



Table S1. Properties of 6 ScELIPs Unigenes.

Predicted Number of Amino Acid	Predicted pI	Predicted Molecular Mass (kDa)	Conserved
			Domain
13021	212	5.58	Chloro_a_b-bind
40120	236	9.09	Chloro_a_b-bind
40121	236	9.33	Chloro_a_b-bind
68225	207	9.57	Chloro_a_b-bind
16576	94	10.39	Chloro_a_b-bind
8044	94	6.71	Chloro_a_b-bind

Table S2. Sequences information for construction of the phylogenetic tree.

	Gene	Amino Acid	Accession Number
<i>AtELIP1</i>	<i>ELIP1</i>	151	U89014
<i>AtELIP2</i>	<i>ELIP2</i>	152	Z97336
<i>Syntrichia ruralis-A</i>	<i>ELIPa</i>	212	AY034890
<i>Syntrichia ruralis-B</i>	<i>ELIPb</i>	224	AY034891
<i>Setaria italica</i>	<i>ELIP</i>	181	XP_004955632
<i>Zea mays</i>	<i>ELIP</i>	192	ACG46269
<i>Panicum miliaceum</i>	<i>ELIP</i>	197	RLN34913.1
<i>Oryza sativa</i>	<i>ELIP</i>	187	BAD30330
<i>Brachypodium distachyon</i>	<i>ELIP</i>	193	XP_010228291.1
<i>Dendrobium catenatum</i>	<i>ELIP</i>	192	XP_020674324
<i>Apostasia shenzhenica</i>	<i>ELIP</i>	196	PKA64958.1
<i>Elaeis guineensis</i>	<i>ELIP</i>	189	XP_010923519.1
<i>Phoenix dactylifera</i>	<i>ELIP</i>	193	XP_008786056.1
<i>Solanum tuberosum</i>	<i>ELIP</i>	197	XP_006363471
<i>Medicago truncatula</i>	<i>ELIP</i>	197	XP_013469748.1
<i>Gossypium raimondii</i>	<i>ELIP</i>	193	XP_012487200.1
<i>Morus notabilis</i>	<i>ELIP</i>	195	XP_010107710
<i>Capsella rubella</i>	<i>ELIP</i>	196	XP_006298609.1
<i>Brassica rapa</i>	<i>ELIP</i>	191	XP_009148406.1
<i>Selaginella moellendorffii</i>	<i>ELIP</i>	197	XP_024536558
<i>Sphagnum fallax</i>	<i>ELIP</i>	253	Sphfalx0001s0155.1
<i>Onoclea sensibilis</i>	<i>ELIP</i>	230	AAB25012
<i>Marchantia polymorpha</i>	<i>ELIP</i>	227	PTQ40288
<i>Physcomitrella patens ELIP12</i>	<i>ELIP12</i>	225	A9TAX2
<i>Physcomitrella patens ELIP8</i>	<i>ELIP8</i>	325	EDQ69484
<i>Physcomitrella patens ELIP11</i>	<i>ELIP11</i>	110	A9S3S8

<i>Physcomitrella patens</i> <i>ELIP7</i>	<i>ELIP7</i>	140	A9TL19
<i>Physcomitrella patens</i> <i>ELIP6</i>	<i>ELIP6</i>	135	A9RSF4
<i>Physcomitrella patens</i> <i>ELIP10</i>	<i>ELIP10</i>	220	A9SZ27
<i>Physcomitrella patens</i> <i>ELIP4</i>	<i>ELIP4</i>	249	A9TIL7
<i>Physcomitrella patens</i> <i>ELIP9</i>	<i>ELIP9</i>	225	A9T6B6
<i>ScELIP1</i>	<i>ScELIP1</i>	236	KM363766
<i>ScELIP2</i>	<i>ScELIP2</i>	207	KM363767

Table S3. Primer information for RT-qPCR of high light treatment of plantlets.

