

SCL15 (1) M-----K  
 BnSCL1 (1) M-----K  
 SCL27 (1) MPLSFERFOGEGV FGLSSSSSFYSDSQKIWSNQDKTEAKQEDLGYVVG-GFLPEPTSVLDAI  
 SCL22 (1) MPLPFFQFOGKGV LGFLDSSSSSPGYKIWANPEKLGHRVEEDLCFVVNNGGFS EPTSVLDSV  
 SCL6 (1) MPLPFFEFOGKGLSCFSSF-SSSFPQPPSSPLLSHRKARGGEEEEEE-VPAAEPTSVLDSI

SCL15 (3) IPASSPQDTINNNNTNSTDNSH-----LSMDEHVMRSMDWDSIMKELIELD---  
 BnSCL1 (3) IQASSPQDNQPSNTINNSTDNSH-----LSMDEHAMRSMDWDSIMKELIEND---  
 SCL27 (61) RSPSPLASYSSITTLSSSHGGG GTTVTNTVTAGDDNNNKC SQMGLDGLLGVLSASSPG  
 SCL22 (62) RSPSPFVSSITTLSSSHGGGPS CGG-----AAAATFS GAGKCDQMGFEDLLGVLSGGSPG  
 SCL6 (60) ISPTSSSIVSSSHGGNSAVGGG-----DATTTEQCGAIGLGDWHEQVPHD---

SCL15 (49) DSAPNSIKTGF-----TTTITDSTI---L  
 BnSCL1 (49) DSAPYQLQPS-----S  
 SCL27 (122) EQSILRLIMDPGSAFVDFDPGFVFGSGSPVAPVSDNSNLLCNFPFQEIINPAEA---L  
 SCL22 (118) EQSIFRLIMAGDVVDPGSE---FVGFDIGSGSDPVIDNPNPLFGYGFPPQNAFEEEEKFQL  
 SCL6 (106) HEQSILGLIMG-----DSTIDPS---L

SCL15 (71) PLYA---VDSNLEGFDPQIQPSD-----FESSSDVYVPGNQITIGYGFNS-----  
 BnSCL1 (61) ---FNLVFPD-----IDS SDVYVPGPNQITIGYGFNS-----  
 SCL27 (180) INPSNHCLFYNPFLSFP AKRFNSG--SLHQPVFPLSDPD PGHDPVRRQHQFQFPFYHNNQQQ  
 SCL22 (176) SINPNPGFFSDPESSFP AKRLNSG-----QPGSCHLQWVFPFSDPGHESHDP--  
 SCL6 (124) ELNS---ILQTSFTFHSDSYSSPCFGVVDTGFGLDHHSVPPSHVSGLLINQSQTHY TQNP-

SCL15 (112) -----LDSV DNGGFDFIEDLIRVVD CVESDEL-----QLAQVVL SRL  
 BnSCL1 (89) -----LDSV DNGGFDFIEDLIRVVD CVESDEL-----HLAHVVL S QL  
 SCL27 (240) QFPSSSSSTAVAMVPVSPGMAGDDQSV IIEQLFNAAELI GHTGNNGDHTV LAQGILARL  
 SCL22 (223) -----FLTTPK IAG-EDQNDQDQSAV IIDQLFSAAEITINGGDN--NPV LAQGILARL  
 SCL6 (181) ----AAIFYGHHHTPPPAKRINPGPVGIT EQLVKAAEVIESDT-----CLAQGILARL

