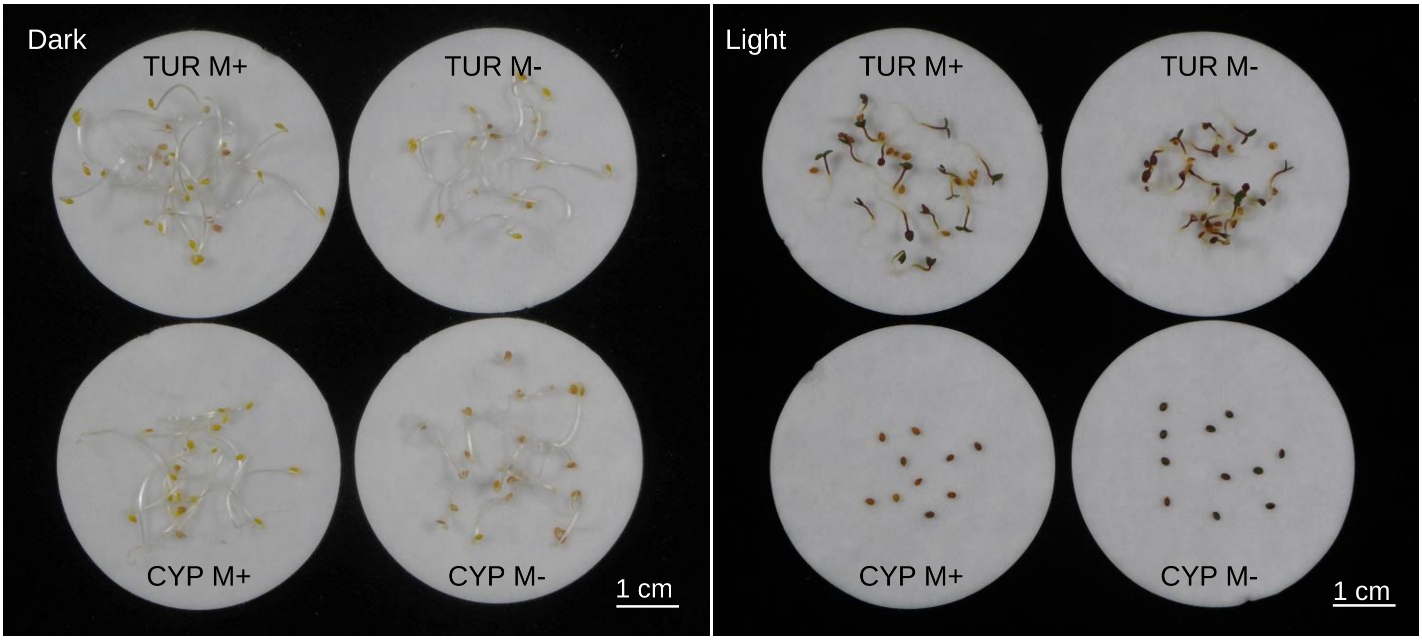

Supporting Figure 1. Germination of dimorphic seed types in response to light. Germination of mucilaginous (M+) and non-mucilaginous (M-) seeds were tested from TUR and CYP accessions in dark or under white light (100 µmol m^{-2} s^{-1}). Images were taken 7 days after imbibition.

