

Supplemental Data

Figure 1

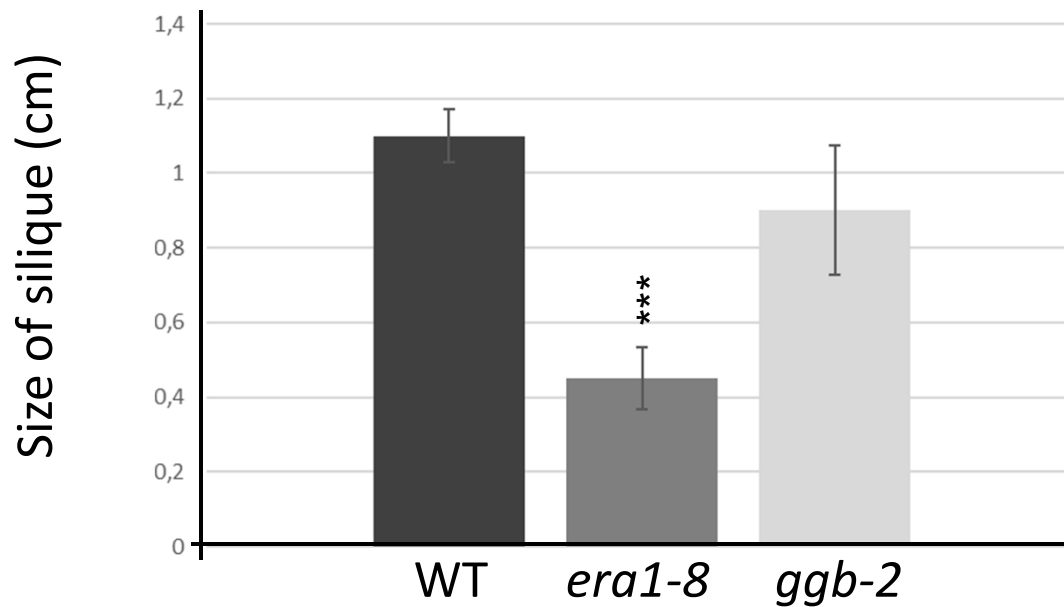


Fig. 1: Silique size measurement of WT, *era1-8* and *ggb-2* plants. *** P value < 0.001 (Student's *t*-test).