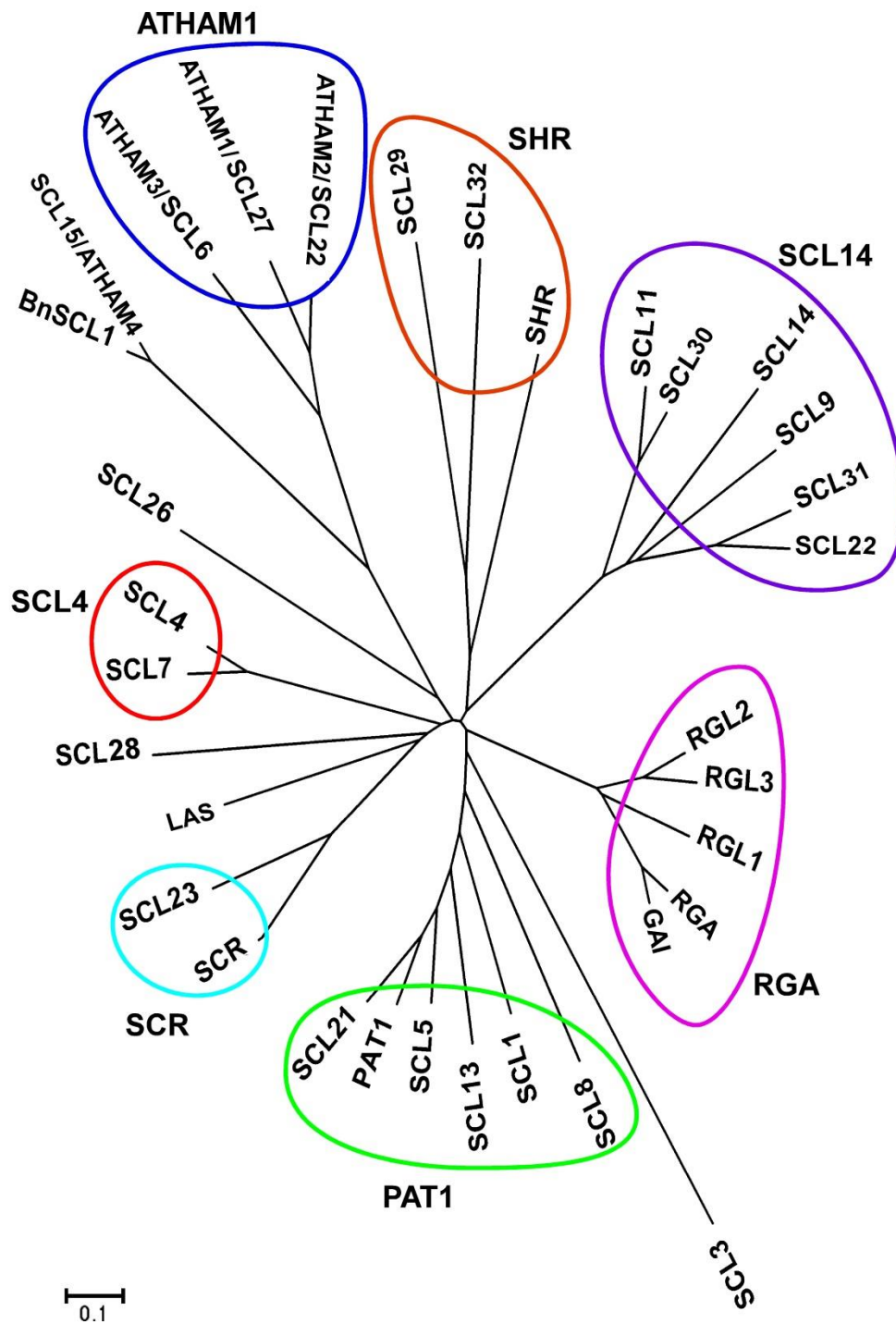
SCL15 (149) NORLRS PA-----GRPLQRAAFYFKEALGSFLTGSNRNIRLSSWSEIVQRIRAIKEYS  
 BnSCL1 (126) NORLQ TSA-----GRPLQRAAFYFKEALGSLLTGSNRN--QLFSWSDIVQKIRAIKEFS  
 SCL27 (301) NHHLNTSSNH-----KSPFORAAASHIAEALLSLIHNESSPF--LITPENLILRTAAYRSFS  
 SCL22 (274) NHHLNNNDDTNNNPKP PFHRAASYITEALHSLIQDSSLSFP SLPSPQNLIFRTAAYRAFS  
 SCL6 (231) NQQLSSPV-----GKPLERAAAFYFKEALNNLLHNVSQT----LNFYSLIFKIAAYKSFS

SCL15 (203) GISPIPLFSHFTANQAILDSLSSQSSSPFVHVVDPEIIGFGGQYASIMREIATEKSVSGGF--  
 BnSCL1 (178) GISPIPLFSHFTANQAILDSLSSQSSSPFVHVVDPEIIGFGGQYASIMREIAEK SANGGF--  
 SCL27 (355) ETSPFLQFVNFTANQITILESCNESGFDR--IHIIDFDI GYGGQWASLIQELAGKRNRRSS--  
 SCL22 (335) ETSPFLQFVNFTANQITILESFEGFDR--IHIIDFDI GYGGQWASLIQELAGKRNRRSS--  
 SCL6 (281) EISPVLFQFANFTSNQAILLESFHGFHR--LHIIDFDI GYGGQWASIMQELVLRDNAA PLS-

SCL15 (262) ----LRVTAVV--AEECAVETRLVKENITQFAAEMKIRFQIEFVLMKTFEMLSFKAI---  
 BnSCL1 (237) ----LRVTAVV--AEDCAVETRLVKENITQFAAEMKIRFQIEFVLMKTFEILSFKAI---  
 SCL27 (415) ASSLKLTVFAPFPSTVSLDEFELRFTTEENLKT FAGEVKIPFEIETLLSVEILLNPAWPL--SL  
 SCL22 (391) APSLKITAFASF--STVSLDEFELRFTTEENLRSFAGE TGV SFEIETLLNMEILLNPTYWPLSLF  
 SCL6 (338) ---LKITVFAF--ANHDQLELGF TQNLKHFAS EINI SLLTQVLSLDLLGSLSWP----

