

Journal of Experimental Botany Supplementary Information

Article title: *Aethionema arabicum*: a novel model plant to study the light control of seed germination

Authors: Zsuzsanna Mérai, Kai Graeber, Per Wilhelmsson, Kristian K. Ullrich, Waheed Arshad, Christopher Grosche, Danuše Tarkowská, Veronika Turečková, Miroslav Strnad, Stefan A. Rensing, Gerhard Leubner-Metzger, Ortrun Mittelsten Scheid

The following Supplementary Information is available for this article:

- Fig. S1** Germination of dimorphic seed types in response to light.
- Fig. S2** Heatmap of all 87 genes light-regulated in *Aethionema arabicum* CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM (reads per kilobase of transcript per million mapped reads) values.
- Fig. S3** Identification of the Arabidopsis orthologue of *Aethionema* AA18G00108 as GA2ox3. (A) Gibberellin 2-oxidase family phylogeny based on protein sequences. (B) Synteny of GA2ox3 position in the genome of Arabidopsis and *Aethionema*.
- Fig. S4** Accumulation of GA forms in *Aethionema arabicum* TUR and CYP seeds under dark and light conditions.
- Fig. S5** Identification and alignments of phytochromes in *Aethionema arabicum*. (A) Phylogenetic tree of phytochromes. (B-F) Phytochrome A, B, C, D, E protein alignments of three *Aethionema arabicum* accessions.
- Fig. S6** Alignment of PIL5/PIF1 protein sequence of three *Aethionema arabicum* accessions.
- Table S1** Information about geographic origin of *Aethionema arabicum* accessions.
- Table S2** List of primers used for quantitative RT-PCR analysis.
- Table S3** List of *Aethionema* accession numbers used for this study.
- Dataset S1** List of differentially expressed *Aethionema arabicum* genes in TUR Dark versus TUR Light.
- Dataset S2** List of differentially expressed *Aethionema arabicum* genes in CYP Dark versus CYP Light.
- Dataset S3** List of differentially expressed *Aethionema arabicum* genes in CYP Dark versus TUR Dark.
- Dataset S4** List of differentially expressed *Aethionema arabicum* genes in CYP Light versus TUR Light.
- Dataset S5** List of common differentially expressed *Aethionema arabicum* genes in CYP Light versus TUR Light and TUR Dark versus TUR Light.

Dataset S6 List of target genes of Arabidopsis PIL5/PIF1 and transcriptional changes of orthologues in the Aethionema experiments.

Dataset S7 List of plant species for which protein sequences were considered for phylogenetic tree constructions.

Supplementary Figure Legends

Fig. S1 Germination of dimorphic seed types in response to light. Germination of mucilaginous (M+) and non-mucilaginous (M-) seeds were tested from TUR and CYP accessions in dark or under white light ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$). Images were taken 7 days after imbibition.

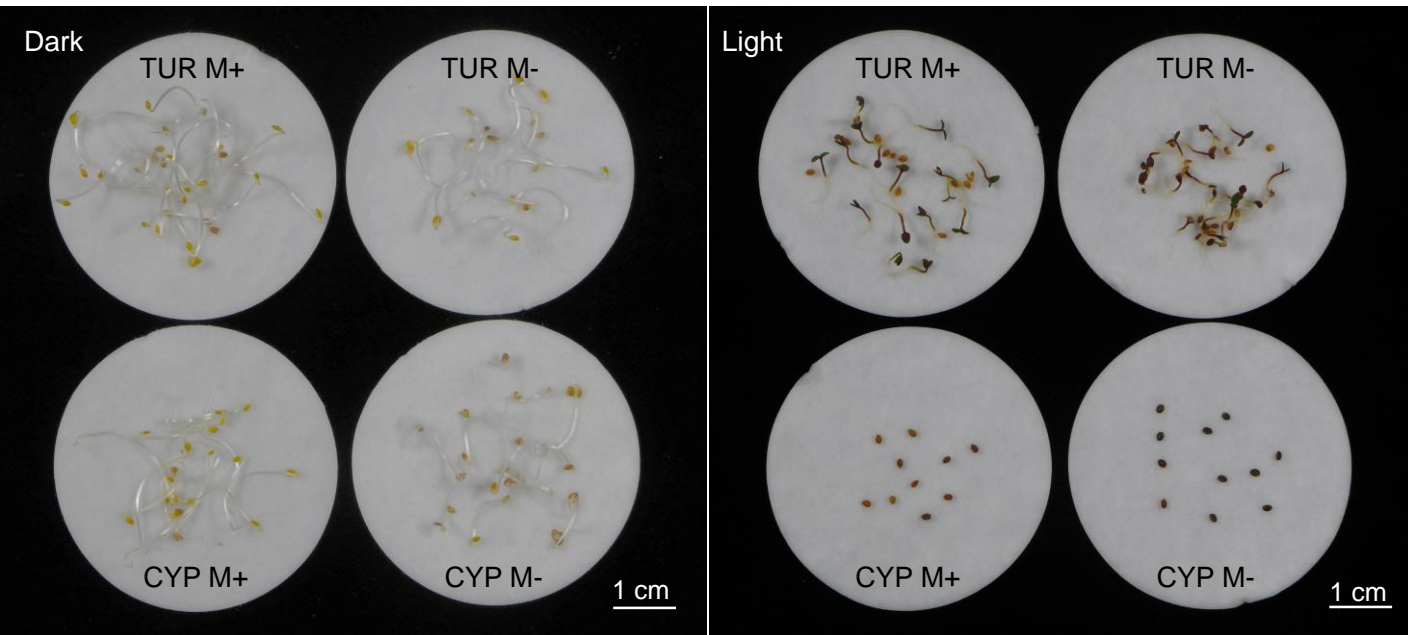
Fig. S2 Heatmap of all 87 genes light-regulated in CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM values.