Aethionema accession	TAIR10DESCRIPTION
AA31G00304	ARATHwo_AT1G76600.1
AA18G00108	gibberellin 2-oxidase
AA18G00131	NA
AA6G00020	delay of germination 1
AA7G00013	alpha/beta-Hydrolases superfamily protein
AA21G00250	Matrixin family protein
AA96G00113	cytochrome P450, family 94, subfamily B, polypeptide 3
AA6G00035	Protein of unknown function, DUF584
AA31G00340	ARATHwo_AT1G76250.1
AA118G00057	ARATHwo_AT4G33980.2
AA9G00199	RING/U-box superfamily protein
AA53G01387	Integrase-type DNA-binding superfamily protein
AA35G00052	DRE-binding protein 2A
AA659G00001	RING/U-box superfamily protein
AA4G00240	Ethylene insensitive 3 family protein
AA13G00009	flavanone 3-hydroxylase
AA44G00071	Protein of unknown function (DUF1118)
AA60G00062	plasma membrane intrinsic protein 2
AA11G00062	UDP-Glycosyltransferase superfamily protein
AA65G00216	Protein of unknown function, DUF584
AA24G00057	ARATHwo_AT3G44450.1
AA4G00193	NA
AA62G00022	Histone superfamily protein
AA26G00398	sequence-specific DNA binding transcription factors
AA33G00153	basic leucine-zipper 2
AA57G00148	Leucine-rich repeat (LRR) family protein
AA26G00194	rhamnose biosynthesis 3
AA65G00256	extensin-like protein
AA39G00541	ADP-ribosylation factor A1F
AA40G00565	GAST1 protein homolog 4
AA297G00002	arabinogalactan protein 31
AA44G00506	Leucine-rich repeat (LRR) family protein
AA10G00399	UDP-glucose 6-dehydrogenase family protein
AA53G00911	Ferritin/ribonucleotide reductase-like family protein
AA31G00563	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AA466G00003	Eukaryotic aspartyl protease family protein
AA26G00651	cell elongation protein / DWARF1 / DIMINUTO (DIM)
AA44G00016	calnexin 1
AA53G01423	leucine-rich repeat/extensin 1
AA30G00236	NA
AA7G00012	beta-xylosidase 2
AA44G00068	RPA70-kDa subunit B
AA90G00040	UDP-glucosyl transferase 71C3