Gene	Sequence	GeneBank Accession	
<i>OHP2</i>	Forward TCTTCGACAGCTTCGTCGTCT	NM_103122	one helix protein
	Reverse GAGGCTCCGGAGAGTAGGA		
<i>OHP</i>	Forward TGAGCTCGTCGCCGTATCT	NM_120290.3	one helix protein
	Reverse GCGGCTCTGACAACGAAAGG		
<i>SEP2</i>	Forward TGGCGATTAGCCGAGAACGG	NP565524	stress enhanced protein 2
	Reverse CACCATCTCCGCCGTCTTT		
<i>LHCB4.2</i>	Forward ATCGACGCCGTTTCAGCCAT	NM_111728	PS II CP29 antenna protein
	Reverse GCCAAGAGTGGCGAGCATTG		
<i>LHCA2</i>	Forward CTGTCTCCAGGCCAGATGCG	NM_116012	PS I antenna protein
	Reverse CACCAGGGAGGCTACCGTCT		
<i>PSBS</i>	Forward GGGAGCCATTGGAGCTCTCG	NM_103552	PS II CP22 antenna protein
	Reverse GAGACCGAGGGCAGATCGGA		
<i>PSBD</i>	Forward TGATGGAGTCGCCGGTGTA	NP_051054	PS II D2 protein
	Reverse AAGCGGTTAGCGGTGACCAT		
<i>ScELIP1</i>	Forward GGCTATGCTGGATTCTGTGT	KM363766	
	Reverse GACGCCAGGAACCAGATCAA		
<i>ScELIP2</i>	Forward GCAATGATCGGACTTGTGCG	KM363767	
	Reverse ACGGATTGTTCACAGCAGGT		
<i>a-TUB</i>	Forward GATGTACCGTGGTGATGTC		
	Reverse GAGCCTCTGAAAATTCTCC		

