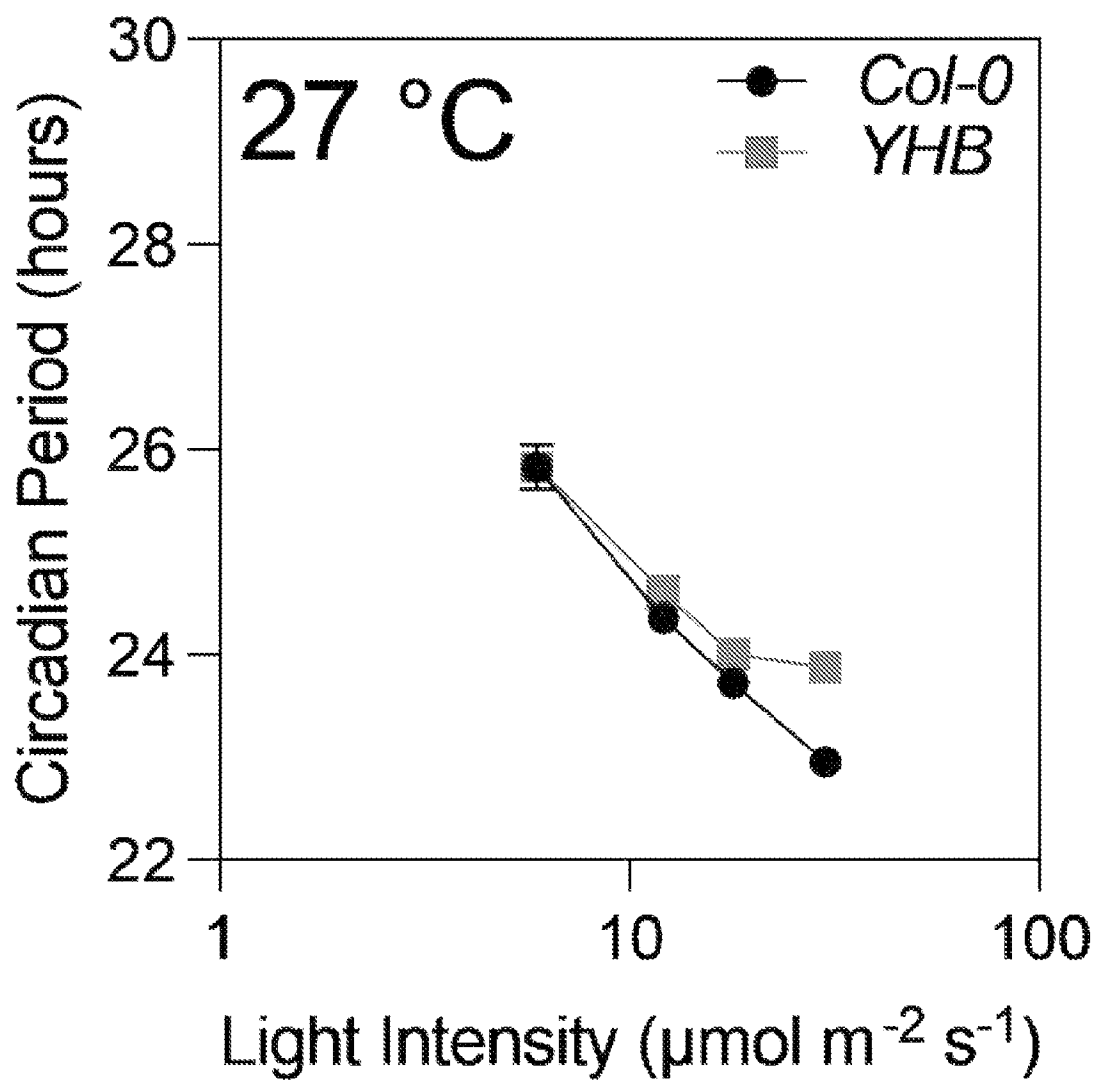


FIG. 12A

