SUPPLEMENTAL TABLE:

Table S1. Primer sequences

Primer Name	**Sequence 5' to 3'**
Primer F1 (PBL13)	ATGGTTTTGTGTTTCCAAGATC
Truncation RV	GTAATCTTTGATGTCTTGGAGAACGG
GABI RV	AAGACTTGTCTCTTTAACTTCC
SALK RV	CCATCAAGATCAAGAAGTTTAACG
pbl13 SALK_203557 RP	GTGACCATGGATGTAATTTGCGGTTC
pbl13 SALK_203557 LP	CTACCTCAAGAAGTCGTCGTCCTC
LbB1.3	ATTTTGCCGATTTCGGAAC
At5g35580 GABI LP	CTCCAGCTGTTAGAGACGTCG
At5g35580 GABI RP	CAAGGCGATGATACACATGTG
GABi_TDNA_o8409	ATATTGACCATCATACTCATTGC
At5g35580CACCF	CACCATGGTTTTGTGTTTCCA
At5g35580 -stop R	GTACCGTTCCCCTCCGGCCTCGTT
PBL13 K111A F	CTCAGCCCGTTGCCGTTGCTCTTCTTGATCTTGATG
PBL13 K111A R	CATCAAGATCAAGAAGAGCAACGGCAACGGGCTGAG
EF-1a_F	CTGGATTCGAGGGAGACAACATG
EF-1a_R	GCACCGTTCCAATACCACCAATC
PR1 qF	CGGAGCTACGCAGAACAACT
PR1 qR	CTCGCTAACCCACATGTTCA
BamHI PBL13 FW	GGATCCATGGTTTTGTGTTTCCAAGATCC
PBL13 XhoI RV	CTCGAGTCAGTACCGTTCCCCTCCG
NdeI RIPK-F	GTTACGCATATGGCGGTGAAGAAG
BamHI RIPK-R with stop	AGGATCCTTAGTACCGTTCCCCAC