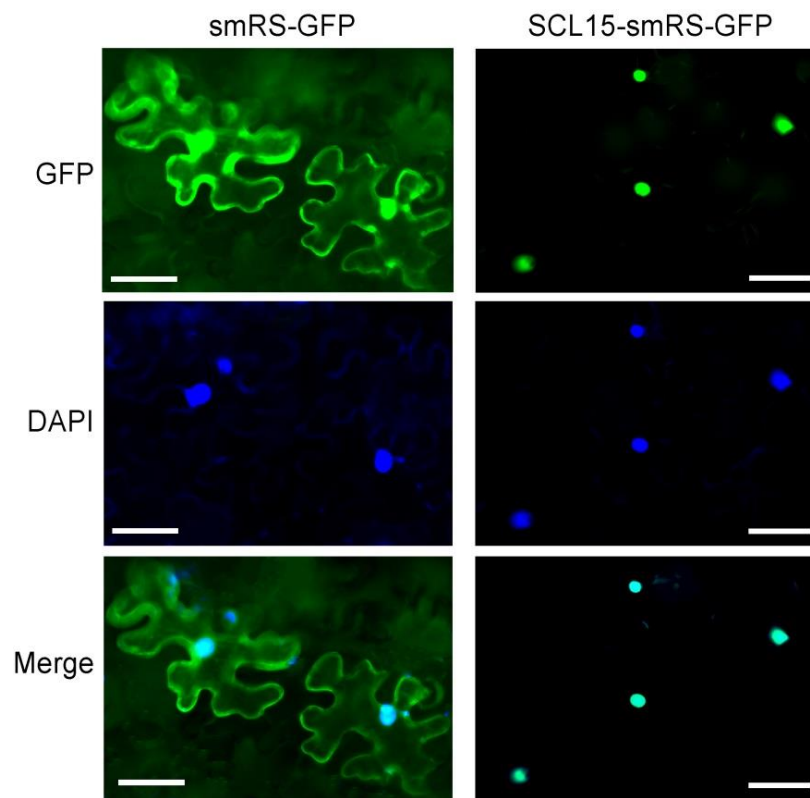
SCL15 (313) RFVFGERTV VLI--SPALFRRISGITDFVNNLRRVSPKV VVFDVSEGWTEIAGSGSFRREF  
 BnSCL1 (288) RFVFGERTV VLI--SPALFRRVIGIAEFVNNLGRVSPNV VVFDVSEGCTETAGSGSFRREF  
 SCL27 (475) RSSEKEAIAVNI PVNSVASGYLPLILRFLKQLS-----FNIVVCSDRGCDRN--DAPFPNAV  
 SCL22 (451) RSSEKEAIAVNI PISSMVSGY LPLILRFLKQLS-----FNVVCSDRS CD RN--NDAPFPNGV  
 SCL6 (389) NSSEKEAIAVNI--SAASF SHLPLMLRFVKHLS-----FTLIVCSDRGCEFT--DLFESQQL



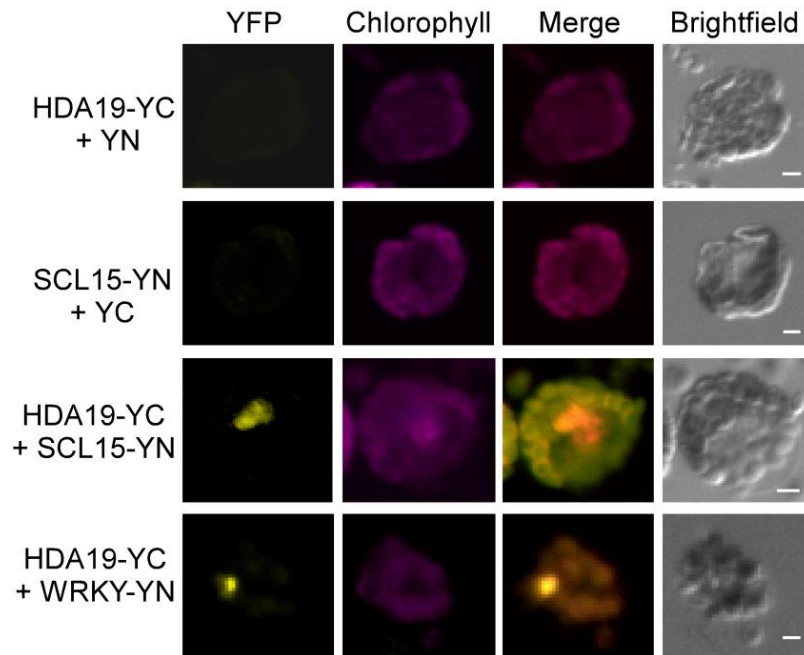


**Supplementary Figure 2. Phylogenetic analysis of the GRAS family proteins in *Arabidopsis*.** The tree was generated using the neighbour-joining algorithm with MEGA version 5<sup>46</sup>. Six major clades or groups are noted: ATHAM1, PAT1, RGA, SCL4, SCL14, SCR and SHR. Proteins and their accession numbers are as follows: SCL1 (At1g21450), SCL3 (At1g50420), SCL4 (At5g66770), SCL5 (At1g50600), SCL6 (also designated as LOM3 or AtHAM3 (At4g00150), SCL7 (At3g50650), SCL8 (At5g52510), SCL9

(At2g37650), SCL11 (At5g59450), SCL13 (At4g17230), SCL14 (At1g07530), SCL15/ATHAM4 (At4g36710), SCL21 (At2g04890), SCL22/AtHAM2 (At3g60630), SCL23 (At5g41920), SCL26 (At4g08250), SCL27 (also designated as LOM1 or AtHAM1) (At2g45160), SCL28 (At1g63100), SCL29 (At3g13840), SCL30 (At3g46600), SCL31 (At1g07520), SCL32 (At3g49950), SCL33 (At2g29060), GAI/RGA2 (At1g14920), LAS (At1g55580), PAT1 (At5g48150), RGA/RGA1 (At2g01570), RGL1 (At1g66350), RGL2 (At3g03450), RGL3 (At5g17490), SCR (At3g54220), SHR (At4g37650). *Brassica napus* BnSCL1 (AY66405) is also included for comparison. Scale bar represents 0.1 amino acid substitutions.