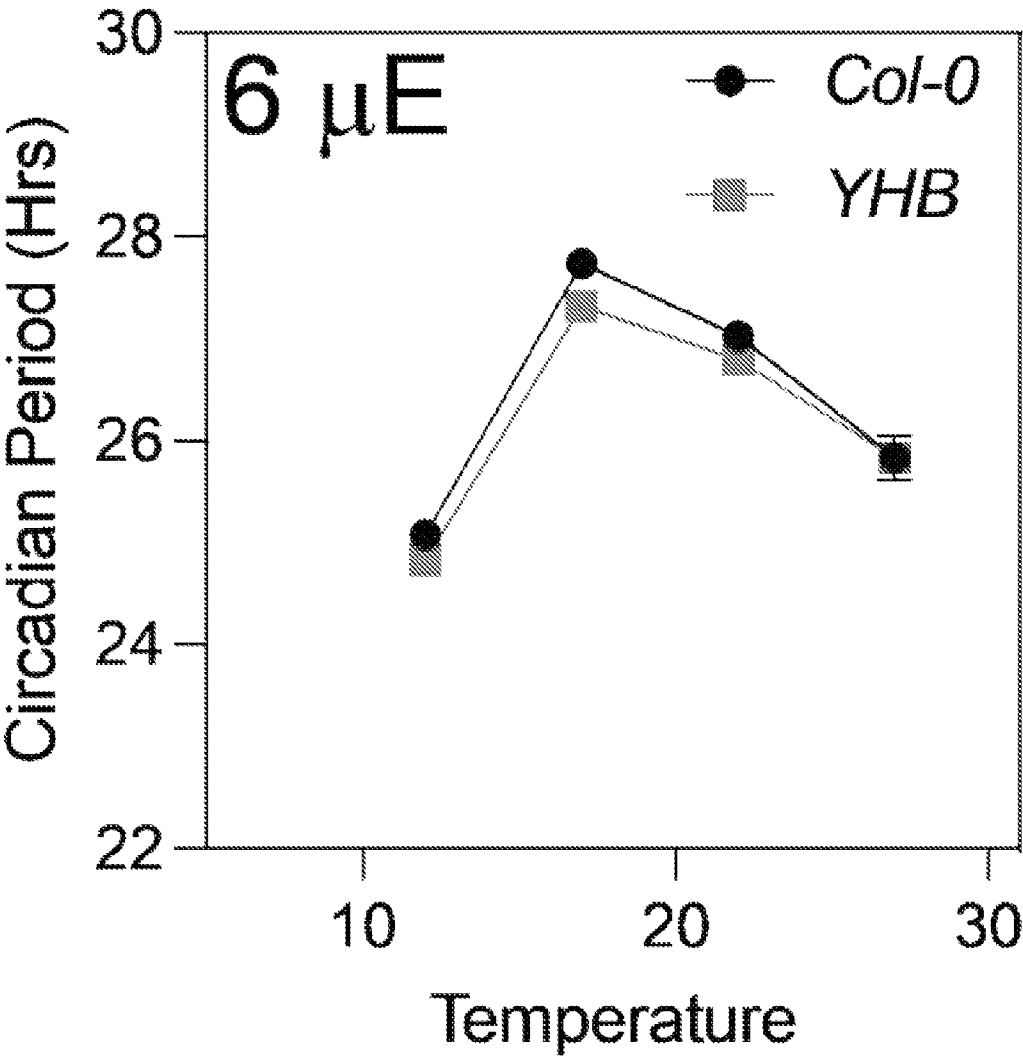


FIG. 12B

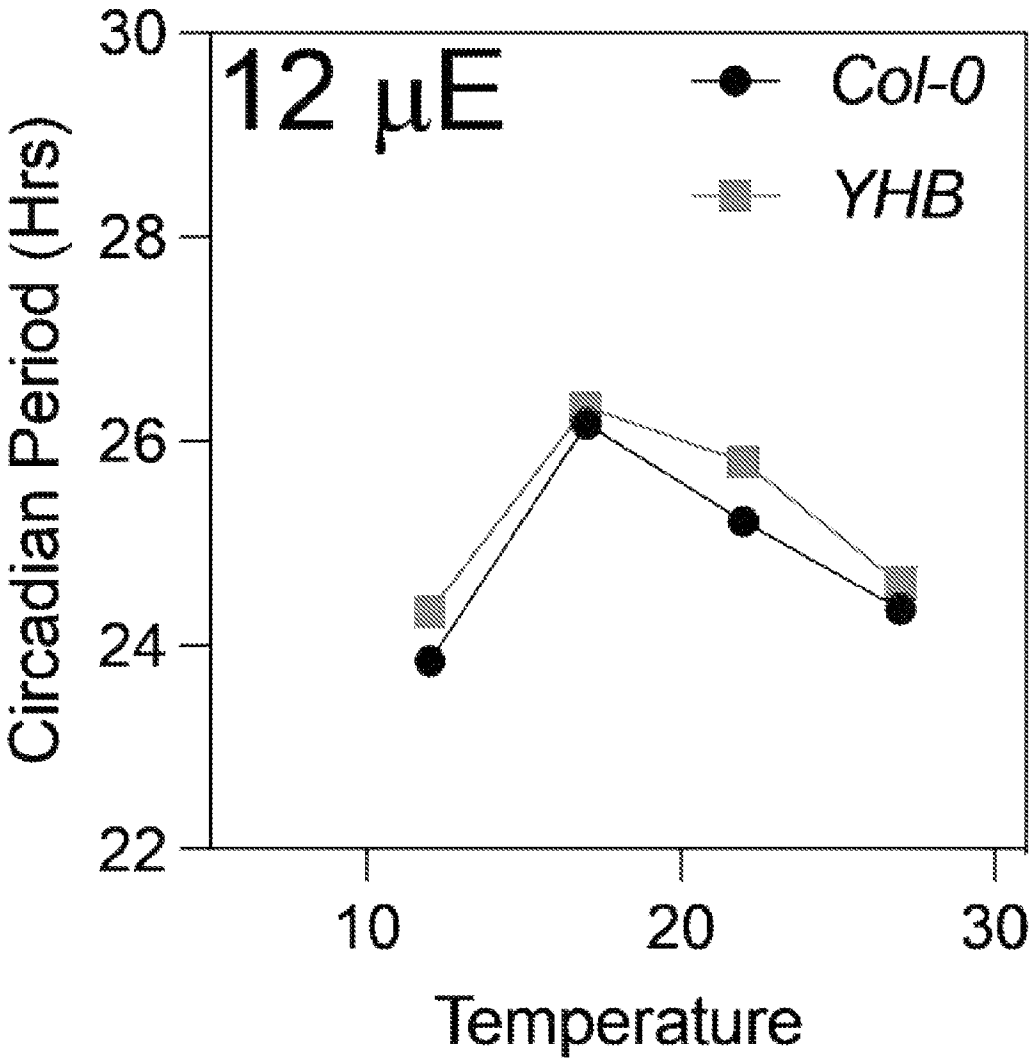


