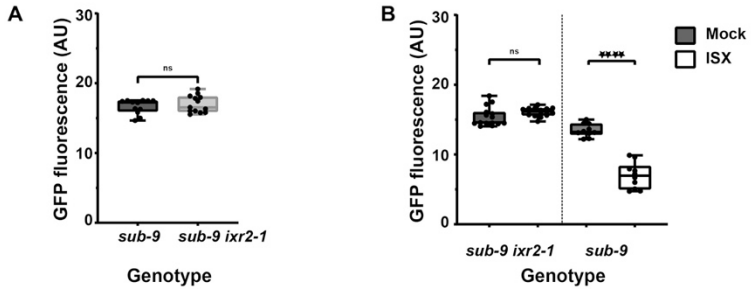

Fig. S1. Effect of isoxaben treatment on pSUB::SUB:EGFP expression. (A) Quantification of signal intensity of the pSUB::SUB:EGFP reporter in seven-day-old *sub-9* and *sub-9 i xr 2-1* plate-grown seedlings. Imaging parameters between both genotypes were identical. Box and whisker plots are shown. n ≤ 15. No statistical significance difference was observed (unpaired t-test with Welch's correction, two-tailed P values). The experiment was performed three times with similar results. (B) Quantification of signal intensity of the pSUB::SUB:EGFP reporter in seven-day-old plate-grown *sub-9* and *sub-9 i xr 2-1* seedlings transferred to plates containing 600 nM isoxaben for 8 hours. Imaging parameters between both genotypes were identical. Box and whisker plots are shown. 10 >n ≤ 15. No statistical significance difference was observed for treated or untreated sub-9 ixr2- 1 seedlings (****, P < 0.0001; one-way ANOVA followed by post hoc Tukey's multiple comparison test). The experiment was performed three times with similar results.

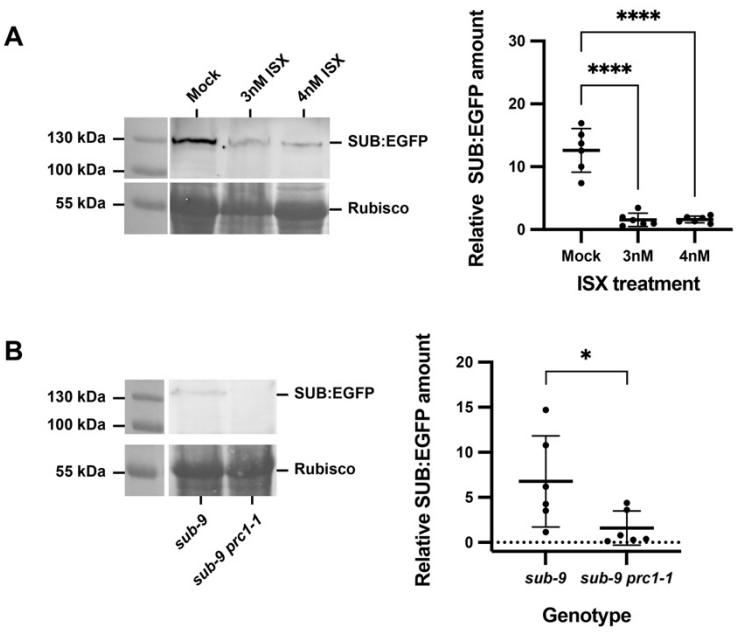

Fig. S2. Western blot analysis of pSUB::SUB:EGFP expression. (A) Left panel: Western blot depicting SUB:EGFP expression levels in seven-day-old plate-grown *sub-1* pSUB::SUB:EGFP seedlings exposed to mock or increasing amounts of isoxaben (ISX) using an anti-GFP antibody. The upper row shows the SUB:EGFP signal. The bottom row shows Ponceau staining depicting Rubisco bands as loading control. The experiment was performed twice with three biological replicates each. Right panel: quantification of signal intensity of all the biological replicates. SUB:EGFP signal intensity in each lane was normalized using the respective loading control. Mean +/- SD are indicated. Asterisks indicate statistical significance (****, $P < 0.0001$; one-way ANOVA followed by post hoc Tukey's multiple comparison test). (B) Western blot depicting SUB:EGFP expression levels in seven-day-old plate-grown *sub-9* pSUB::SUB:EGFP or *sub-9 prc1-1* pSUB::SUB:EGFP seedlings using an anti-GFP antibody. The upper row shows the SUB:EGFP signal. The bottom row shows Ponceau staining depicting Rubisco bands as loading control. The experiment was performed twice with three biological replicates each. Right panel: quantification of signal intensity of all the biological replicates. SUB:EGFP signal intensity in each lane was normalized using the respective loading control. Mean +/- SD are indicated. Asterisks indicate statistical significance (*, $P < 0.05$; two-tailed unpaired t test).

