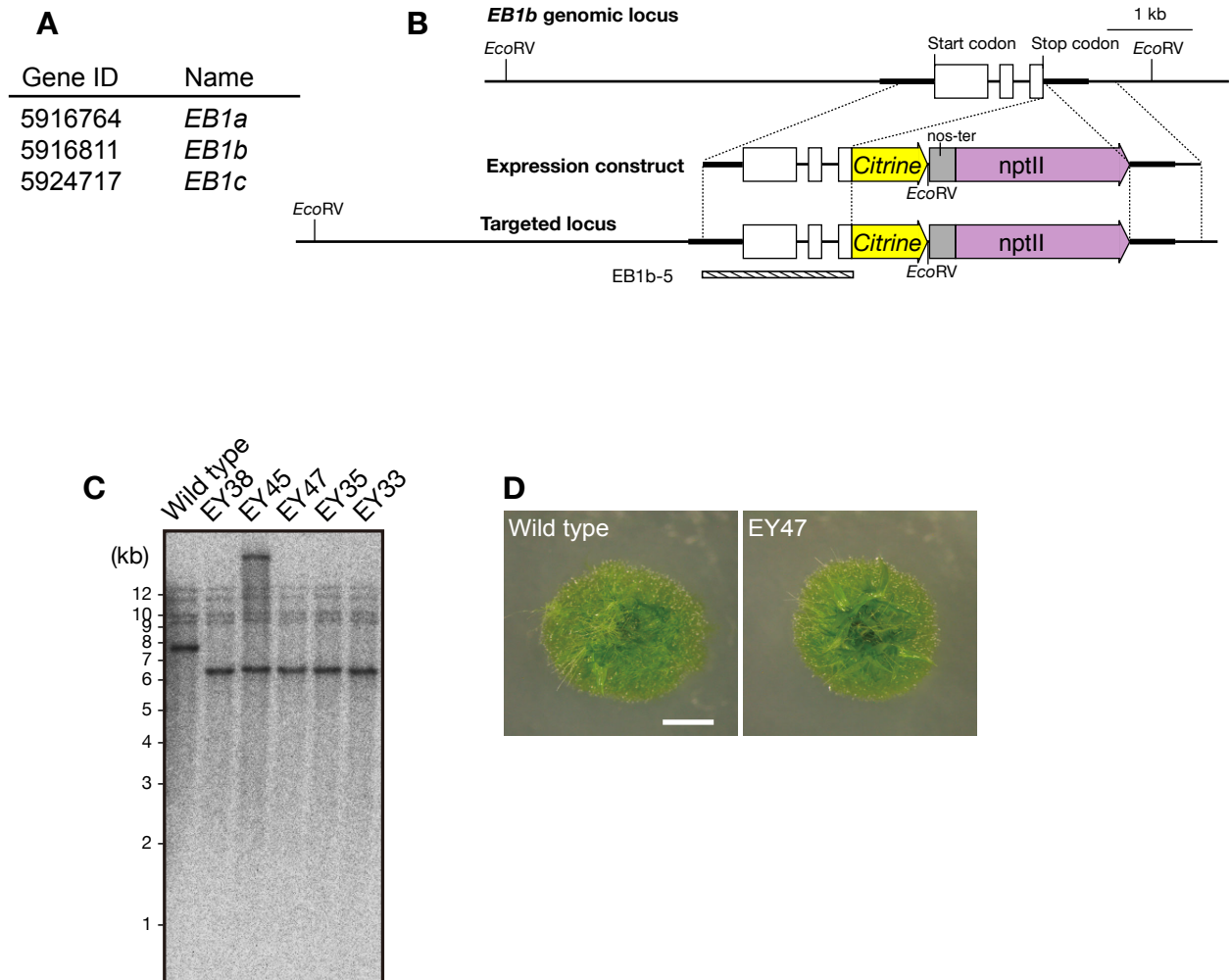


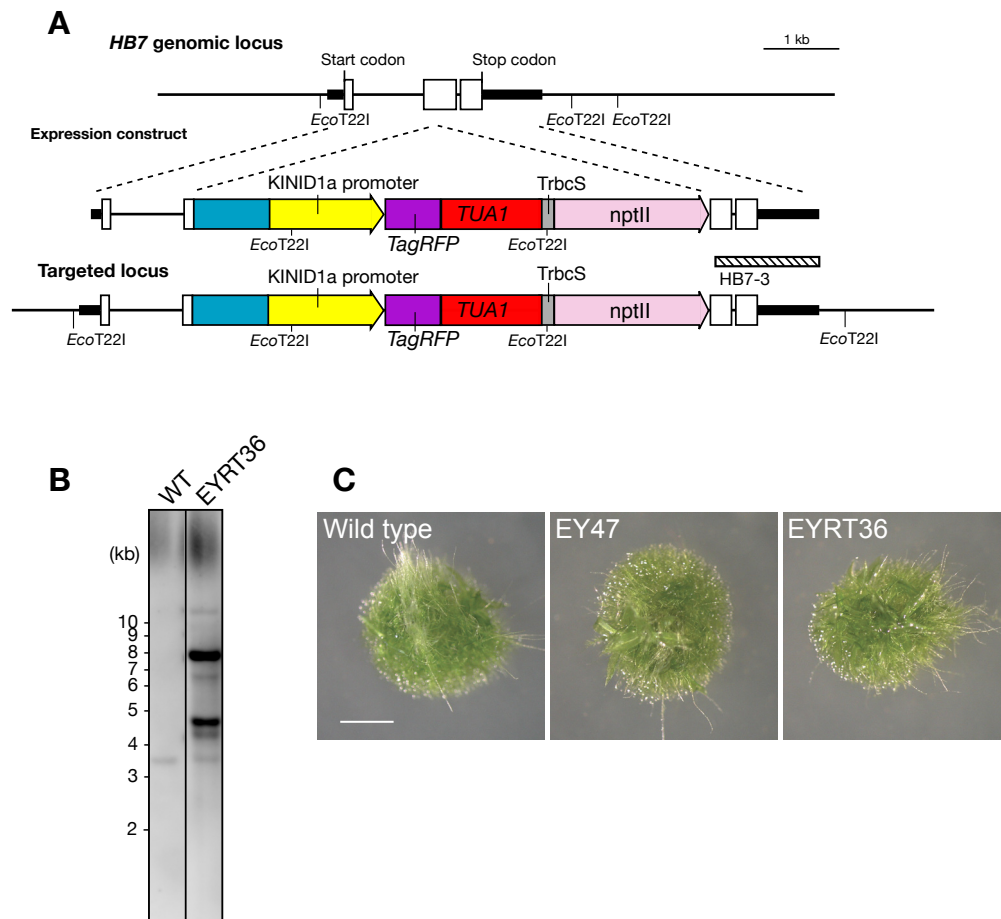
**Supplemental Figure 1.** Distribution of sGFP- $\alpha$ -tubulin in a Caulonemal Apical Cell.

(A) sGFP fluorescence image. (B) Bright field image. The both images are maximum Z-projection of 11 planes (1  $\mu$ m-intervals). The arrow indicates the intense MT bundles in an apical dome. Scale bar = 20  $\mu$ m.