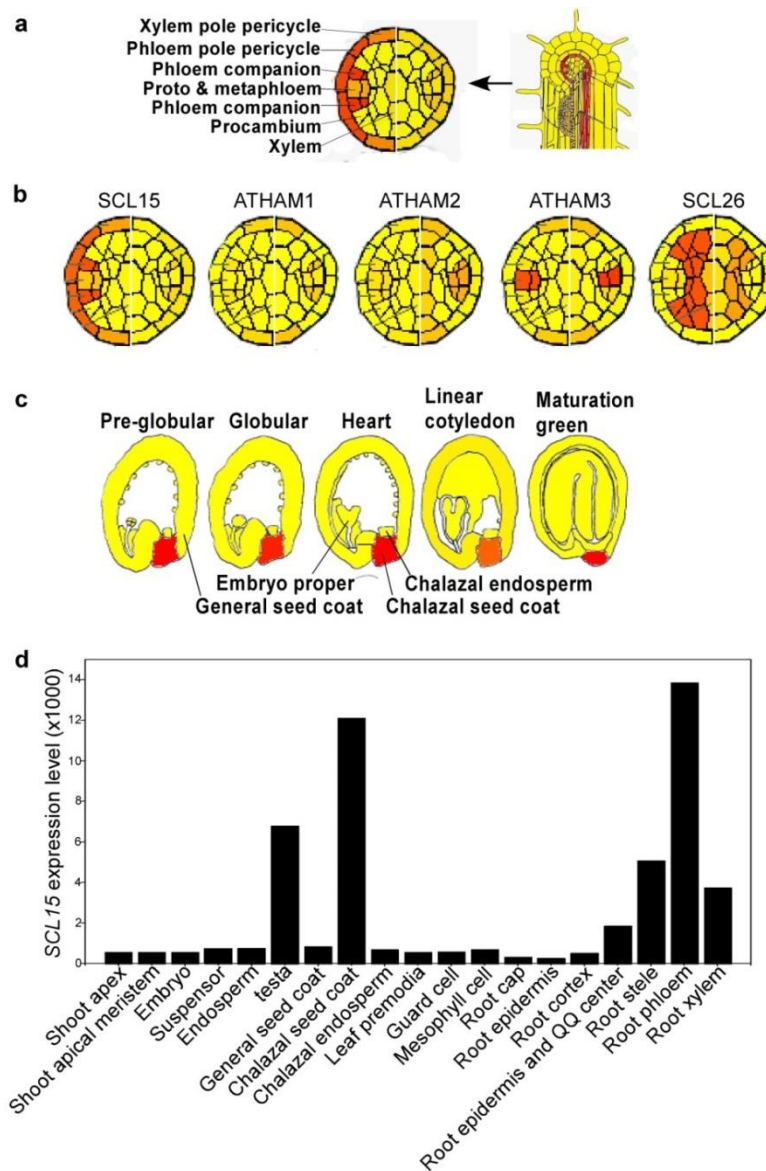


**Supplementary Figure 3. Subcellular localization of SCL15.** A green GFP fluorescent signal is present in the nuclei of tobacco leaf epidermal cells when a translational fusion between SCL15 and the soluble-modified red-shifted green fluorescent protein (smRS-GFP) (*35Spro::SCL15:smRS-GFP*) was introduced. *35Spro::smRS-GFP* was used as a negative control. Bars=10  $\mu$ m.



**Supplementary Figure 4. BiFC analysis of SCL15 interaction with HDA19 in**

***Arabidopsis mesophyll protoplasts.*** Co-expression of SCL15 fused with the N-terminus of YFP (YN) or HDA19 fused with the C-terminus of YFP (YC) with empty vector YC or YN was used as a negative control and co-expression of HDA19-YC and WRKY38-YN served as a positive control for the BiFC assay. Bars = 5  $\mu$ m.