Figure 2

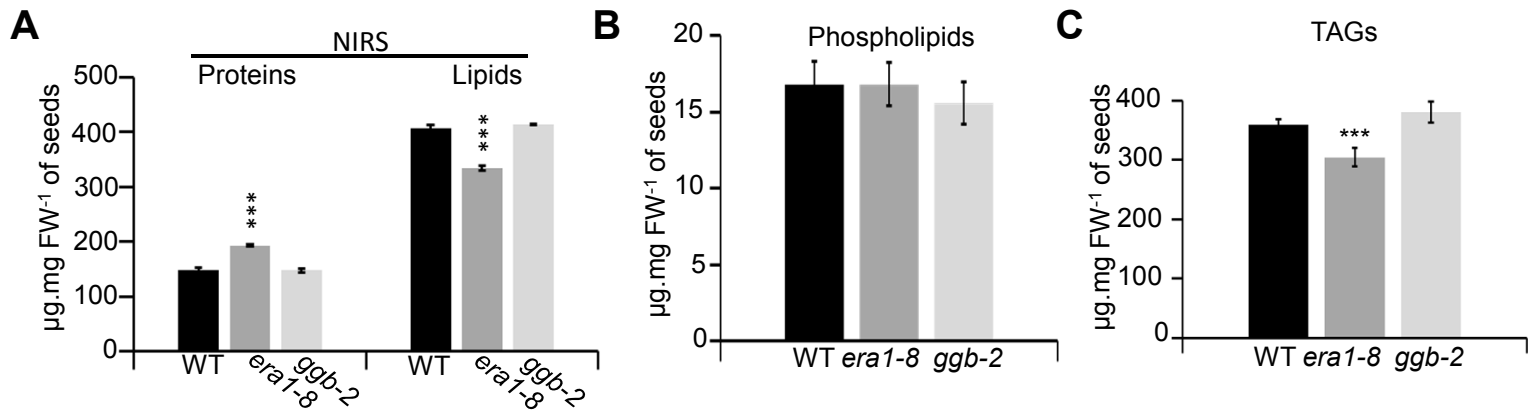


Fig. 2: Proteins and lipids content expressed per mg of seeds. (A) Results of NIRS analyses. (B) Total phospholipids contents per mg of seeds. (C) TAG contents per mg of seed. Data represent mean $\pm$ SE. *** p -value < 0.001 (Student's t -test). FW, Fresh weight.

