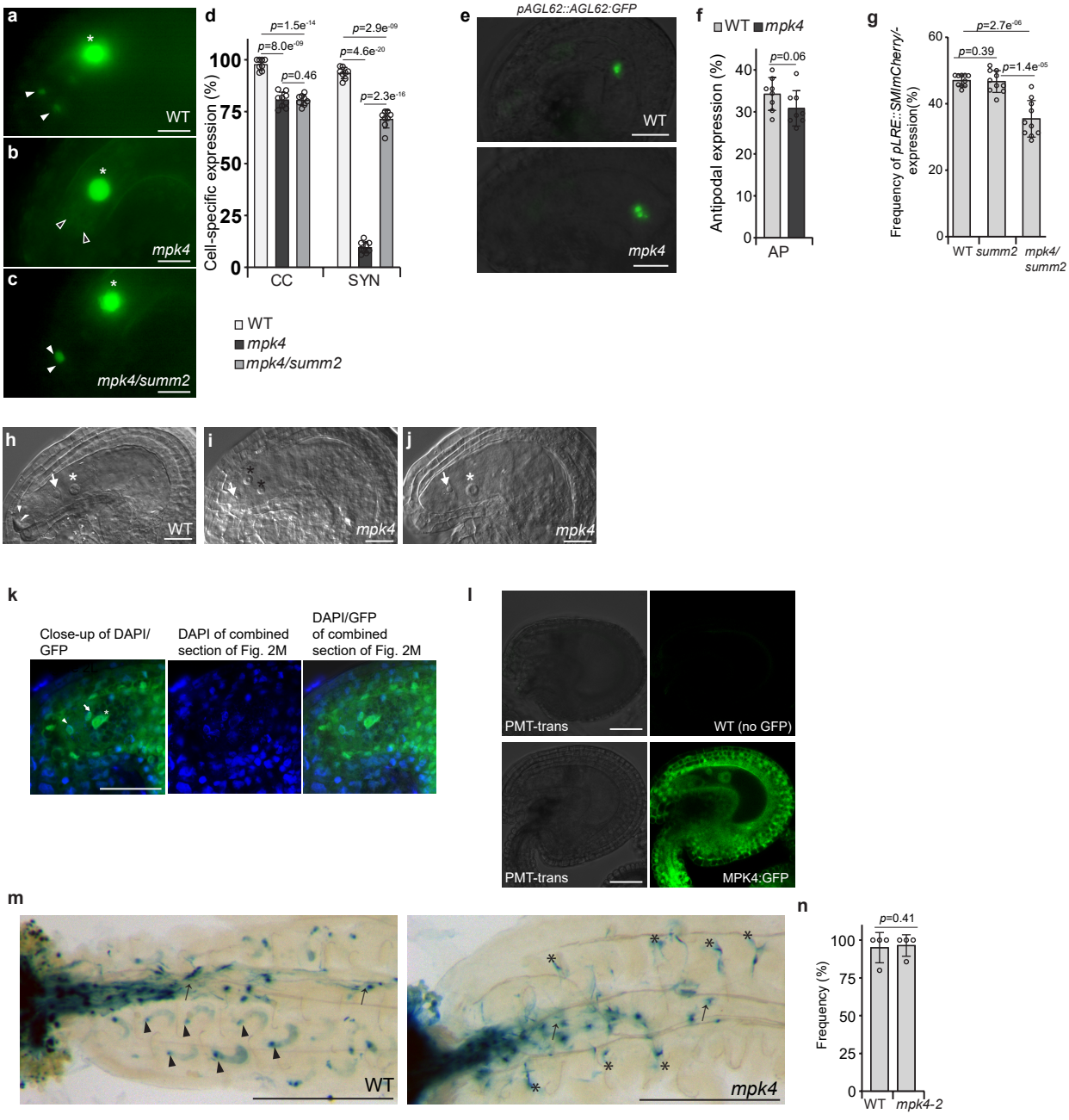


Supplementary Figure 1

Supplementary Figure 1. Characterization of the premature synergid degeneration and the MPK4:GFP localization

a-d Localization (a-c) and quantification (d) of the female gametophyte reporter *pHD2B::GFP:HD2B/+* in WT (n=263), *mpk4* (n=310) and *mpk4/summ2* (n=283). Error bars show ± SD.

e-f Localization and occurrence of the antipodal marker *pAGL62::AGL62:GFP/-* (WT, n=249; *mpk4*, n=195). Error bars show ± SD. White arrowhead, synergid; black arrowhead, degenerating synergid; white arrow, egg cell; white asterisk, central cell nucleus; Scale bars, 20 µm

g Frequency of *pLRE::SMImCherry/-* expression in WT (n=338), *summ2* (n=332) and *mpk4/summ2* (n=314). See also **Figure 4o-p**. Error bars show ± SD.