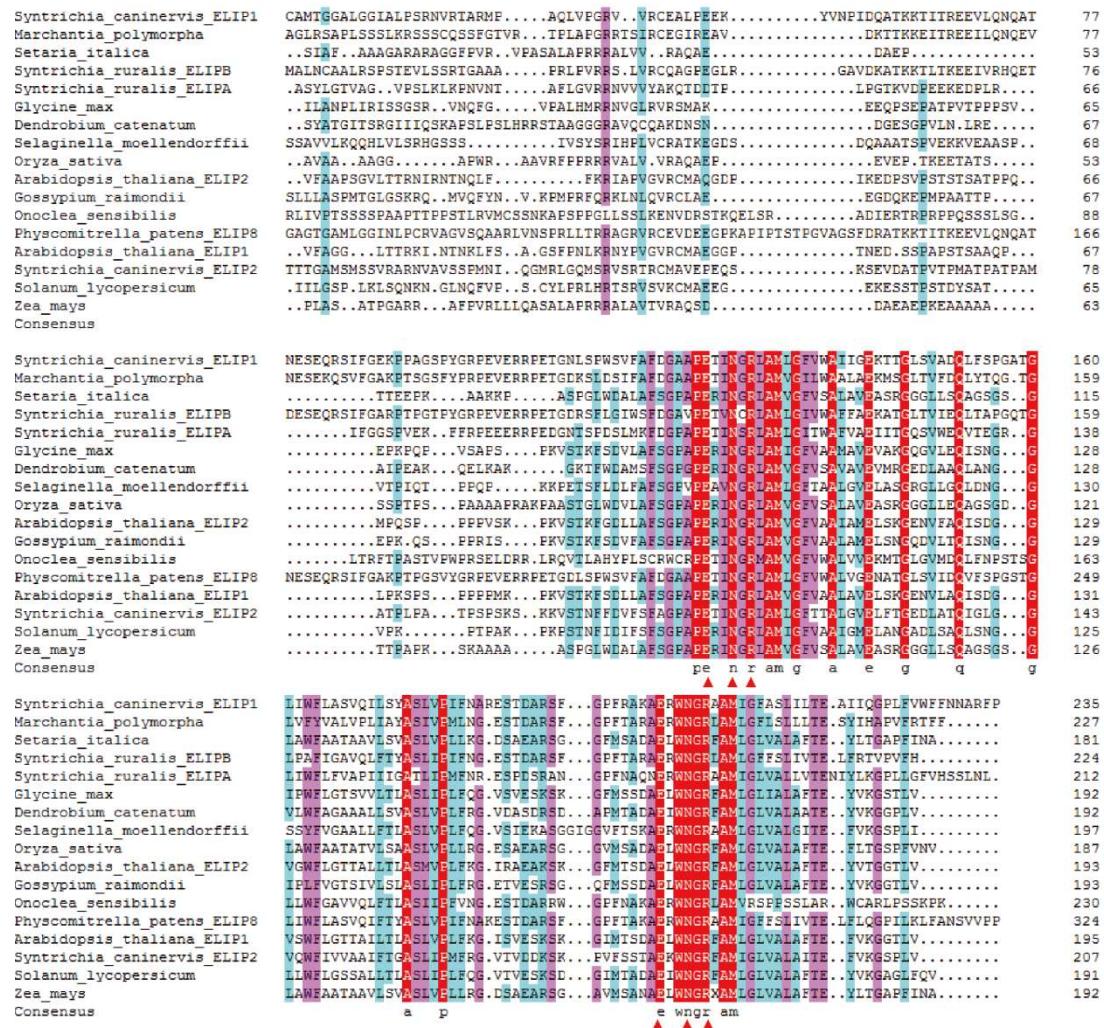


Figure S1. The amino acid sequences alignment of ELIPs by MEGA 7.0. *ScELIP1* and *ScELIP2* have conserved amino acids (triangular symbol) to known ELIP proteins.

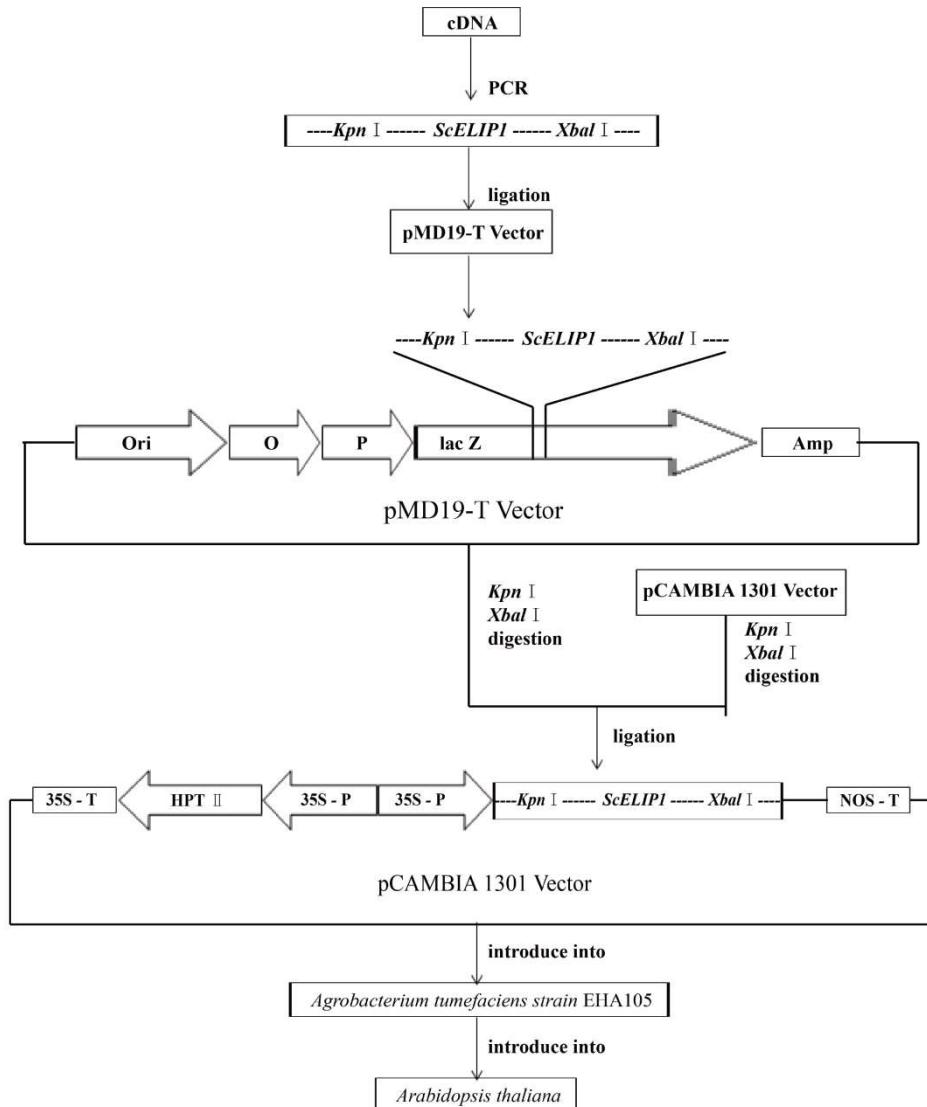
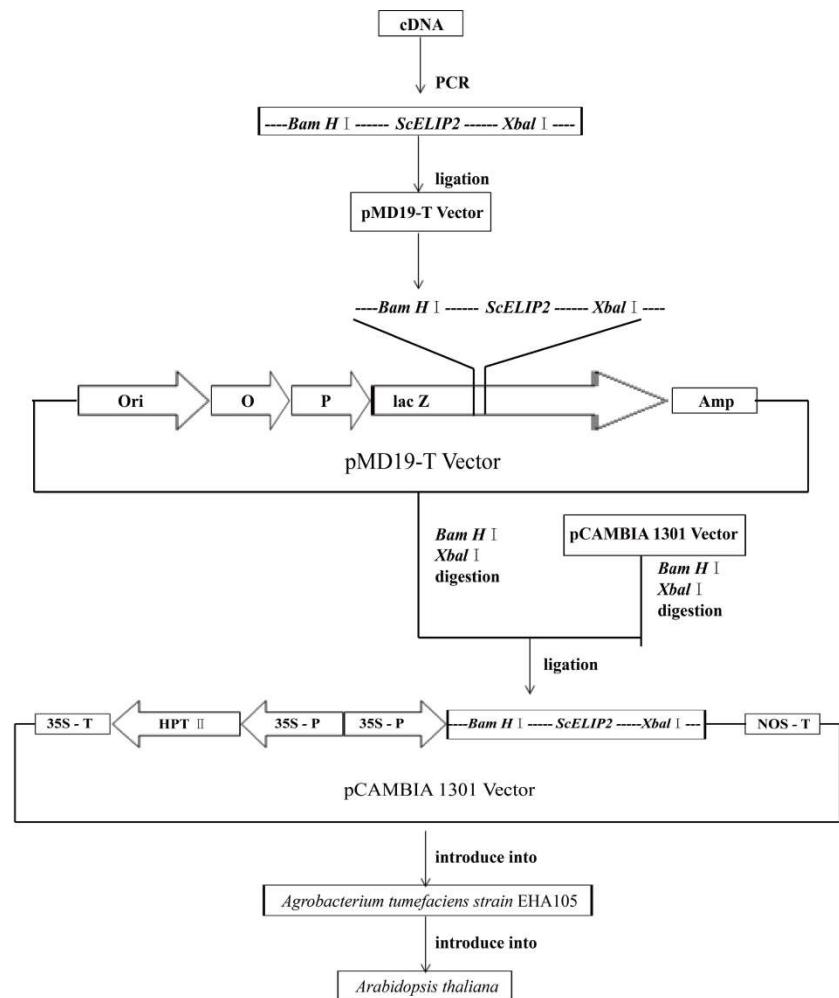