AA32G00601	homolog of yeast CDT1 A
AA21G00074	phy rapidly regulated 1
AA21G00008	uv-b-insensitive 4
AA428G00003	cytochrome P450, family 83, subfamily B, polypeptide 1
AA108G00006	Pectin lyase-like superfamily protein
AA17G00061	Protein of unknown function (DUF581)
AA805G00002	PYR1-like 4
AA398G00001	FASCICLIN-like arabinogalactan 2
AA32G00222	S-adenosylmethionine synthetase 2
AA44G00517	ARATHwo_AT5G13100.1
AA26G00318	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
AA53G01380	O-methyltransferase family protein
AA8G00033	SKU5 similar 17
AA26G00339	GDSL-like Lipase/Acylhydrolase superfamily protein
AA21G00251	GATA transcription factor 2
AA8G00303	FRA8 homolog
AA35G00022	expansin A2
AA8G00179	Plant invertase/pectin methylesterase inhibitor superfamily protein
AA8G00110	sulfurtransferase 18
AA26G00453	purple acid phosphatase 17
AA61G00301	phy rapidly regulated 2
AA26G00278	Ran BP2/NZF zinc finger-like superfamily protein
AA6G00288	RING/U-box superfamily protein
AA25G00031	ARATHwo_AT5G54970.1
AA32G00244	Heat shock protein DnaJ with tetratricopeptide repeat
AA26G00148	Subtilase family protein
AA87G00204	NA
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AA166G00005	Leucine-rich repeat (LRR) family protein
AA61G00462	FASCICLIN-like arabinogalactan-protein 10
AA8G00274	Stress responsive A/B Barrel Domain
AA19G00337	Glycosyl hydrolase superfamily protein
AA19G00338	Glycosyl hydrolase superfamily protein
AA53G01128	zinc finger protein 4
AA53G01281	early nodulin-like protein 8
AA21G00283	protein binding
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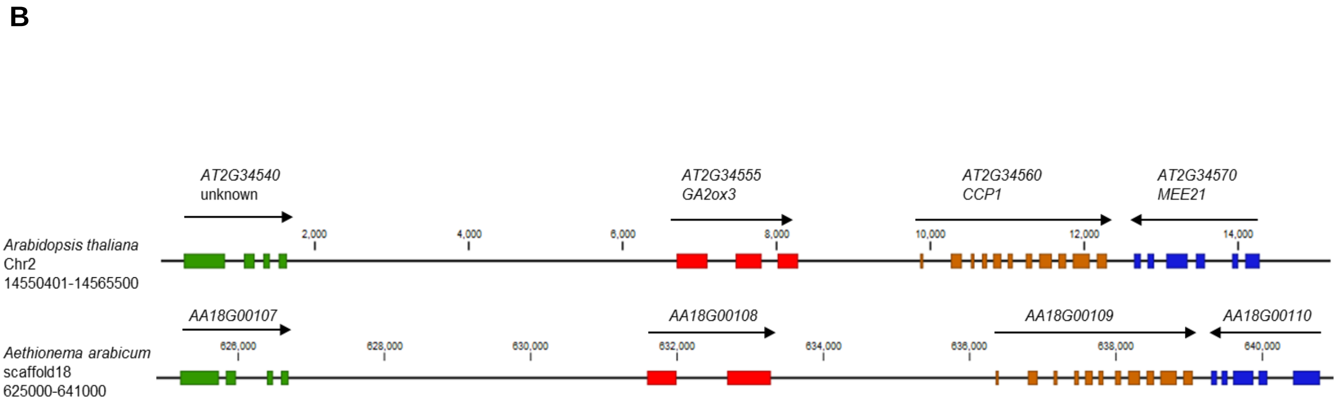
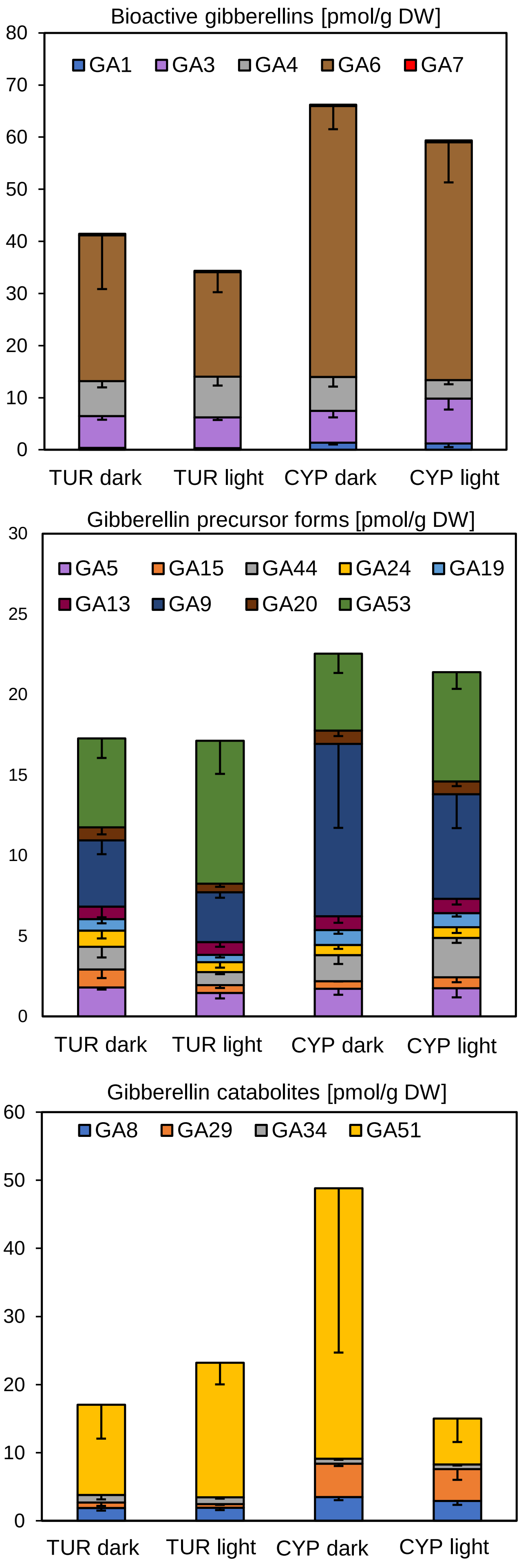
Supporting Figure 2. Heatmap of all 87 genes light-regulated in CYP seeds and differentially expressed in light-exposed TUR and CYP seeds based on RPKM values.

