

**Supplemental Figure S1.** *Fusarium* disease score ratings system. Following *F. oxysporum* infection, plants were given a disease score rating ranging from 0 to 5. (0) No symptoms, (1) minimal symptoms, 1 leaf chlorotic, (2) >1 leaf chlorotic, minimal necrosis, (3) >50% chlorosis and necrosis, (4) extensive necrosis, stunting, (5) dead.



**Supplemental Figure S2. Analysis of** *Ibd20* **T-DNA mutants.** (A) *LBD20* expression was examined in shoot and root tissue of wild-type (WT) and *Ibd20* plants. Both *Ibd20* alleles had either non-detectable or trace levels of *LBD20*. (B) *Thi2.1* expression was examined in WT and *Ibd20* shoot tissue 6 h post mock or MeJA treatment. Gene expression levels are relative to the internal control  $\beta$ -actin genes. The average of three biological replicates consisting of pools of thirty to forty plants is shown with SE. Asterisks indicate values that are significantly different (\*\**P*<0.01, \**P*<0.05 Student's *t*-test) from WT in the same tissue or treatment.



Supplemental Figure S3. *PDF1.2* and *PR4* expression in wild-type versus *Ibd20* plants following MeJA treatment. Expression of the JA-defense marker genes *PDF1.2* and *PR4* was examined in wild-type (WT) and *Ibd20* (A) root or (B) shoot tissue 6 h post mock or MeJA treatment. Gene expression levels are relative to the internal control  $\beta$ -actin genes. The average of three biological replicates consisting of pools of thirty to forty plants is shown with SE. Asterisks indicate values that are significantly different (\**P*<0.05 Student's *t*-test) from WT. Similar results were obtained in independent experiments.



Supplemental Figure S4. LBD20 is a repressor of a subset of JA-regulated defense genes following *Fusarium* infection. Expression of JA-response genes was examined in wild-type (WT) and *lbd20* (A) root or (B) shoot 48 h post mock or *F. oxysporum* (Fo) inoculation. Gene expression levels are relative to the internal control  $\beta$ -actin genes. The average of three biological replicates consisting of pools of thirty to forty plants is shown with SE. *PDF1.2* and *PR4* were induced similarly in both WT and *lbd20* shoots (data not shown).





WΤ

LBD20-OX



LBD20-OX-1LBD20-OX-2LBD20-OX-3LBD20-OX-4WT backgroundIbd20 background

**Supplemental Figure S5. Plants over-expressing** *LBD20* **have altered leaf morphology and fertility.** (A) Range in severity of phenotypes in T1 plants over-expressing *LBD20* under a dual 35S promoter (*LBD20-OX*) compared to wild-type (WT). 26% of T1 plants died due to deformed growth, and 22% produced little or no seed. (B) Leaf morphology of *LBD20-OX* plants in a wild-type (WT) or *Ibd20* background carrying a single copy insertion of the 35S::*LBD20* transgene and used for gene expression and *Fusarium* infection experiments.

Gene	Locus	Forward primer sequence 5'-3'	Reverse primer sequence 5'-3'
	(AGI)		
ACT-8	At1g49240		GAGGATAGCATGTGGAACTGAGAA
(reference)			
ACT-2	At3g18780		GATGGCATGGAGGAAGAGAGAAAC
(reference)			
ACT-7	At5g09810		GAGGAAGAGCATTCCCCTCGTA
(reference)			
ACT-		AGTGGTCGTACAACCGGTATTGT	
universal			
(reference)			
LBD20	At3g03760	GGCTCAAGCTAGGCTCTCTG	ATTGCACCACCGATAACTCC
PDF 1.2	At5g44420	TTTGCTGCTTTCGACGCAC	CGCAAACCCCTGACCATG
Thi2.1	At1g72260	CTCAGCTGATGCTACCAATGAGC	GCTCCATTCACAATTTCACTTGC
VSP2	At5g24770	CCTA AAGA ACG AC AC CG TCA	TCGGTCTTCTCTGTTCCGTA
PR4	At3g04720	TGCTACATCCAAATCCAAGCCT	CGGCAAGTGTTTAAGGGTGAAG
MYC2	At1g32640	TCATACGACGGTTGCCAGAA	AGCAACGTTTACAAGCTTTGATTG

## Supplemental Table S1. RT-Q-PCR primers used in gene expression analyses.