**Supplementary Figure 5. Expression patterns of *SCL15* in specific cells and tissue**

**types. (a)** *SCL15* expression in roots. Note the transcript abundance of *SCL15* is high in

the phloem system of vascular tissues, particularly in the phloem companion cells and

pericycle cells. **(b)** Comparison of cell type-specific expression patterns in *Arabidopsis*

roots between *SCL15* and other members of the ATHAM1 clade as shown in

Supplementary Figure 2. **(c)** *SCL15* expression in developing seeds showing marked

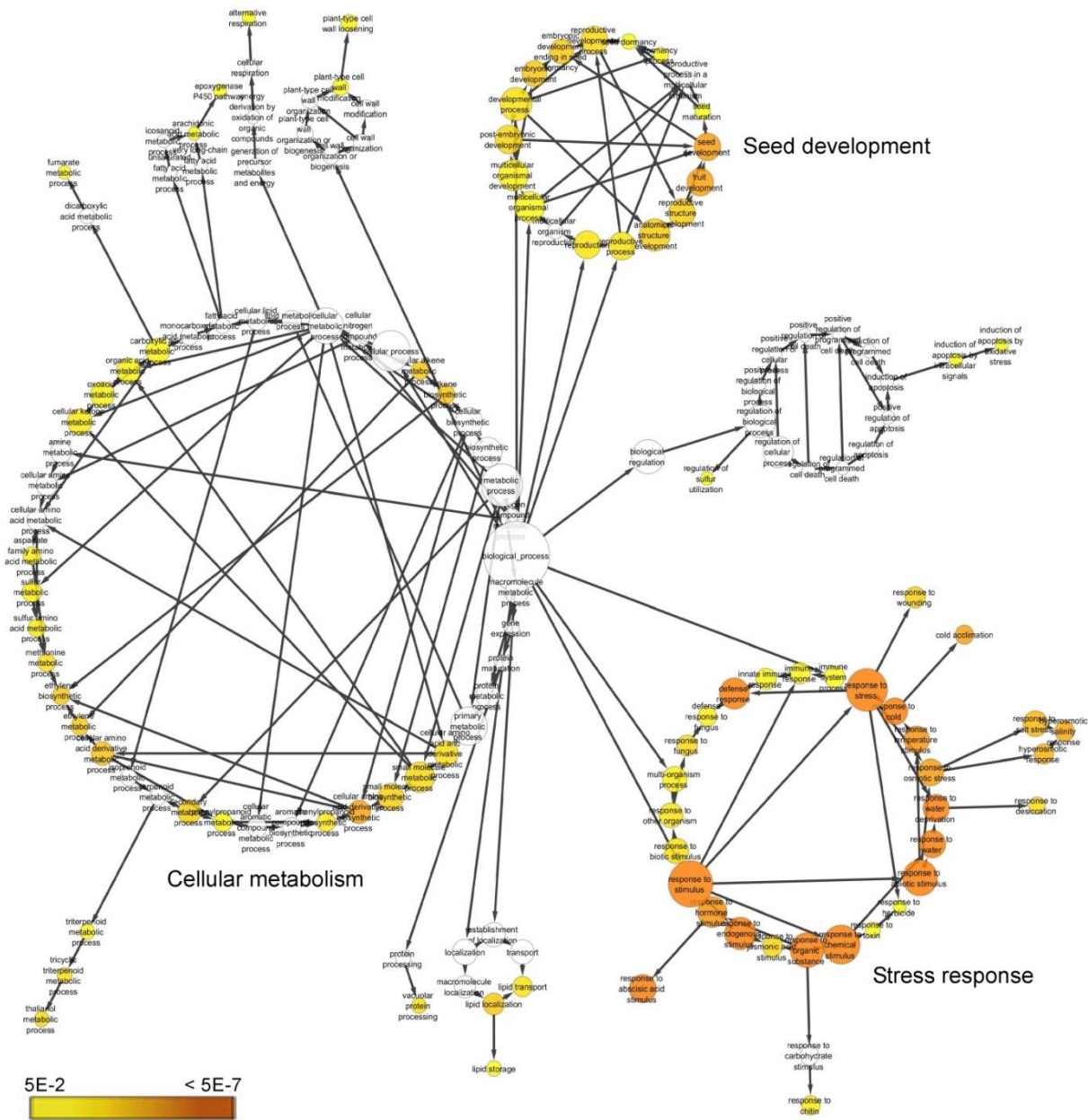
expression in chalazal seed coat. **(a to c)** Data used are retrieved from the BAR

*Arabidopsis* eFP browser (<http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi>).