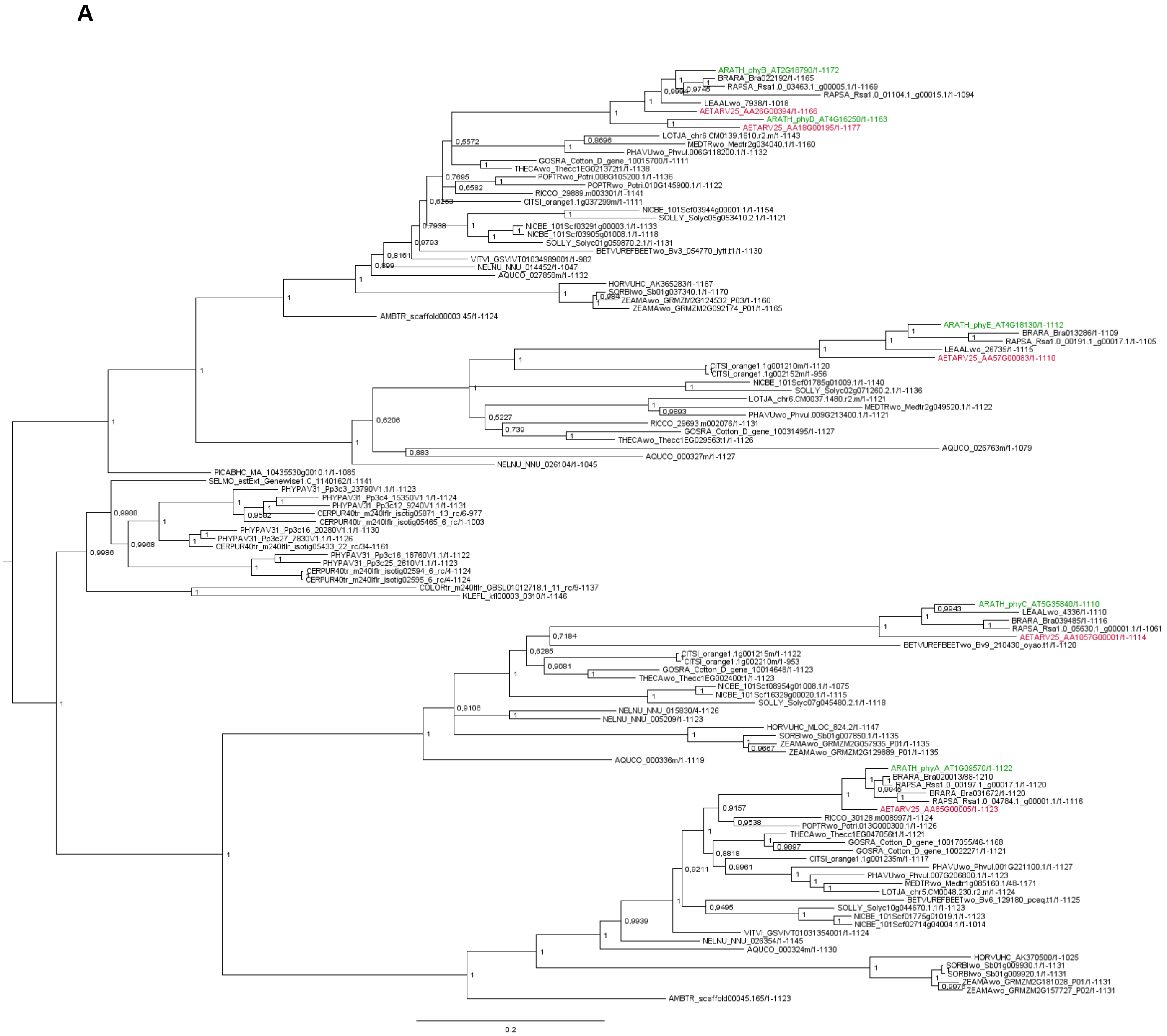
Supporting Figure 3



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.*