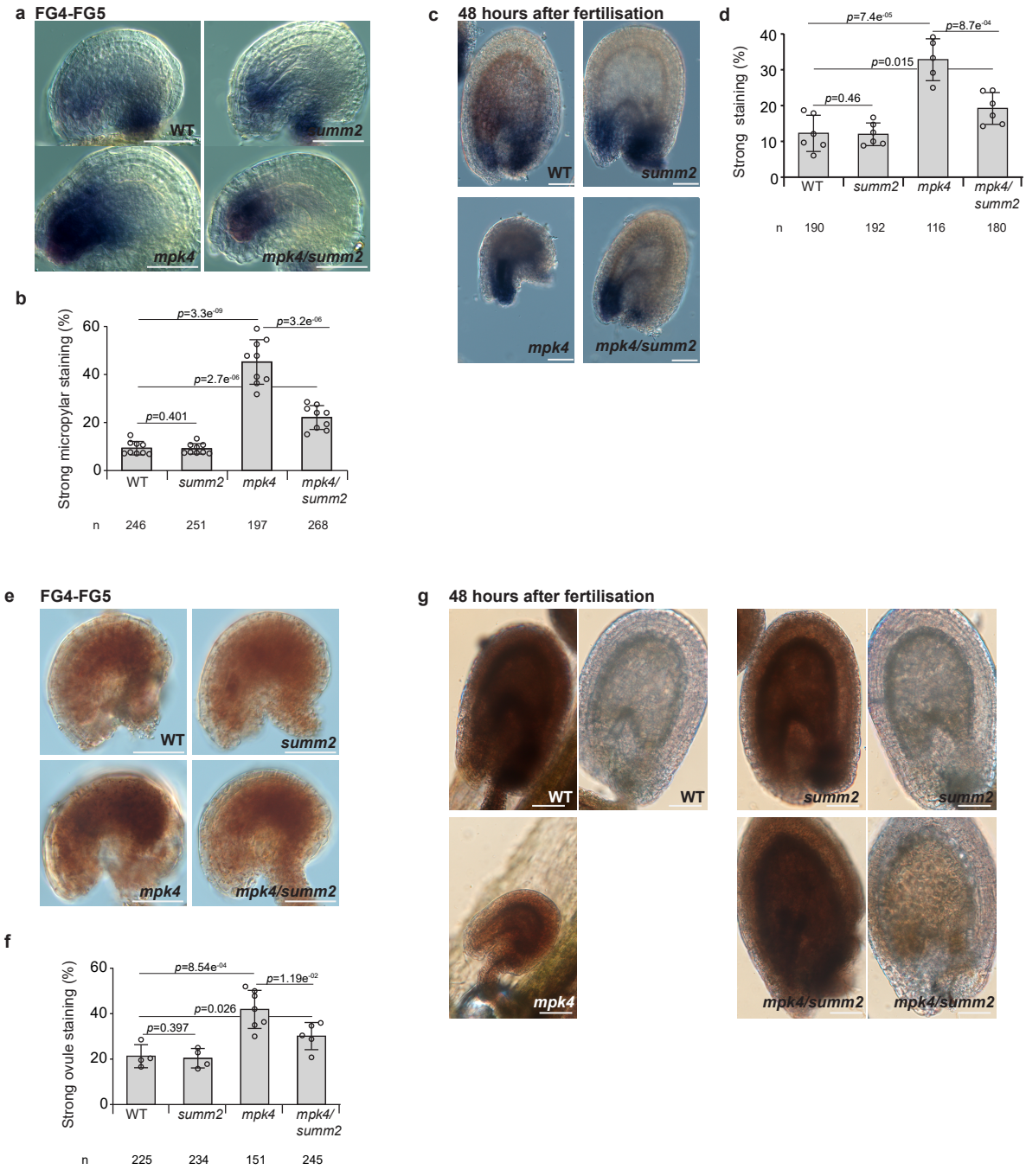
h-j Differential-contrast microscopy of WT (h) and *mpk4* (i-j) female gametophyte. Representative images are depicted of three biological replicates. Scale bars, 20 µm.

k MPK4:GFP localization in synergid, egg cell, CC and sporophytic ovule tissue, co-localized with the nuclei staining dye 4′,6-diamidino-2-phenylindole DAPI, **also see Figure 2n**. Scale bars, 20 µm

l Evaluation of MPK4:GFP signal intensity against a WT control without carrying a GFP-reporter.

