

ABA importers ABCG17 and ABCG18 redundantly regulate seed size in *Arabidopsis*

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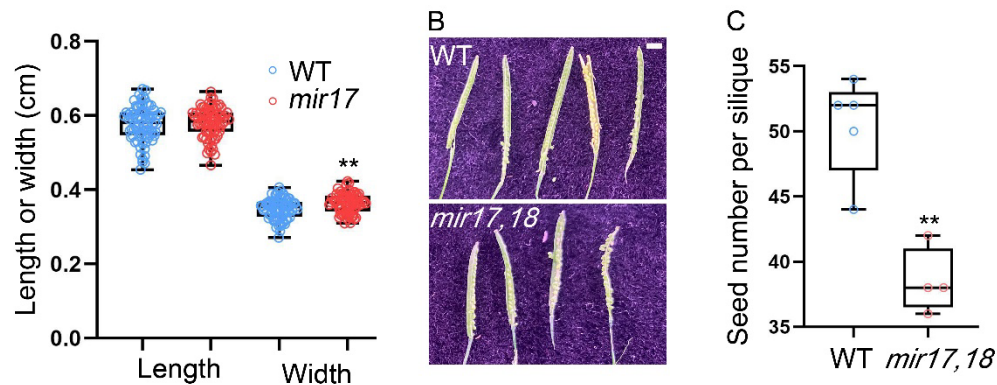
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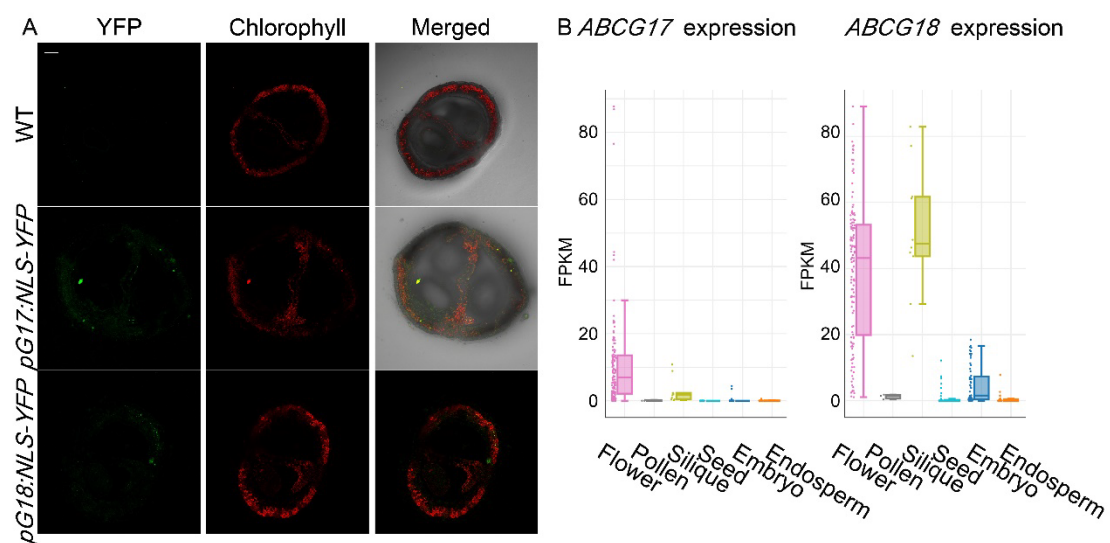
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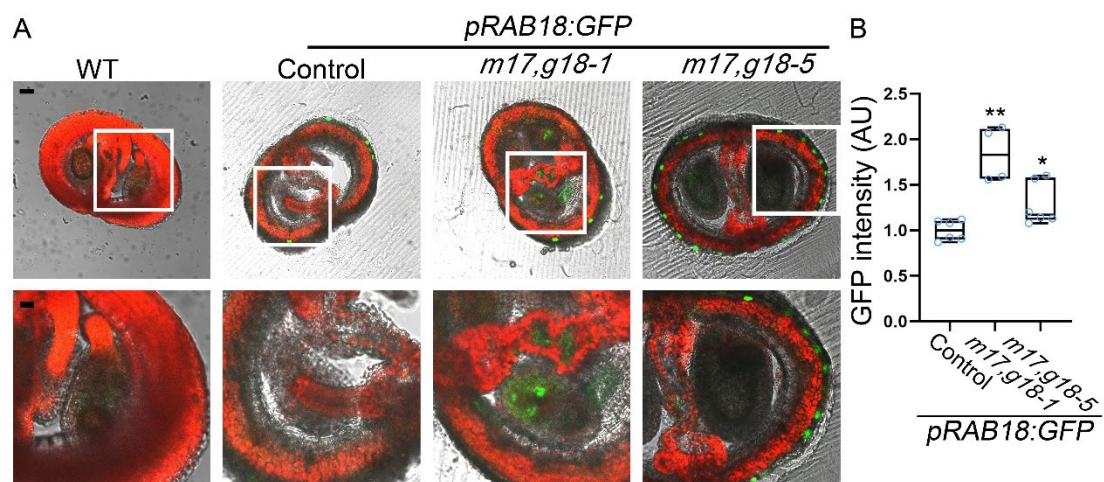
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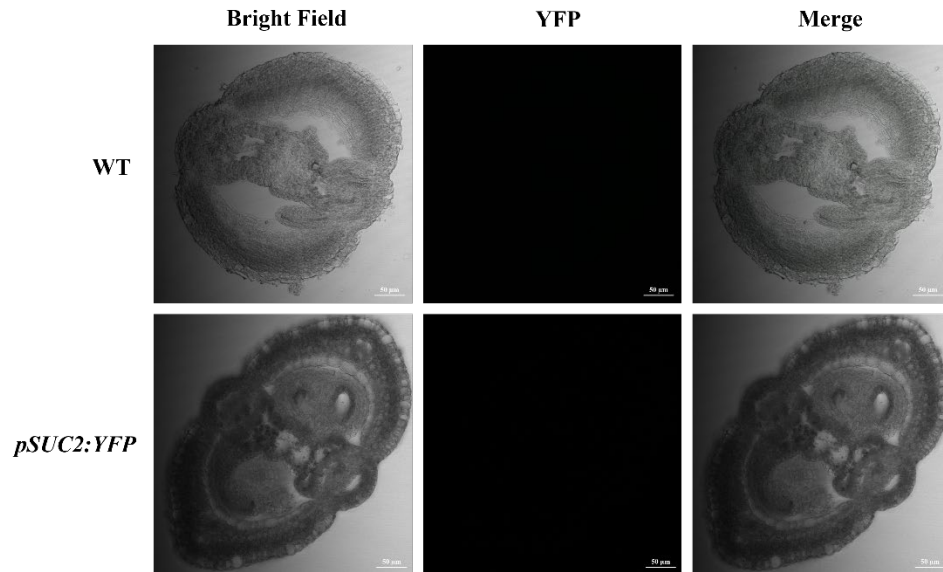
Sup. Fig. 1. Double knockdown of *ABCG17* and *ABCG18* contains reduced seed number per each silique compared to WT. **A**, Seed length and width of the indicated genotypes. $n \geq 73$. P value < 0.01, Student's t test. **B**, Images of siliques of the indicated genotypes. Scale bar = 1 mm. **C**, Average ($\pm$ SD) seed number of each silique of the indicated genotypes. $n \geq 4$, **, P value < 0.01, Student's t test.



