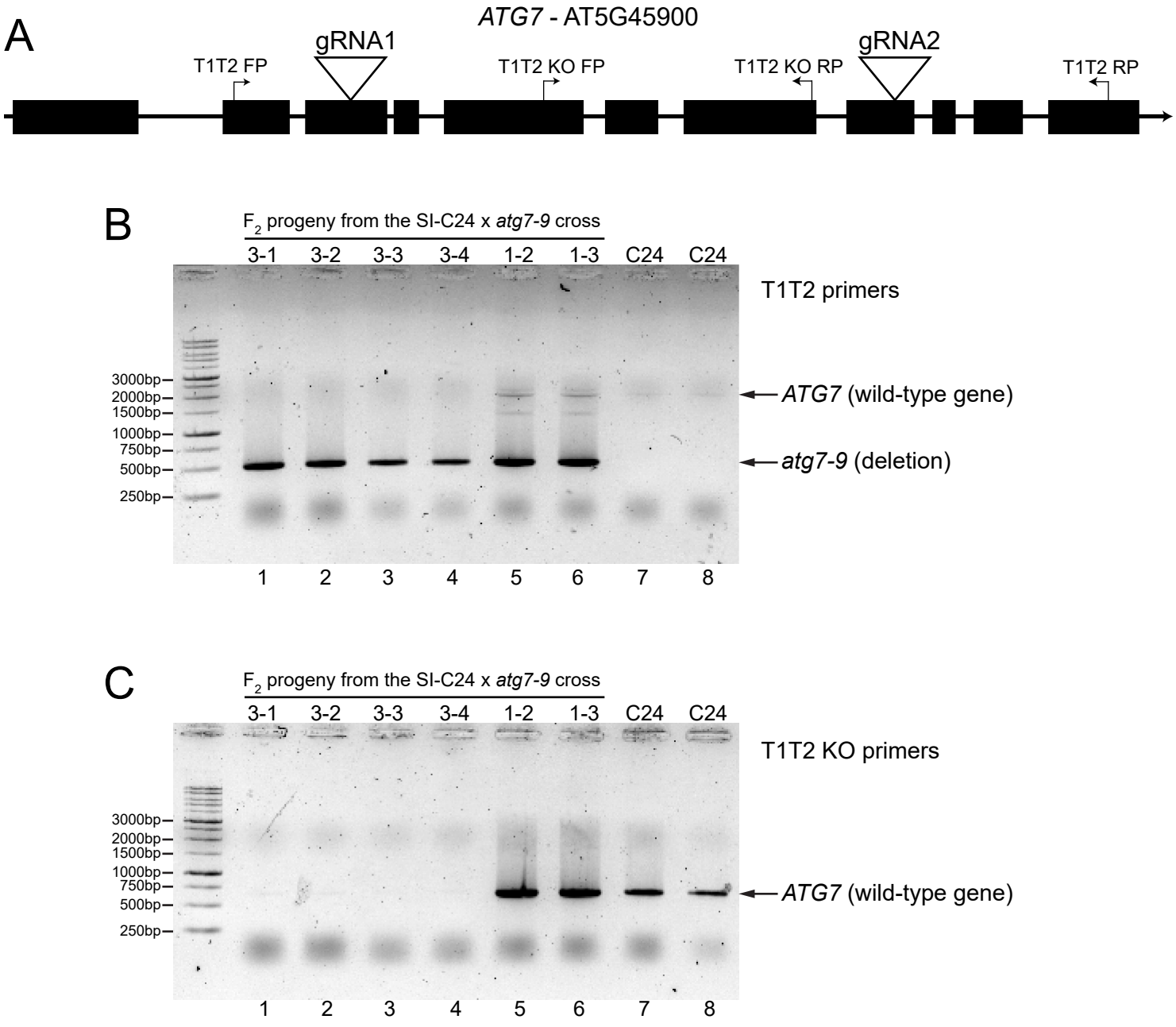
