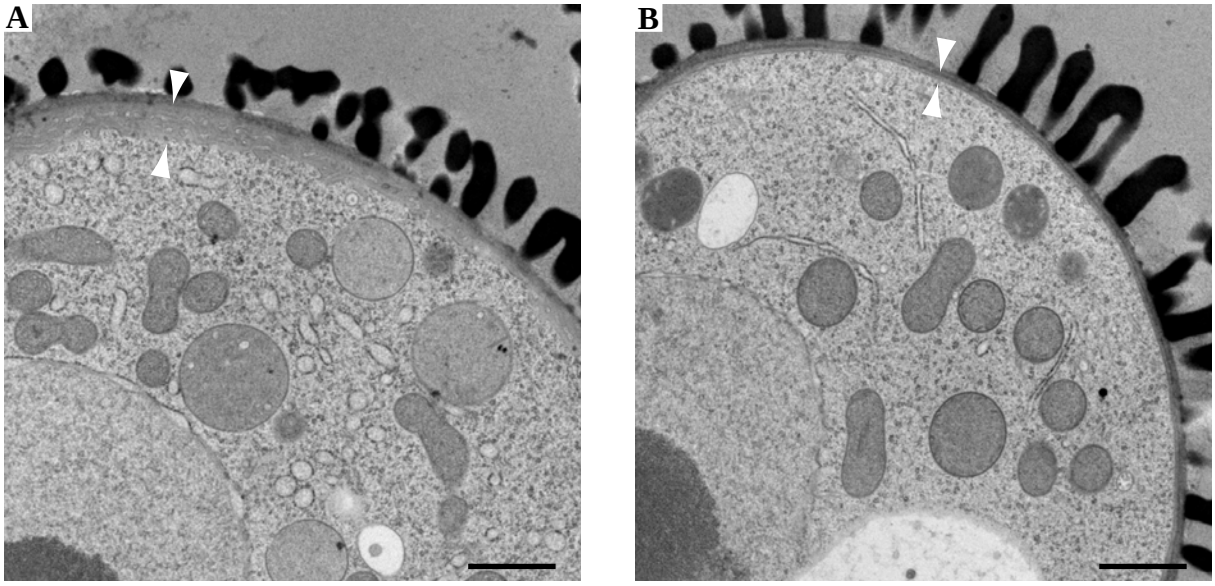
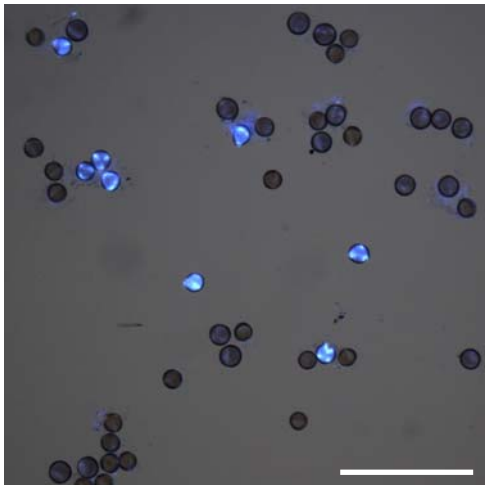
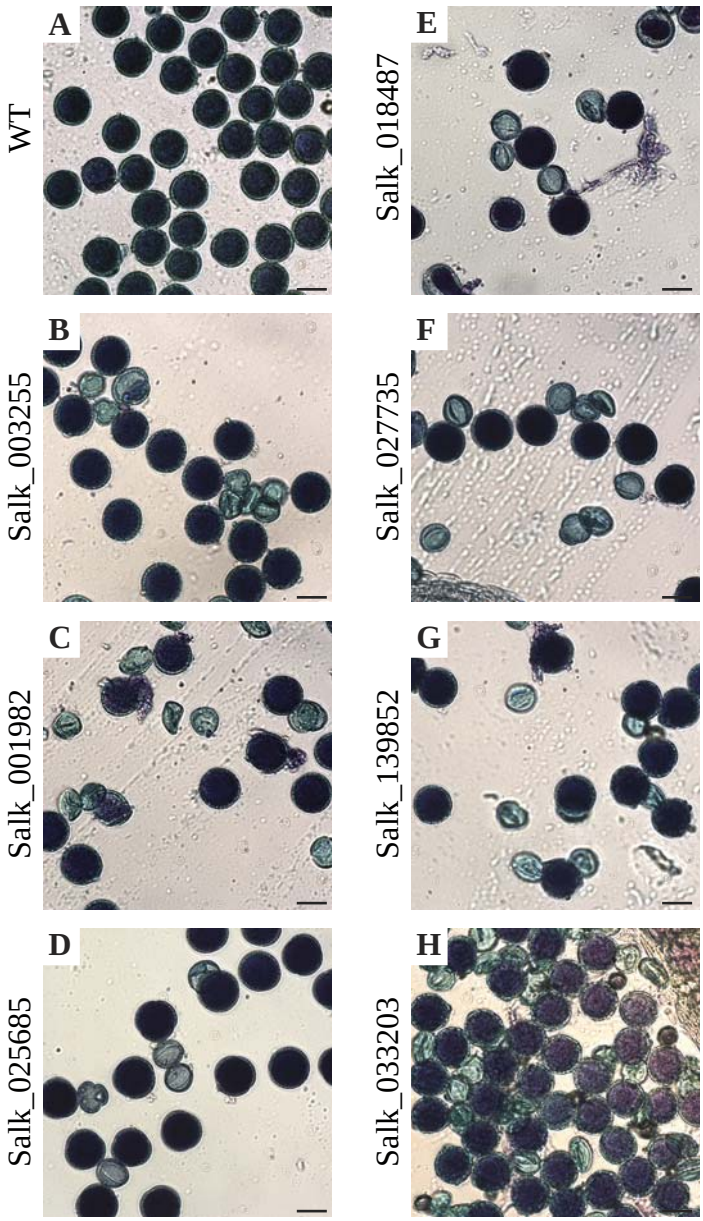


