

Supplementary Fig. S1. Schematic representation of *jaz* **T-DNA insertion lines.** Shown are details of T-DNA insertion lines used in this study. The exact location of the T-DNA inserts is not depicted and are not to scale. UTRs, exons and introns are represented by grey bars, black bars and raised lines, respectively.



jaz1 jaz2 jaz3 jaz4 jaz5 jaz6 jaz7 jaz8 jaz9 jaz11 jaz12

Supplementary Fig. S2. Screening of jaz T-DNA insertion lines in *F. oxysporum* disease assays. jaz T-DNA insertion lines were screened in *F. oxysporum* disease assays and survivorship recorded relative to wild-type plants at 21-days post inoculation. Shown is the average of two biological replicates \pm SE (n=55). Asterisks indicate values that are significantly different (***P*<0.01 Student's *t*-test) from WT.





Supplementary Fig. S3. Detection of seed aborts in *jaz7-1D* and confirmation of *jaz7-1*. (A) Siliques of *jaz7-1D* and WT were examined for seed aborts with a 1:3 ratio (7:19) of aborts (indicated by arrows) to normal ovules observed in *jaz7-1D*. (B) Primers specific to the first or second exon of *JAZ7* were used to screen for full or truncated transcripts derived from the *jaz7-1* T-DNA line WiscDsLox7H11. *JAZ7* transcript 5' to the T-DNA insertion site was detected at levels similar to Col-0 however, it is unlikely 5' *JAZ7* transcripts would produce a truncated protein as non-polyadenylated transcripts would be degraded if not correctly processed. No transcript was detected with primers specific to the second exon (3' to T-DNA insertion site). Values are averages \pm SE of three biological replicates consisting of pools of 10 plants. Gene expression levels are relative to the internal control *B-actin* genes.

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Supplementary Fig. S4. Ectopic over-expression of JAZ7 in wild-type plants.

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(A) Basal JAZ7 expression in 355:JAZ7 overexpression (JAZ7-OX) lines. Values are averages \pm SE of three biological replicates consisting of pools of 10-20 plants. Shown also is fold increase in JAZ7 expression over wild-type (WT). Gene expression levels are relative to the internal control β -actin genes. (B) Phenotypes of jaz7 mutant lines. (C) Basal expression of JA-marker genes was examined in shoot tissue of wild-type (WT), jaz7-1D and 355:JAZ7 over-expression (JAZ7-OX) plants. Values are averages \pm SE of three biological replicates consisting of pools of 10 plants. Gene expression levels are relative to the internal control β -actin genes. (D-E) (D) Root growth on control media and (E) sensitivity of WT, jaz7-1D, jaz7-1 and JAZ7-OX seedlings to MeJA 7-days post germination. Values are averages \pm SE of three biological replicates consisting of pools of 10-15 seedlings. (F-G) *F. oxysporum* disease assays with (F) necrotic leaves per plant at 14-days post inoculation and (G) survival rates at 28-days. Values are averages \pm SE (n=40). Asterisks indicate values that are significantly different (***P*<0.01, **P*<0.05, Student's *t*-test) from WT. Similar results were obtained in independent experiments.



Supplementary Fig. S5. Backcrossed F2 *jaz7-1D* seedlings have short roots and are JAhypersensitive. (A-D) Growth of wild-type (Col-0), *jaz7-1D*, *jaz7-1* and F₂ seedlings from a cross between Col-0 and *jaz7-1D* on (A) control media and (B) MeJA (50 uM) containing media 7-days post germination. (C-D) F₂ seedlings segregated 2:1 for heterozygous *jaz7-1D*:WT root lengths under control and MeJA treatments. F₂ Seedlings with *jaz7-1D* root phenotype were significantly different from WT but not from *jaz7-1D*. Root elongation of each line when grown on control media or media containing MeJA was calculated as a percentage relative to control treatment. Values are averages \pm SE of 10-15 seedlings. Values that differed significantly from the WT were identified by the one-way Anova and Dunnet's post-hoc test (***P*<0.01, **P*<0.05). Similar results were obtained in an independent experiment.