**(d)** *SCL15* expression in specific tissues. Data used are derived from Genevestigator

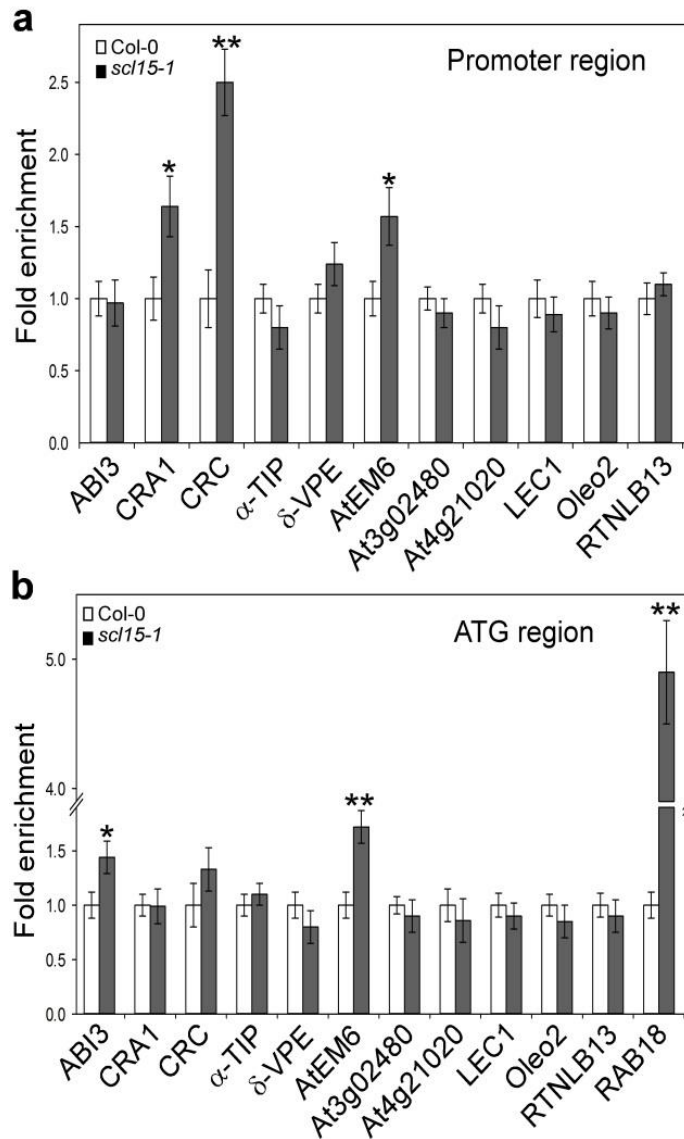
(<https://www.genevestigator.com/gv/plant.jsp>).



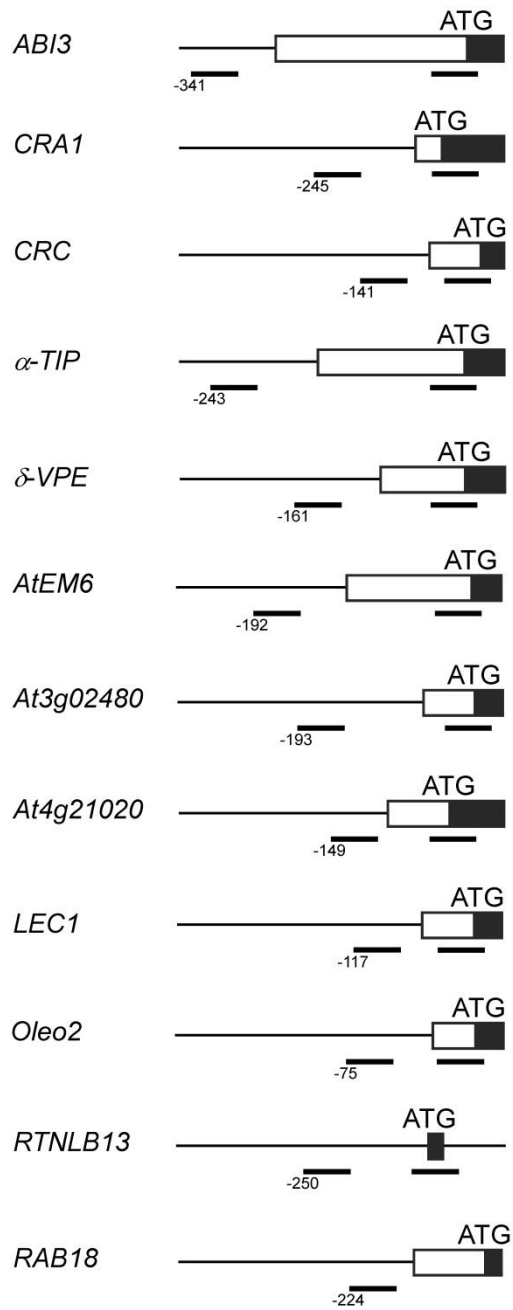


**Supplementary Figure 6. Overrepresentation of gene ontology categories among genes up-regulated in *scf15* mutant seedlings.** BiNGO analysis representing overrepresented categories of the ontology Biological Process among the genes that are more than three-fold (FDR  $\leq 0.05$ ) up-regulated in the *scf15-1* mutant plants compared to wild type (Supplementary dataset 1). The two most overrepresented GO categories are shown. The size of the nodes is proportional to the number of genes annotated to that node. Coloured nodes ranging from yellow to dark orange represent the levels of significance of the overrepresented GO terms with *P* values from  $5E-2$  to  $5E-7$ . White nodes represent GO terms that are not significantly overrepresented. Statistical testing was as described by Maere et al.<sup>34</sup>.