Figure 3

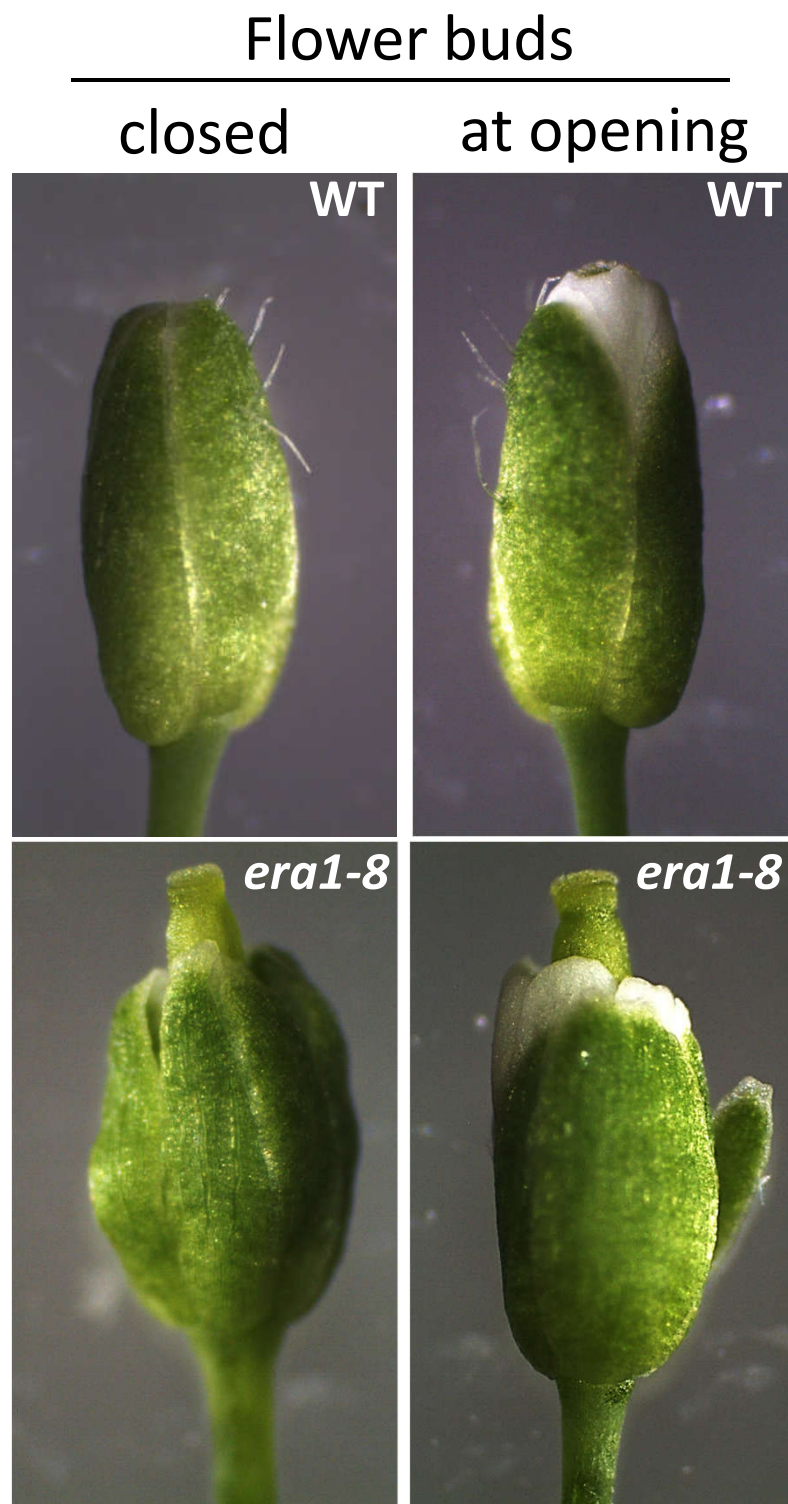


Fig. 3: Flower buds of WT and *era1-8* showing protruding pistils of *era1-8* before