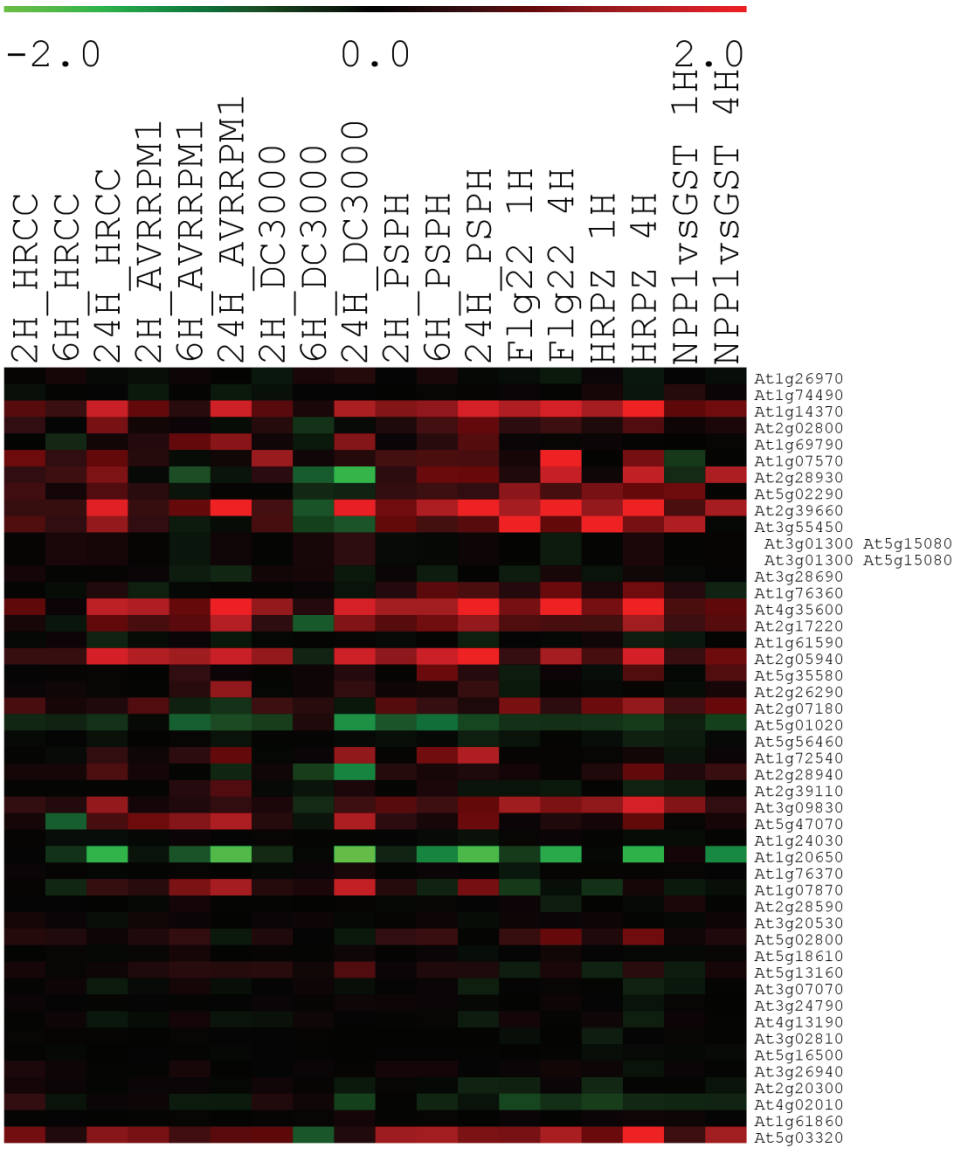

Figure S1. RLCK VIIs expression in response to biotic stresses

Analysis of AtGenExpress Biotic Stress data reveals several RLCK VII members are transcriptionally regulated in response to treatment with pathogens or elicitors. Pathogen treatments include avirulent *Pto* DC3000 *hrcC*-, avirulent Pto DC3000 (AvrRpm1), and the non-host pathogen *Pseudomonas syringae* pv. *phaseolicola*. Elicitor treatments include the bacterial PAMP flg22, the bacterial elicitor HrpZ, and the oomycete elicitor NPP1. Heat map displays the log2 transformed ratio of treatment to control samples. Twenty four genes were found to be at least 1.5 fold up-regulated in one or more conditions. Seven genes were found to be at least 1.5 fold down-regulated in one or more conditions.