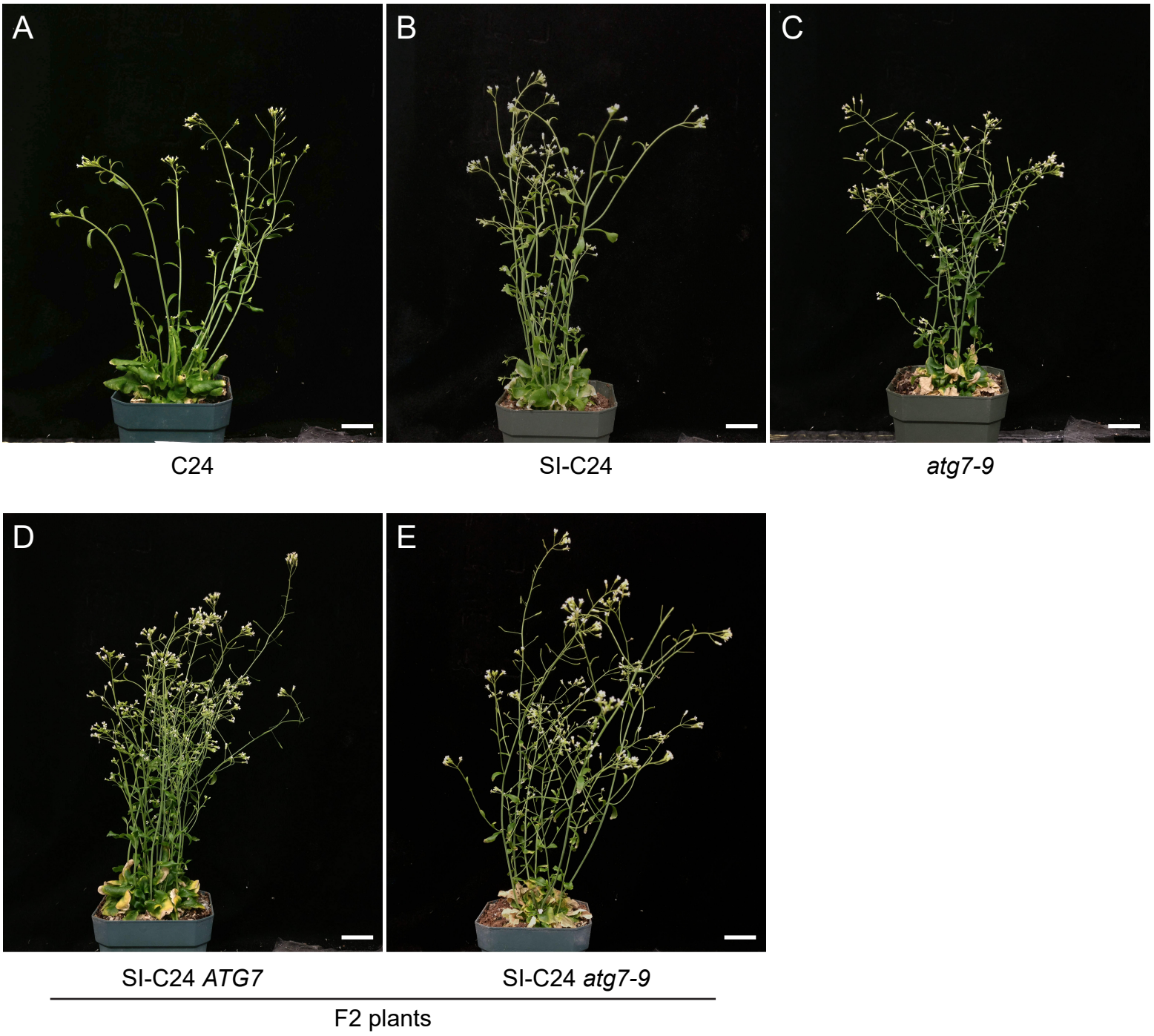