Figure S2. 35S-*ScELIP1* vector construction strategy.

**Figure S3.** 35S-*ScELIP2* vector construction strategy.**Figure S4.** Verification of transgenic Agrobacterium by bacterium PCR. Lane 1-5 positive transgenic clones for *ScELIP1*, lane 6-10 positive transgenic clones for *ScELIP2*. Lane 1 and 6 Agrobacterium used for transforming *Atelip* mutant.

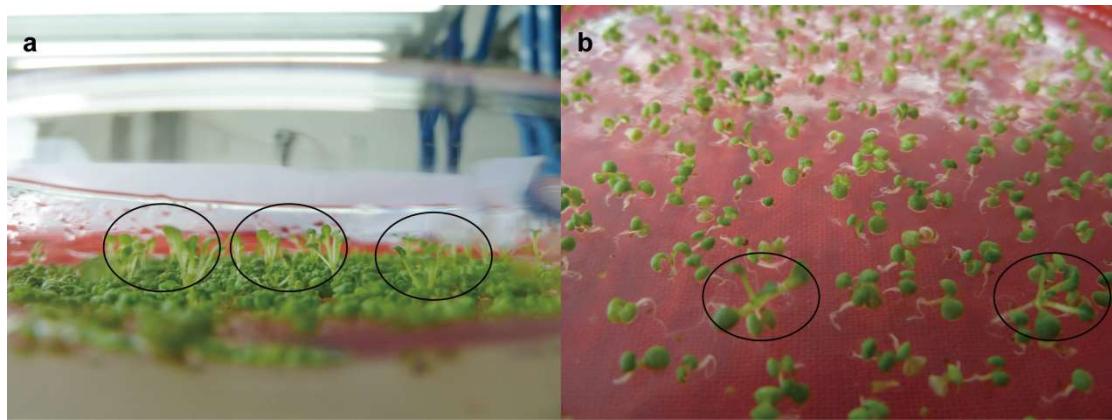


Figure S5. Hygromycin selection of transgenic *Arabidopsis thaliana*. The plantlets in the circles are positive transgenic lines which have emergent green leaves which stay green, the negative plants have cotyledon emergence but subsequently turn yellow or white after ten days.