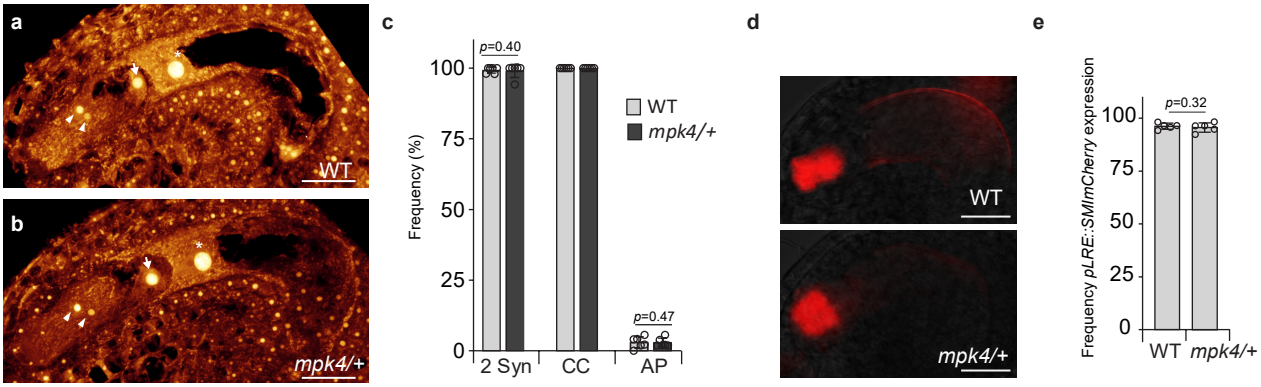
m-n GUS-stained PT tracking through the transmitting tract in WT and *mpk4*. Flowers of WT and *mpk4* were pollinated with *pLAT52::GUS*-expressing pollen and the growth of the PT within the maternal tissue was evaluated after 24 hours. Images show regular growth of the PT in the transmitting tract/ pistil in WT and *mpk4*, yet, ovule-targeting in *mpk4* is affected (Black asterisk). Black arrowhead, PT-arrival and burst in the FG; black arrow, PT in the transmitting tract of the pistil. Shown are the results of 4 biological replicates. Error bars show ± SD.

Statistical significance was analyzed by one-way ANOVA. Source data and further statistical analysis are provided in the source data file.



