

## **Journal of Experimental Botany Supplementary Information**

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

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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.

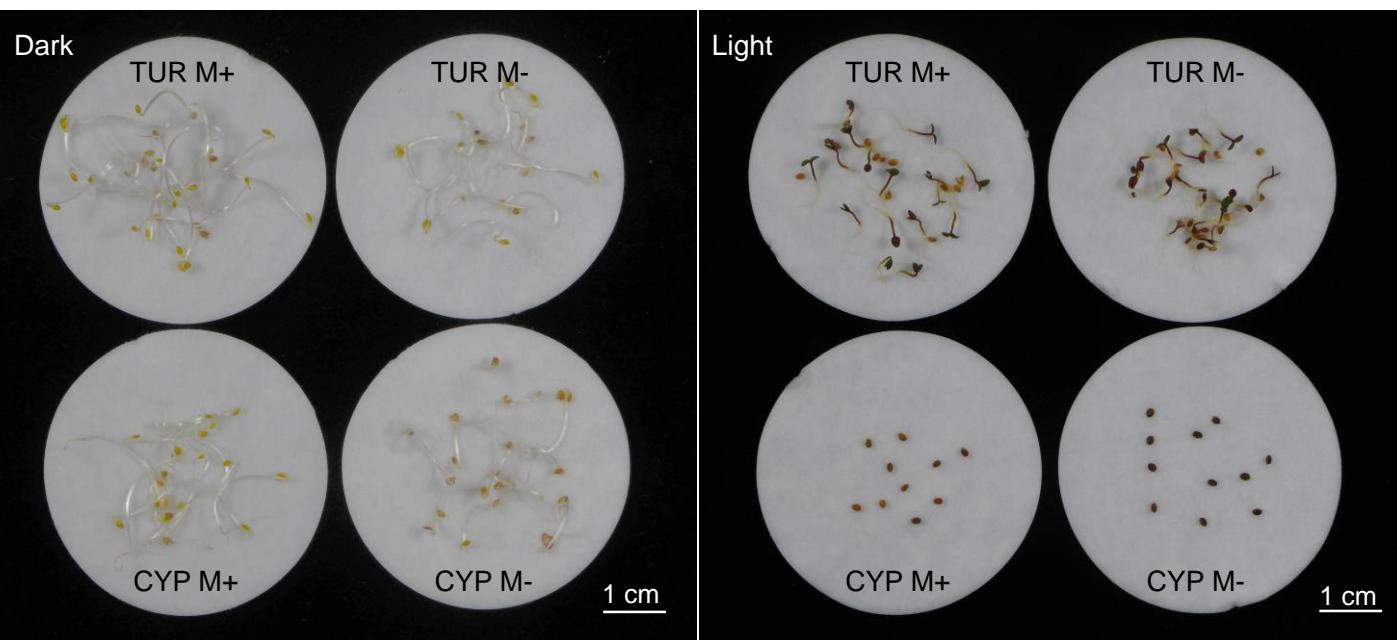
**Fig. S2** Heatmap of all 87 genes light-regulated in CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM values.