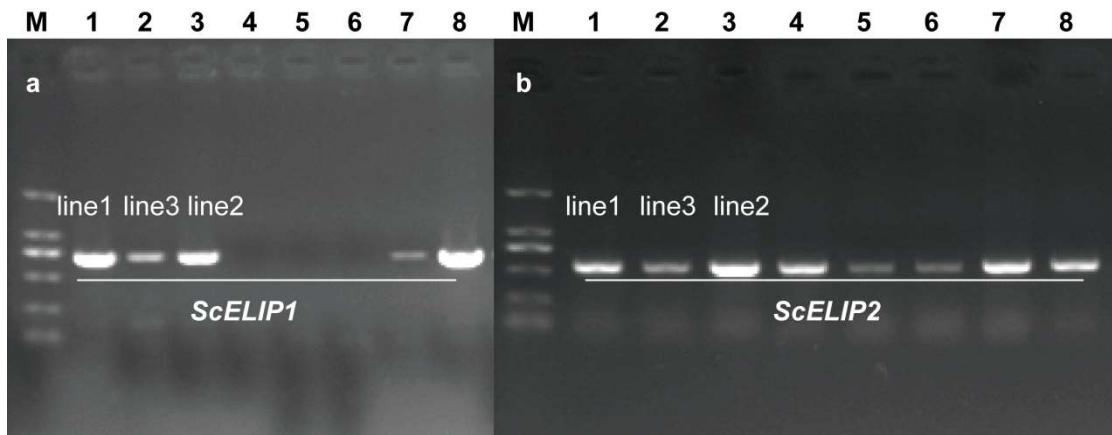


Figure S6. RT-PCR validation of T3 transgenic lines.

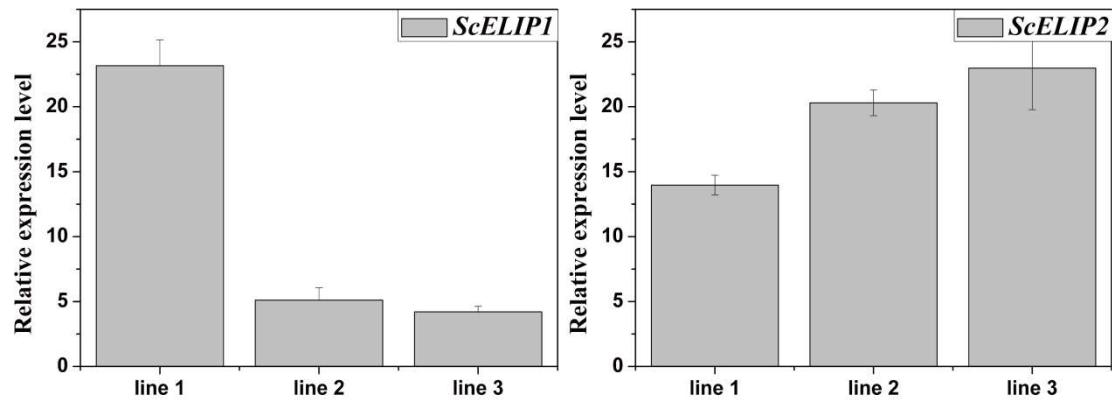


Figure S7. Quantitative real time PCR expression level analysis of *ScELIP1* and *ScELIP2* transgenic lines. Error bars represent the SD of three biological repeats. Relative expression values were obtained from $2^{-\Delta\Delta Ct}$ comparing WT and the transgenic lines with the *Atelip* mutant respectively.