and at flower opening (visible petals).

Figure 4

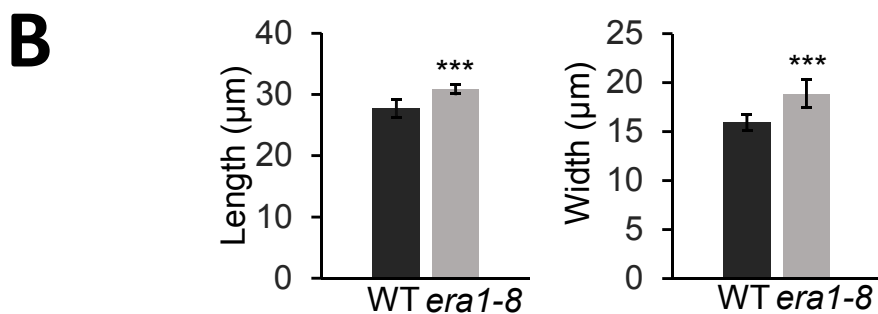
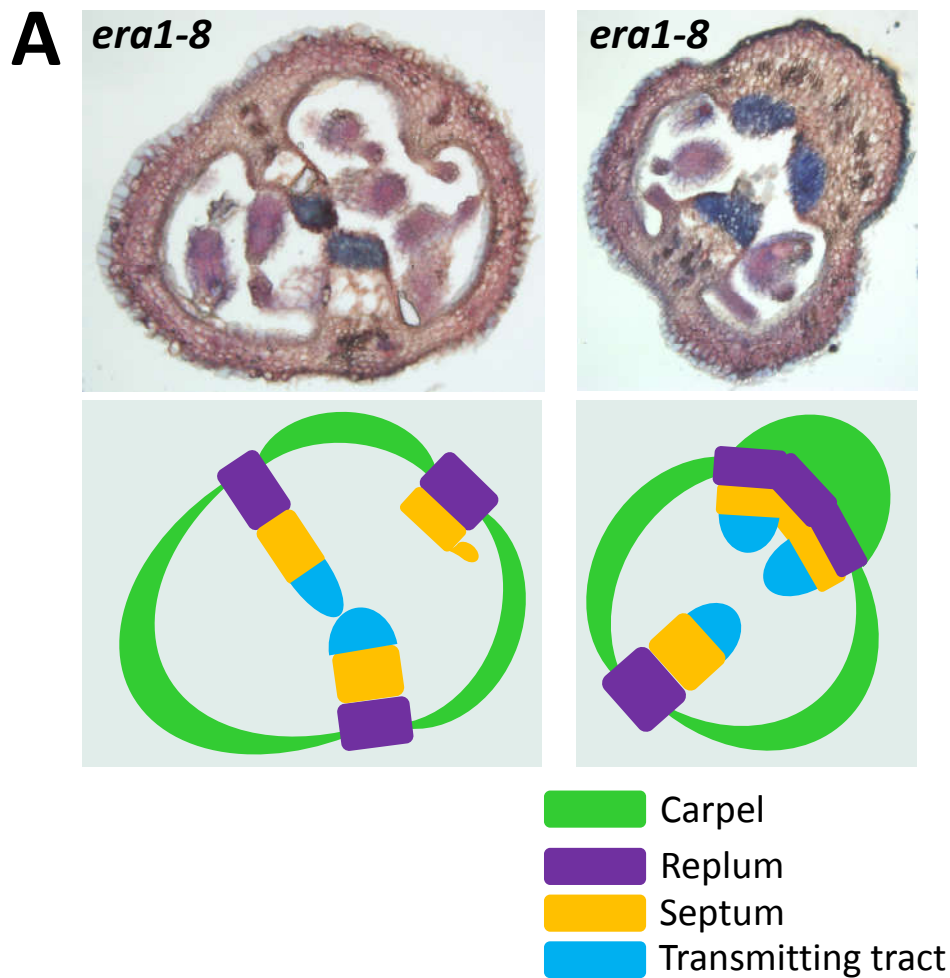