Fig. S3 Identification of the *A. thaliana* orthologue of *Ae. arabicum* AA18G00108 as GA2ox3. **(a)** Phylogenetic tree of gibberelin2-oxidases using Bayesian inference (2000000 generations, standard deviation of split frequencies 0.063371) and allows clear assignment of *Ae. arabicum* orthologues. Sequences of *A. thaliana* (ARATH) and *Ae. arabicum* (AETAR) are marked in green and red, respectively. For detailed assignment of five letter code see Supplemental Dataset 7. **(b)** Synteny of GA2ox3 position in the genome of *A. thaliana* and *Ae. arabicum*.

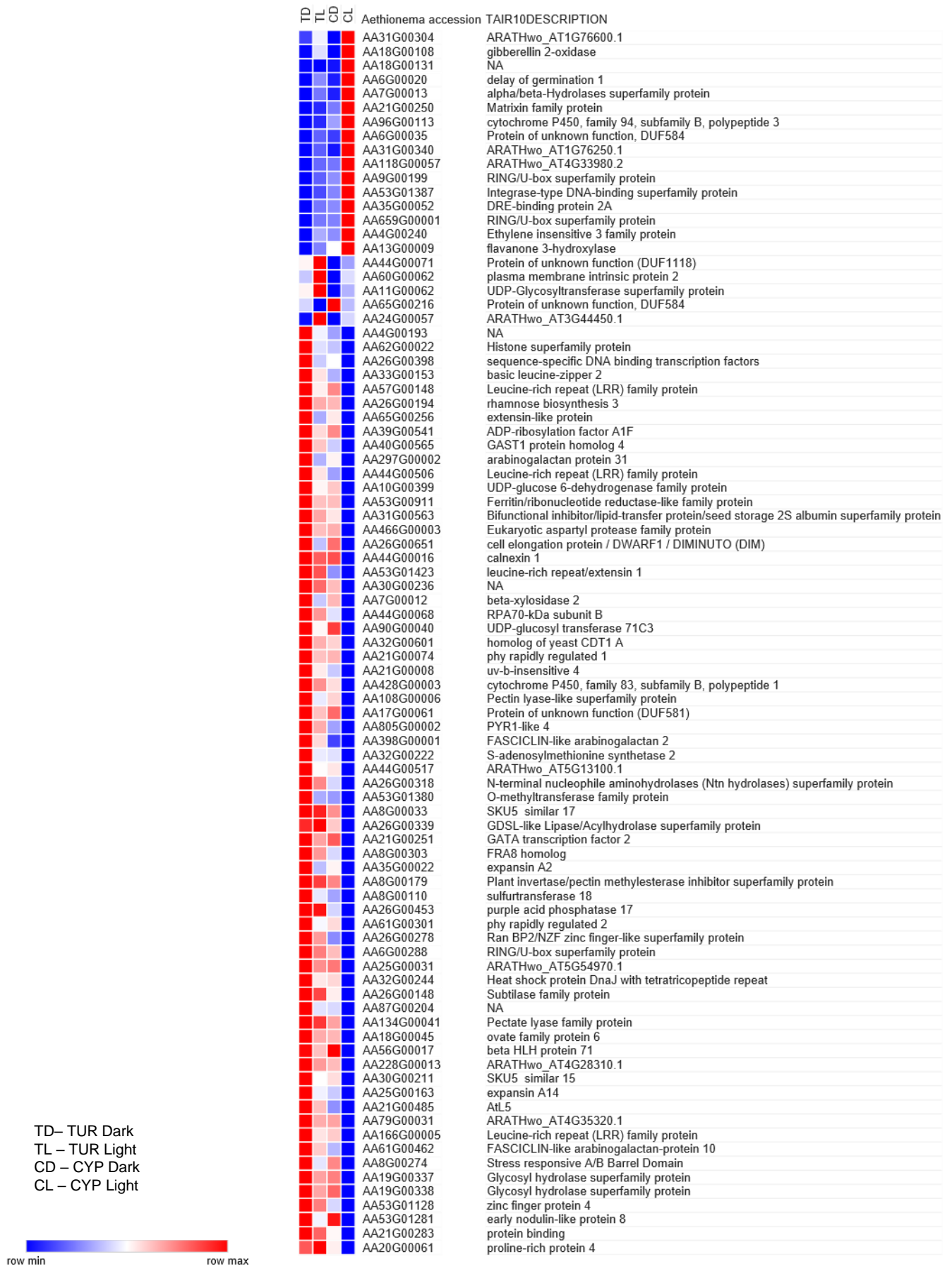
Fig. S4 Accumulation of GA forms in *Ae. arabicum* TUR and CYP seeds under dark and light conditions.

Fig. S5 Identification and alignments of phytochromes in *Ae. arabicum*. **(a)** Phylogenetic tree of phytochromes using Bayesian inference (1688500 generations, standard deviation of split frequencies 0.009992) and allows clear assignment of *Ae. arabicum* orthologues. Sequences of *A. thaliana* (ARATH) and *Ae. arabicum* (AETAR) are marked in green and red, respectively. For detailed assignment of five letter code see Supplemental Dataset 7. **(b-f)** Phytochrome protein alignments of three *Ae. arabicum* accessions. Germination of TUR seeds is light-insensitive while CYP and KM2397 both have light inhibited germination.

Fig. S6 Alignment of PIL5/PIF1 protein sequence of three *Ae. arabicum* accessions. Germination of TUR seeds is light-insensitive while CYP and KM2397 both have light inhibited germination.

