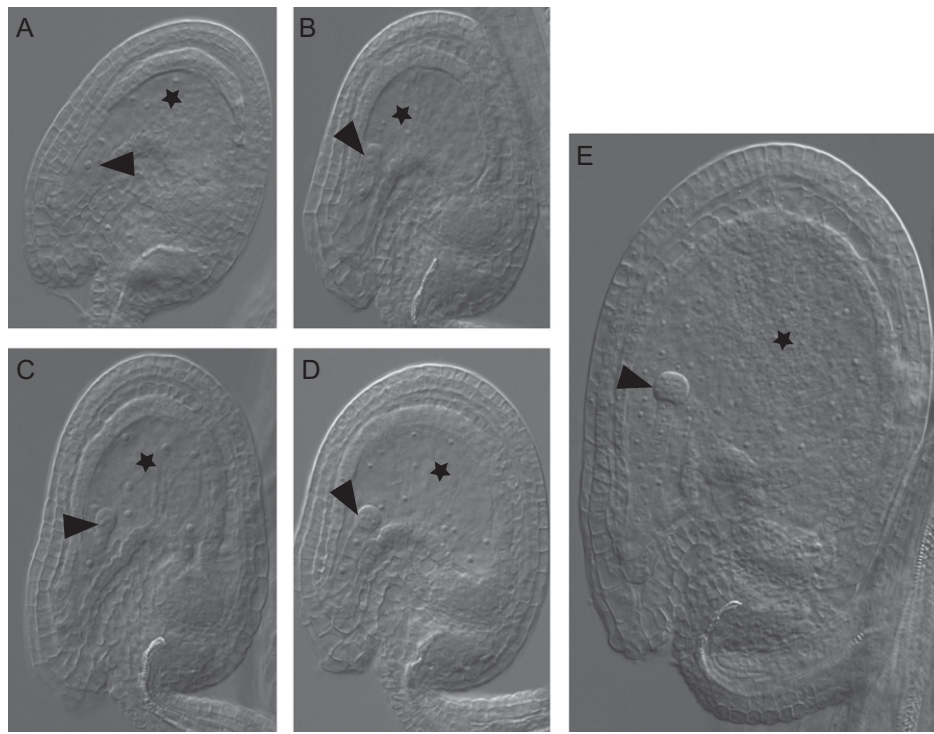


Supporting Information

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F

Genotype	Embryo (%)					Endosperm (%)								unfer-tilized	n
	Zygote	1 nuc	2 nuc	4 nuc	>4 nuc	1 nuc	2 nuc	4 nuc	8 nuc	16 nuc	32 nuc	>32 nuc			
<i>fiona/FIONA</i>	4.4%	7.0%	3.2%	4.4%	69.6%	1.3%	0.6%	5.1%	5.7%	3.8%	3.2%	69.0%	11.4%	158	
<i>FIONA/FIONA</i>	0.0%	0.0%	0.7%	0.7%	88.5%	0.0%	0.0%	0.0%	0.0%	0.0%	0.7%	89.2%	10.1%	148	

Fig. S1. *FIONA* is required for embryo and endosperm development. (A-D) *fiona* mutants arrested at the zygote stage (A) or one- (B), two- (C), or four- (D) celled embryo stage. (E) Normal seed of the same silique. (F) Frequencies of different embryo and endosperm arrests in *fiona/FIONA* vs. *FIONA/FIONA* plants. Arrowhead, embryo; star, endosperm; nuc, nucleate.