**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.

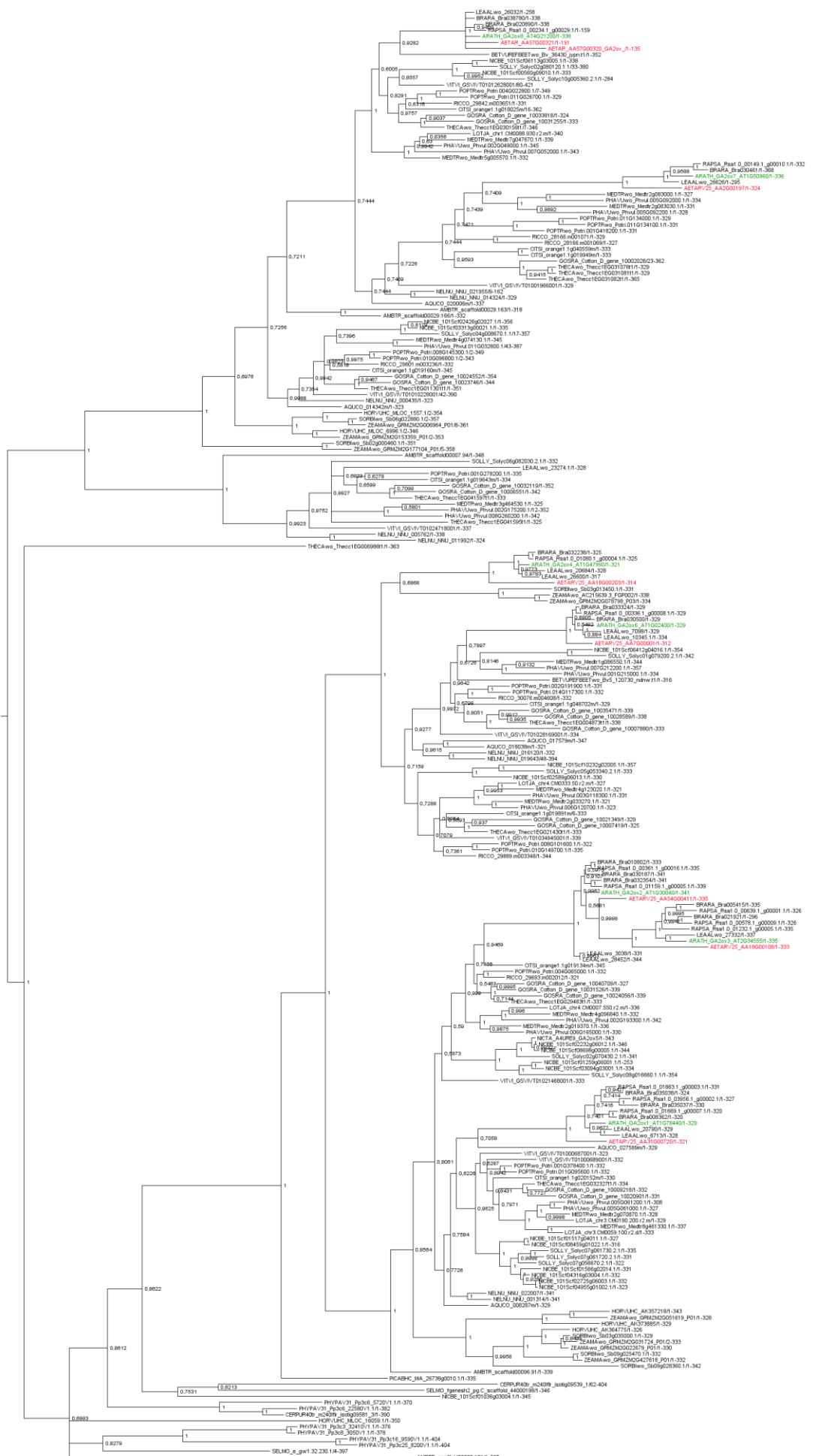


**Supporting Figure 1.** Germination of dimorphic seed types in response to light. Germination of mucilaginous (M+) and non-mucilaginous (M-) seeds were tested from TUR and CYP accessions in dark or under white light ( $100 \mu\text{mol m}^{-2} \text{s}^{-1}$ ). Images were taken 7 days after imbibition.