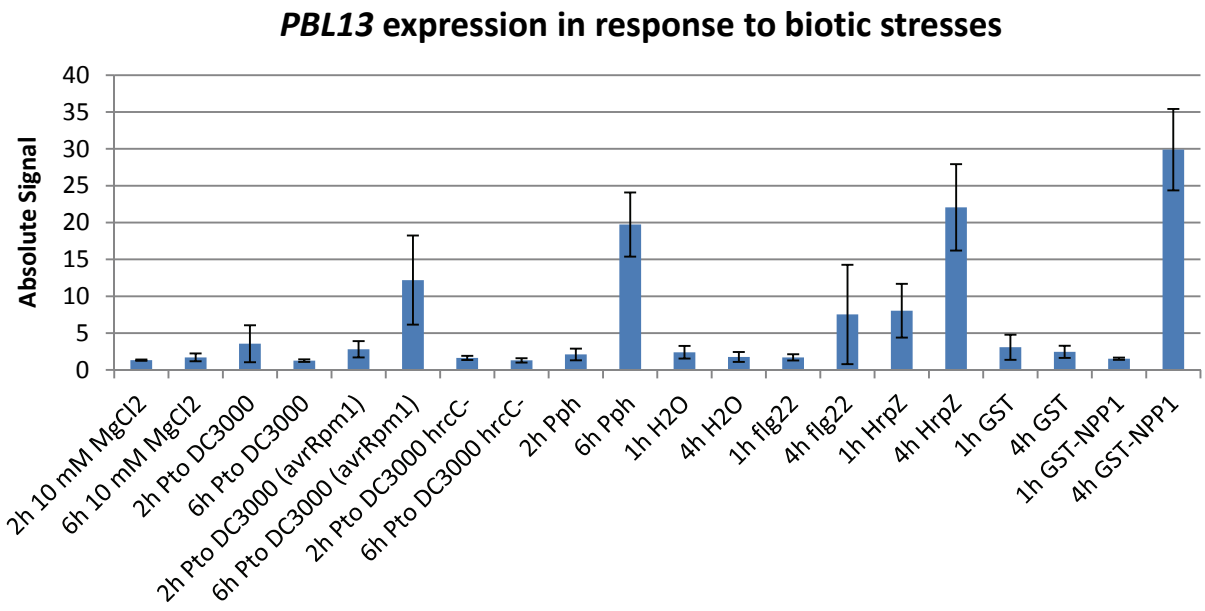

Figure S2. *PBL13* is differentially regulated in response to biotic stresses

PBL13 expression data obtained from the Arabidopsis eFP Browser (Winter et al., 2007). Five-week-old Col-0 plants were syringe infiltrated with bacterial pathogens resuspended in 10 mM $MgCl_2$ or elicitors resuspended in water. *PBL13* is upregulated in response to treatment with avirulent *Pto* DC3000 (AvrRpm1), the non-host pathogen *P. syringae* pv. *phaseolicola*, the bacterial derived elicitor HrpZ, and the oomycete derived elicitor NPP1. Measurement indicates absolute quantification of the signal.