Supplemental Figure S1. Generation of the *ATG7* CRISPR/Cas9 deletion mutation in the C24 accession.

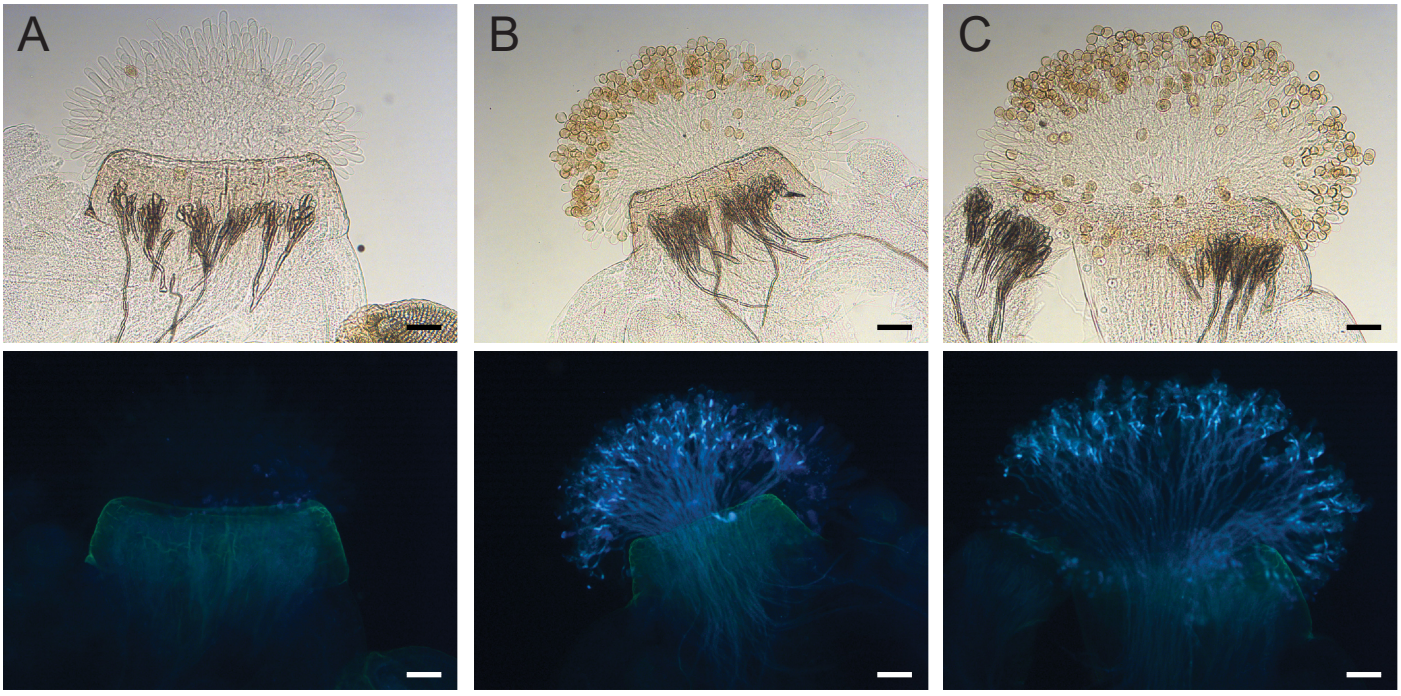
A, Schematic of the *ATG7* gene showing the location of the two gRNAs targeting exon 3 and exon 8 for the CRISPR/Cas9-mediated deletion in the C24 accession. The sites of the genotyping primers are also shown (T1T2 and T1T2 KO).

B, The *atg7-9* deletion was detected using primers flanking the gRNA cut sites (T1T2 FP, T1T2 RP). The top band is the wild-type *ATG7* gene and the bottom band is the *atg7-9* mutation (internal deletion of the region between exon 3 and exon 8).

C, Homozygotes for the *atg7-9* mutation were confirmed using primers in the internal region deleted in *atg7-9* (T1T2 KO FP, T1T2 KO RP). The F_2 progeny in lanes 1 to 4 are homozygous for the *atg7-9* mutation, while those in lanes 5 and 6 are heterozygotes. Lanes 7 and 8 are wild-type C24 plants.