normal arrested

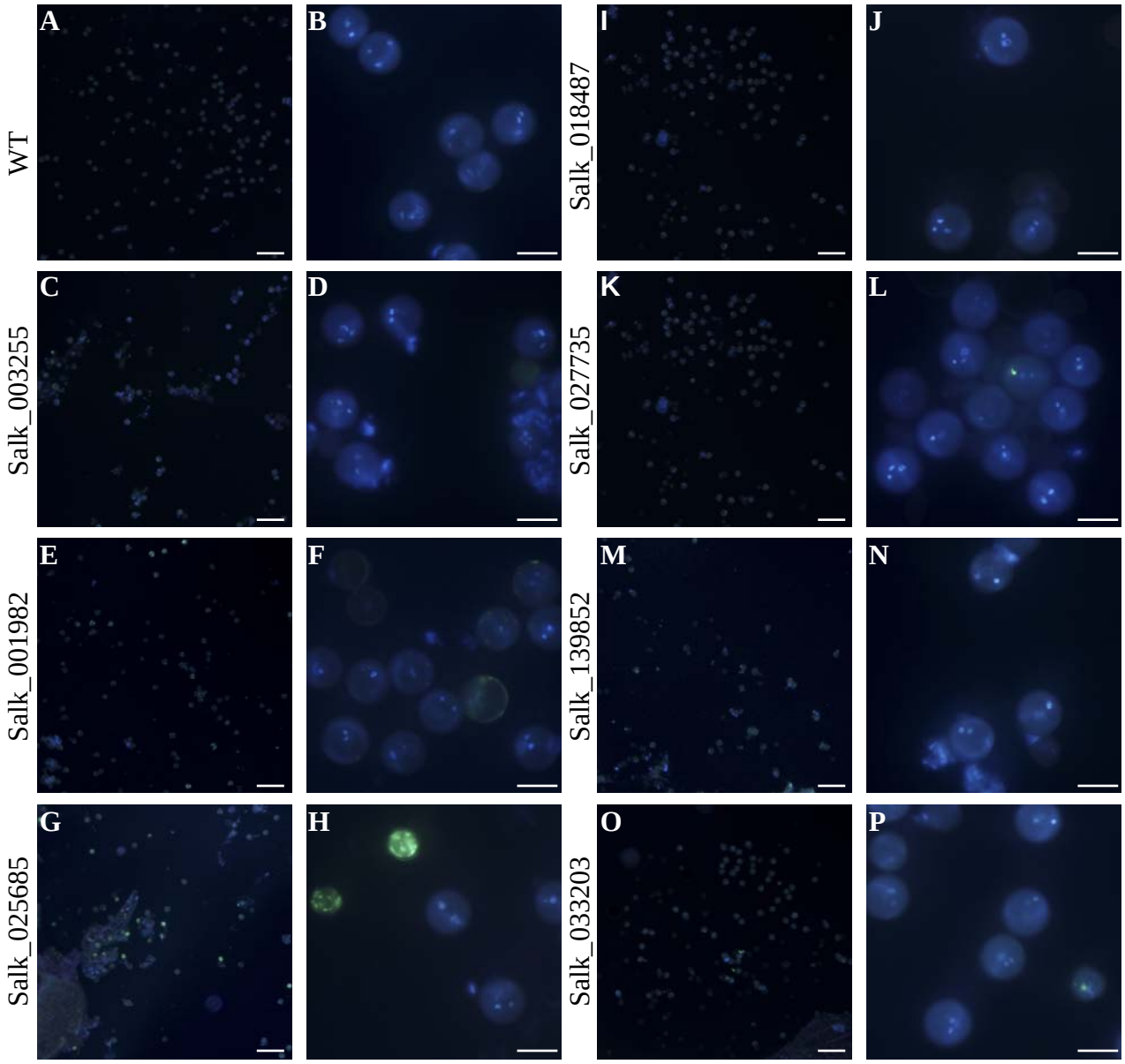
Supplemental Figure 1: *drp2ab* pollen grains arrest at the polarized microspore stage
Electron micrographs of normally developing (A) and arrested (B) pollen grains from a *drp2AaBb* anther at the late polarized microspore stage. White arrowheads indicate the width of the intine. Arrested grains were recognized by the presence of a smooth, thin intine layer (see figure 8A,B). Scale bars: 1 μm.