FIG. 12C

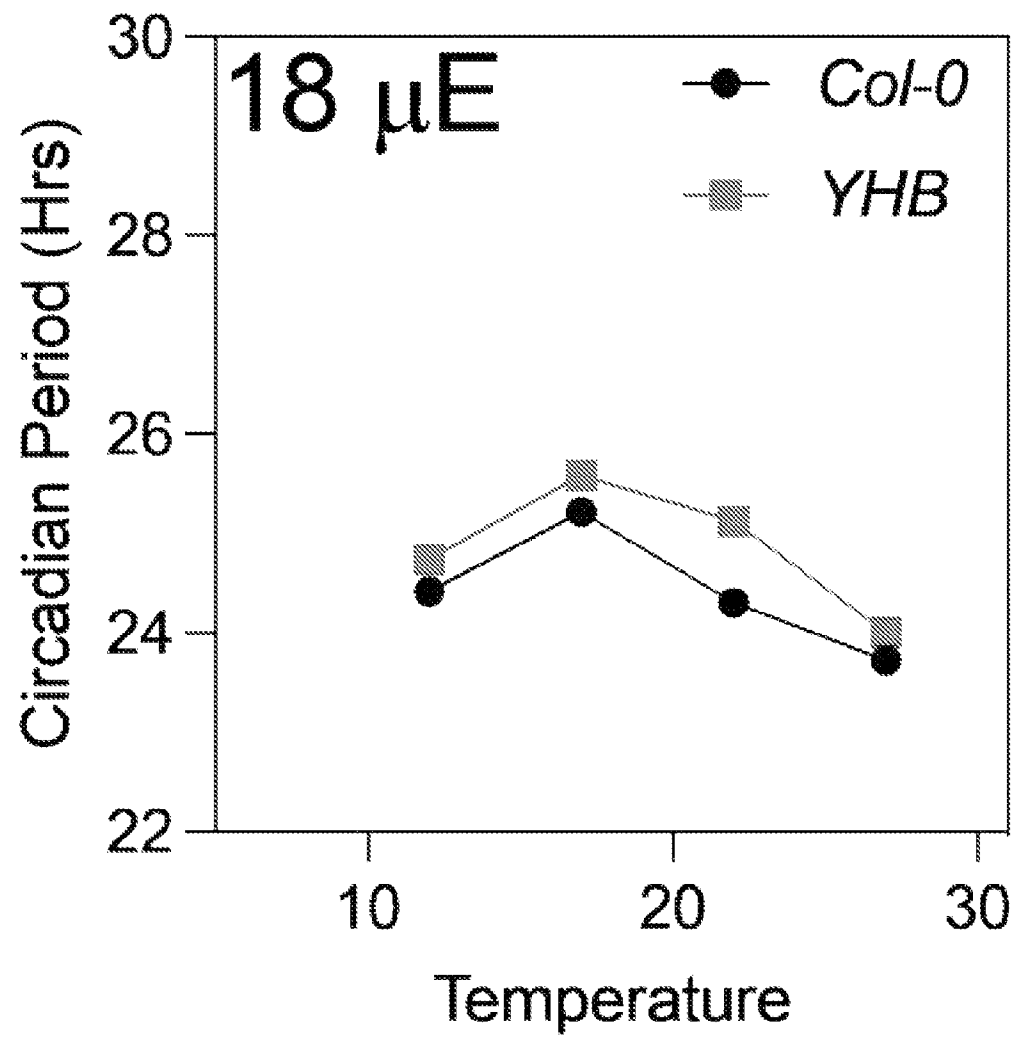