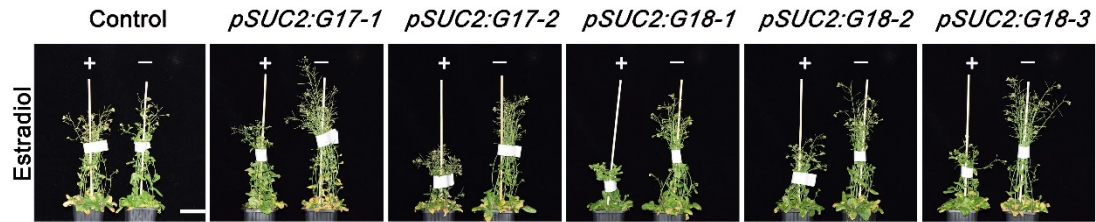
Sup. Fig. 2. *ABCG17* and *ABCG18* are expressed in valves in the early seed developing stage. **A**, Images of *pABCG17:NLS-YFP* (*pG17:NLS-YFP*) and *pABCG18:NLS-YFP* (*pG18:NLS-YFP*) reporters in siliques at 4 DAP. YFP signal (green) is detected in valves. Chlorophyll autofluorescence in red. Scale bar = 50 μ m. **B**, Expression levels of *ABCG17* and *ABCG18* at different tissues, obtained from online RNA-Seq data (<http://ipf.sustech.edu.cn/pub/athrna/>). FPKM stands for Fragments Per Kilobase of transcript per Million mapped reads.