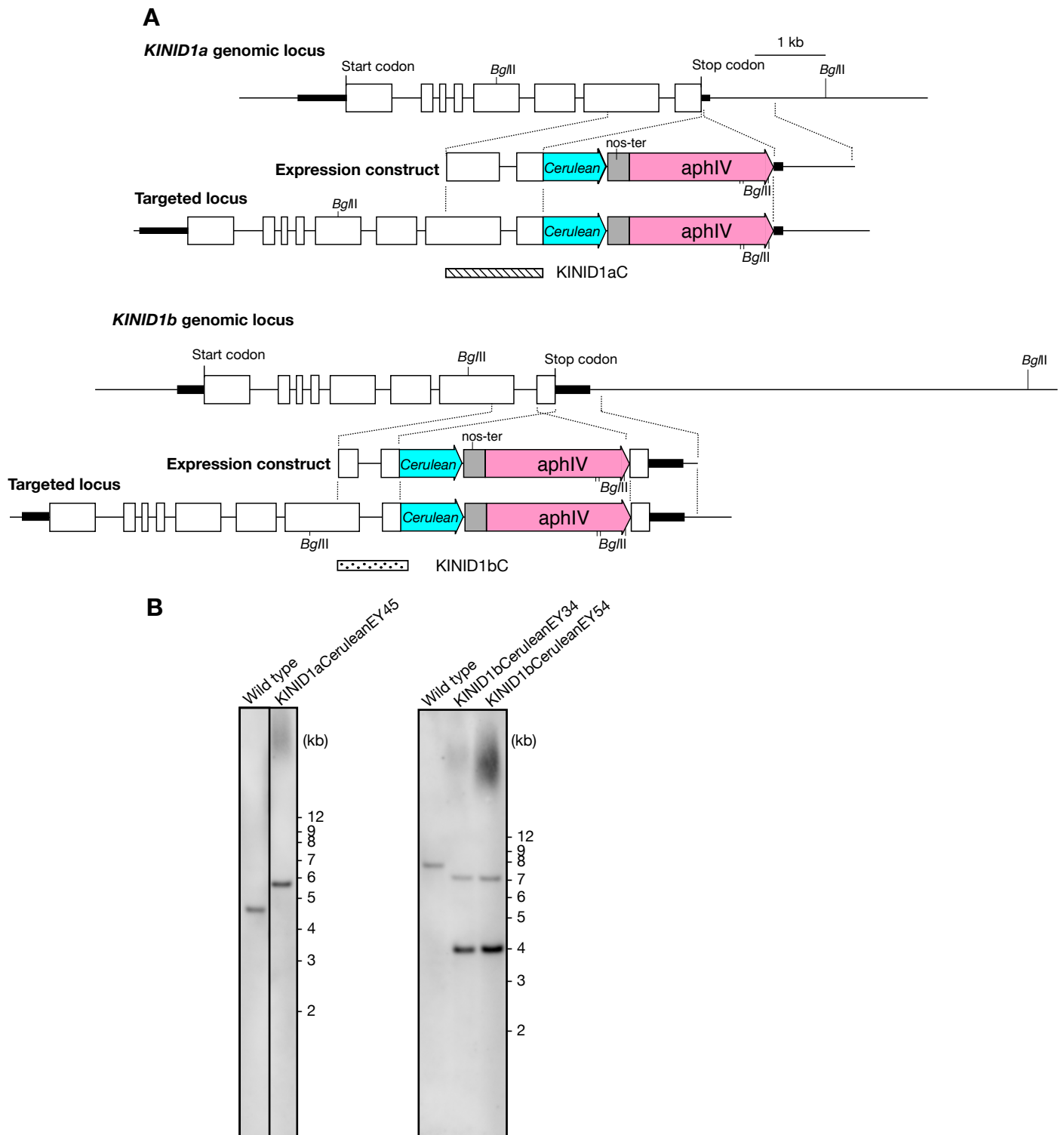
**Supplemental Figure 2.** Generation of the Lines Expressing EB1b-Citrine.

(A) Gene ID and *Physcomitrella patens* *EB1* homologs. (B) Schematics of the targeting of the *EB1b* locus. White boxes represent *EB1b* coding regions. Thick and thin lines indicate 5' and 3' untranslated regions, and genomic regions, respectively. A probe used for DNA-blot analyses is indicated by a hatched box. A yellow arrow represents the *Citrine* coding region (Griesbeck et al., 2001) and a purple arrow represents the neomycin phosphotransferase expression cassette (*nptII*; pTN182 [AB267705]). (C) DNA gel-blot analysis of the targeted lines. Genomic DNA of the wild type and targeted lines was digested with *EcoRV* and hybridized with a EB1b-5 probe. (D) Protonemal colonies of the wild type and the EY47 line. Scale bar = 5  $\mu$ m.