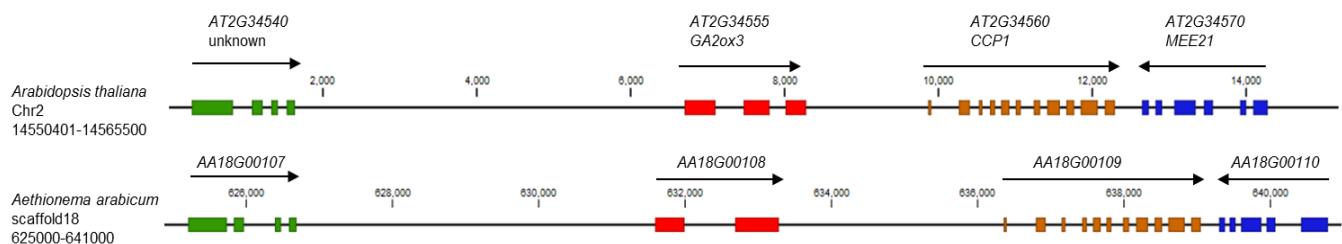


**Supporting Figure 2.** Heatmap of all 87 genes light-regulated in CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM values.

A

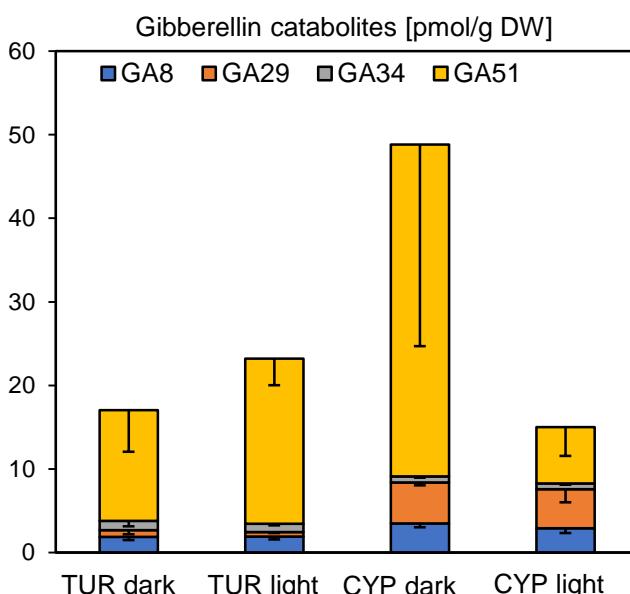
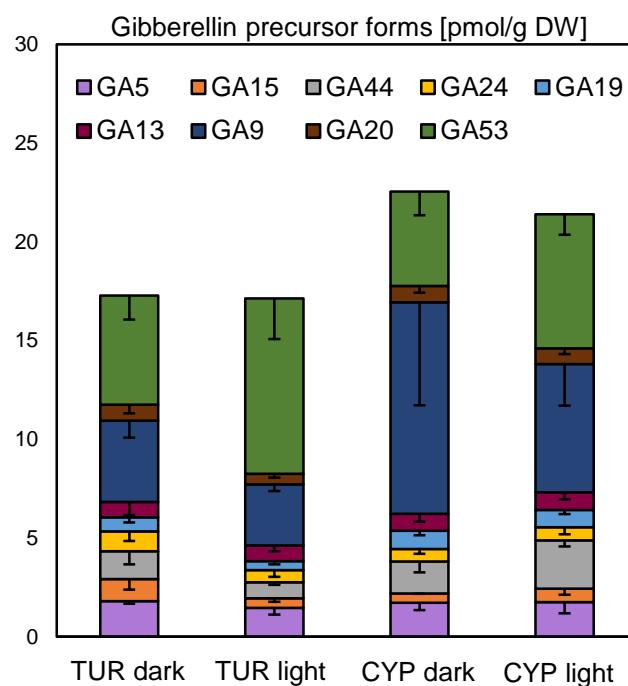
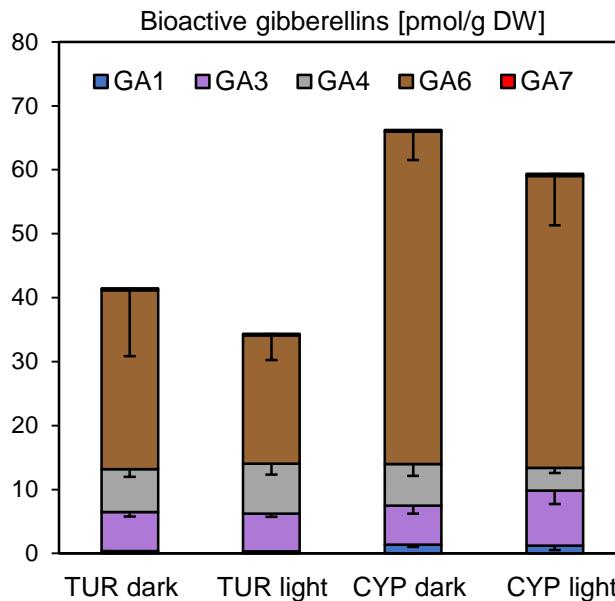