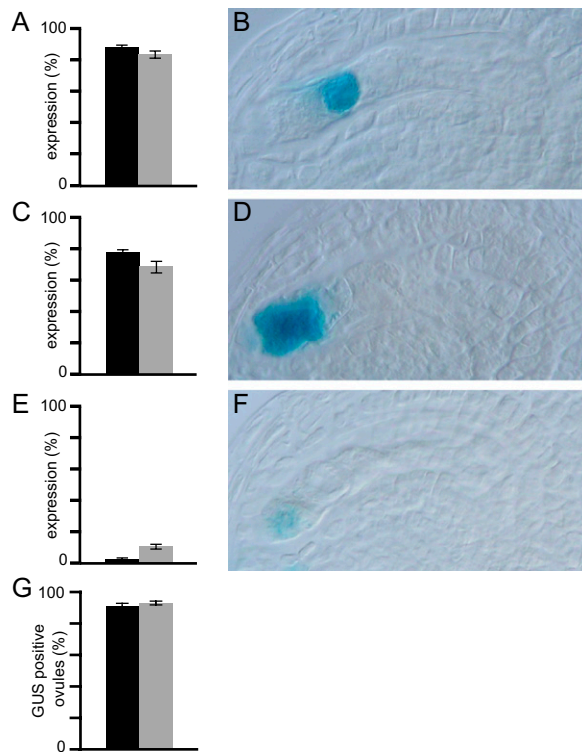


Fig. S2. Expression of egg and synergid cell markers in wild-type and *fiona* gametophytes. (A) Frequencies of ovules expressing ET1119 (1); $n = 375$ for wild type, $n = 579$ for *fiona/FIONA*. (B) Expression of the egg cell marker ET1119. (C and E) Frequencies of ovules showing normal (C) and weak (E) expression of ET2634 (1); $n = 396$ for wild type, $n = 401$ for *fiona/FIONA*. Gametophytes were analyzed 2 d after emasculation. Black bar, wild type; gray bar, *fiona/FIONA*. (D and F) Normal (D) and weak (F) expression of the synergid marker ET2634. (G) Frequencies of GUS-positive ovules in *FIONA/FIONA* (black bar) and *fiona/FIONA* (gray bar) plants, after fertilization with pollen from *pAt5g40260::GUS* (2) plants; $n = 283$ for wild type, $n = 300$ for *fiona/FIONA*. Error bars, mean \pm SEM.

- Gross-Hardt R, et al. (2007) LACHESIS restricts gametic cell fate in the female gametophyte of Arabidopsis. *PLoS Biol* 5:e47.
- Yu HJ, Hogan P, Sundaresan V (2005) Analysis of the female gametophyte transcriptome of Arabidopsis by comparative expression profiling. *Plant Physiol* 139:1853–1869.

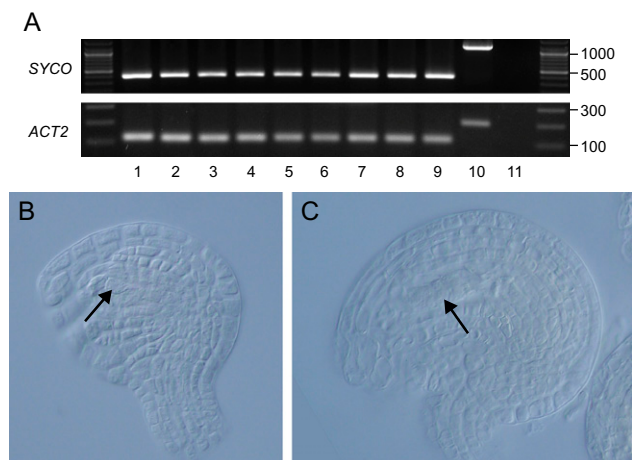


Fig. S3. Expression analysis of SYCO in the sporophyte and during early stages of female gametophyte development. (A) Semiquantitative RT-PCR analysis of SYCO and ACT2 transcripts from cDNAs of 1, seedlings; 2, leaves; 3, stem; 4, roots; 5, flower buds; 6, open flowers; 7, inflorescences; 8, young siliques; 9, old siliques; 10, genomic DNA; and 11, water control. Amplification of SYCO and ACT2 was performed with 35 and 27 cycles, respectively. (B and C) *pSYCO::NLS_GUS* expression cannot be detected during early stages of female gametophyte development (arrow).