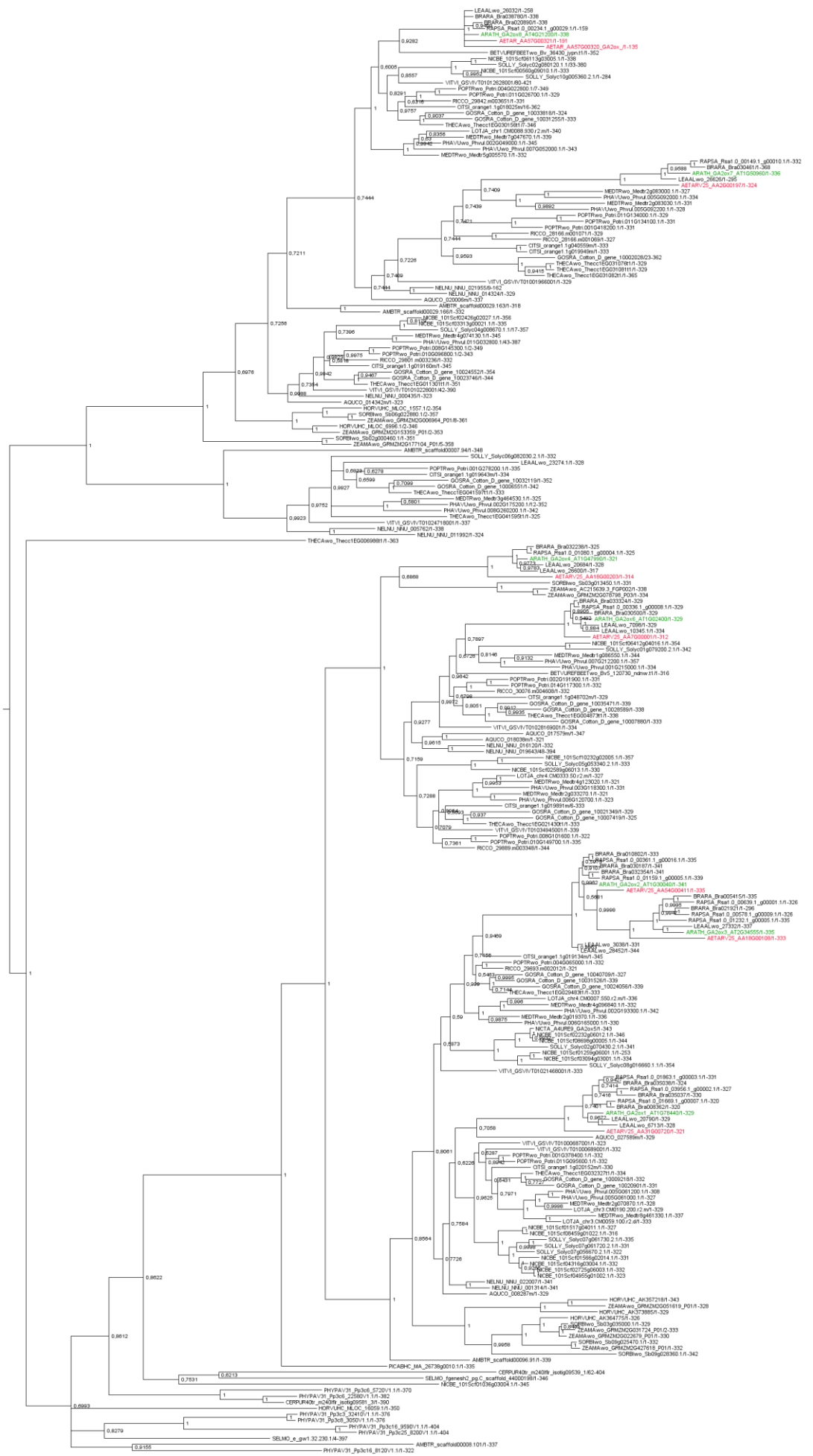


Supporting Figure 1. Germination of dimorphic seed types in response to light. Germination of mucilaginous (M+) and non-mucilaginous (M-) seeds were tested from TUR and CYP accessions in dark or under white light ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$). Images were taken 7 days after imbibition.

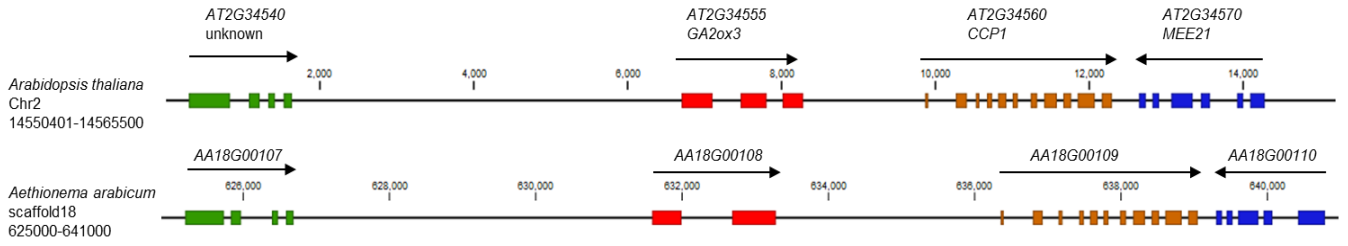


Supporting Figure 2. Heatmap of all 87 genes light-regulated in CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM values.