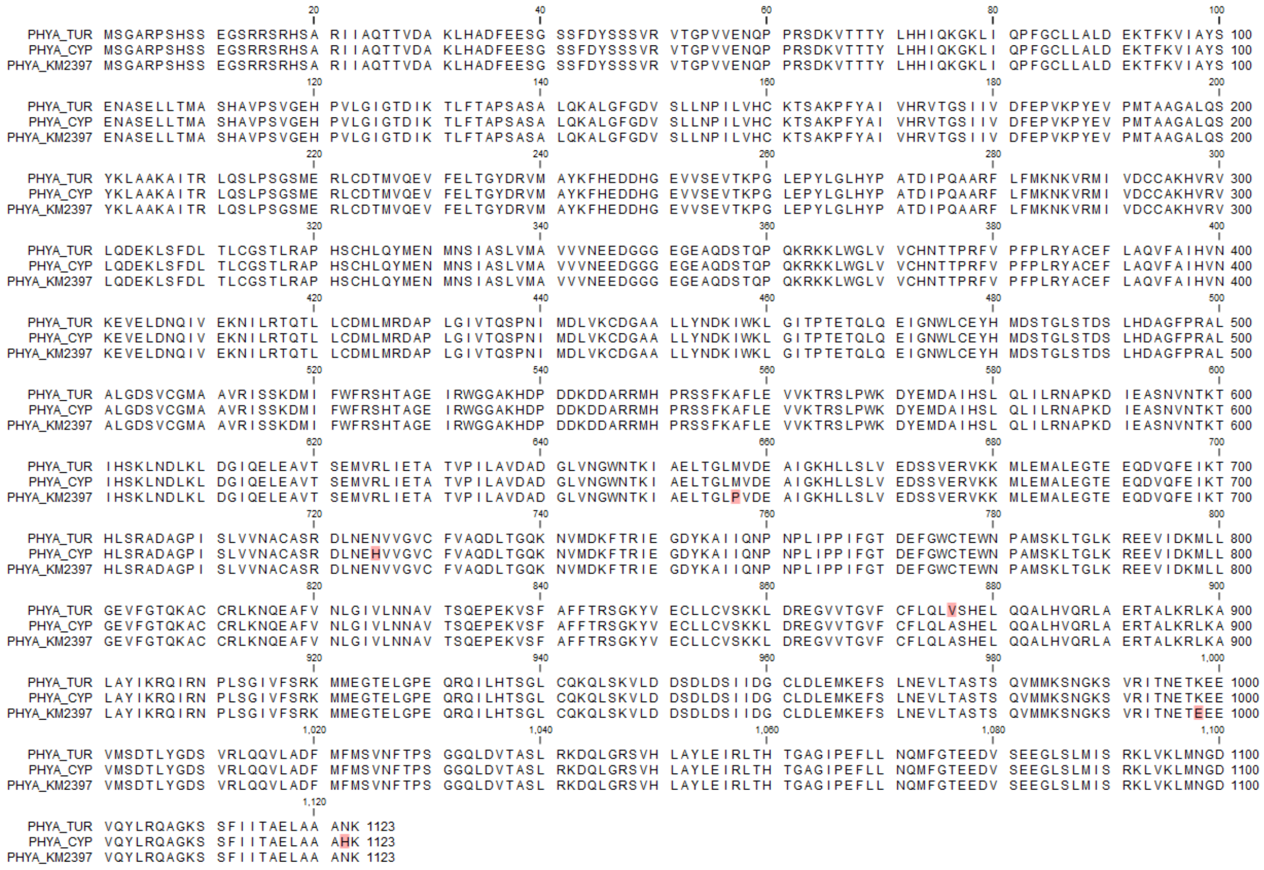


Supporting Figure 4. Accumulation of GA forms in *Ae. arabicum* TUR and CYP seeds under dark and light conditions.