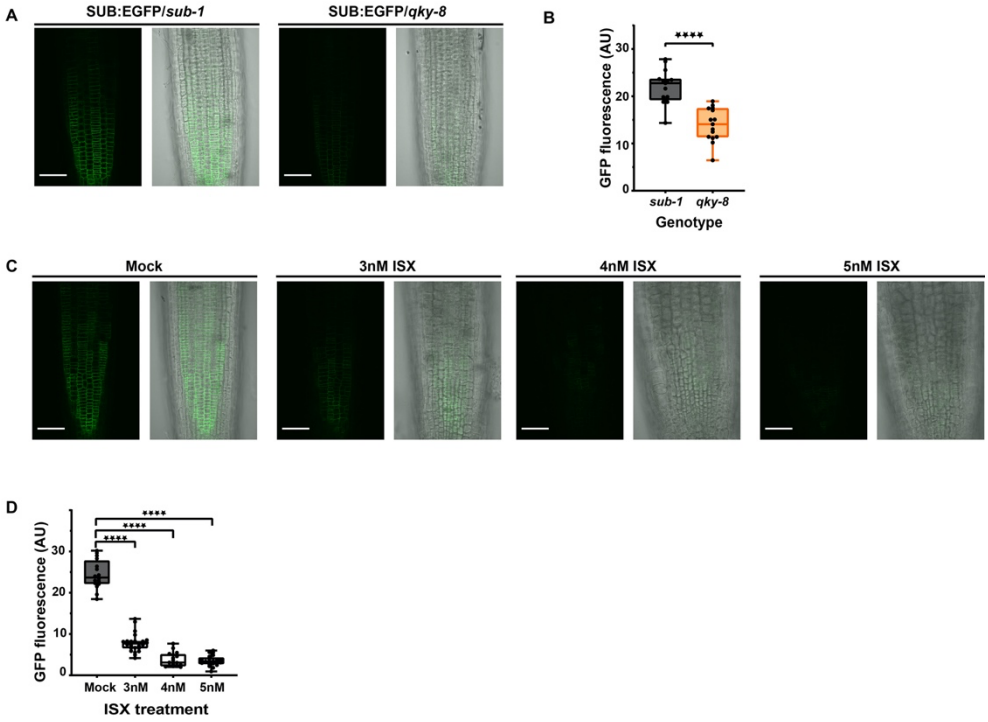

Fig. S3. Effect of isoxaben treatment on pSUB::SUB:EGFP expression pattern in *qky-8*. (A,C) show confocal micrographs depicting optical sections through roots of seven-day-old seedlings. (A) Signal intensity of a functional pSUB::SUB:EGFP reporter in *sub-1* and *qky-8* genetic background. Note the reduction of signal in *qky-8*. (B) Quantification of the data shown in (A). Box and whisker plots are shown. n =15. Asterisks represent statistical significance (****, $P < 0.0001$; unpaired t-test with Welch's correction, two-tailed P values). The experiment was performed three times with similar results. (C) Signal intensity of a functional pSUB::SUB:EGFP reporter in *qky-8*. Continuous treatments are indicated. Duration of treatment and treatment are indicated. Imaging parameters between mock and isoxaben treatments were identical. Note the reduced signal in isoxaben-treated seedlings. (D) Quantification of the data shown in (C). Box and whisker plots are shown. $16 \leq n \leq 25$. Asterisks represent statistical significance (****, $P < 0.0001$; one-way ANOVA followed by post hoc Tukey's multiple comparison test). The experiment was performed three times with similar results. Scale bars: 50 µm.

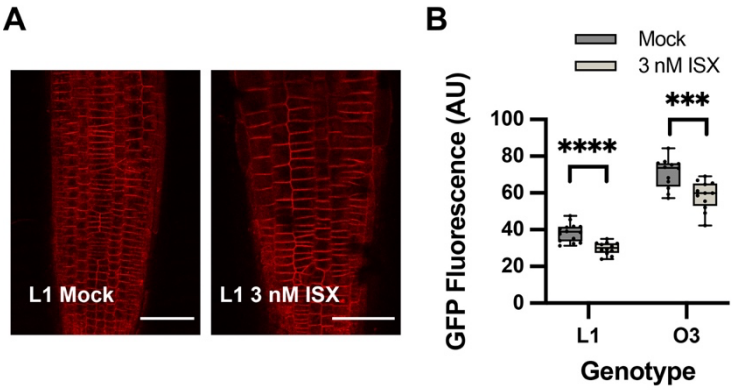

Fig. S4. Effect of isoxaben treatment on SUB:mCherry overexpression. The two independent Col lines homozygous for the pUBQ::SUB:mCherry construct (L1, O3) also carry the pGL2::GUS:EGFP reporter. Genotype and treatment are indicated. (A) Representative confocal micrographs depicting SUB:mCherry signal in optical sections through roots of seven-day-old L1 seedlings grown for five days on regular MS plates followed by exposure to mock or 3 nM isoxaben for 48 hours. Imaging parameters between mock and isoxaben treated seedlings were identical. (B) Quantification of the data shown in (A). Box and whisker plots encompassing all data points are shown. 12 ≤ n ≤ 14. In both lines a small but statistically significant decrease in signal intensity was observed upon exposure to isoxaben (****, P < 0.0001; ***, P < 0.002; unpaired t tests with Welch correction). The experiment was performed twice with similar results. Scale bars: 50 µm.