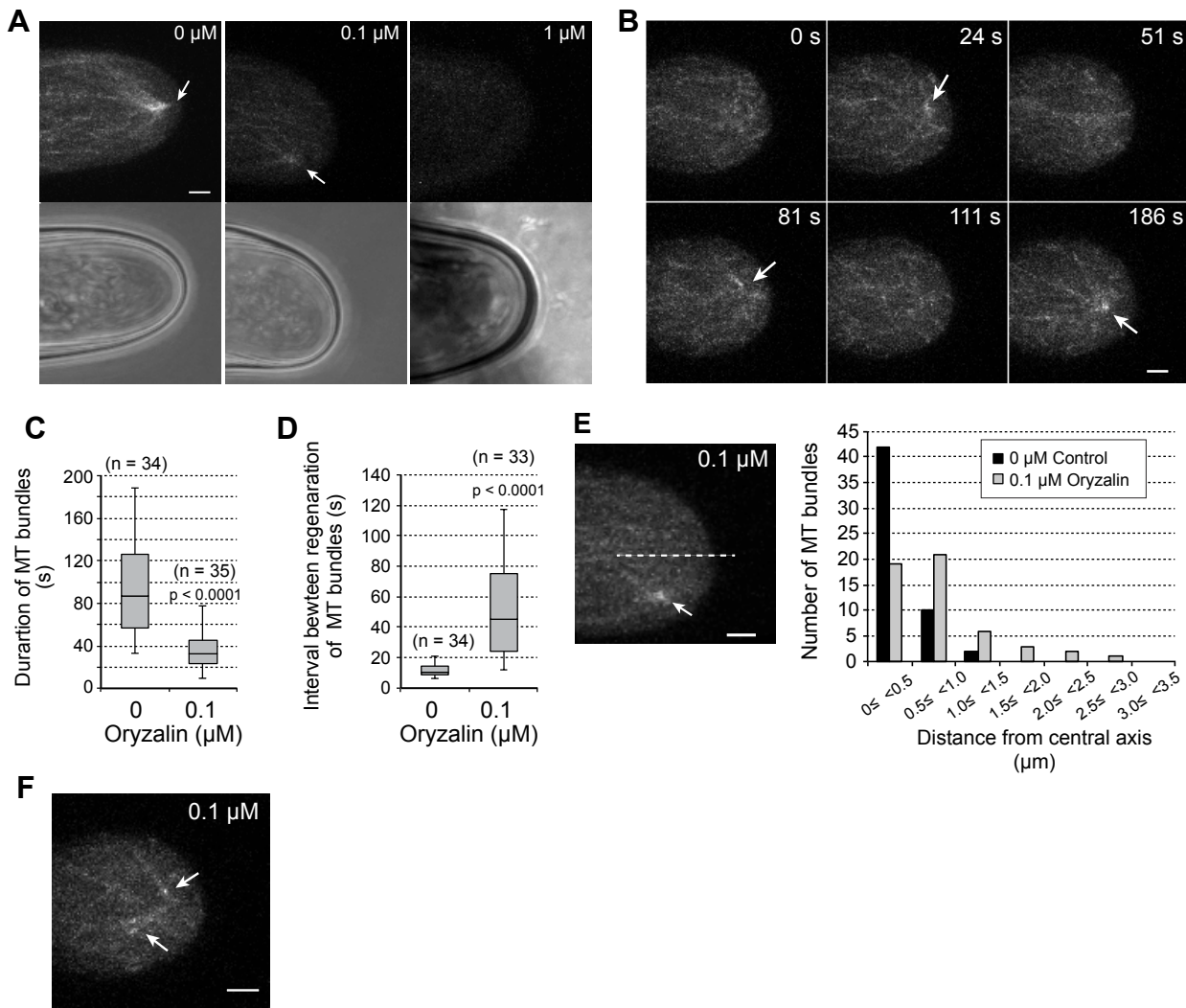
**Supplemental Figure 3.** Generation of the Lines Co-expressing EB1b-Citrine and TagRFP- $\alpha$ -tubulin.

(A) A schematic for the insertion into the *HB7* locus of a DNA fragment containing the *KINID1a* promoter (yellow arrow; Kubo et al., 2013), TagRFP (magenta box; Merzlyak et al., 2007), *Physcomitrella patens*  $\alpha$ -tubulin gene *TUA1* (red box; AB096718), a *Pea rbcS* terminator (*TrbcS*; gray box), and a neomycin phosphotransferase II expression cassette (*nptII*; pink arrow; Nishiyama et al., 2000). A blue box represents the vector region of TN90. Open boxes and thick lines represent *HB7* coding and untranslated regions, respectively. The probe used in (B) is indicated as a hatched line. (B) DNA gel-blot analysis of the insertion lines. Genomic DNA was digested with *EcoT221*. (C) Protonemal colonies of the wild type, EY47 and EYRT36 lines. Scale bar = 5  $\mu$ m.