Fig. 4: Ovary organization and pollen grain measurement. (A) A photo gallery of *era1-8* 3-carpels ovaries with their representative diagram. Tissues are stained with neutral red and alcian blue. (B) Length and width measurement of WT and *era1-8* pollen used to calculate pollen volume in Fig. 9E.

Figure 5

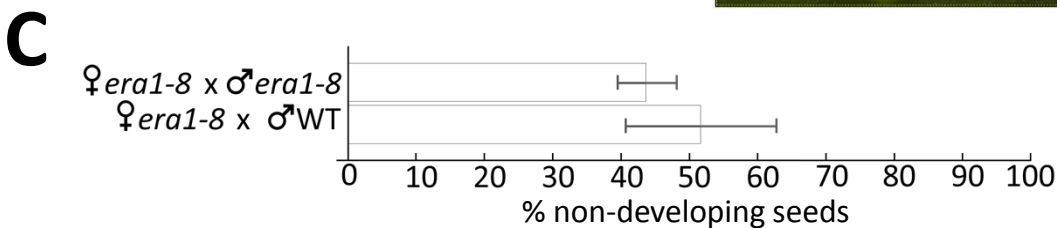
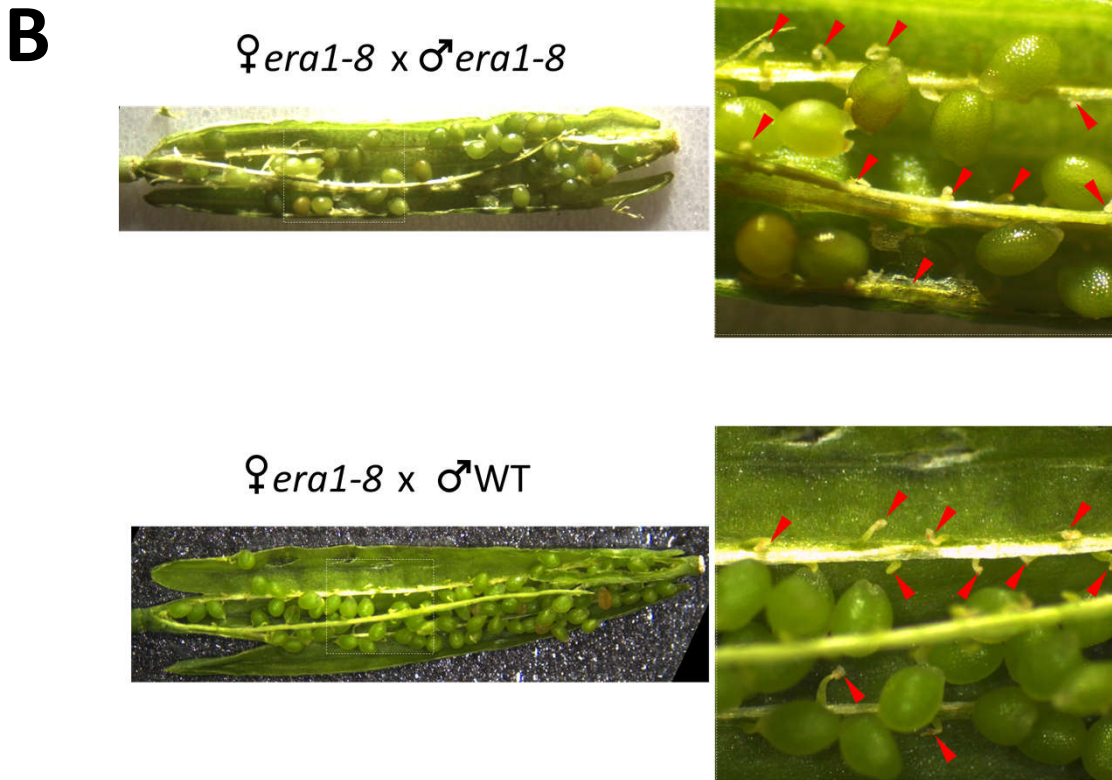
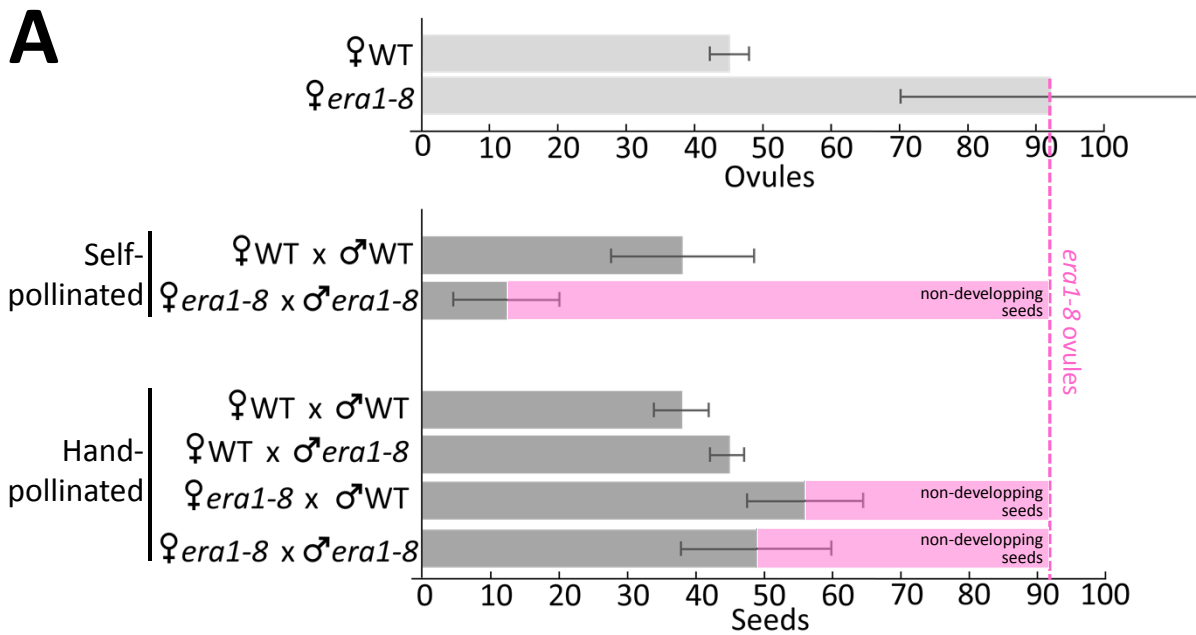


Fig. 5: Quantification of *era1-8* seed production and non-developing seeds. (A) Graphs summarizing data presented Fig. 6C (ovules), Fig. 6D (seeds, self-pollination) and Fig. 9B (seeds, hand-pollinated) with estimated *era1-8* non-developing seeds (pink). (B) Dissection of siliques obtained after handmade pollination with the indicated crosses (i.e. *era1-8* pistils with *era1-8* or *WT* pollen). On the right, closer views showing aborted ovules (red arrowheads). (C) Quantification of non-developing seeds in the indicated hand-pollinated crosses (n=20).