A

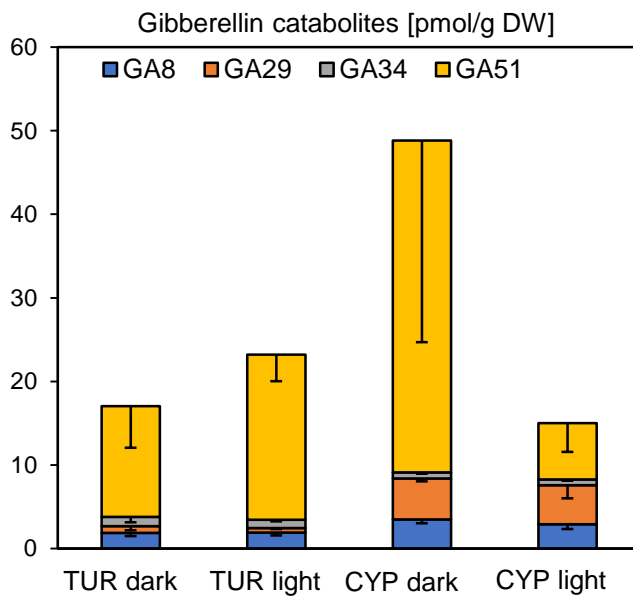
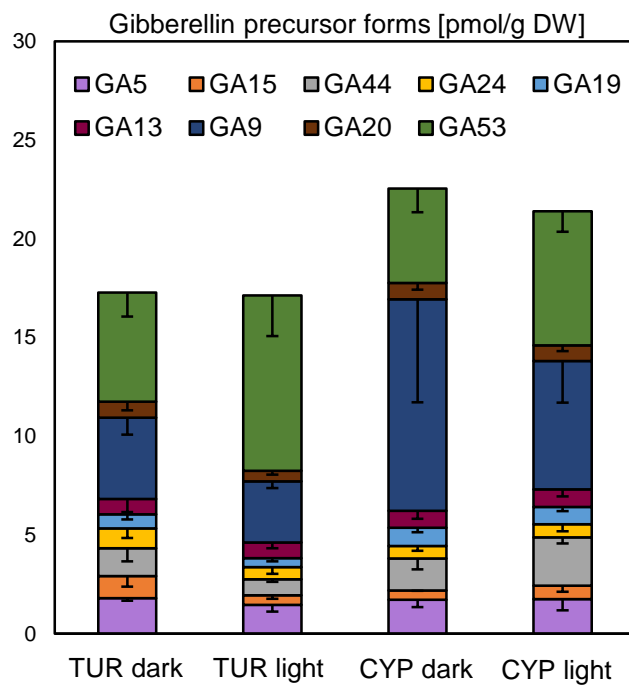
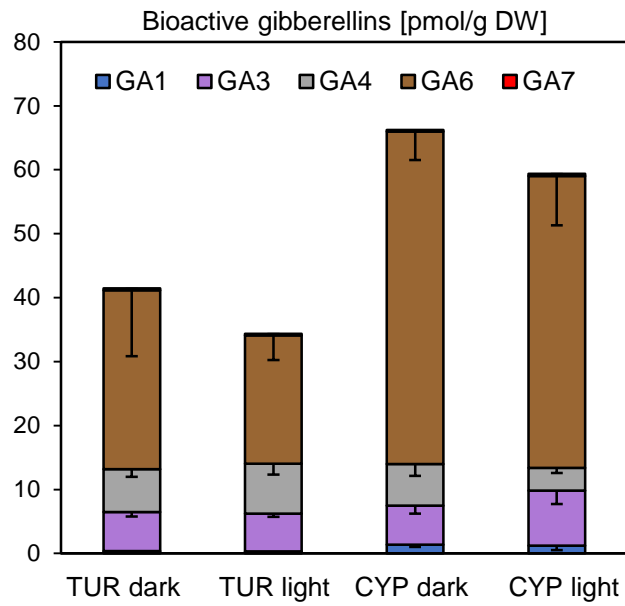


Supporting Figure 3

B

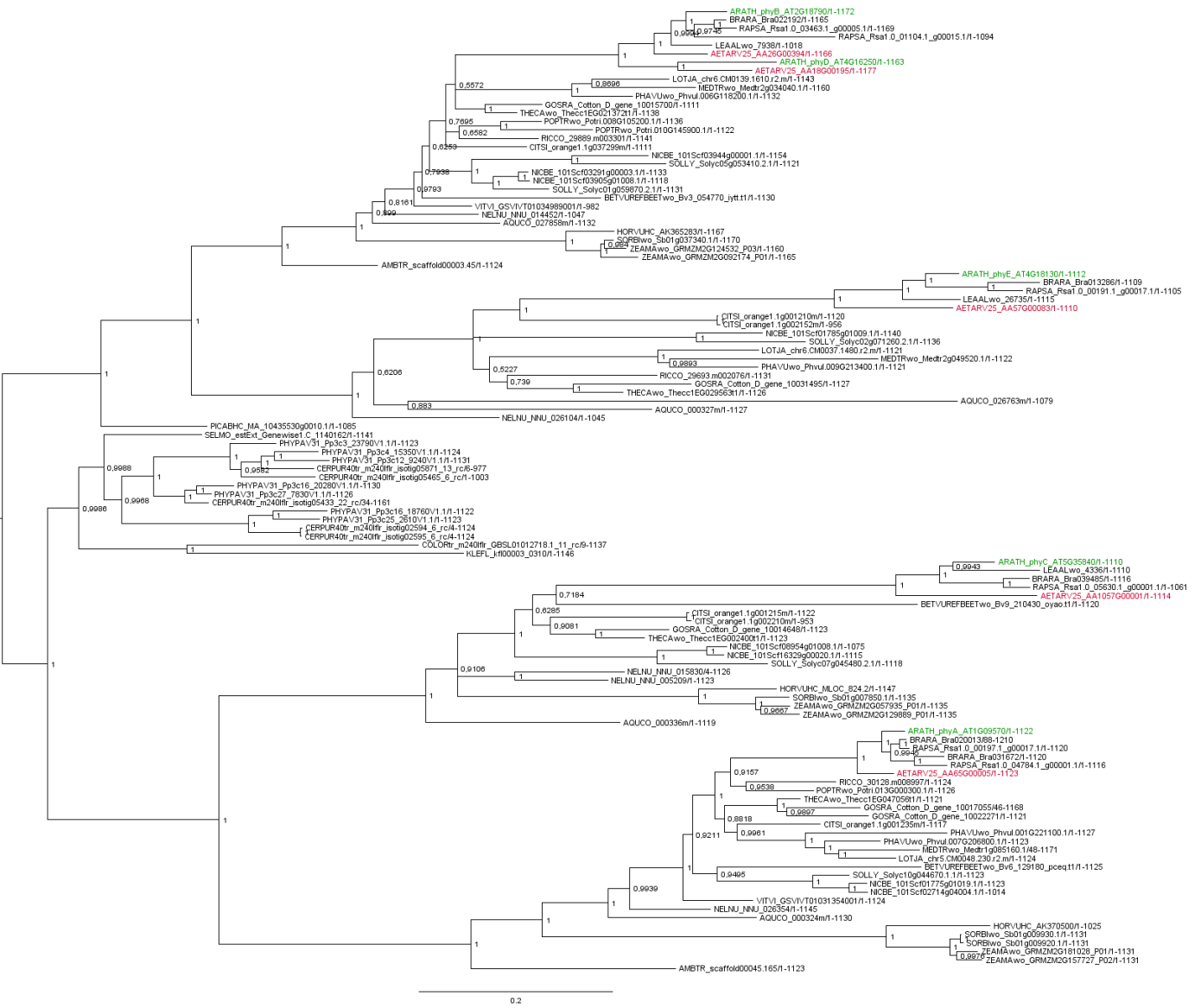
Supporting Figure 3. Identification of the *A. thaliana* orthologue of *Ae. arabicum* AA18G00108 as *GA2ox3*.