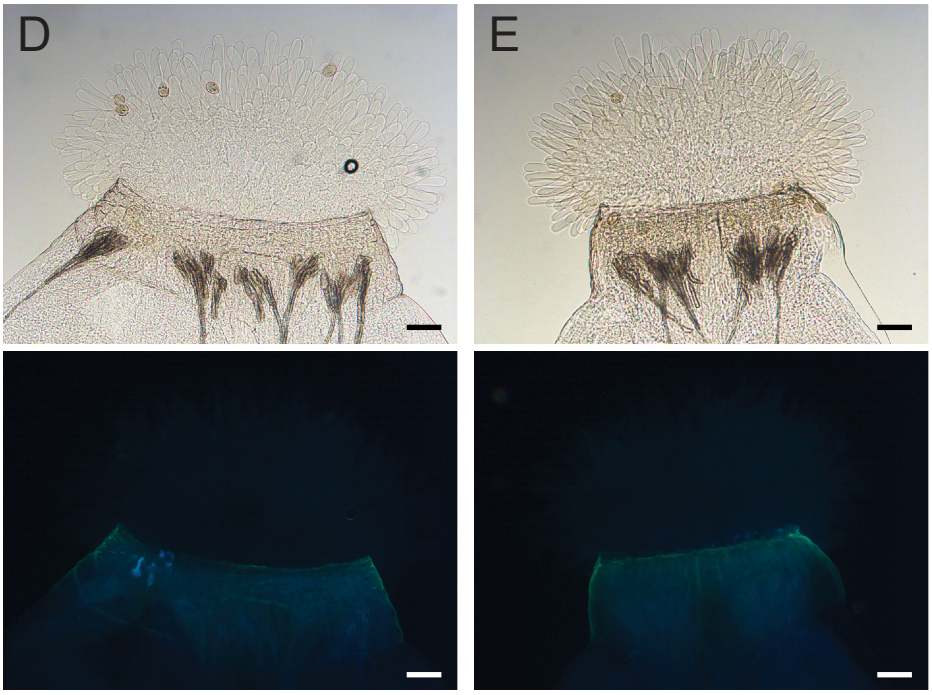
Supplemental Figure S2. Representative images of flowering plants for the SI-C24 and *atg7-9* mutant plants in the C24 accession.
A-C, shows wild-type C24, SI-C24 and *atg7-9* C24 mutant plants.
D-E, shows the F_2 plants from the SI-C24 x *atg7-9* cross. All plants shown are SI-C24 and segregating for the *atg7-9* mutation as indicated by the genotypes.
Scale bar = 2cm.