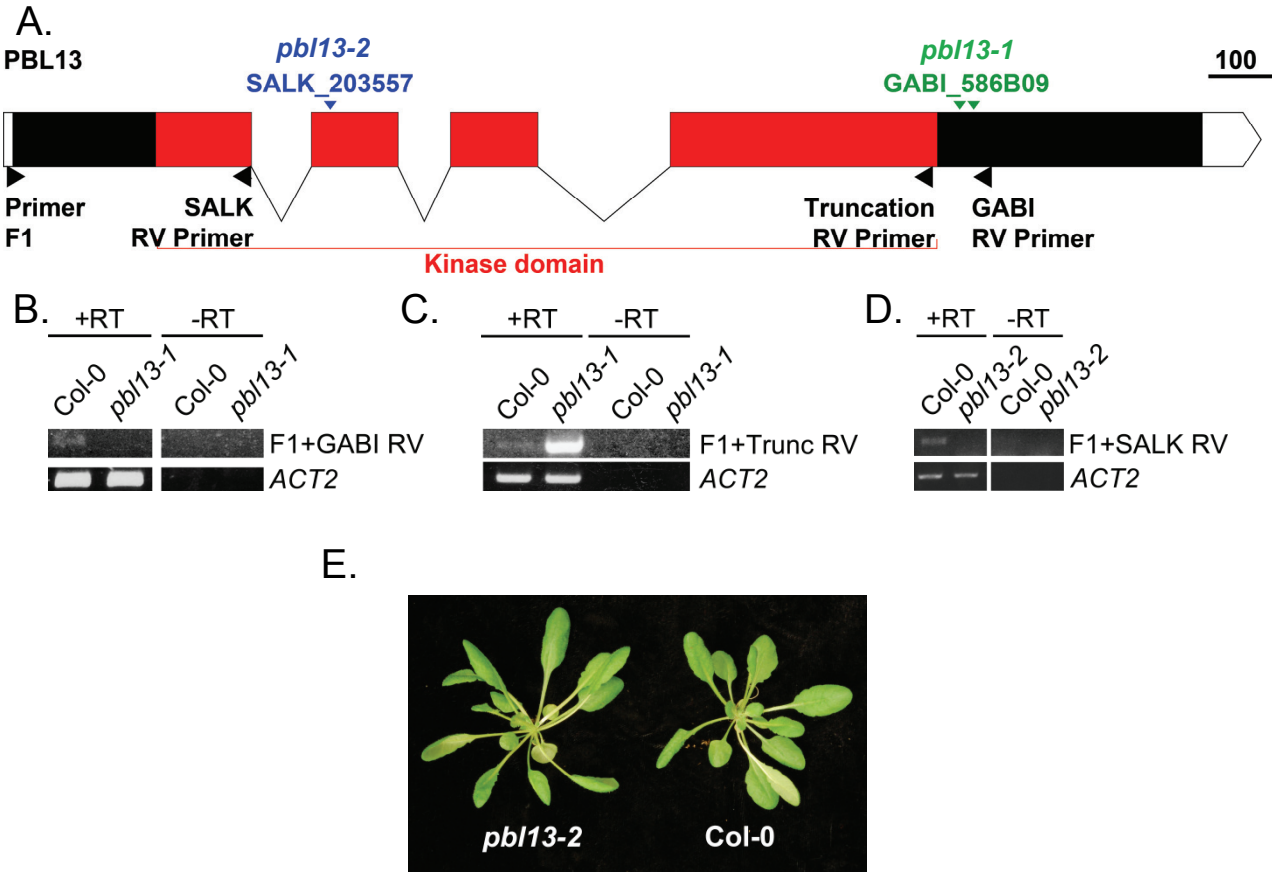

Figure S3. *pbl13-2* is a true knockout and is morphologically similar to wild type Col-0
A, Diagram of T-DNA insertions within *PBL13* and location of primer binding sites. GABI_586B09 has two tandem inverted T-DNA insertions immediately downstream of the kinase coding region. The kinase domain is indicated in red. B, The GABI_586B09 T-DNA insertion line *pbl13-1* does not express full length *PBL13*. RT = reverse transcriptase, *ACT2* = *ACTIN 2* (*AT3G18780*). C, The GABI_586B09 T-DNA insertion line *pbl13-1* expresses a truncated form of *PBL13*. The expression of truncated *PBL13* is higher than wild type *PBL13* in Col-0. D, The SALK_203577 T-DNA insertion line *pbl13-2* is a true knockout. The PBL13 transcript upstream of the T-DNA insertion cannot be detected. E, *pbl13-2* does not exhibit gross morphological differences from wild type Col-0.

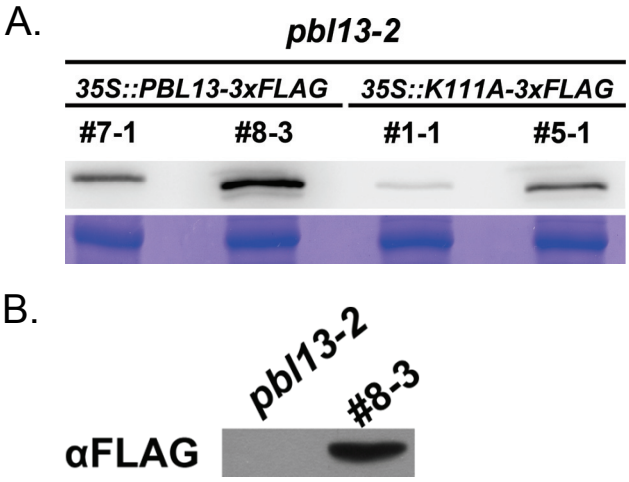

Figure S4. PBL13-3xFLAG expression in transgenic lines
A, Detection of the PBL13-3xFLAG transgene expression in individual T3 complementation lines. Ten micrograms of protein were loaded per lane. Equal protein loading was determined by coomassie staining. PBL13 was detected by anti-FLAG immunoblotting. B, αFLAG-HRP (Sigma) does not detect cross reacting bands in the *pbl13-2* background.