Figure 6

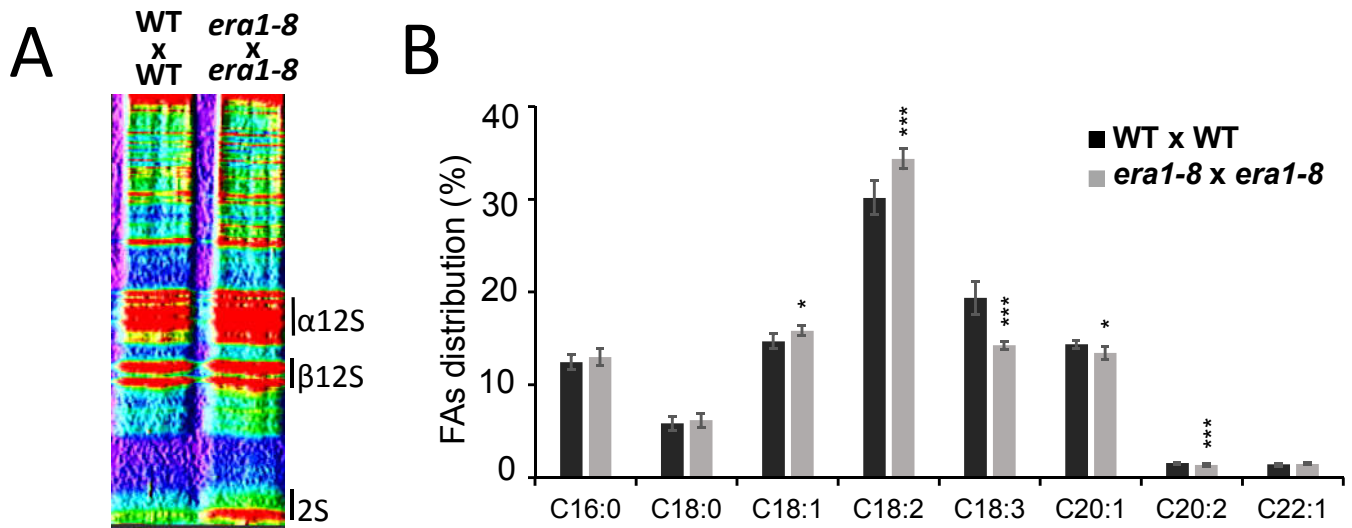


Fig. 6: Seed contents after hand pollination. (A) 15% SDS-PAGE of seed total protein extracts. The picture of silver-nitrate stained gel of the Fig. 9G was recolored with the ImageJ interactive surface plot Plugin. (B) Total distribution of FAs shown in Fig. 9H.