(a) Phylogenetic tree of gibberelin2-oxidases using Bayesian inference (2000000 generations, standard deviation of split frequencies 0.063371) and allows clear assignment of *Ae. arabicum* orthologues. Sequences of *A. thaliana* (ARATH) and *Ae. arabicum* (AETAR) are marked in green and red, respectively. For detailed assignment of five letter code see Supplemental Dataset 7. (b) Synteny of *GA2ox3* position in the genome of *A. thaliana* and *Ae. arabicum*.



Supporting Figure 4. Accumulation of GA forms in *Ae. arabicum* TUR and CYP seeds under dark and light conditions.

A



			20		40		60		80	
PHYE_TUR	MGFETSSSSA	SNMKPLTDSK	PKSNTAQYSA	DAGLFADFDD	SIYTGKSFNY	SKSMISQPIG	VTDDHITAYL	GNIQRGGFVQ	PFGCLLAVEE	90
PHYE_CYP	MGFETSSSSA	SNMKPLTDSK	PKSNTAQYSA	DAGLFADFDD	SIYTGKSFNY	SKSMISQPIG	VTDDHITAYL	GNIQRGGFVQ	PFGCLLAVEE	90
PHYE_KM2397	MGFETSSSSA	SNMKPLTDSK	PKSNTAQYSA	DAGLFADFDD	SIYTGKSFNY	SKSMISQPIG	VTDDHITAYL	GNIQRGGFVQ	PFGCLLAVEE	90
		100		120		140		160		180
PHYE_TUR	SSFCVVGYS	NCIELLGLCV	ASSSHCNCFE	GKGLIGIDAR	TFFTPSSSDS	LAKASSFTEI	SLLNPVLVHS	KTTQKPFYAI	LHRIDAGLVI	180
PHYE_CYP	SSFCVVGYS	NCIELLGLCV	ASSSHCNCFE	GKGLIGIDAR	TFFTPSSSDS	LAKASSFTEI	SLLNPVLVHS	KTTQKPFYAI	LHRIDAGLVI	180
PHYE_KM2397	SSFCVVGYS	NCIELLGLCV	ASSSHCNCFE	GKGLIGIDAR	TFFTPSSSDS	LAKASSFTEI	SLLNPVLVHS	KTTQKPFYAI	LHRIDAGLVI	180
		200		220		240		260		280
PHYE_TUR	DLEPTRSGDP	AMTLAGAVQS	QKLAVRAISR	LQSLPGGDIG	ALCDTVVEDV	QKLTGYDRVM	VYQFHEDDHG	EVVSEIRRS	LEPYLGLHYP	270
PHYE_CYP	DLEPTRSGDP	AMTLAGAVQS	QKLAVRAISR	LQSLPGGDIG	ALCDTVVEDV	QKLTGYDRVM	VYQFHEDDHG	EVVSEIRRS	LEPYLGLHYP	270
PHYE_KM2397	DLEPTRSGDP	AMTLAGAVQS	QKLAVRAISR	LQSLPGGDIG	ALCDTVVEDV	QKLTGYDRVM	VYQFHEDDHG	EVVSEIRRS	LEPYLGLHYP	270
		300		320		340		360		380
PHYE_TUR	ATDIPQAARF	LFKQNRVRMI	CDCNATPVKV	IQSDELKRPL	CLVNSTLRSP	HACHTQYMAN	MGSIASLVLA	IVIKTKDSSK	LWGLVVGHH	360
PHYE_CYP	ATDIPQAARF	LFKQNRVRMI	CDCNATPVKV	IQSDELKRPL	CLVNSTLRSP	HACHTQYMAN	MGSIASLVLA	IVIKTKDSSK	LWGLVVGHH	360
PHYE_KM2397	ATDIPQAARF	LFKQNRVRMI	CDCNATPVKV	IQSDELKRPL	CLVNSTLRSP	HACHTQYMAN	MGSIASLVLA	IVIKTKDSSK	LWGLVVGHH	360
		380		400		420		440		460
PHYE_TUR	SPRYVSFPLR	YACEFLMQAF	GLQLHMLQL	TSQLAEKKAM	RTQTLLCDML	LRDVTSAIVT	QSPGIMDLVK	CDGAALYYNG	RCWLGVGTPN	450
PHYE_CYP	SPRYVSFPLR	YACEFLMQAF	GLQLHMLQL	TSQLAEKKAM	RTQTLLCDML	LRDVTSAIVT	QSPGIMDLVK	CDGAALYYNG	RCWLGVGTPN	450
PHYE_KM2397	SPRYVSFPLR	YACEFLMQAF	GLQLHMLQL	TSQLAEKKAM	RTQTLLCDML	LRDVTSAIVT	QSPGIMDLVK	CDGAALYYNG	RCWLGVGTPN	450
		460		480		500		520		540
PHYE_TUR	ESQVKDLVKW	LIENHGDSGT	LTTDSLVDAG	YPDASLFGDA	VCGIAAAGIS	SKDFLIWFRS	NTASAIKWGG	AKHHPKDKDD	DERMHPRSSF	540
