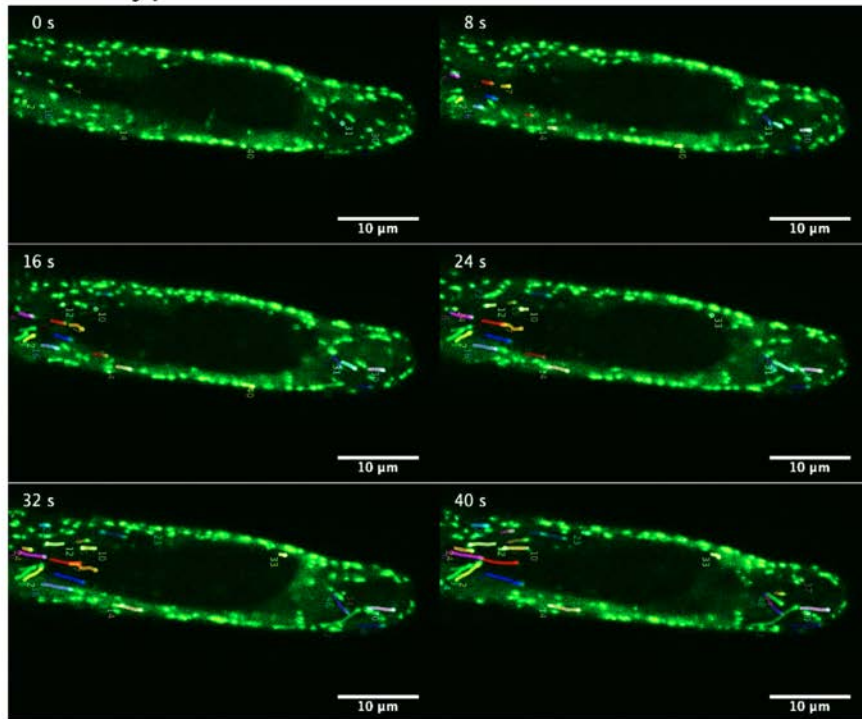
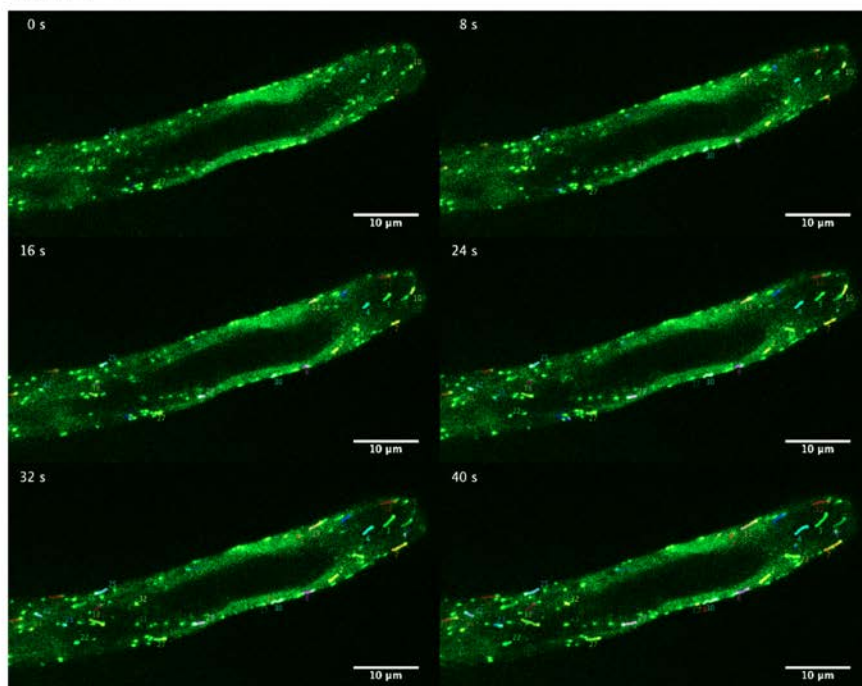