Figure 7

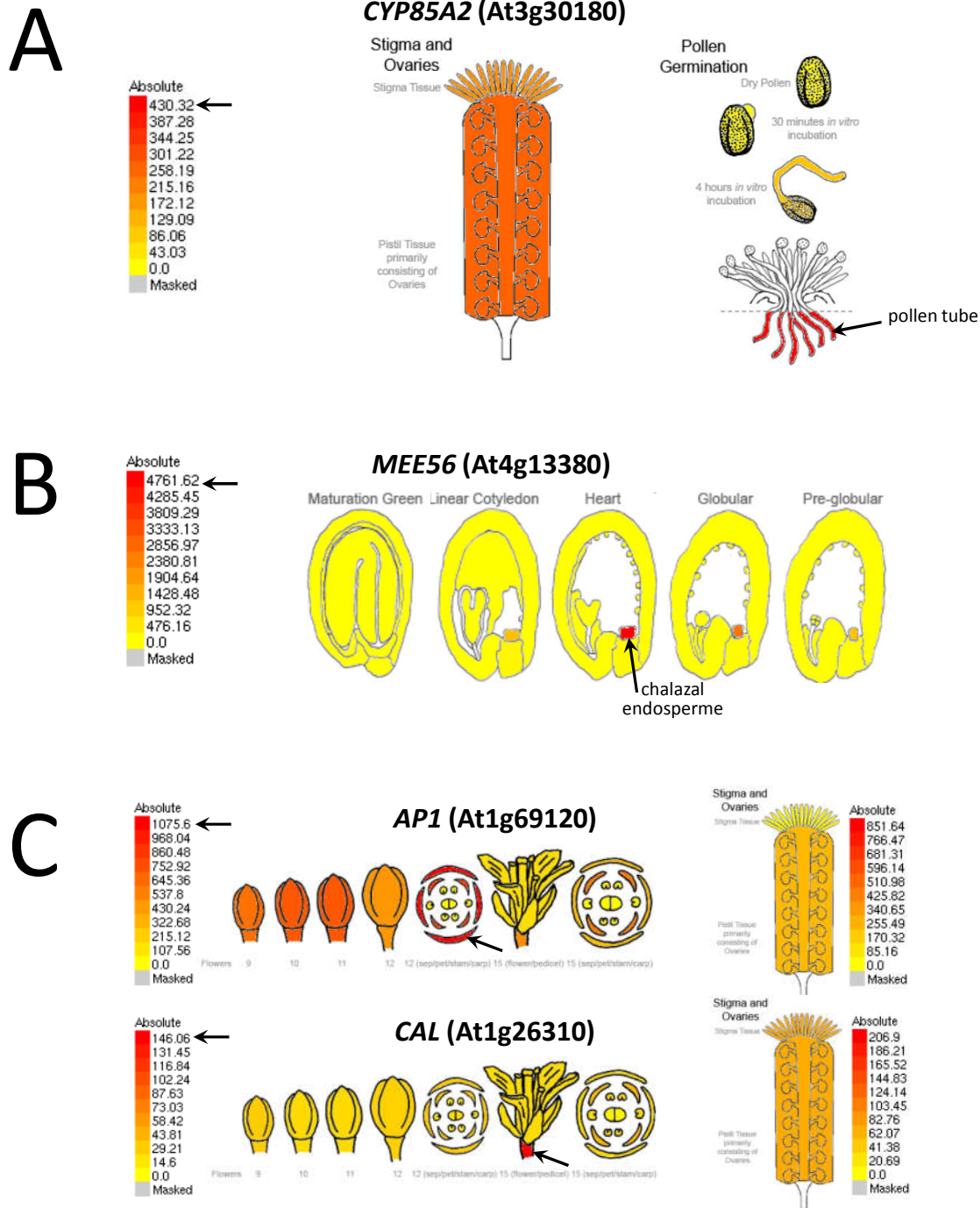


Fig. 7: Screen shots of the BioArray Ressource Arabidopsis eFP Browser (<http://bar.utoronto.ca/>) for indicated CaaX-protein encoding loci. (A) *CYP85A2* expression pattern recovered from the Tissue Specific data source. (B) *MEE56* expression pattern recovered from the Seed data source. (C) *AP1* and *CAL* expression pattern recovered from the Developmental Map and Tissue Specific data sources. Arrows indicate maximum expression level reach in a data source.

Figure 8

%	At2S1	At2S2	At2S3	At2S4	At2S5	CRA1	CRB/CRU2	CRC/CRU3	CRD
C	31,481	31,528	31,855	31,530	31,279	31,257	31,612	31,413	31,868
H	49,486	49,496	49,325	49,643	49,886	49,605	49,625	49,377	49,349
N	8,984	9,003	8,986	9,057	8,942	9,479	9,099	9,377	8,921
O	9,478	9,414	9,333	9,245	9,361	9,569	9,438	9,661	9,673
S	0,571	0,560	0,501	0,526	0,533	0,090	0,226	0,173	0,188

Percentage of atomic composition of individual 2S albumins (pink) and 12S globins (blue)

%	At2S+At12S	At2S	At12S	At2S/At12S
C	31,536	31,534	31,537	1,000
H	49,532	49,567	49,489	1,002
N	9,094	8,994	9,219	0,976
O	9,463	9,366	9,585	0,977
S	0,374	0,538	0,169	3,179

Average (percent) of atomic composition of 2S albumins (pink) and 12S globins (blue). At2S/At12S ratio is significantly different (black).