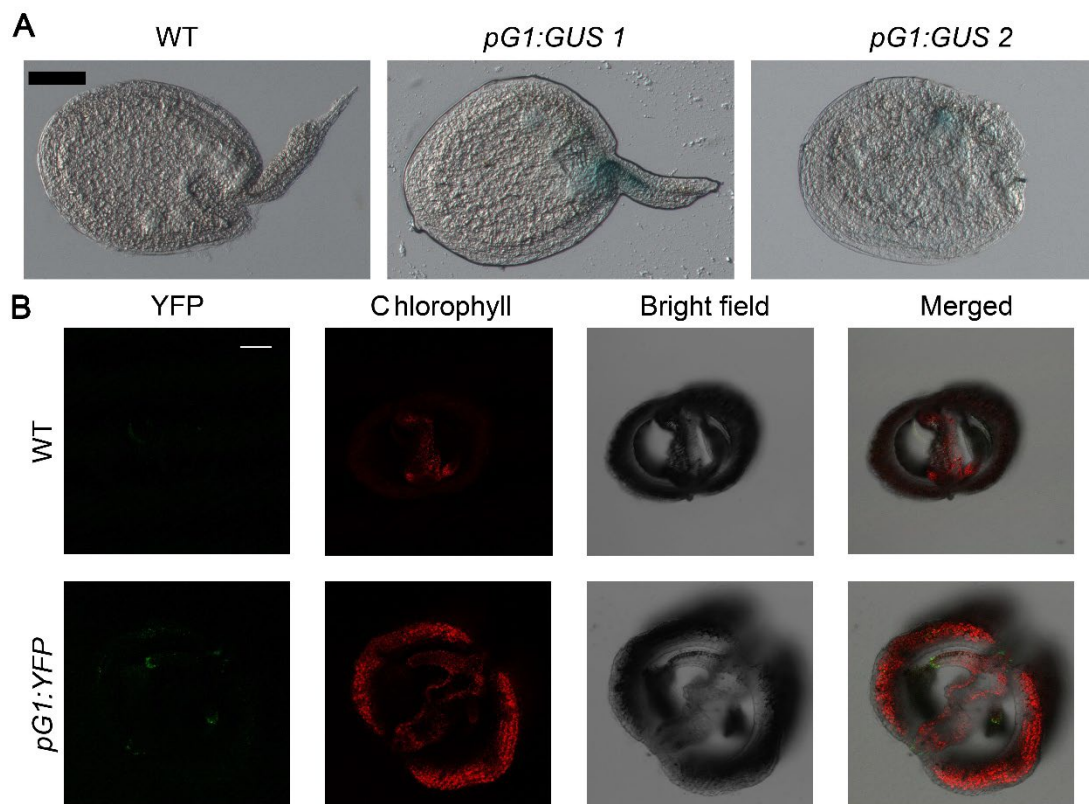
Sup. Fig. 3. Double knockdown of *ABCG17* and *ABCG18* leads to changes in ABA response in the valves. **A**, *pRAB18:GFP* signal in *mir17,g18* and Control siliques at 4 DAP. *mir17,g18* is *mir17* (*amiRNA-ABCG17*) transformed into the background of *abcg18-1* T-DNA insertion line. Shown are two independent transformation lines (#1 and #5). Green is GFP fluorescent signal, and red is chlorophyll. Scale bar = 50 μ m. **B**, Average ($\pm$ SD) GFP intensities in indicated lines. $n \geq 4$; *, P value < 0.05, **, P value < 0.01, Student's t test.