### Wild Type

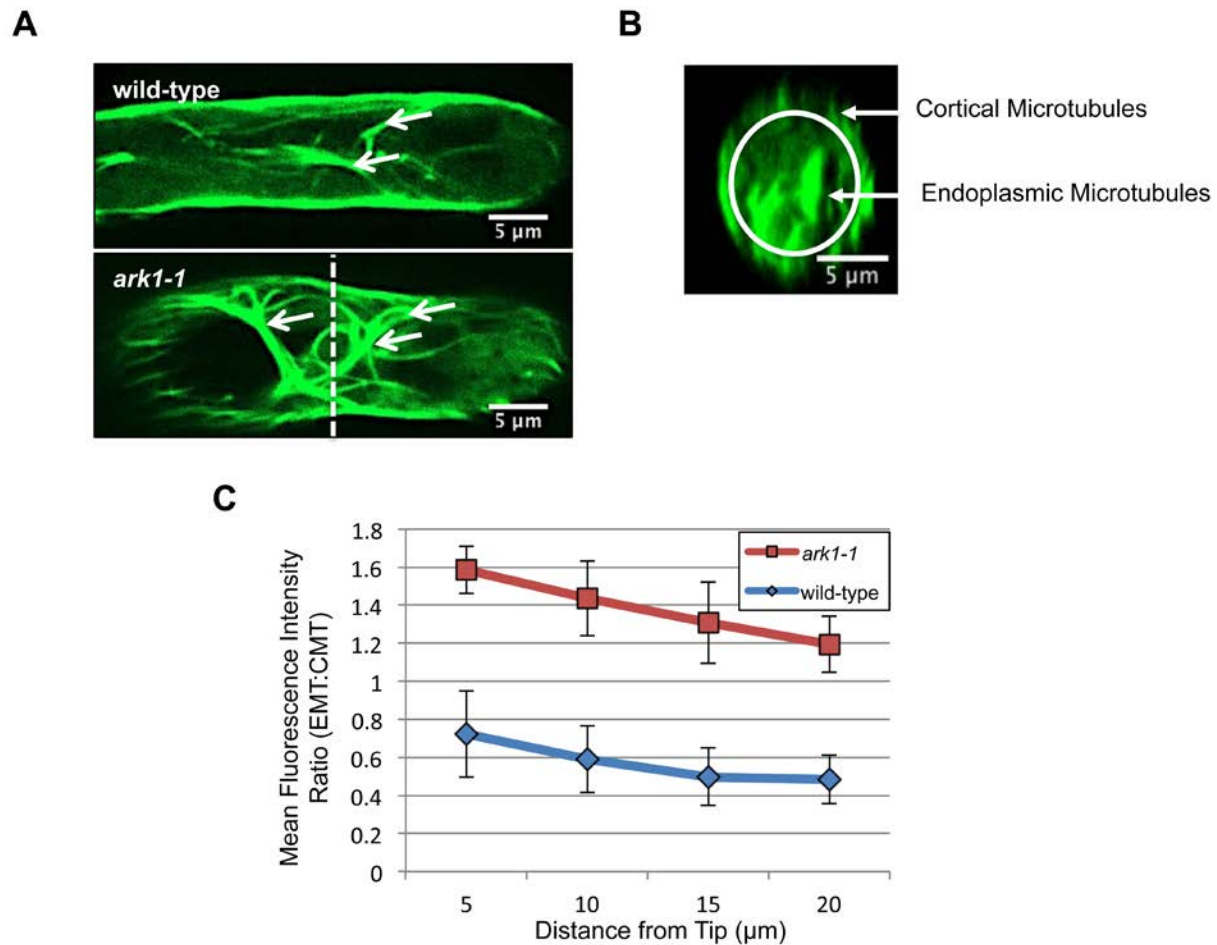


### *ark1-1*



**Supplemental Figure 1.** EB1b-GFP velocity is slower in *ark1-1* root hairs than in wild-type root hairs.

Montage of spinning-disc laser confocal time-lapse micrographs of EB1b-GFP in wild-type (top) and *ark1-1* (bottom) root hairs showing both cortical and endoplasmic microtubule plus-ends. The colored lines represent the EB1b-GFP trajectories with wild type showing faster EB1b-GFP movement than *ark1-1*. Images were acquired every 8 s and represent the medial plane of the root hair. Scale bars represent 10 μm. Images represent Supplemental Movies 1 and 2 online. Representations of these montages can be found in Figures 1D and 1E.