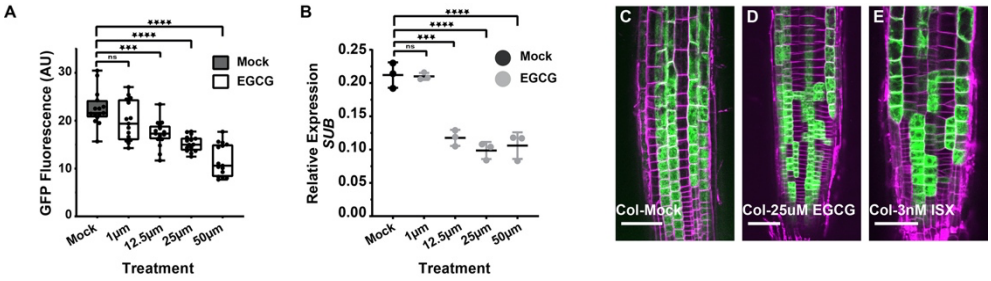

Fig. S5. Effects of EGCG treatment on pSUB::SUB:EGFP, *SUB* and pGL2::GUS:EGFP expression patterns. (A) Box and whisker plot shows quantification of signal intensity of the pSUB::SUB:EGFP reporter upon continuous exposure of plate-grown seedlings to mock or to indicated amount of EGCG treatment (n=15). Asterisks represent statistical significance (***, P < 0.0006; ****, P < 0.0001; one-way ANOVA followed by post hoc Tukey's multiple comparison test). The experiment was performed three times with similar results. (B) Relative transcript levels of *SUB* in seven-days-old seedlings exposed to mock or EGCG for indicated amount and time. Expression was detected by qPCR. Mean ± SD is shown, n=3. Asterisks represent statistical significance (***, P < 0.0006; ****, P < 0.0001; one-way ANOVA followed by post hoc Tukey's multiple comparison test). The experiment was performed three times with similar results. (C-E) confocal micrographs depicting optical sections through roots of seven-day-old seedlings showing the pGL2::GUS:EGFP expression pattern. Genotypes and/or treatments are indicated. 10/10 (C), 13/15, (D) 11/14 (E) root analyzed showed this pattern. Scale bars: 50 µm.

Supplementary Materials and Methods

Plant genetics

To generate the *sub-9 ixr2-1* double mutant F2 progeny of a parental cross between *sub-9* and *ixr2-1* were genotyped to select the double mutants. To generate the *pSUB::SUB:EGFP sub-9 ixr2-1* and *pSUB::SUB:EGFP sub-9 prc1-1* lines, the previously reported pSUB::SUB:EGFP plasmid was transformed into *sub-9*. Homozygous complementing T3 *pSUB::SUB:EGFP sub-9* was crossed into *sub-9 prc1-1* and *sub-9 ixr2-1* double mutants, respectively, and the F2 progeny was screened for double mutants with pSUB::SUB:EGFP expression and further propagated to obtain homozygous F3 lines. The *sub-9* pGL2::GUS:EGFP and *prc1-1* pGL2::GUS:EGFP lines were obtained by crossing the reporter line pGL2::GUS:EGFP into *sub-9* and *prc1-1*.

Table S1. Primers used in this study

Primer name	Sequence
R1(at4g33380) LP	5'- TGAAGGAGAGGAAGAGCCTGAGGAA -3'
R1(at4g33380) RP	5'-CCCCATCTCACTGCAGCACCAC -3'
R2 At2g28390 LP	5'-AGATTGCAGGGTACGCCTTGAGG-3'
R2 At2g28390 RP	5'- ACACGCATTCCACCTTCCGCG -3'
R3 At5g46630 LP	5'- CCAAATGGAATTTCAGGTGCCAATG -3'
R3 At5g46630 RP	5'- CAATGCGTACCTTGAGAAAACGAAC-'3
SUB(AT1G11130) LP	5'- GTTTGGATCTTTGACCTAGACGA-3'
SUB(AT1G11130) RP	5'- CAAGTTATTAATCGCCGAAACAT-3'