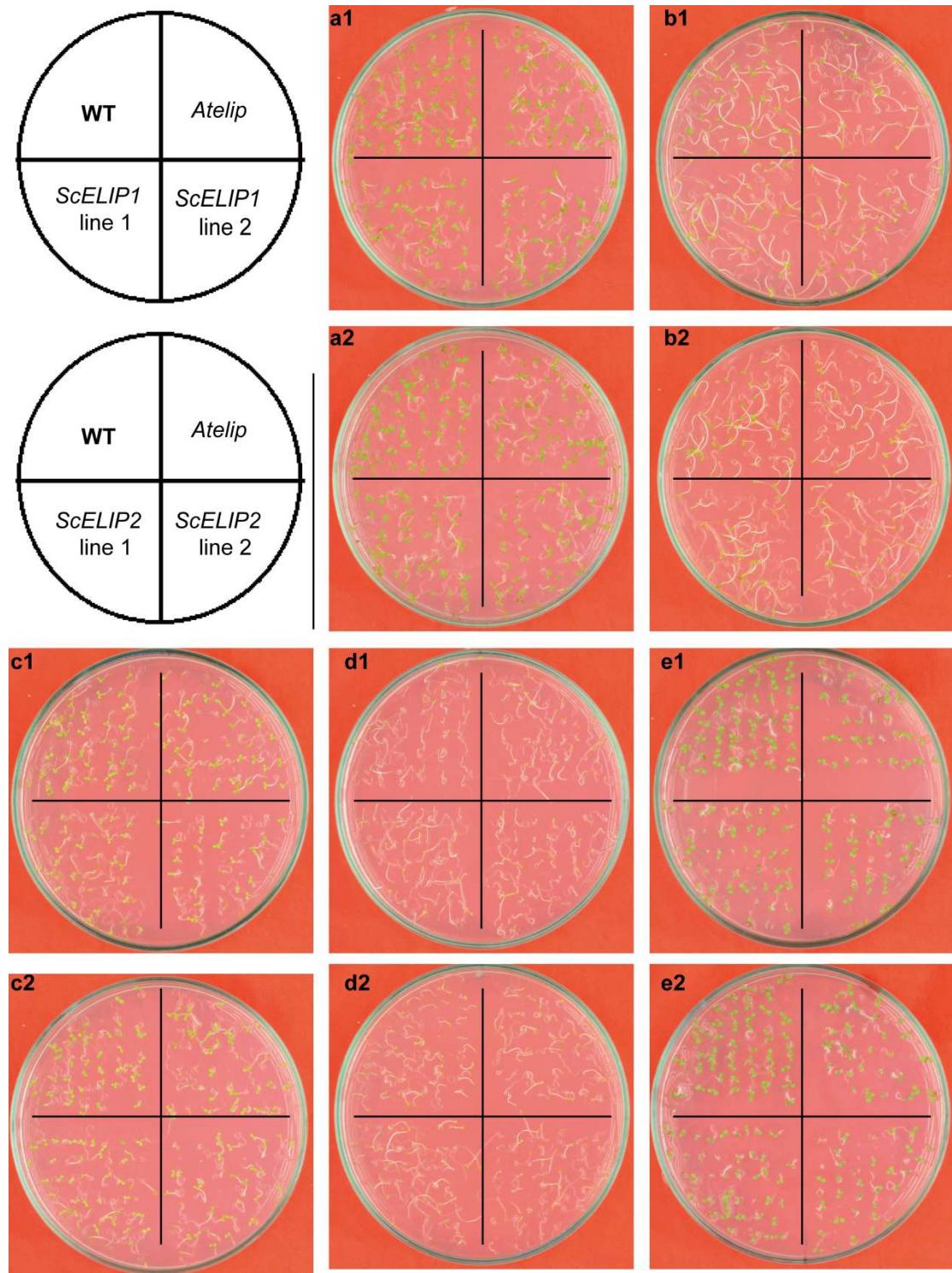


Figure S8. Seed germination phenotypes for Col-0 WT, *Atelip* mutant and 35S-*ScELIP* lines under different light treatments. Images, labeled a-e, depict the phenotypic response of the four genotypes to the various light treatments. Control condition (a1,a2); Red light alone (b1,b2); Blue light alone (c1,c2); UVB alone (d1,d2); High light alone (e1,e2).