Supplemental Figure 2: Ectopic callose deposition in pollen from *DRP2A/drp2a-4; DRP2B/drp2b-4* anthers
Developing pollen at the tricellular stage of development from *DRP2A/drp2a-4; DRP2B/drp2b-4* anthers was stained with DAPI to label the nuclei (faint dark blue) and aniline blue to label callose (bright white/blue) and viewed under fluorescent optics. Scale bar: 100 μm.



Supplemental Figure 3: Alexander staining of pollen lethal mutants
Developing pollen at the bicellular and tricellular stage of development from the F1 progeny of a cross between WT Ler and either WT Col (A) or a Salk insertional allele (B-H) was stained with Alexander's Stain to determine pollen viability and viewed by light microscopy. Scale bars: 20 μm.



Supplemental Figure 4: Aniline blue staining of pollen lethal mutants
Developing pollen at the bicellular and tricellular stage of development from the F1 progeny of a cross between WT Ler and either WT Col (A-B) or a Salk insertional allele that shows pollen lethality upon outcrossing (C-P) was stained with DAPI to label the nuclei (blue) and aniline blue to label callose (yellow-green) and viewed under fluorescent optics. Scale bars: 100 μm in (A,C,E,G,I,K,M,O) and 20 μm in (B,D,F,G,H,J,L,N,P).

genotype	*WT*	*drp2AaBB*	*drp2AABb*	*drp2AaBb*	N=
expected %	≤25	≥25	≥25	≤25	
WT ♀ X *drp2AaBb* ♂	19	46	34	0.5	198
drp2AaBb ♀ X *WT* ♂	18	43	39	0	120

Table S1: Analysis of progeny from *drp2AaBb/WT* reciprocal crosses

The genotype of F1 progeny from reciprocal crosses between DRP2A/drp2a-1; DRP2B/drp2b-2 and WT plants was determined by PCR amplification using allele-specific primers. Percentage of offspring recovered with each genotype is indicated, and compared to the percentage that would be expected if there were no transmission defects. The ≤ and ≥ symbols reflect potential minor deviations from the expected percentages due to the possibility of a small degree of linkage between DRP2A and DRP2B, which are found on opposite arms of chromosome 1.

primer	sequence (5' > 3')
747	gatctttgccggaaaacaattggagg
748	cgacttgtcattagaaagaaagagat
774	aacgtccgcaatgtgttattaagttgtc
858	taacctgttacgtttacccctttacattgcagct
859	atccactcgttcttgtcgactacactctca
861	actgtttctggtaacggtctcttcgtcttt
865	tccatgagacaaagtctttcagaaggct
926	gggtgatggttcacgtagtgggccatcg
962	gctgataattcctactg
964	ctgatgatgaaggagaaaaatc
968	ctctcagattcgatgaagcag
1055	gacgaagacacacacagac
1056	ccaaactcatatatatgtgtctctc
1160	gatgttttgtattcttcatctcttcgttc
1161	tgcgttagatttagaggtaaaactcatt
1162	acacacacagacaaacaaatcctagctta

primer	sequence (5' > 3')
1163	tagtagacaggacaacacaaagtggttac
1164	cttctctccatatatgtgctttcttcat
1165	taacagttcgaagaattaaagtgagacaa
1171	atcgttttacatgaaaatatataatgtgg
1172	ttcttataatgattgatttatgtacctttga
1055	gacgaagacacacacagac
1056	ccaaactcatatatatgtgtctctc
1160	gatgttttgtattcttcatctcttcgttc
1161	tgcgttagatttagaggtaaaactcatt
1162	acacacacagacaaacaaatcctagctta
1163	tagtagacaggacaacacaaagtggttac
1164	cttctctccatatatgtgctttcttcat
1165	taacagttcgaagaattaaagtgagacaa
1171	atcgttttacatgaaaatatataatgtgg
1172	ttcttataatgattgatttatgtacctttga

Table S2: Oligonucleotides used in this study