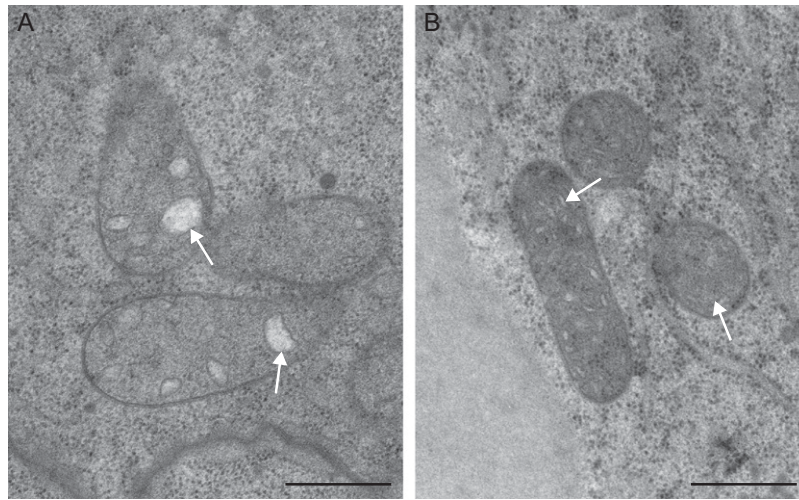


Fig. 54. *pMEA::SYCO_GFP* rescues the mitochondrial defect in *syco* central cells. (A) Central cell mitochondria from *syco-1/SYCO*. (B) Central cell mitochondria from *syco-1/syco-1 pMEA::SYCO_GFP*. White arrow, cristae. (Scale bars, 500 nm.)

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yAAC2p -----MSS 3
AtAAC2 MVEQTQHPHILQKVSGQLLSSSVSQDIRGYASASKRPATYQKHAAYGNYSNAAFQYPLVA 60
      : :

yAAC2p NAQVKTPLPP---APAPKKESNFLIDFLMGGVSAAVAKTAASPIERVKLLIQNQDEMLK 59
AtAAC2 ASQIATTTSPVFVQAPGEKGFNFNAIDFMMGGVSAAVSKTAAAPIERVKLLIQNQDEMLK 120
      **: . . *   ** . * : ** ** : ***** : ***** : ***** : *****

yAAC2p QGTLDRKYAGILDGCFKRTATQEGVISFWRGNTANVIRYFPTQALNFAFKDKIKAMFGFKK 119
AtAAC2 AGRLTEPYKGIKIDCFGRITRDEGIGSLWRGNTANVIRYFPTQALNFAFKDYFKRLEFNFK 180
      * * . * ** ** * * : **: . : ***** : ***** : * : * . **

yAAC2p E-EGYAKWFAGNLSGGAAGALSLLFVYSLDYARTRLAADSKSSKGG-ARQFNGLIDVY 177
AtAAC2 DKDGYKWFAGNLSGGAAGASSLLFVYSLDYARTRLANDSKSAKGGGERQFNGLVDVY 240
      : : ** ***** * * ***** : ** : ** * : ** : **

yAAC2p KKTLSKSDGVAGLYRGFLPSVVGIVVYRGLYFGMYDSLKPLLLTGSLEGSFLASFLLGWVV 237
AtAAC2 KKTLSKSDGIAGLYRGNISGAGIIVYRGLYFGLYDSVKPVLTTGDLQDSFFASFALGWLI 300
      ***** : ***** * . ** : ***** : ** : ** : ** : * : ** : ** : ** : ** : ** : ** : ** : **

yAAC2p TTGASTCSYPLDTRRRMMTSGQAVKYDGAFDCLRKIVAAEGVSLFKGCGANILRGVA 297
AtAAC2 TNGAGLASYPIDTRRRMMTSGEAVKYKSSFDQFSQIVKKEGAKSLFKGAGANILRAVA 360
      * . ** . : ** : ***** : ***** : ** : ** : ** : ** : ** : ** : ** : ** : ** : ** : **

yAAC2p GAGVISMVDQLQMILFGKFKF--- 318
AtAAC2 GAGVLAGYDKLQIVFGKKGSGGA 385
      **** : : ** : ** : ** : ** : ** :

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Fig. 55. Alignment of *Saccharomyces cerevisiae* Aac2 (yAac2p) and *Arabidopsis* AAC2 (AtAAC2) protein sequences. The position of the dominant mutation A199D is shown in red. Sequence alignment was performed with ClustalW2, using default parameters. Asterisks (*) indicate conserved residue; colons (:) indicate conserved substitution; periods (.) indicate semiconserved substitution.