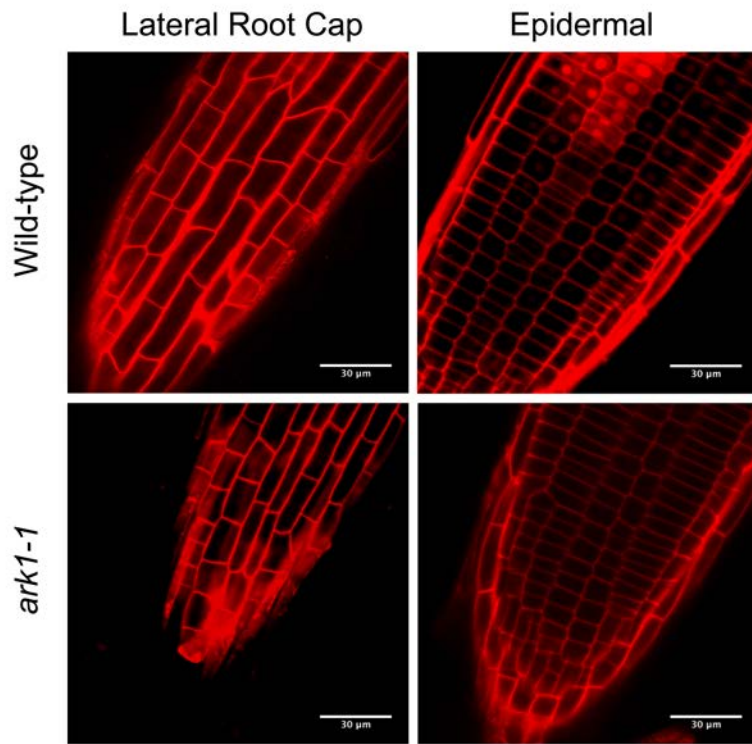


**Supplemental Figure 2.** Endoplasmic microtubules are more abundant in *ark1-1* than in wild-type root hairs.

**(A)** Endoplasmic bundles are indicated by arrows. Spinning disc confocal images of the mid-plane of elongating root hairs. Scale bars represent 5  $\mu\text{m}$ .

**(B)** Cross-section of the *ark1-1* root hair indicated by the dashed-line in (A). The white circle divides the cortical and endoplasmic region used for analysis in (C). Scale bar represents 5  $\mu\text{m}$ .

**(C)** Graph showing an increase in endoplasmic microtubule bundles relative to cortical microtubules in *ark1-1* root hairs. The ratio of mean fluorescent intensity of microtubules between the endoplasmic to cortical region was calculated (indicated in (B)). Endoplasmic bundles are highest at the tip and decrease as you move further away. 19 wild-type and 13 *ark1-1* root hairs were measured. Images were analyzed according to (Sakai et al., 2008). Data and bars represent mean and standard deviation, respectively.



**Supplemental Figure 3.** Cell and tissue patterns are not affected in *ark1-1* root tips.

Confocal images of propidium iodiodide-stained root tips of the lateral root cap (left) and epidermal cells (right). The size of cells and cell plate placement are not altered in *ark1-1* (bottom) relative to wild-type (top).

Forward Primer (5'→3')	Reverse Primer (5'→3')	PCR Product
AAA AAA GCA GGC TGG ACG ATG ATC AAG AGA TG	AGA AAG CTG GGT TAT ATA TCT TTA CAC ATA AGT TGT ACA GTG	Full length ARK1 genomic
AAA AAA GCA GGC TTG AAG AGA TAG AAC CAT GAG TTC GTC AAA TTC CTC C	AGA AAG CTG GGT AGC TTG AGA AGT AAG GGT TTG TTT TG	Full length ARK1 CDS
AAA AAA GCA GGC TTG AAG AGA TAG AAC CAT GAG TTC GTC AAA TTC CTC C	AGA AAG CTG GGT ACT GAC CAG ATA ACG AC	ARK1ΔARM CDS
AAA AAA GCA GGC TTG GAT GGA ATT TGA TTA TGA TTA TGA GAG TTT G	AGA AAG CTG GGT AGC TTG AGA AGT AAG GGT TTG TTT TG	ARK1ΔMotor CDS
AAA AAA GCA GGC TTG AAG AGA TAG AAC CAT GAG AGC TAC CAT GGC	AGA AAG CTG GGT AGC TTG AGA AGT AAG GGT TTG TTT TG	ARM CDS

**Supplemental Table 1.** List of primer sequences used for various *ARK1* constructs. CDS = coding sequence.