PHYE_CYP	ESQVKDLVKW	LIENHGDSGT	LTTDSLVDAG	YPDASLFGDA	VCGIAAAGIS	SKDFLIWFRS	NTASAIKWGG	AKHHPKDKDD	DERMHPRSSF	540
PHYE_KM2397	ESQVKDLVKW	LIENHGDSGT	LTTDSLVDAG	YPDASLFGDA	VCGIAAAGIS	SKDFLIWFRS	NTASAIKWGG	AKHHPKDKDD	DERMHPRSSF	540
		560		580		600		620		640
PHYE_TUR	KAFLEVVKCR	SLPWEVSEIN	AIHSLQLIMR	ESFHNMQETS	SKAVSSNVMA	KDANELTSFV	CEMVRMIETA	TAPIFGVDSL	GCINGWNKKI	630
PHYE_CYP	KAFLEVVKCR	SLPWEVSEIN	AIHSLQLIMR	ESFHNMQETS	SKAVSSNVMA	KDANELTSFV	CEMVRMIETA	TAPIFGVDSL	GCINGWNKKI	630
PHYE_KM2397	KAFLEVVKCR	SLPWEVSEIN	AIHSLQLIMR	ESFHNMQETS	SKAVSSNVMA	KDANELTSFV	CEMVRMIETA	TAPIFGVDSL	GCINGWNKKI	630
		640		660		680		700		720
PHYE_TUR	AEITGLQASE	AMGKSLINDI	VQGESRADLE	SLLSKALQGE	EENKVMKLKLR	KFGQSNLDS	SSGAAAACV	IVNACTSRDS	AGKIIIVCVFV	720
PHYE_CYP	AEITGLQASE	AMGKSLINDI	VQGESRADLE	SLLSKALQGE	EENKVMKLKLR	KFGQSNLDS	SSGAAAACV	IVNACTSRDS	AGKIIIVCVFV	720
PHYE_KM2397	AEITGLQASE	AMGKSLINDI	VQGESRADLE	SLLSKALQGE	EENKVMKLKLR	KFGQSNLDS	SSGAAAACV	IVNACTSRDS	AGKIIIVCVFV	720
		740		760		780		800		820
PHYE_TUR	QDITGEKAI	TDRFIRLQGD	YKTIIVQSLNP	LIPPIFASDQ	NACCSEWNA	MEKLTGWSKH	EVIKMLPGE	VFGVLCKVKC	QDSLTKFLSI	810
PHYE_CYP	QDITGEKAI	TDRFIRLQGD	YKTIIVQSLNP	LIPPIFASDQ	NACCSEWNA	MEKLTGWSKH	EVIKMLPGE	VFGVLCKVKC	QDSLTKFLSI	810
PHYE_KM2397	QDITGEKAI	TDRFIRLQGD	YKTIIVQSLNP	LIPPIFASDQ	NACCSEWNA	MEKLTGWSKH	EVIKMLPGE	VFGVLCKVKC	QDSLTKFLSI	810
		820		840		860		880		900
PHYE_TUR	LYQISGQIS	ESSLFGFFNR	EGNYIESSLT	ANKSTNSEGK	VVGCFFFLQI	IKKESCISTR	SNLNLTYIRQ	EIKNPLNGIR	FAHKLESSE	900
PHYE_CYP	LYQISGQIS	ESSLFGFFNR	EGNYIESSLT	ANKSTNSEGK	VVGCFFFLQI	IKKESCISTR	SNLNLTYIRQ	EIKNPLNGIR	FAHKLESSE	900
PHYE_KM2397	LYQISGQIS	ESSLFGFFNR	EGNYIESSLT	ANKSTNSEGK	VVGCFFFLQI	IKKESCISTR	SNLNLTYIRQ	EIKNPLNGIR	FAHKLESSE	900
		920		940		960		980		1,000
PHYE_TUR	ISESQROFLK	TSDACEKQIT	TIIDGMDLKS	IEEGKSELKT	EEFHLGSILD	AIIISQVMIML	RERHSQKLE	IPEEIKNLSL	FGDGVRLQLI	990
PHYE_CYP	ISESQROFLK	TSDACEKQIT	TIIDGMDLKS	IEEGKSELKT	EEFHLGSILD	AIIISQVMIML	RERHSQKLE	IPEEIKNLSL	FGDGVRLQLI	990
PHYE_KM2397	ISESQROFLK	TSDACEKQIT	TIIDGMDLKS	IEEGKSELKT	EEFHLGSILD	AIIISQVMIML	RERHSQKLE	IPEEIKNLSL	FGDGVRLQLI	990
		1,000		1,020		1,040		1,060		1,080
PHYE_TUR	LADLLRNIVN	HSPFPNSWIG	IKISGSKNLD	DCCIHLQFRI	IHPGKGLPLE	IVNDMFGIED	GWVTPDGLGL	KLSRKLLEQM	KGSVSVYRED	1080
PHYE_CYP	LADLLRNIVN	HSPFPNSWIG	IKISGSKNLD	DCCIHLQFRI	IHPGKGLPLE	IVNDMFGIED	GWVTPDGLGL	KLSRKLLEQM	KGSVSVYRED	1080
PHYE_KM2397	LADLLRNIVN	HSPFPNSWIG	IKISGSKNLD	DCCIHLQFRI	IHPGKGLPLE	IVNDMFGIED	GWVTPDGLGL	KLSRKLLEQM	KGSVSVYRED	1080
		1,100		1,120		1,140		1,160		1,180
PHYE_TUR	DCCFFHVDLQ	LRTKTSDETR	GVETKSQKFF							1110
PHYE_CYP	DCCFFHVDLQ	LRTKTSDETR	GVETKSQKFF							1110
PHYE_KM2397	DCCFFHVDLQ	LRTKTSDETR	GVETKSQKFF							1110