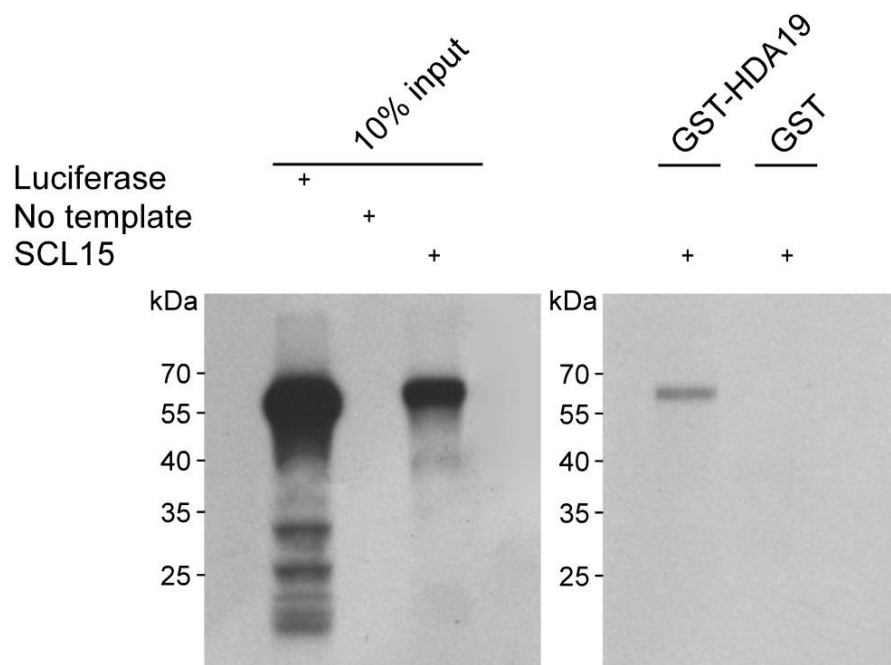




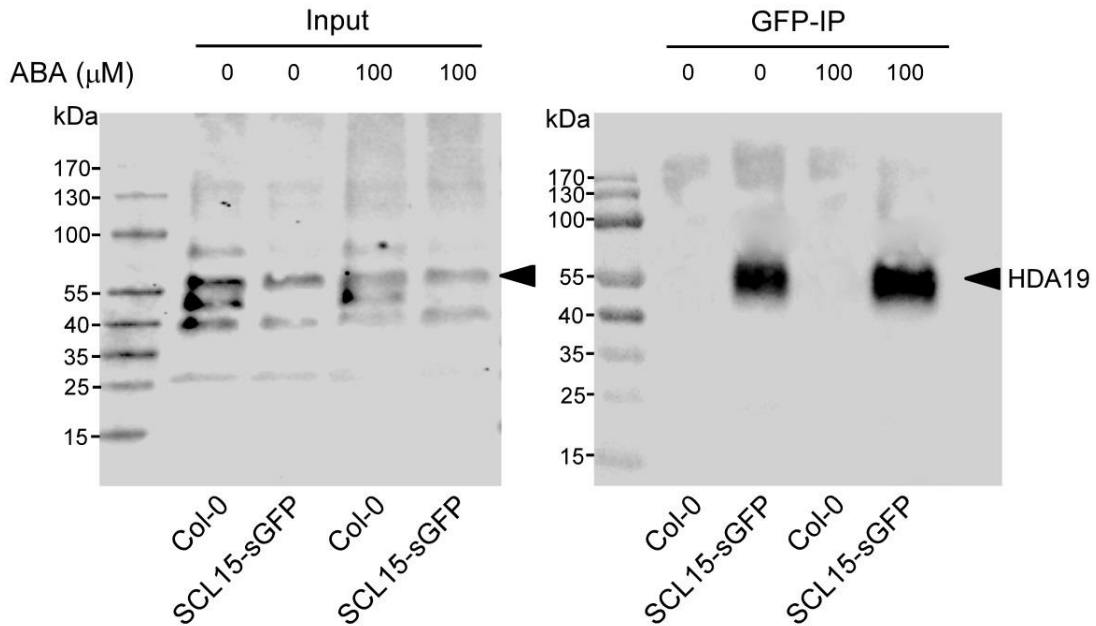
**Supplementary Figure 7. ChIP analysis of H4ac levels for the ectopically-expressed seed maturation genes in wild-type Col-0 and the *scl15-1* seedlings. (a) Relative H4K5K8K12K16ac levels at the proximal promoter regions. (b) Relative H4K5K8K12K16ac levels at the ATG regions. The fold enrichment of *scl15-1* (black bars) relative to the wild type (white bars) is shown and the values are means  $\pm$  SD of three biological replicates (Student's *t*-test, \* $P < 0.05$ , \*\* $P < 0.01$ ).**