## Supporting Figure 3

**B**

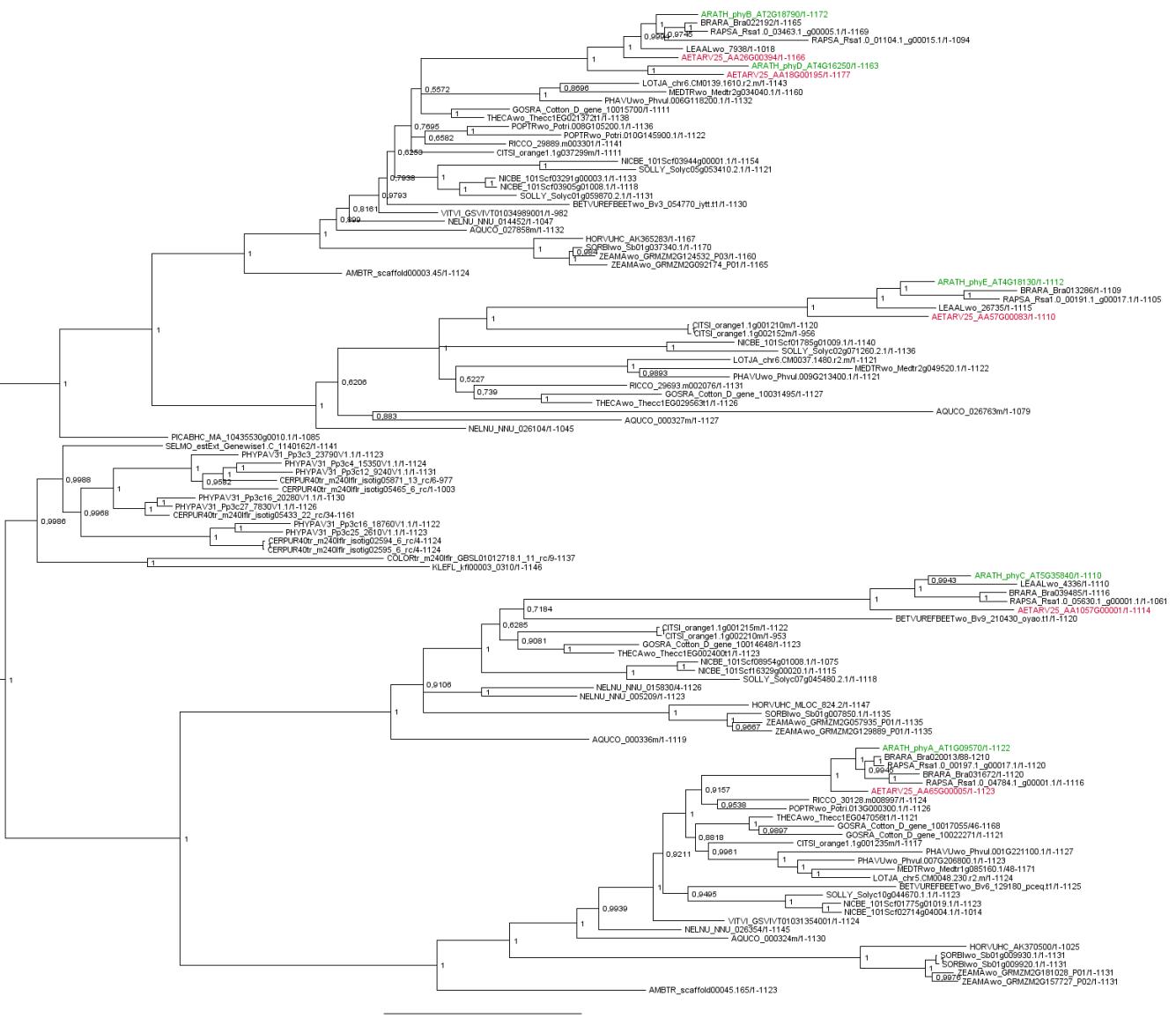
**Supporting Figure 3.** Identification of the *A. thaliana* orthologue of *Ae. arabicum* AA18G00108 as *GA2ox3*.