Sup. Fig. 4. *SUC2* is not expressed in the developing seed. YFP signal, driven by *pSUC2*, is not detected in developing seeds, 4-days after pollination. Scale bar = 50 μ m.



Sup. Fig. 5. Phloem-specific expression of *ABCG17* or *ABCG18* leads to reduced growth. Images of 45-day-old estradiol-treated vs. mock-treated WT, *pSUC2:ABCG17*, and *pSUC2:ABCG18* plants. *G17* and *G18* indicates for *ABCG17* and *ABCG18*. Scale bar = 5 cm. + indicates for 5 μ m estradiol treatment, - indicates for mock treatment.



Sup. Fig. 6. *ABCG1* is weakly expressed in the zygote. **A**, Images of GUS stained WT and *pABCG1:GUS* seeds at 4 DAP. Scale bars = 100 μ m. **B**, Images of 4 DAP WT and *pABCG1:NLS-YFP* silique with YFP (*pG1:YFP*) signal in green and chlorophyll in red. Scale bar = 50 μ m.

Table S1. T-DNA insertions.

Gene	Gene accession	T-DNA line	Insertion
<i>ABCG17</i>	<i>AT3G55100</i>	CS332619	Chr3 20421138
<i>ABCG18</i>	<i>AT3G55110</i>	SALK_100187	Chr3 20425486
<i>ABCG1</i>	<i>AT2G39350</i>	SALK_061511	Chr2 16431923

Table S2. Primers used for genotyping T-DNA lines.

Gene	Primer name	Primer sequence (5'-3')
<i>abcg17</i> CS332619	<i>abcg17</i> -LP	GCAGAACAGCTTCGTAGGGATACT
	<i>abcg17</i> -RP	TGATGCATTAGCAGGACA
	BP	ATTTTGCCGATTTCGGAAC
<i>abcg18-1</i> SALK_100187	<i>abcg18-1</i> -LP	AGAAGAGACCCCAAGCTAACG
	<i>abcg18-1</i> -RP	TCACAGAGTTCGCACTTGATG
	BP	ATTTTGCCGATTTCGGAAC
<i>abcg1</i> SALK_061511	<i>abcg1</i> -LP	GTCAATAAAACCCATTTCGCC
	<i>abcg1</i> -RP	ACTTCTCGGGAGACGAAACTC
	BP	ATAATAACGCTGCGGACATCTACATTTT

Table S3. Cloning primers.

Promoter/gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>pABCG17</i>	CACCTCACGCCCTCTTATTCTT GCTTCC	TCACGCCCTCTTATTCTTGC TTCC
<i>pABCG18</i>	CACCTCACGCCCTCTTATTCTT GCTTCC	TCACGCCCTCTTATTCTTGC TTCC
<i>ABCG17 CDS</i>	CACCATGCTGCAAAGAGACGC CGT GATC	TCACGCCCTCTTATTCTTGC TTCC
<i>ABCG18 CDS</i>	CACCATGCCACGTGTTTCGGC GGAAATT	TCACGTCCTCTTATTCTTAC TCCC
<i>ABCG1 CDS</i>	CTCCACCGTCATCACCGTA	CAACATCACACTAGGAACC ACAC
<i>pABCG1</i>	GGAGGTGAAGTCCTGCTTTAA TGAGATATGCGAG	CGAGCCATGGCGCGCCAC CCTTACAATAG

Table S4. amiRNA sequences.

Targeted gene	amiRNA sequences
<i>ABCG17</i>	TTATTTGTCCTGCTAACGCAT
<i>ABCG18</i>	TAAGATAAACGTTTCCGGCAA
<i>ABCG17,18</i>	TGTTTAGAGTTACCGTGGCTT