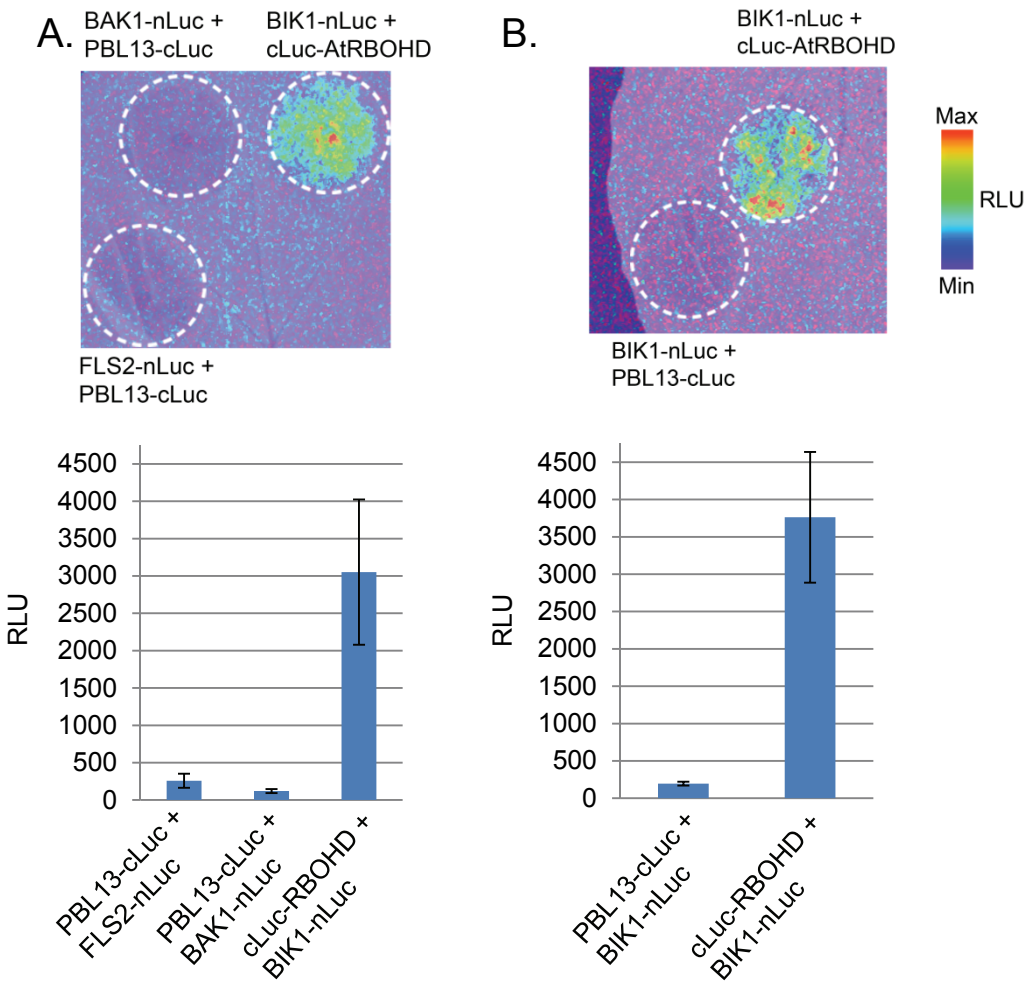

Figure S5. PBL13 does not associate with FLS2, BAK1, or BIK1 by split-luciferase complementation imaging.

PBL13 fails to associate with members of the FLS2 complex in *N. benthamiana*. BIK1 association with RBOHD is used here as a positive control. Constructs were transiently expressed in *N. benthamiana* and luminescence was detected after treatment with 1 mM luminol solution. A, visualization of luminescence with a CCD camera. B, quantification of luminescence using a luminometer. Error bars indicate standard deviation.

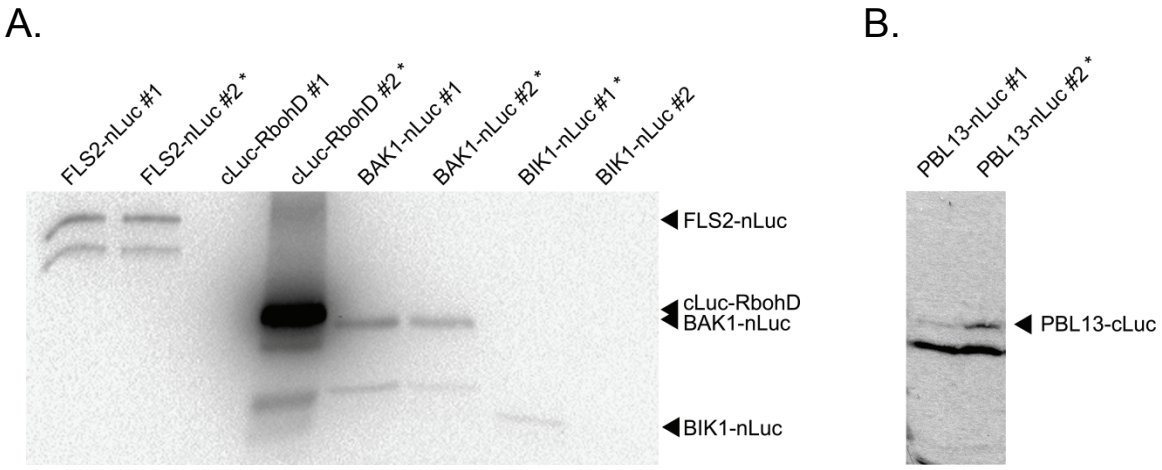

Figure S6. Luciferase-fusion proteins express in Nicotiana benthamiana
A, B, Detection of luciferase-fusion proteins after transient coexpression in *Nicotiana benthamiana*. Asterisks denote *Agrobacterium* clones used in this study. Proteins were detected with anti-luciferase primary antibody (Sigma) and goat anti-rabbit-HRP secondary (BioRad).