(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



Supporting Figure 5

B

20 40 60 80 100  
PHYA\_TUR MSGARPSSH S EGSRRSRHSA R IIIAQTTVDA KLHADFEESO SSFDYSSSVR VTGPPVVENQ PRSDKVTTTY LHHI1QKGKLI QPFGCLLALD EKTFKVIAYS 100  
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420 440 460 480 500  
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520 540 560 580 600  
PHYA\_TUR ALGDSVCGMA AVRISSKDML FWFRSHTAG E IRWGGAHKDP DDKDARRMH PRSSFKAFLE VVKTRSLPKW DYEMDA1HSL QL1LNRNAPKD IEASNVNTKL 600  
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C

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1.020 1.040 1.060 1.080 1.100  
PHYB\_TUR GNVVNA1VSQ AMFLLRERGL QL1RDI1PNEI KSI1AVYGDQI R1QQLLAEFL LS1I1RYAPSO EWVE1HLRQA PKQ1TDGFSS IRTEFRMACP GEGLPPELVR 1100  
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1.120 1.140 1.160

Supporting Figure 5

D

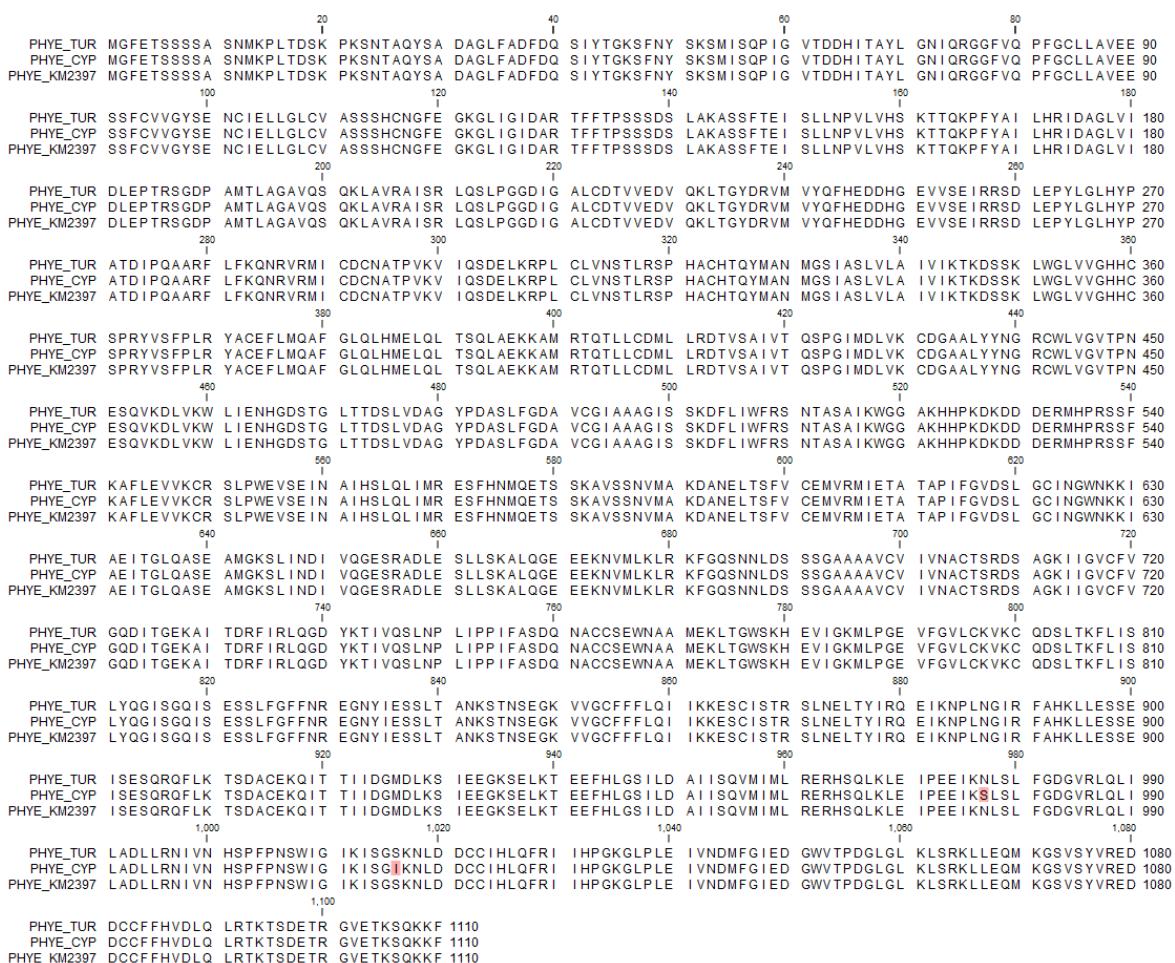
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 200 220 240 260 280  
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 PHYC\_CYP RLWGLVVCCHH SNPRFVSFL RYACELLMQV FTAOINKEVE SALLVKEKHI LOTQSVLCDM FFRNAPIGIV TESPNIMDLV KCDGAALCYR 450  
 PHYC\_KM2397 RLWGLVVCCHH SNPRFVSFL RYACELLMQV FTAOINKEVE SALLVKEKHI LOTQSVLCDM FFRNAPIGIV TESPNIMDLV KCDGAALCYR 450  
 480 500 520 540 560  
 PHYC\_TUR DKFWLLGITP TEIQRDIDI WVLKNNECKT GFTTESLMES GYPGASGLGE SVCGMAMVFI SEKDFLFWFR SGTAKQIKWG GARHDPNRD 540  
 PHYC\_CYP DKFWLLGITP TEIQRDIDI WVLKNNECKT GFTTESLMES GYPGASGLGE SVCGMAMVFI SEKDFLFWFR SGTAKQIKWG GARHDPNRD 540  
 PHYC\_KM2397 DKFWLLGITP TEIQRDIDI WVLKNNECKT GFTTESLMES GYPGASGLGE SVCGMAMVFI SEKDFLFWFR SGTAKQIKWG GARHDPNRD 540  
 580 600 620 640 660  
 PHYC\_TUR GKRMRHPRSSF KAFMEVIRWK SEA WVDMEMD AINSQLIIK GSLQEHSKT D NVNPSMDNRV OKVDELCVIL NEMVRLIDTA AVPIFAVDAS 630  
 PHYC\_CYP GKRMRHPRSSF KAFMEVIRWK SEA WVDMEMD AINSQLIIK GSLQEHSKT D NVNPSMDNRV OKVDELCVIL NEMVRLIDTA AVPIFAVDAS 630  