♂SI-Col-0 x
♀SI-Col-0

♂Col-0 x
♀Col-0

♂Col-0 x
♀SI-Col-0



♂SI-Col-0 x
♀SI-Col-0 *ATG7*

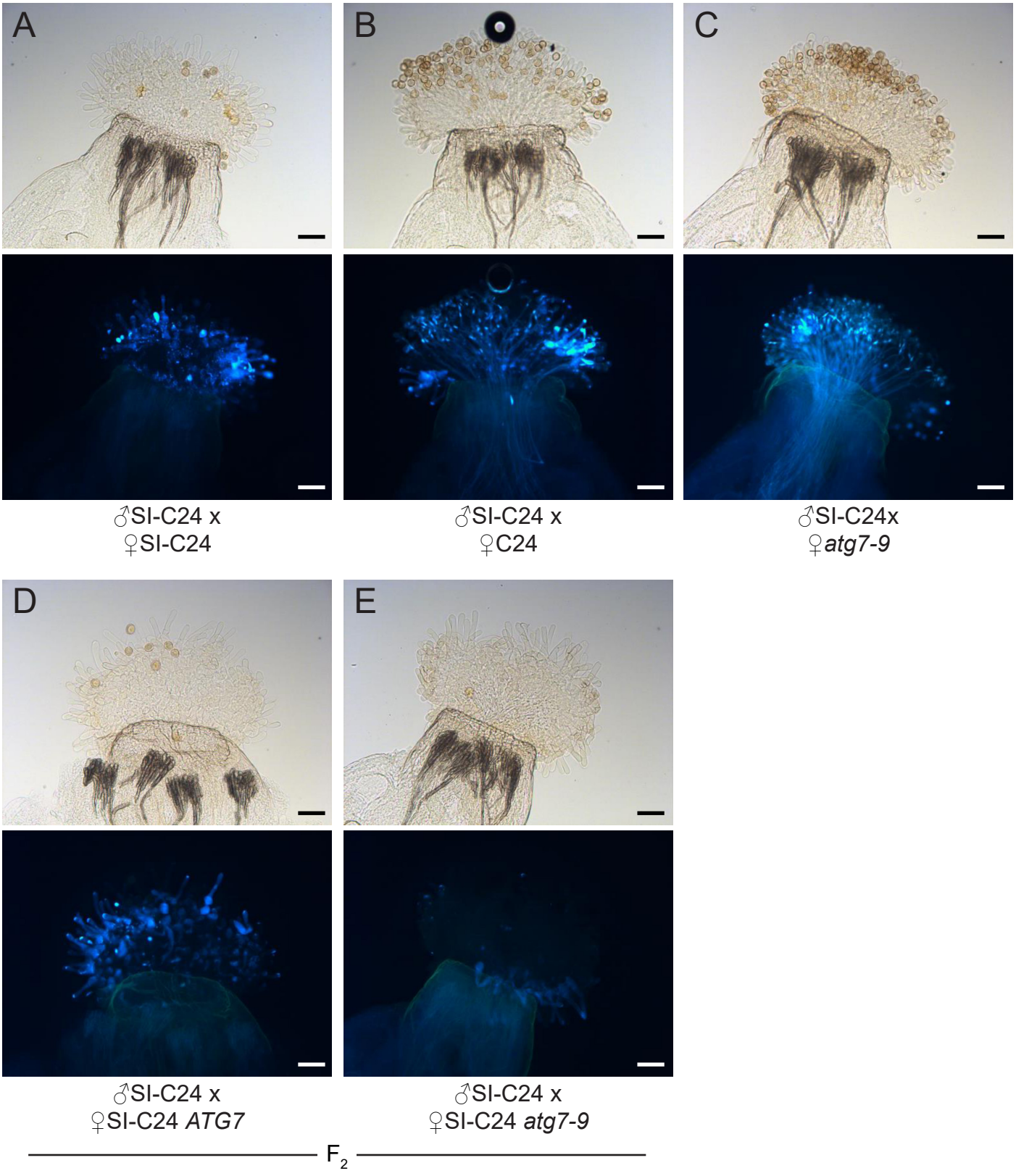
♂SI-Col-0 x
♀SI-Col-0 *atg7-2*

F_2

Supplemental Figure S3. Representative images of aniline blue-stained pistils at 2 hrs following pollination with SI-Col-0 or Col-0 pollen.

A-E, All stigmas were hand-pollinated with SI-Col-0 pollen or wild-type Col-0 pollen as indicated and collected at 2 hours post-pollination for aniline blue staining. The genotypes of the pistils are indicated for each panel.

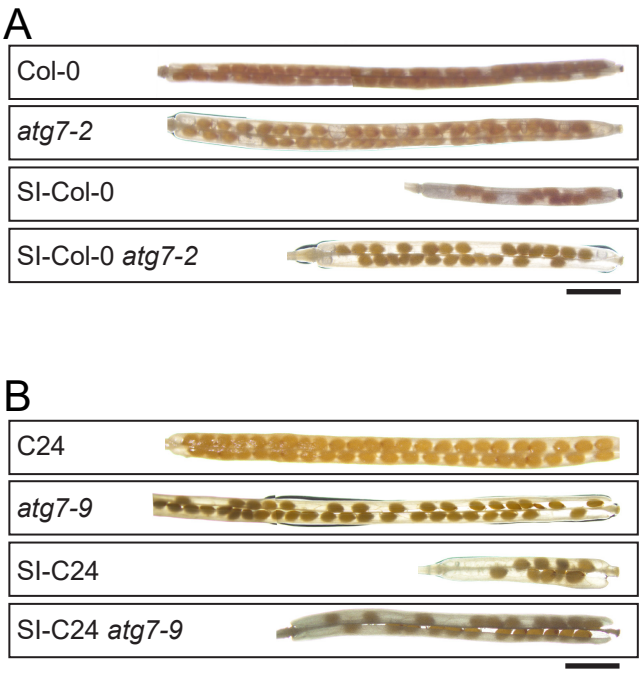
For each panel, top image = brightfield, bottom image = aniline blue. Scale bar = 100μm.