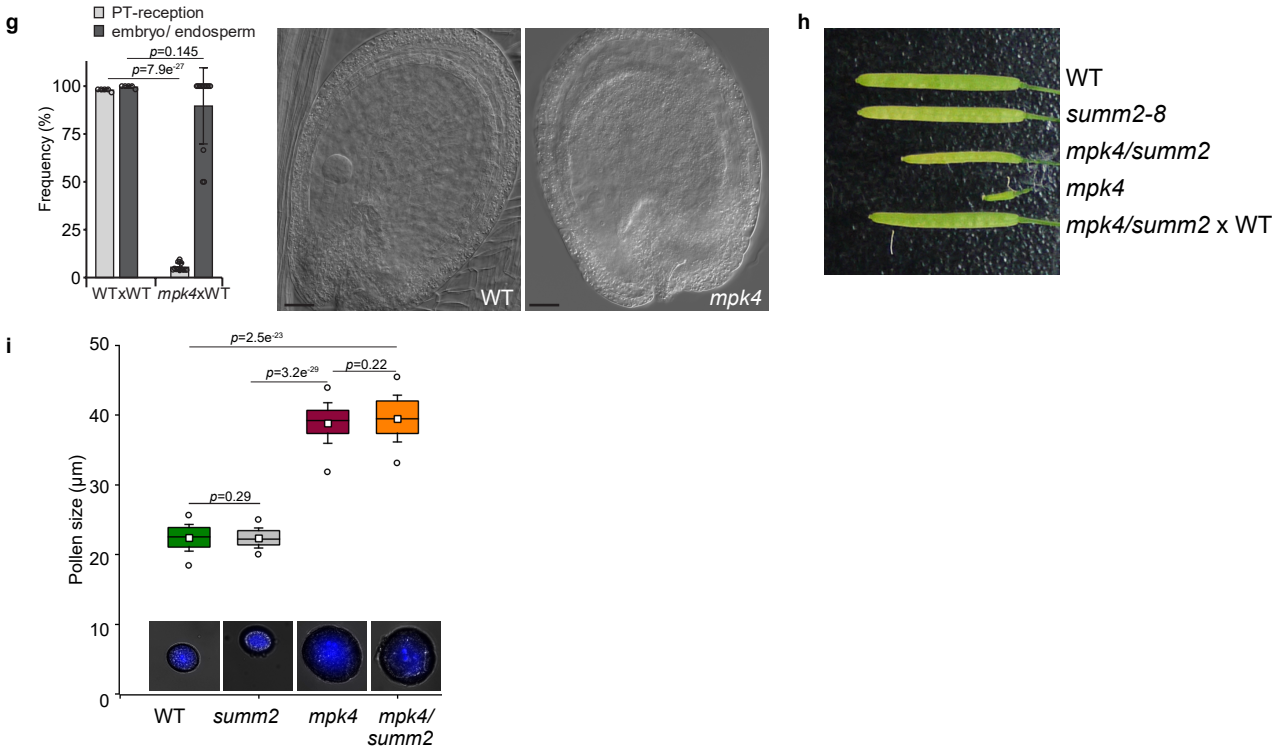
Supplementary Figure 2

Supplementary Figure 2. Analysis of reactive-oxygen species levels before and after fertilization
a-g NBT-staining (a-d) and DAB staining (e-g) at the FG4-FG5 developmental stage and 48 hours after fertilization. Depicted are the results and representative images of three biological replicates. Statistical significance was analyzed by one-way ANOVA. Error bars show ± SD. Source data and further statistical analysis are provided in the source data file. Scale bars, 30 µm.



f *mpk4-2* transmission efficiency

		determined			expected		
Transmission	**cross**	**+/+**	***mpk4-2*/+**	***mpk4-2*/*mpk4-2***	**+/+ (%)**	***mpk4-2*/+ (%)**	***mpk4-2*/*mpk4-2***
selfed	-/+ x -/+	91 (28.4%)	171 (53.5%)	58 (18.1%)	25.0	50.0	25.0



Supplementary Figure 3

Supplementary Figure 3. Characterization of the heterozygote *mpk4* mutant
a-c The occurrence of synergids, central cell and antipodals in WT (n=298) and *mpk4*/+ (n=304), see also **Supplementary movies 7-8**. Depicted are the results and representative images of three biological replicates. Error bars show ± SD. Scale bars, 30 µm.
d-e The expression of the *pLRE::SM1-mCherryGolgie* reporter in the synergids in WT (n=268) and *mpk4*/+ (n-279). Depicted are the results and representative images of three biological replicates. Error bars show ± SD. Scale bars, 20 µm.
f Transmission efficiency of the self-crossed heterozygote *mpk4* mutant.
g Frequency of embryo/endosperm formation in WT (n=302) and *mpk4*/- (n=304) after the reception of WT-pollen tubes. Three biological replicates analyzed. Error bars show ± SD. Scale bars, 30 µm.
h Representative siliques of WT, *summ2-8*, *mpk4/summ2*, *mpk4*, and *mpk4/summ2* pollinated with WT pollen.
i Pollen size of WT, *summ2*, *mpk4/summ2,* and *mpk4*. Boxes represent the 25th and 75th percentiles, and the inner rectangle highlights the median, whiskers show the SD, and outliers are depicted by dots (Min/max range). Statistical significance was analyzed by one-way ANOVA. Analyzed were three biological replicates. Source data and further statistical analysis are provided in the source data file.

Supplementary Table 1

Primer used in this study:		
mpk4-LP	GTGACAATGCAAGAAGATACGTTAGACAGC	Genotyping *mpk4-2*
mpk4-RP	CTTGAAATATCTACAGAGTTGGTGTG	Genotyping *mpk4-2*
LBb1	ATTTTGCCGATTTCGGAAC	T-DNA, genotyping *mpk4-2*
91s	TTTCTGTATCAGTTGTTGCGTG	Genotyping *mpk4-3*, base pair exchange determination by sequencing: GaGGATTTCGGG
91as	TCTAACGTATCTTCTTGCATTGTC	Genotyping *mpk4-3*, GaGGATTTCGGG
LB3	atctgaatttcataaccaatctcgatacac	T-DNA, genotyping *summ2-8*
90s	ATGGGAGCTTGTTTAACACTCTCG	Genotyping *summ2-8*
87as	CCAATGGAAGCTTTCTCAGC	Genotyping *summ2-8*