 PHYC\_KM2397 GKRMRHPRSSF KAFMEVIRWK SEA WVDMEMD AINSQLIIK GSLQEHSKT D NVNPSMDNRV OKVDELCVIL NEMVRLIDTA AVPIFAVDAS 630  
 680 700 720 740 760  
 PHYC\_TUR GVINGWNSKA AEVTGLAVEQ AIGKSLSDLV EEDSVTTVNN I LNLALQGS ERGAEIJKS FGPKRKSSPI DLVINTCCSR DTMRNVLGVC 720  
 PHYC\_CYP GVINGWNSKA AEVTGLAVEQ AIGKSLSDLV EEDSVTTVNN I LNLALQGS ERGAEIJKS FGPKRKSSPI DLVINTCCSR DTMRNVLGVC 720  
 PHYC\_KM2397 GVINGWNSKA AEVTGLAVEQ AIGKSLSDLV EEDSVTTVNN I LNLALQGS ERGAEIJKS FGPKRKSSPI DLVINTCCSR DTMRNVLGVC 720  
 780 800 820 840 860  
 PHYC\_TUR FIGQDVTKQK KLFESYSRVR EDYARIMWKPK STLIPIFM PNPVGCTEWN DAMQKLSGIK REEAVEKLLL GEVFTLDDYG CRLKDHDTLV 810  
 PHYC\_CYP FIGQDVTKQK KLFESYSRVR EDYARIMWKPK STLIPIFM PNPVGCTEWN DAMQKLSGIK REEAVEKLLL GEVFTLDDYG CRLKDHDTLV 810  
 PHYC\_KM2397 FIGQDVTKQK KLFESYSRVR EDYARIMWKPK STLIPIFM PNPVGCTEWN DAMQKLSGIK REEAVEKLLL GEVFTLDDYG CRLKDHDTLV 810  
 880 900 920 940 960  
 PHYC\_TUR KLRIALNAVS SGENVEKLFF GFYHREGNFV EALLSTNKKT DIEGKVTVGL CFLQVPSPEL QCALQVQQIS EKAMACALDK LAYLRQEVNM 900  
 PHYC\_CYP KLRIALNAVS SGENVEKLFF GFYHREGNFV EALLSTNKKT DIEGKVTVGL CFLQVPSPEL QCALQVQQIS EKAMACALDK LAYLRQEVNM 900  
 PHYC\_KM2397 KLRIALNAVS SGENVEKLFF GFYHREGNFV EALLSTNKKT DIEGKVTVGL CFLQVPSPEL QCALQVQQIS EXAMACALDK LAYLRQEVNM 900  
 980 1000 1020 1040 1060  
 PHYC\_TUR PENAI AFLQN LHHSGLSD EOKWLRTNII CREQLAKVIS DSDLEGIEEG YGELSLNEFS LEESLEAVVK QVMELSDERK VQILCDYPEE 990  
 PHYC\_CYP PENAI AFLQN LHHSGLSD EOKWLRTNII CREQLAKVIS DSDLEGIEEG YGELSLNEFS LEESLEAVVK QVMELSDERK VQILCDYPEE 990  
 PHYC\_KM2397 PENAI AFLQN LHHSGLSD EOKWLRTNII CREQLAKVIS DSDLEGIEEG YGELSLNEFS LEESLEAVVK QVMELSDERK VQILCDYPEE 990  
 1080 1100  
 PHYC\_TUR VSSIRLYGDY LRLQQISET LSCSLSLFTP FKGLSVSFV I ARVEAIGRR TKRVHLEFRI IHPAPGLPG LENEMFKPLR KGTSEGGL 1080  
 PHYC\_CYP VSSIRLYGDY LRLQQISET LSCSLSLFTP FKGLSVSFV I ARVEAIGRR TKRVHLEFRI IHPAPGLPG LENEMFKPLR KGTSEGGL 1080  
 PHYC\_KM2397 VSSIRLYGDY LRLQQISET LSCSLSLFTP FKGLSVSFV I ARVEAIGRR TKRVHLEFRI IHPAPGLPG LENEMFKPLR KGTSEGGL 1080