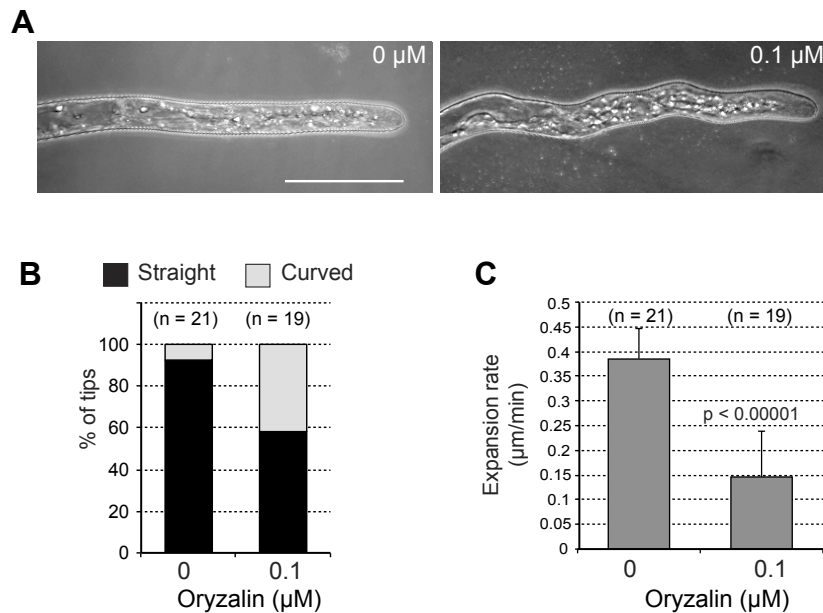
**Supplemental Figure 4.** Generation of the Lines Co-expressing *KINID1a*-Cerulean and EB1b-Citrine and the Lines Co-expressing *KINID1b*-Cerulean and EB1b-Citrine.

(A) Schematics of targeting the *KINID1a* and *KINID1b* loci. White boxes represent the *KINID1a* and *KINID1b* coding regions. Thick and thin lines indicate the 5' and 3' untranslated regions, and genomic regions, respectively. Probes used in (B) are indicated by hatched and dotted boxes. Cyan arrows denote Cerulean (Rizzo et al., 2004). A gray box and a pink arrow indicate the nos terminator (nos-ter; Nishiyama et al., 2000) and the neomycin phosphotransferase II expression cassette (nptII; Nishiyama et al., 2000), respectively. (C) DNA gel-blot analyses of targeted lines. Genomic DNA of the wild type, *KINID1a*-Cerulean (right panel), and *KINID1b*-Cerulean (left panel) was digested with *Bgl*II.



**Supplemental Figure 5.** Application of a MT-depolymerizing Drug, oryzalin, Leads to Aberrant Formation and Maintenance of the Intense MT Bundles in Apical Domes of Caulonemal Apical Cells.

**(A)** Distribution of sGFP- $\alpha$ -tubulin in an apical dome of a caulonemal apical cell of the line expressing sGFP- $\alpha$ -tubulin, GTU193, in the absence and presence of 0.1  $\mu\text{M}$  and 1  $\mu\text{M}$  oryzalin. Arrows indicate the MT bundles. **(B)** Dynamics of sGFP- $\alpha$ -tubulin in an apical dome of a caulonemal apical cell of GTU193 in the presence of 0.1  $\mu\text{M}$  oryzalin. The images were acquired every 3 min and representative images are shown. The images are a maximum Z-projection of 10 planes (0.8  $\mu\text{m}$ -intervals). Arrows indicate the MT bundles. **(C)** Measurement of the appearance duration of the intense MT bundle in apical domes of caulonemal apical cells of GTU193 in the absence or presence of 0.1  $\mu\text{M}$  oryzalin. A graph shows box-plot medians and 25th/75th percentiles.  $p < 0.0001$ , unpaired  $t$ -test between the absence and presence of oryzalin. **(D)** Measurement of the interval duration between the generation of the intense MT bundles in apical domes of caulonemal apical cells of GTU193 in the absence or presence of 0.1  $\mu\text{M}$  oryzalin. A graph shows box-plot medians and 25th/75th percentiles.  $p < 0.0001$ , unpaired  $t$ -test between the absence and presence of oryzalin. **(E)** Distribution of intense MT bundles in apical domes. The left image shows a MT bundle (arrow) positioned from a central axis (a dotted line) in an apical dome of GTU193 in the presence of 0.1  $\mu\text{M}$  oryzalin. The graph indicates the number of MT bundles relative to the distance from the central axis on the apical domes. **(F)** Multiple MT bundles in an apical dome of GTU193 in the presence of 0.1  $\mu\text{M}$  oryzalin. Arrows indicate the MT bundles. Scale bars = 2  $\mu\text{m}$ .