Supporting Figure 5. Identification and alignments of phytochromes in *Ae. arabicum*. (a) Phylogenetic tree of phytochromes using Bayesian inference (1688500 generations, standard deviation of split frequencies 0.009992) and allows clear assignment of *Ae. arabicum* orthologues. Sequences of *A. thaliana* (ARATH) and *Ae. arabicum* (AETAR) are marked in green and red, respectively. For detailed assignment of five letter code see Supplemental Dataset 7. (b-f) Phytochrome protein alignments of three *Ae. arabicum* accessions. Germination of TUR seeds is light-insensitive while CYP and KM2397 both have light inhibited germination.

			20		40		60		80			
PIL5/PIF1_TUR	MNHFVPDFE I	DDDYTNP I	SS	SLNLRPKP I	IM	AENEDDLME	LLWHNGQLF	IQEDEMSSWL	HYP LREDDFC	SDLFNSVSST	SQPQHVSTAP	90
PIL5/PIF1_KM2397	MNHFVPDFE I	DDDYTNP I	SS	SLNLRPKP I	IM	AENEDDLME	LLWHNGQLF	IQEDEMSSWL	HYP LREDDFC	SDLFNSVSST	SQPQHVSTAP	90
PIL5/PIF1_CYP	MNHFVPDFE I	DDDYTNP I	SS	SLNLRPKP I	IM	AENEDDLME	LLWHNGQLF	IQEDEMSSWL	HYP LREDDFC	SDLFNSVSST	SQPQHVSTAP	90
	100			120		140		160		180		
PIL5/PIF1_TUR	NVSTAPNVS N	VSTAPNVSTA		PNVFTAPNVS	I	IATNVSNQTS	QITS AKPLVR	NFINFSRFRG	NFTGDKIESG	PSISKSVIRE	STQVNPSESD	180
PIL5/PIF1_KM2397	NVSTAPNVS X	VSTAPNVSTA		PNVFTAPNVS	I	IATNVSNQTS	QITS AKPLVR	NFINFSRFRG	NFTGDKIESG	PSISKSVIRE	STQVNPSESD	180
PIL5/PIF1_CYP	NVSTAPNVS N	VSTAPNVSTA		PNVFTAPNVS	I	IATNVSNQTS	QITS AKPVR	NFINFSRFRG	NFTGDKIESG	PSISKSVIRE	STQVNPSESD	180
	200			220		240		260		280		
PIL5/PIF1_TUR	LTRVDVNRET	VNCGSSSDVA		GENAFNFAIN	R	RK GKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TATATVNEKK	RKEKEAIDET	270
PIL5/PIF1_KM2397	LTRVDVNRET	VNCGSSSDVA		GENAFNFAIN	R	RK GKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TATATVNEKK	RKEKEAIDET	270
PIL5/PIF1_CYP	LTRVDVNRET	VNCGSSSDVA		GENAFNFAIN	R	RK GKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TAT VNEKK	RKEKEAIDET	268
	280			300		320		340				
PIL5/PIF1_TUR	ESRSEETRAG	RGSTSTKRSR		AAEVHNLSE R	K	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQVFT	347	
PIL5/PIF1_KM2397	ESRSEETRAG	RGSTSTKRSR		AAEVHNLSE R	K	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQVFT	347	
PIL5/PIF1_CYP	ESRSEETRAG	RGSTSTKRSR		AAEVHNLSE R	K	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQ LFT	345	

Supporting Figure 6. Alignment of PIL5/PIF1 protein sequence of three *Ae. arabicum* accessions. Germination of TUR seeds is light-insensitive while CYP and KM2397 both have light inhibited germination.

Table S1 Information about geographic origin of *Aethionema arabicum* accessions

ID number	Species	Origin	Region	Altitude	Seed source
KM2491	<i>Aethionema heterocarpum</i>	Israel	Golan Heights, Mt. Hermonit	1100 m	S. Cohen
KM2614	<i>Aethionema heterocarpum</i>	Turkey	Belen/Hatay	700 m	K. Mummenhoff
KM2496	<i>Aethionema carneum</i> (Banks & Sol.) Fedts	Israel	Philistine Plain	39 m	A. Singer, Israel Plant Gene Bank 21673
KM2397	<i>Aethionema arabicum</i> Andr. Ex DC.	Turkey	Elazığ, Harput	1200 m	E. Schranz
Iran8458	<i>Aethionema arabicum</i> Andr. Ex DC.	Iran	Mt. Dizin, Karaj	~2600 m	S. Mohammadin
Iran8456-1	<i>Aethionema arabicum</i> Andr. Ex DC.	Iran	Mt. Touchal, Tehran	~2600 m	S. Mohammadin
Iran8456-2	<i>Aethionema arabicum</i> Andr. Ex DC.	Iran	Mt. Touchal, Tehran	~2600 m	S. Mohammadin