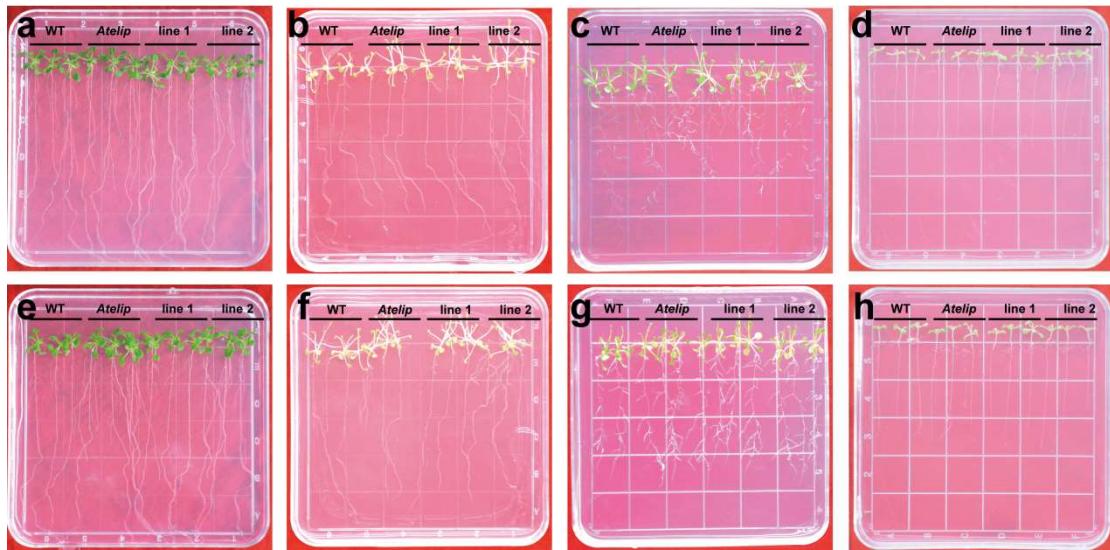


Figure S9. Phenotypic response of Col-0 WT, *Atelip* mutant and 35S-*SceLIP1* and 35S-*SceLIP2* after seven days of exposure to different light treatments. Row 1, WT, *Atelip* mutant, 35S-*SceLIP1* transgenic lines. Row 2, WT, *Atelip* mutant, 35S-*SceLIP2* transgenic lines. Control conditions (**a, e**), Red light alone (**b, f**), Blue light alone (**c, g**), UVB alone (**d, h**).

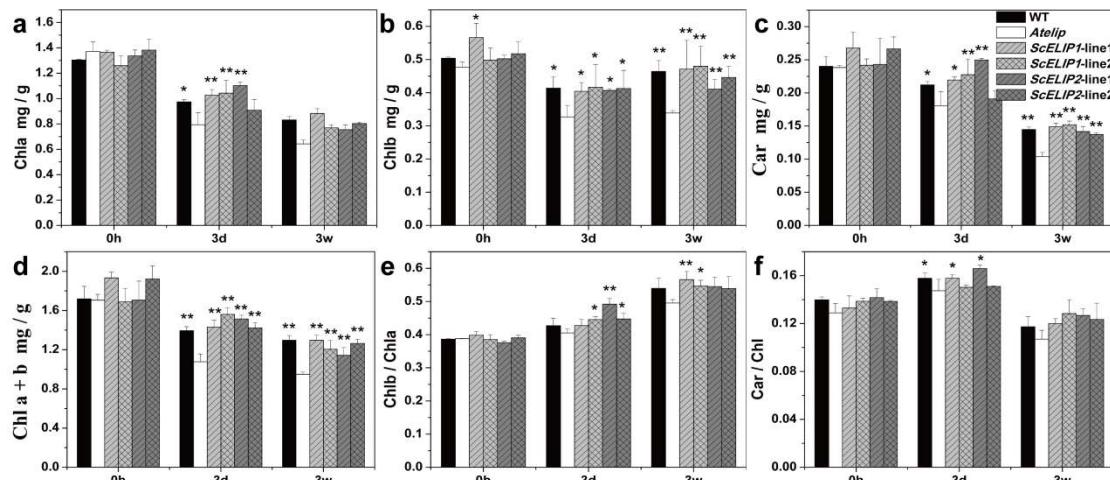


Figure S10. The change of chlorophyll content of WT, *Atelip* and transgenic lines at 0 h, 3 days and 3 weeks high light stress (1000 $\mu\text{mol}/\text{m}^2/\text{s}$). Error bars represent the SD of three biological repeats. *, P < 0.05; **, P < 0.01. P-values were obtained from Dunnett's T3 test comparing WT and the transgenic lines with the *Atelip* mutant respectively.