**Supplemental Figure 6.** Application of an MT-depolymerizing Drug, oryzalin, Leads to both Mis-direction and Reduced Expansion Rate of Tip Growth.

**(A)** Shape of caulonemal apical cells in the line expressing sGFP- $\alpha$ -tubulin, GTU193, in the presence of 0.1  $\mu\text{M}$  oryzalin. **(B)** Proportion of tips showing straight and curved shapes. The straight or curved sets of tip shape are referred to as “Straight” or “Curve”, respectively. **(C)** Expansion rate of tip growth for caulonemal apical cells of GTU193 in the presence of 0.1  $\mu\text{M}$  oryzalin. The expansion rate was measured by time-lapse imaging (interval 3 s, duration 340 s).  $p < 0.0001$ , unpaired  $t$ -test between the control line and the mutants. Error bars indicate SD. Scale bar = 20  $\mu\text{m}$ .

**Supplemental Table 1. Primers Used in This Work**

Primer	Sequence
PpEB1bF1	5'-GTGTCGACTAGTATTTGTTTCCTCGG-3'
PpEB1bR1	5'-ATCCTCTAAAAGATCCTTACTGTCGTCGTC-3'
PpEB1bF2	5'-TGGCGGCCGCACTATTACTCGCAGCCAAG-3'
PpEB1bR2	5'-ACCCGCGGTACTCGTCATGATCGGGC -3'
tagRFPstart	5'-ATCTTGGTGAGTAAAGGTGAAGAGTTG -3'
tagRFPend	5'-GTTCAATTTGTGACCTAGCTTGGA -3'
API1pF1	5'-CTCGGTACCTTTTGTGTTGAGGAGGTTTTACTTTTTTG -3'
API1pR1	5'-CGCACCCGACGGCTCTGTTTTAA-3'
tagRFPstartF2	5'-GGGATGGTGAGTAAAGGTGAAGAGTTGATTAAAG-3'
PpTUArApaI	5'-TGAGGGCCCTCAGTAGTCGTCGTCCTCC-3'
aph4F1	5'-TACTCCAAAAATGTCAAAGATACAGTCTCA-3'
aph4R1	5'-TAGTTTTGATCTTGAAAAGATCTTTTATCTTTAG-3'
CeruF1	5'-TAACTTCGTATAGCATAATTATACGAAGT-3'
CeruR1	5'-GGGGGGCAATTCTCATGTTTGACAGCTTATC -3'
PpHB7-3for	5'-AACAAGCTTGAGCCCGAGAG-3'
PpHB7-3rev	5'-CCTGGTTGCTTTTCCCAGAG-3'
229-2p4	5'-CAGCCTTCAAATCAGTGTCCC-3'
api1R400ClaI	5'-CAGAAAAGGATCGATAGACCTGGCC-3'
api1LF10	5'-CTCGAGGGTGGTGCCATTTCCGA-3'
api1LR390HindIII	5'-CTTAAGCTTGGGAGACATCATCGATGC-3'
M13-21	5'-TGTAACGACGGCCAGT-3'
api1R3940ClaI	5'-AGAAATGTATCGATGCAGCGAG-3'
sGFP-	5'-TCGCCGACACGCTGAACTTGTG-3'

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