Table S2 List of primers used for quantitative RT-PCR analysis

Name	Nucleotide sequence
AearACT2_for	AATTGAGCATGGTGTGGTCA
AearACT2_rev	GCTCTTCAGGAGCAATACGG
AearUBQ10_for	GAGGATGGCCGAACATTG
AearUBQ10_rev	TGCCCGTTAGGGTTTTGA
AearAPC2_for	TCTCCTGCAATCGAGGACTT
AearAPC2_rev	GCAGTGAGCAACCGGTATTT
AearNCED5_for	GCCGTTTGATCTTGACGCTC
AearNCED5_rev	ACGGAGTTTAGTTTACGGCGT
AearNCED6_for	GCTTCTTCAGCTCTCGACAA
AearNCED6_rev	GAACCGTTGGATCAGTCGGT
AearNCED9_for	TCCTTTTCTCCGATCAAACCTCT
AearNCED9_rev	TCGAATTCGAGGATTTGGGGA
AearABA1_for	GGAGGAGAAGAAAGGGGAGA
AearABA1_rev	ATCCTTTCTTTTTTCGCAGCA
AearABA2_for	AACATGGCGCAAGAGTCTG
AearABA2_rev	TGGATGAAACAAGCCTCCTT
AearABA3_for	TGGAAGAATTTCTTGAGGAATTTGGA
AearABA3_rev	TCTTGAATTCGGTGTACGGA

AearCYP707A2_for	GCGGTTCCAACAAAGAAAAC
AearCYP707A2_rev	GAGTGGCGAAGAAGGAATTG
AearGA3ox1_for	TCTTCGTCACCTCCCTGACT
AearGA3ox1_rev	GATGAGCGGGAGAGTTGTGT
AearGA3ox2_for	CCCATCCAATACACATTCCA
AearGA3ox2_rev	GCCTTGGCTGAGAAAAGAAG
AearGA2ox2_for	TCACAGCCCCTCACTTTAGA
AearGA2ox2_rev	GGCTTCTGGGTCGGTTAAAT
AearGA2ox3_for	CGCGTCTCTCTTAACCCAAC
AearGA2ox3_rev	TCACATGCCTTGACCATTTG
AearRGA_for	GTCCTCGGCTACAAGGTCAG
AearRGA_rev	TGAGGGAATCCATCTTCAGG
AearGAI_for	TGGTGGTGCTTCTGTACCTG
AearGAI_rev	TCATCCATGTGACCACCATC
AearRGL2_for	GGACCCTGCAACAATACCAT
AearRGL2_rev	CCACGCCTTCAACTTCCTTA
AearSOM_for	CCGCGAAAATTGATATCTCC
AearSOM_rev	TCGATTTGATTTCTCACCA
AearDAG1_for	GCAATTACTCCCCAATAACAACA
AearDAG1_rev	GTTTGCGTTTTCGTTTGAG
AearDAG2_for	GGAACAACAACAACAACAATGA
AearDAG2_rev	CTACCGGAGATGGATGTGGT
AearJMJ20_for	ATGGGAATCGAGATTGTTGG
AearJMJ20_rev	CGGCTGGTTTTTATGCAAGT
AearJMJ22_for	GGGAATGAGCGACCTGATTA
AearJMJ22_rev	TCACTGCATTCCAAGCAGAC
AearPAR1_for	CTCTAGCAACTCCCGACACC
AearPAR1_rev	TCTCCAACAATCTCCGTTTTG
AearPAR2_for	CGTCACTTCAGCGAGTGAAA
AearPAR2_rev	TTCCCGGA ACTATTGTCTGC
AearDOG1_for	CGCGTCACTAAGCGATCTAAC
AearDOG1_rev	GCCGCGTCTTCTTG TAGACTT
AearABI3_for	ATGGCGGAAACCTTCCTTAT
AearABI3_rev	GAGGAAGAGGAGGAGGAGGA
AearABI4_for	CTCAACGCAAACGCAAAGGT
AearABI4_rev	TCACGGATTT CAGCAACCCA
AearABI5_for	GAACGCCGAAGAAAACAATC
AearABI5_rev	TCAACCCGGTTTGGTACATT

Table S3 List of Aethionema accession numbers used for this study

Name	Accession number
<i>AearNCED5</i>	AA54G00417
<i>AearNCED6</i>	AA78G00012
<i>AearNCED9</i>	AA31G00716
<i>AearABA1</i>	AA8G00025
<i>AearABA2</i>	AA32G01008
<i>AearABA3</i>	AA37G00095
<i>AearCYP707A2</i>	AA32G00787
<i>AearGA3ox1</i>	AA37G00176
<i>AearGA3ox2</i>	AA31G00895
<i>AearGA2ox2</i>	AA54G00411
<i>AearGA2ox3</i>	AA18G00108
<i>AearRGA</i>	AA14G00090
<i>AearGAI</i>	AA53G00639
<i>AearRGL2</i>	AA10G00264
<i>AearPIL5</i>	AA33G00286
<i>AearSOM</i>	AA7G00098
<i>AearDAG1</i>	AA61G00535
<i>AearDAG2</i>	AA21G00391
<i>AearJMJ20</i>	AA5G00018
<i>AearJMJ22</i>	AA283G00008
<i>AearPAR1</i>	AA21G00074
<i>AearPAR2</i>	AA61G00301
<i>AearDOG1</i>	AA6G00020
<i>AearABI3</i>	AA109G00007
<i>AearABI4</i>	AA29G00257
<i>AearABI5</i>	AA60G00170
<i>AearPHYA</i>	AA65G00005
<i>AearPHYB</i>	AA26G00394
<i>AearPHYC</i>	AA1057G00001
<i>AearPHYD</i>	AA18G00159
<i>AearPHYE</i>	AA57G00083