Supplemental Figure S4. Representative images of aniline blue-stained pistils at 2 hrs following pollination with SI-C24 or C24 pollen.

A-E, All stigmas were hand-pollinated with SI-C24 pollen or wild-type C24 pollen as indicated and collected at 2 hours post-pollination for aniline blue staining. The genotypes of the pistils are indicated for each panel.

For each panel, top image = brightfield, bottom image = aniline blue. Scale bar = 100μm.



Supplemental Figure S5. Representative images of cleared siliques used in seed counting for control and SI plants with the *atg7* mutation.
Siliques were harvested at 2-weeks post-pollination following manual pollination with **A,** SI-Col-0 pollen or **B,** SI-C24 pollen on pistils with the indicated genotypes (Seed count graphs are shown in Figure 5). For the longer siliques, two images were combined to cover the entire silique. Scale bar = 2 mm.

Supplemental Table S1. Primer Sequences		
Primer Name	Primer Sequence	Used for
C24 atg7-9 target site 1 with BsaI and gRNA scaffold	ATTATTGGTCTCTAAACCTGCTTGTAATGATTGGCGCC AATCTCTTAGTCGACTCTACCAATA	Generating *atg7-9* deletion in C24
C24 atg7-9 target site 2 with BsaI and gRNA scaffold	ATATATGGTCTCGATTGCATATCATCAGACAGAGAGG GTTTTAGAGCTAGAAATAGCAAGTTAAAAT	
C24 *atg7-9* T1T2 FP	CGTTCCCTGCGTTTGTACTT	Assessing *atg7-9* deletion
C24 *atg7-9* T1T2 RP	GAATTGTCGCCTTTTGCATT	
C24 *atg7-9* T1T2 KO FP	ATGAGATGGCGAGCATTACC	Assessing atg7-9 homozygosity
C24 *atg7-9* T1T2 KO RP	CATGGCGCATTACCATGTAG	
BastaR FP	CGGAGAGGAGACCAGTTGAG	Basta Resistance Screening
BastaR RP	GAGCTGGCAACTCAAAATCC	
atg7-2 FP	TGCTAATTCCATGGATCCAACAAG	Detecting T-DNA insertion for *atg7-2* (Chung et al., 2010)
atg7-2 RP	GAAGCCACCTAGTGAATATAGTCTATGGAC	
atg7-2 RP-2	TTGACCATCATACTCATTGCTGATCC	Assessing homozygosity of *atg7-2* (Chung et al., 2010)
ATG8-GFP-RT RP1	GGTGAACTTCAAGATCCGCC	Genotyping GFP-ATG8a (Thompson et al., 2005)
GFP-ATG8a RP	ACTCATCCTTGCCTCGAGAGG	
Ah-ARC1 FP	CCGAAGTGCTACAGAGTGGA	Genotyping SI-Col-0 for SI components (Zhang et al., 2019)
Ah-ARC1 RP	TCCGAATCAGAGAACGTGAG	
SCRb FP	ATGAGGAATGCTACTTTCTTC	Genotyping SI-C24 for Al-SCRb (Iwano et al. 2015)
SCRb RP	TAGCAAAATCTACAGTCGCATA	
SRKb FP	ACCAAGATTCACGGTTCAGG	Genotyping SI-C24 for Al-SRKb (Iwano et al. 2015)
SRKb RP	ACGCTGTTCATGTGTCGAAG	
atg5-1 FP	ATACACTTTAGAGGATATCC	Genotyping T-DNA insertion for *atg5-1*
atg5-1 RP	CTGTCTTAACTTGTCCAGCCA	
LB1	GCCTTTTCAGAAATGGATAAATAGCC	