E

20 40 60 80  
 PHYD\_TUR MVSGGGEGS GSGGNRGGKA ASSGLRVAES NHTNSHREQO AQSSATKALR SQNQSQNHTD SKSKAIQQT VDARLHAVFE QSGESGKSF 90  
 PHYD\_CYP MVSGGGEGS GSGGNRGGKA ASSGLRVAES NHTNSHREQO AQSSATKALR SQNQSQNHTD SKSKAIQQT VDARLHAVFE QSGESGKSF 90  
 PHYD\_KM2397 MVSGGGEGS GSGGNRGGKA ASSGLRVAES NHTNSHREQO AQSSATKALR SQNQSQNHTD SKSKAIQQT VDARLHAVFE QSGESGKSF 90  
 100 120 140 160 180  
 PHYD\_TUR YNSNLKTTTN WSSVPEQQIT AYLRSRQGG YIOPFGCLIA VDESTFNIIG YSENAREMLG LMLQSVPSIE NSEVLSIGTD LRSLFKPSSI 180  
 PHYD\_CYP YNSNLKTTTN WSSVPEQQIT AYLRSRQGG YIOPFGCLIA VDESTFNIIG YSENAREMLG LMLQSVPSIE NSEVLSIGTD LRSLFKPSSI 180  
 PHYD\_KM2397 YNSNLKTTTN WSSVPEQQIT AYLRSRQGG YIOPFGCLIA VDESTFNIIG YSENAREMLG LMLQSVPSIE NSEVLSIGTD LRSLFKPSSI 180  
 200 220 240 260 280  
 PHYD\_TUR ILLERAFAVAR E ITLLNPVWI HSKNTRGPFF AILHRDVGVI VIDLEPARTE DPALSIAGAV OSQKLAVRAI SHLQSLPPGD IKLLCDTVE 270  
 PHYD\_CYP ILLERAFAVAR E ITLLNPVWI HSKNTRGPFF AILHRDVGVI VIDLEPARTE DPALSIAGAV OSQKLAVRAI SHLQSLPPGD IKLLCDTVE 270  
 PHYD\_KM2397 ILLERAFAVAR E ITLLNPVWI HSKNTRGPFF AILHRDVGVI VIDLEPARTE DPALSIAGAV OSQKLAVRAI SHLQSLPPGD IKLLCDTVE 270  
 300 320 340 360 380  
 PHYD\_TUR RVRLDTGYDR VMYVKFHEDE HGEVVAETKR DDLEYFGLH YPATDIPQAS RFLFKQNRVR MIVDCHATPV RVVQDDRLLTQ SICLVGSTLR 360  
 PHYD\_CYP RVRLDTGYDR VMYVKFHEDE HGEVVAETKR DDLEYFGLH YPATDIPQAS RFLFKQNRVR MIVDCHATPV RVVQDDRLLTQ SICLVGSTLR 360  
 PHYD\_KM2397 RVRLDTGYDR VMYVKFHEDE HGEVVAETKR DDLEYFGLH YPATDIPQAS RFLFKQNRVR MIVDCHATPV RVVQDDRLLTQ SICLVGSTLR 360  
 400 420 440 460 480  
 PHYD\_TUR APHGCHAQYM ANMGSIASLA MAVIINGNEE DGNVTGGRN SMRLWGLVVC HHTSARCIPI PLRYACEFLM QAFGLQLNME LOLALQVSEK 450  
 PHYD\_CYP APHGCHAQYM ANMGSIASLA MAVIINGNEE DGNVTGGRN SMRLWGLVVC HHTSARCIPI PLRYACEFLM QAFGLQLNME LOLALQVSEK 450  
 PHYD\_KM2397 APHGCHAQYM ANMGSIASLA MAVIINGNEE DGNVTGGRN SMRLWGLVVC HHTSARCIPI PLRYACEFLM QAFGLQLNME LOLALQVSEK 450  
 500 520 540 560 580  
 PHYD\_TUR RVRMLQTLLC DMLLRDSPAV IVTQSPSIMD LVCKNGAFL YQGKYYSLGV APSEAQIDL VEWLLANHAD STGLSTDLSLG DAGYPRASAL 540  
 PHYD\_CYP RVRMLQTLLC DMLLRDSPAV IVTQSPSIMD LVCKNGAFL YQGKYYSLGV APSEAQIDL VEWLLANHAD STGLSTDLSLG DAGYPRASAL 540  
 PHYD\_KM2397 RVRMLQTLLC DMLLRDSPAV IVTQSPSIMD LVCKNGAFL YQGKYYSLGV APSEAQIDL VEWLLANHAD STGLSTDLSLG DAGYPRASAL 540  
 600 620 640 660 680  
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 PHYD\_CYP GDAVCGMAVA YITKKDFLW FRSHTEKEIK WGGAKHHPED KDDGQRMHPR SSFKAFLEV KSRCPWPEDA EMDAIHSLQL ILRDSFKESE 630  
 PHYD\_KM2397 GDAVCGMAVA YITKKDFLW FRSHTEKEIK WGGAKHHPED KDDGQRMHPR SSFKAFLEV KSRCPWPEDA EMDAIHSLQL ILRDSFKESE 630  
 700 720 740 760 780  
 PHYD\_TUR AINNSKAVAG AVQPLGDIQE QEIDEGLGSA REMVRLIETA TVPIFAVDVD GCINGWNAKI AELTGLSVEE AMGRSLVHDL IYKEYEETVD 720  
 PHYD\_CYP AINNSKAVAG AVQPLGDIQE QEIDEGLGSA REMVRLIETA TVPIFAVDVD GCINGWNAKI AELTGLSVEE AMGRSLVHDL IYKEYEETVD 720  
 PHYD\_KM2397 AINNSKAVAG AVQPLGDIQE QEIDEGLGSA REMVRLIETA TVPIFAVDVD GCINGWNAKI AELTGLSVEE AMGRSLVHDL IYKEYEETVD 720  
 800 820 840 860 880  
 PHYD\_TUR KLLSCALKGD EGKVNELKLK TFGPELQKGKA VFVVVNCASS KDYLDNIVGV CFIAQDVTGH KTMVMDKFINI QGDYKAI1HS PNPLIPPIFA 810  
 PHYD\_CYP KLLSCALKGD EGKVNELKLK TFGPELQKGKA VFVVVNCASS KDYLDNIVGV CFIAQDVTGH KTMVMDKFINI QGDYKAI1HS PNPLIPPIFA 810  
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 PHYD\_CYP ADENTCCMEW NTAMEKLTOW PRNEVIKGML VREVFGSCCR LKGPDALTF MIVLHNVMGG QETDKFPFFP FDRRGKFQIQT LTLNKRVNL 900  
 PHYD\_KM2397 ADENTCCMEW NTAMEKLTOW PRNEVIKGML VREVFGSCCR LKGPDALTF MIVLHNVMGG QETDKFPFFP FDRRGKFQIQT LTLNKRVNL 900  
 1000 1020 1040 1060 1080  
 PHYD\_TUR DGKVIGAFCF LQIPSPELQQ ALEIQRROEA ECFSRGKELA YIFQV1KNPL SGLRFTHSM EATLNNEEQK QLLETGVSC M0ISKIVEY 990  
 PHYD\_CYP DGKVIGAFCF LQIPSPELQQ ALEIQRROEA ECFSRGKELA YIFQV1KNPL SGLRFTHSM EATLNNEEQK QLLETGVSC M0ISKIVEY 990  
 PHYD\_KM2397 DGKVIGAFCF LQIPSPELQQ ALEIQRROEA ECFSRGKELA YIFQV1KNPL SGLRFTHSM EATLNNEEQK QLLETGVSC M0ISKIVEY 990  
 1100 1120 1140 1160 1180  
 PHYD\_TUR DVKSIEDGSF KLERTEFLLG NVINAVVSQV MLVLTTERGLQ LIRDPIEIK SMAVYGDOMR LQQLVLAELFS SIIRYAPVKS WVELHLLPV 1080  
 PHYD\_CYP DVKSIEDGSF KLERTEFLLG NVINAVVSQV MLVLTTERGLQ LIRDPIEIK SMAVYGDQMR LQQLVLAELFS SIIRYAPVKS WVELHLLPV 1080  
 PHYD\_KM2397 DVKSIEDGSF KLERTEFLLG NVINAVVSQV MLVLTTERGLQ LIRDPIEIK SMAVYGDQMR LQQLVLAELFS SIIRYAPVKS WVELHLLPV 1080  
 1190 1210 1230 1250 1270  
 PHYD\_TUR KQMADGFSAI HMFMRMACPG EGVPPERVQD MFHSSRWTSP EGLALSICRK ILKLMNGEVQ YIRECERSYF LIILELTIPP KRFNSNTSLTA 1170  
 PHYD\_CYP KQMADGFSAI HMFMRMACPG EGVPPERVQD MFHSSRWTSP EGLALSICRK ILKLMNGEVQ YIRECERSYF LIILELTIPP KRFNSNTSLTA 1170  
 PHYD\_KM2397 KQMADGFSAI HMFMRMACPG EGVPPERVQD MFHSSRWTSP EGLALSICRK ILKLMNGEVQ YIRECERSYF LIILELTIPP KRFNSNTSLTA 1170