Supporting Figure 5

B



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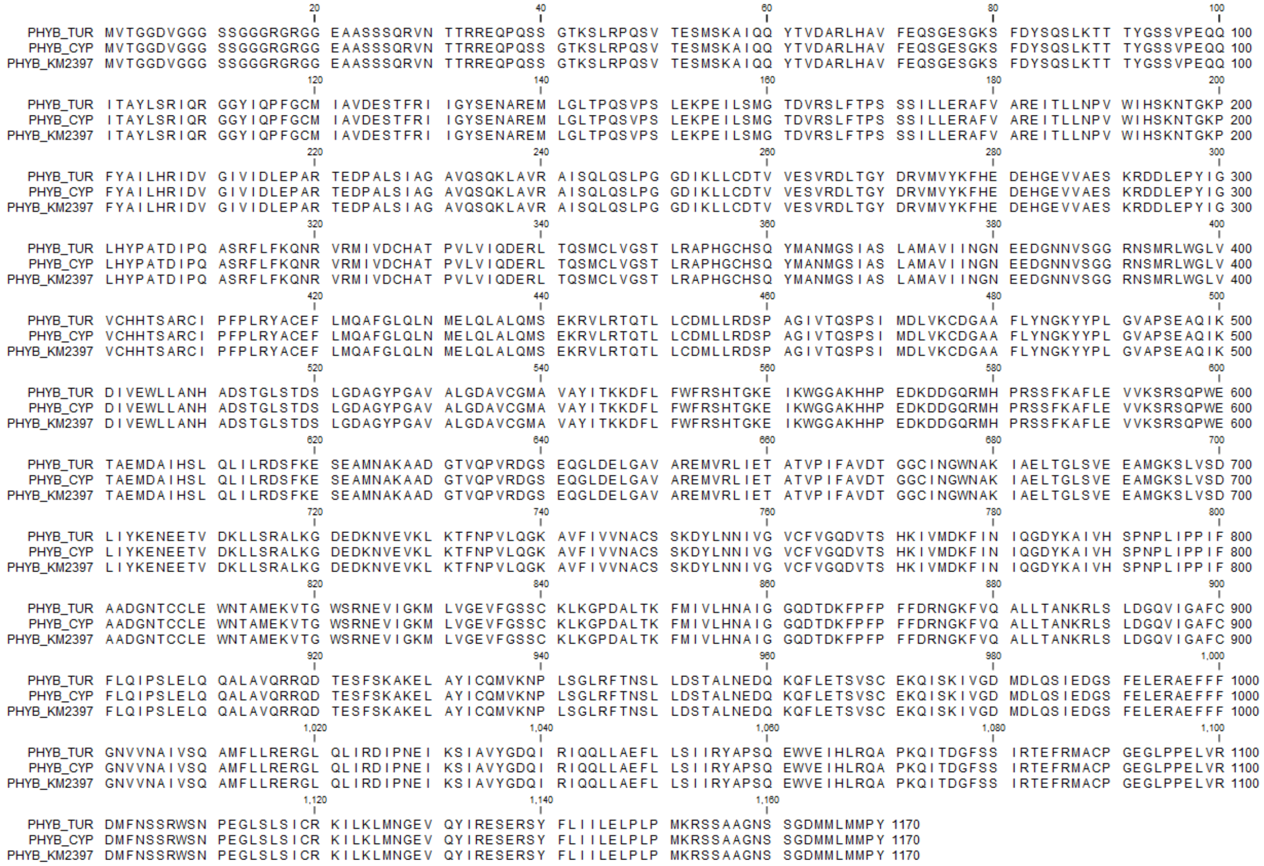

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Supporting Figure 5

D

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Supporting Figure 5

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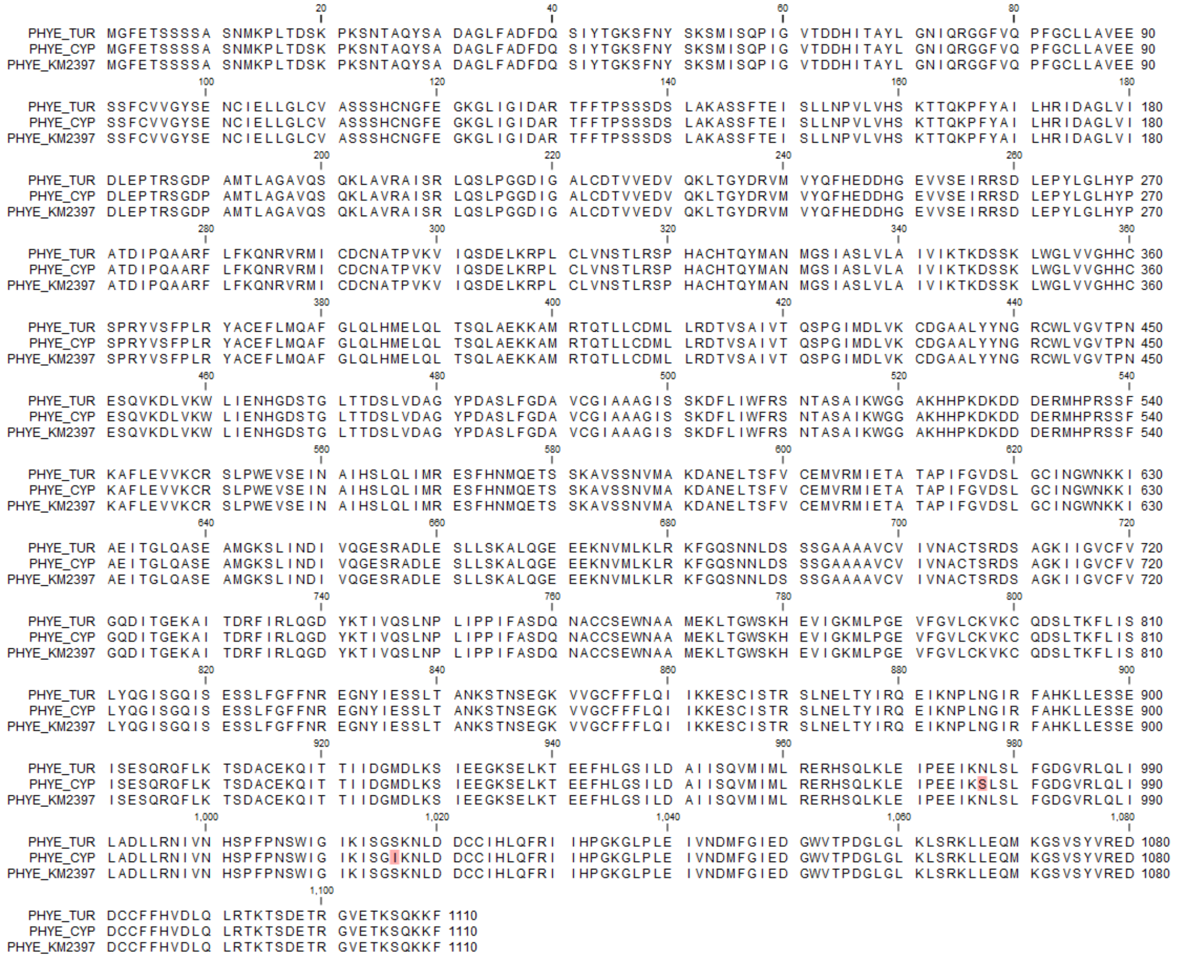