FIG. 12D

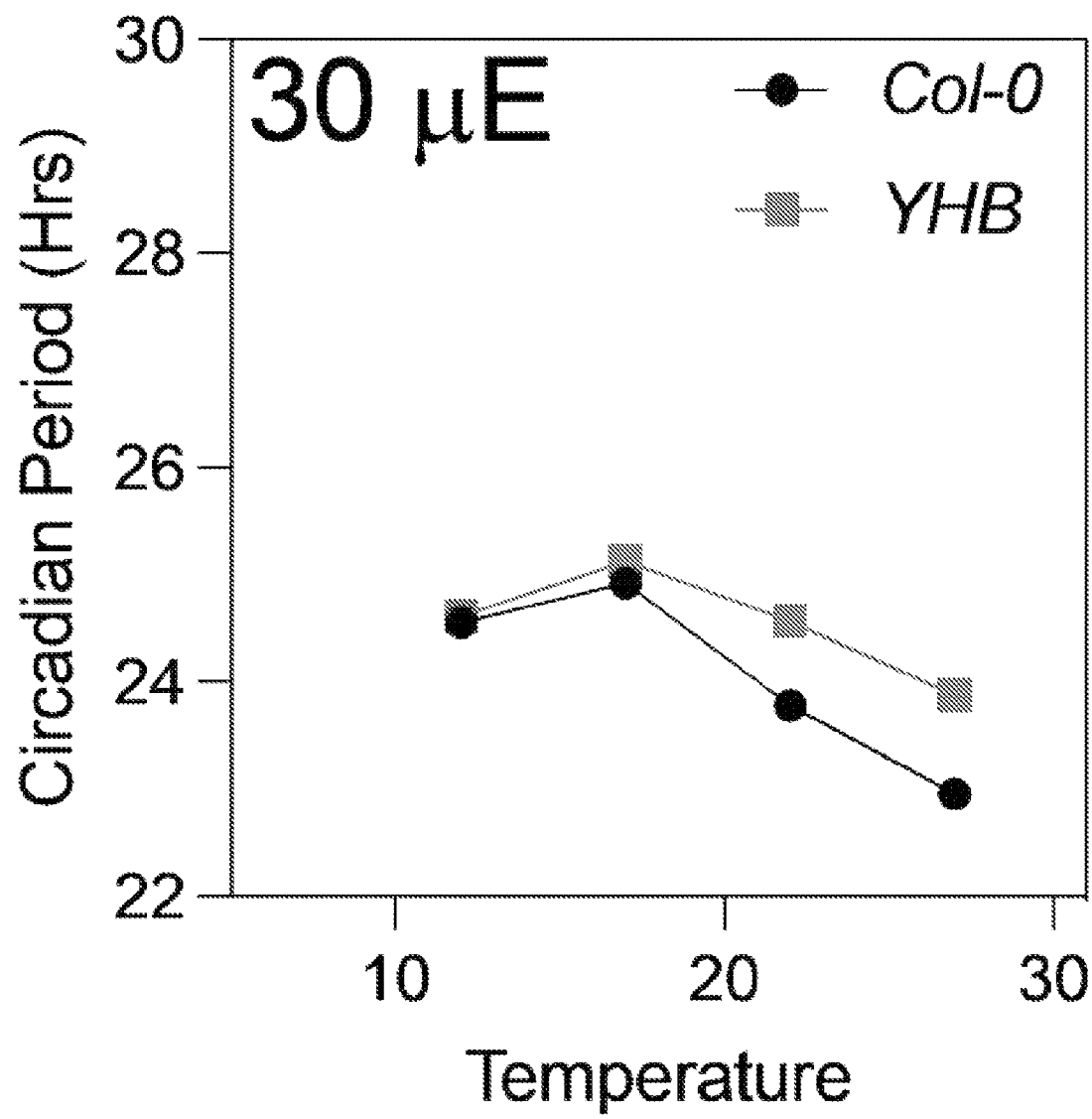


FIG. 13