PHYD\_TUR NIATMPA 1177  
 PHYD\_CYP NIATMPA 1177  
 PHYD\_KM2397 NIATMPA 1177

Supporting Figure 5



**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	MNHFVPD <b>F</b> E I	DDDYTNPISS	SLNLPRKPIM	AENDEDDLME	LLWHNGQNLF	IQEDEMSSWL	HYPLREDDFC	SDLFNSVSST	SQPQHVSTAP	90
PIL5/PIF1_KM2397	MNHFVPD <b>F</b> E I	DDDYTNPISS	SLNLPRKPIM	AENDEDDLME	LLWHNGQNLF	IQEDEMSSWL	HYPLREDDFC	SDLFNSVSST	SQPQHVSTAP	90
PIL5/PIF1_CYP	MNHFVPD <b>F</b> E I	DDDYTNPISS	SLNLPRKPIM	AENDEDDLME	LLWHNGQNLF	IQEDEMSSWL	HYPLREDDFC	SDLFNSVSST	SQPQHVSTAP	90
		100		120		140		160		180
PIL5/PIF1_TUR	NVSTAPNVSN	VSTAPNVSTA	PNVFTAPNVS	IATNVSNQTS	QITSAKPLVR	NFINFSRFRG	NFTGDKIESG	PSISKSIVRE	STQVNPSESD	180
PIL5/PIF1_KM2397	NVSTAPNV <b>X</b>	VSTAPNVSTA	PNVFTAPNVS	IATNVSNQTS	QITSAKPLVR	NFINFSRFRG	NFTGDKIESG	PSISKSIVRE	STQVNPSESD	180
PIL5/PIF1_CYP	NVSTAPNVSN	VSTAPNVSTA	PNVFTAPNVS	IATNVSNQTS	QITSAKP <b>P</b> VR	NFINFSRFRG	NFTGDKIESG	PSISKSIVRE	STQVNPSESD	180
		200		220		240		260		
PIL5/PIF1_TUR	LTRVDVNRET	VNCGSSSDVA	GENAFNFAIN	RKGKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TATATVNEKK	RKEKEAIDET	270
PIL5/PIF1_KM2397	LTRVDVNRET	VNCGSSSDVA	GENAFNFAIN	RKGKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TATATVNEKK	RKEKEAIDET	270
PIL5/PIF1_CYP	LTRVDVNRET	VNCGSSSDVA	GENAFNFAIN	RKGKAVATAN	PTAATAGEIS	GASSSVISKA	DIEPIYLEPA	TAT <b>-</b> VNEKK	RKEKEAIDET	268
		280		300		320		340		
PIL5/PIF1_TUR	ESRSEE <b>TRAG</b>	RGSTSTKRSR	AAEVHNL <b>SER</b>	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQVFT	347	
PIL5/PIF1_KM2397	ESRSEE <b>TRAG</b>	RGSTSTKRSR	AAEVHNL <b>SER</b>	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQVFT	347	
PIL5/PIF1_CYP	ESRSEE <b>TRAG</b>	RGSTSTKRSR	AAEVHNL <b>SER</b>	KRRDRINERM	KALQELIPRC	NKSDKASMLD	EAIEYMKSLQ	LQIQLFT	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	TGCCCGTTAGGGTTTG
AearAPC2_for	TCTCCTGCAATCGAGGACTT
AearAPC2_rev	GCAGTGAGCAACCGGTATT
AearNCED5_for	GCCGTTGATCTGACGCTC
AearNCED5_rev	ACGGAGTTAGTTACGGCGT
AearNCED6_for	GCTTCTTCAGCTCTGACCAA
AearNCED6_rev	GAACCGTTGGATCAGTCGGT
AearNCED9_for	TCCTTTCTCCGATCAAAACCTCT
AearNCED9_rev	TCGAATTGAGGATTGGGA
AearABA1_for	GGAGGAGAAGAAAGGGGAGA
AearABA1_rev	ATCCTTCTTTCGCAGCA
AearABA2_for	AACATGGCGCAAGAGTCTG
AearABA2_rev	TGGATGAAACAAGCCTCCTT
AearABA3_for	TGGAAGAATTCTGAGGAATTGGA
AearABA3_rev	TCTTGAATTGGTGTACGGA

AearCYP707A2_for	GCGGTTCCAACAAAGAAAAC
AearCYP707A2_rev	GAGTGGCGAAGAAGGAATTG
AearGA3ox1_for	TCTTCGTCACCTCCCTGACT
AearGA3ox1_rev	GATGAGCGGGAGAGTTGTGT
AearGA3ox2_for	CCCATCCAATACACATTCCA
AearGA3ox2_rev	GCCTTGGCTGAGAAAAGAAG
AearGA2ox2_for	TCACAGCCCGTCACTTAGA
AearGA2ox2_rev	GGCTTCTGGGTCGGTTAAAT
AearGA2ox3_for	CGCGTCTCTTAACCAAC
AearGA2ox3_rev	TCACATGCCTTGACCATTG
AearRGA_for	GTCCTCGGCTACAAGGTCAG
AearRGA_rev	TGAGGGAATCCATCTTCAGG
AearGAI_for	TGGTGGTGCTTCTGTACCTG
AearGAI_rev	TCATCCATGTGACCACCATC
AearRGL2_for	GGACCCCTGCAACAATACCAT
AearRGL2_rev	CCACGCCCTCAACTCCTTA
AearSOM-for	CCCGGAAAATTGATACTCTCC
AearSOM_rev	TCGATTCGATTCTCACCA
AearDAG1_for	GCAATTACTCCCCAATAACAACA
AearDAG1_rev	GTTTGCCTTGCCTTGAG
AearDAG2_for	GGAACAACAACAACAACAAATGA
AearDAG2_rev	CTACCGGAGATGGATGTGGT
AearJMJ20_for	ATGGGAATCGAGATTGTTGG
AearJMJ20_rev	CGGCTGGTTTTATGCAAGT
AearJMJ22_for	GGGAATGAGCGACCTGATTA
AearJMJ22_rev	TCACTGCATTCCAAGCAGAC
AearPAR1_for	CTCTAGCAACTCCCACACC
AearPAR1_rev	TCTCCAACAACTCCGTTTG
AearPAR2_for	CGTCACTTCAGCGAGTGAA
AearPAR2_rev	TTCCCGGAACTATTGCTGC
AearDOG1_for	CGCGTCACTAACGCGATCTAAC
AearDOG1_rev	GCCCGCTTCTTAGACTT
AearABI3_for	ATGGCGAACCTCCCTTAT
AearABI3_rev	GAGGAAGAGGAGGAGGAGGA
AearABI4_for	CTAACGCAAACGCAAAGGT
AearABI4_rev	TCACGGATTCAGCAACCCA
AearABI5_for	GAACGCCGAAGAAAACAATC
AearABI5_rev	TCAACCCGGTTGGTACATT

**Table S3 List of Aethionema accession numbers used for this study**

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