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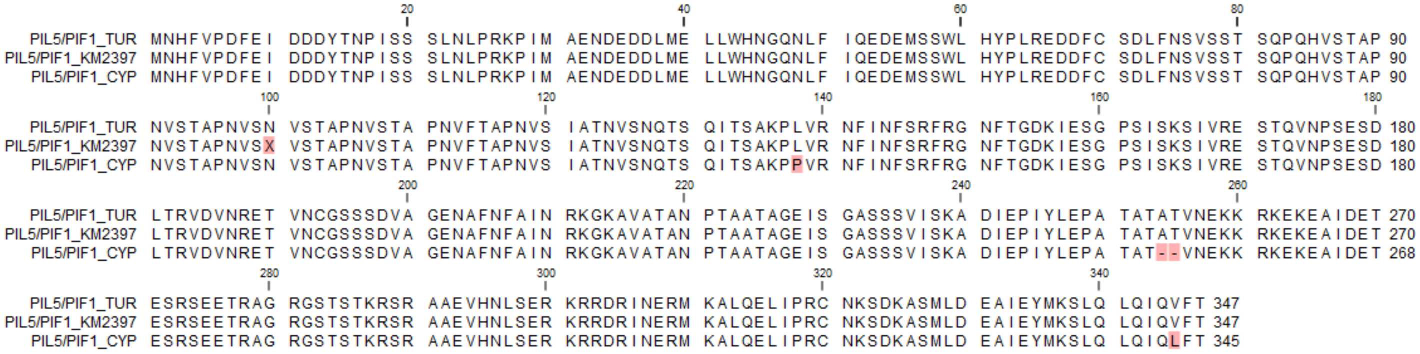
Supporting Figure 5. Identification and alignments of phytochromes in *Ae. arabicum*. (a) Phylogenetic tree of phytochromes using Bayesian inference (1688500 generations, standard deviation of split frequencies 0.009992) and allows clear assignment of *Ae. arabicum* orthologues. Sequences of *A. thaliana* (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.



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                                  |                     |                     |                     |
    PIL5/PIF1_TUR ESRSEETRAG RGSTSTKRSR AAEVHNLSER KRRDRINERM KALQELIPRC NKSDKASMLD EAIEYMKSLQ LQIQVFT 347
 PIL5/PIF1_KM2397 ESRSEETRAG RGSTSTKRSR AAEVHNLSER KRRDRINERM KALQELIPRC NKSDKASMLD EAIEYMKSLQ LQIQVFT 347
    PIL5/PIF1_CYP ESRSEETRAG RGSTSTKRSR AAEVHNLSER KRRDRINERM KALQELIPRC NKSDKASMLD EAIEYMKSLQ LQIQLFT 345
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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.