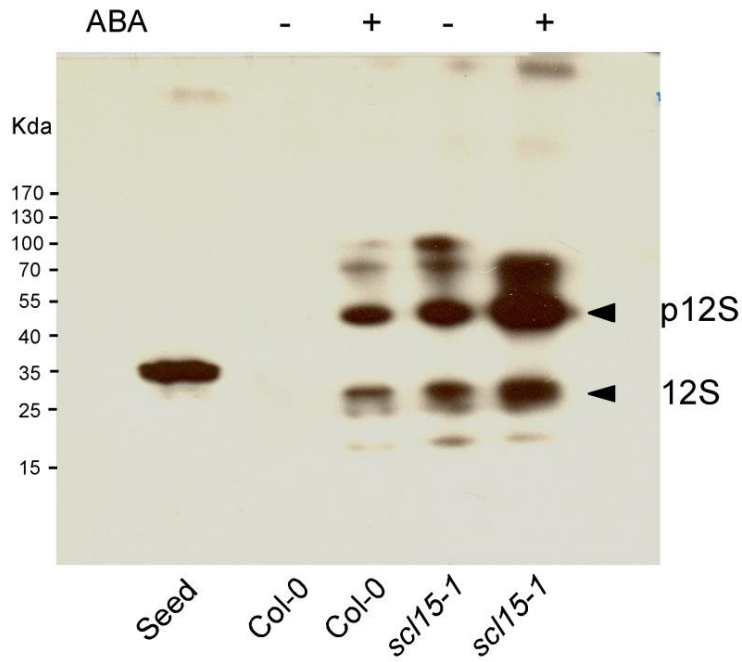
**Supplementary Figure 8. Schematic diagram of the regions examined by ChIP.** The regions that are located at the promoter and translation start (ATG) regions for the up-regulated embryonic genes in *sc15-1* seedlings are indicated.



**Supplementary Figure 9. GST pull-down assay showing interaction of SCL15 with HDA19 *in vitro*.** SCL15 was expressed and radiolabeled using *in vitro* transcription/translation reactions. The translation product (input) was incubated with GST-HDA19 fusion or GST alone.



**Supplementary Figure 10. Co-IP assay in *Arabidopsis* seedlings showing co-precipitation of HDA19 with SCL15-sGFP.** Nuclear extracts (Input) from wild-type Col-0 or homozygous transgenic plants stably expressing *SCL15pro::SCL15-sGFP* treated with or without ABA were immunoprecipitated with a polyclonal anti-GFP antibody (GFP-IP) followed by western blot analysis with polyclonal anti-HDA19 antibodies.



**Supplementary Figure 11. Accumulation of 12S globulin in *scf15-1* seedlings.**

Immunoblot analysis with monoclonal anti-CRA1 antibody showing that accumulation of proglobulin (p12S) and 12S globulin species in *scf15-1* seedlings is increased by ABA treatment (50  $\mu$ M) for 2 d.

**Supplementary Table 1. Selected seed-related genes repressed by SCL15 in seedlings**

Protein	Gene	AGI Code	Fold change
12S globulin	<i>CRA1</i>	At5g44120 <sup>a</sup>	22.36
	<i>CRC</i>	At4g28520 <sup>a</sup>	2.14
Oleosin	<i>OLEO1-L</i>	At2g25890 <sup>a</sup>	10.36
	<i>OLEO2</i>	At5g40420 <sup>a</sup>	4.04
	<i>OLEO3</i>	At5g51210	2.29
Vacuolar processing enzyme	$\delta$ -VPE	At3g20210 <sup>a</sup>	32.51
	$\beta$ -VPE	At1g62710 <sup>a</sup>	3.81
Protein storage vacuole	$\alpha$ -TIP	At1g73190 <sup>a</sup>	14.28
Cysteine peroxiredoxin	<i>PER1</i>	At1g48130 <sup>a</sup>	20.03
Cysteine proteinase		At3g54940 <sup>a</sup>	7.23
		At4g11320 <sup>a</sup>	6.11
Reticulon family protein Late embryogenesis abundant (LEA) protein	<i>RTNLB13</i>	At1g29090	3.75
		At2g23640 <sup>a</sup>	6.38
		At3g17520 <sup>a</sup>	20.78
	<i>Em6</i>	At2g35300 <sup>a</sup>	15.67
		At2g40170 <sup>a</sup>	9.71
		At3g15670	9.27
	<i>M17</i>	At4g21020 <sup>a</sup>	7.09
		At2g41260	6.76
		At3g53040	5.40
		At5g06760	5.27
<i>RAB18</i>	At4g36600	5.27	
	At5g66400 <sup>a</sup>	4.82	
	At1g52690	3.73	
	At1g72100	3.63	
Cupin family protein		At5g44310	3.48
		At2g28490	3.47
		At2g18540	2.66
Carbohydrate metabolic enzyme	<i>BGLU19</i>	At3g21370	24.46
	<i>UGT85A5</i>	At1g22370	4.52
Peroxiredoxin	<i>PER1</i>	At1g48130 <sup>a</sup>	20.03
Protein phosphatase 2C (PP2C)		At5g59220	4.99
		At1g07430	2.92
		At5g51760	2.69
Protease inhibitor		At2g38870	3.69
Pseudogene		At5g35660	3.25
Expansin	<i>EXP2</i>	At5g05290	3.18
	<i>EXPL1</i>	At3g45970	3.46
ABA-responsive protein		At3g02480 <sup>a</sup>	23.45
	<i>ATHVA22B</i>	At5g62490	11.13
	<i>ABI3</i>	At3g24650 <sup>a</sup>	2.34
Embryo-specific protein		At1g05510	4.64
	<i>ATS1/CLO1</i>	At4g26740	2.24
Expressed protein		At5g45690	6.09
		At1g16850	4.53
		At1g78070	3.69
		At5g24130	3.57

<sup>a</sup>Gene expression has been validated by qRT-PCR analysis.