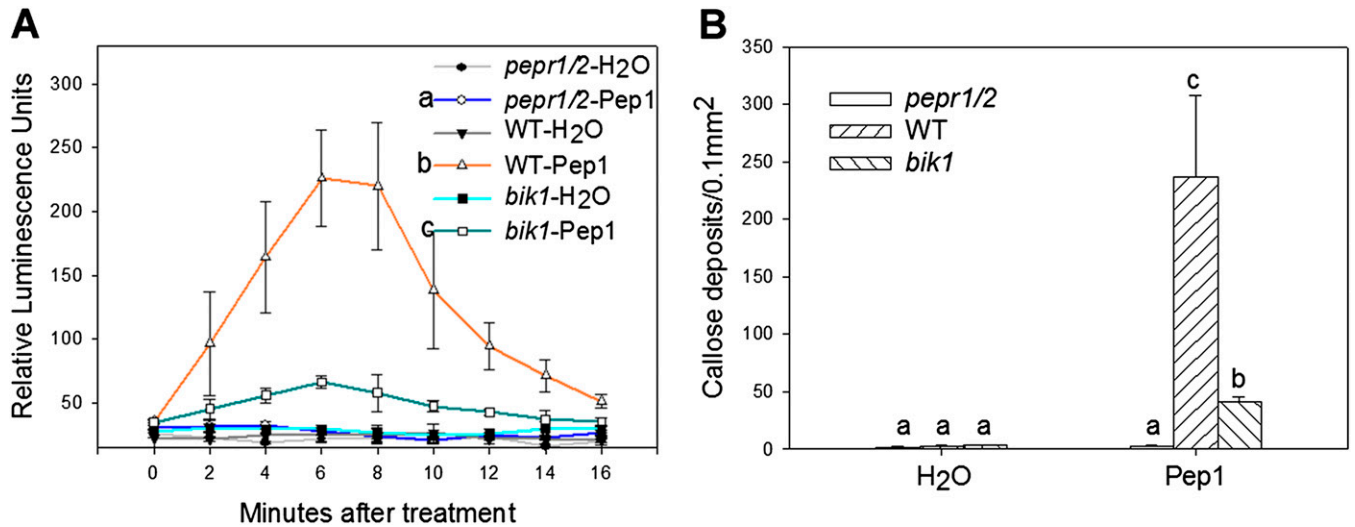
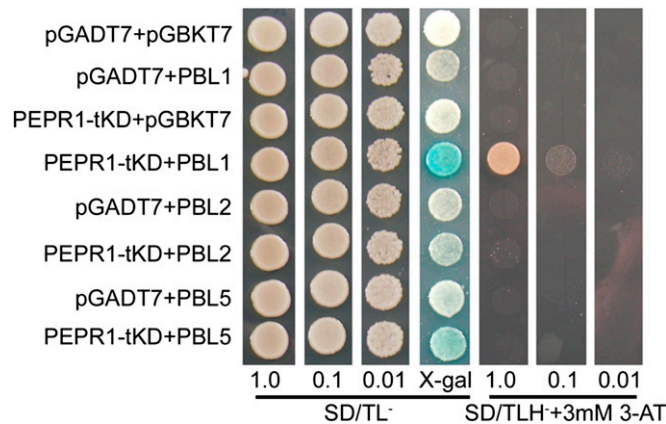


# Supporting Information

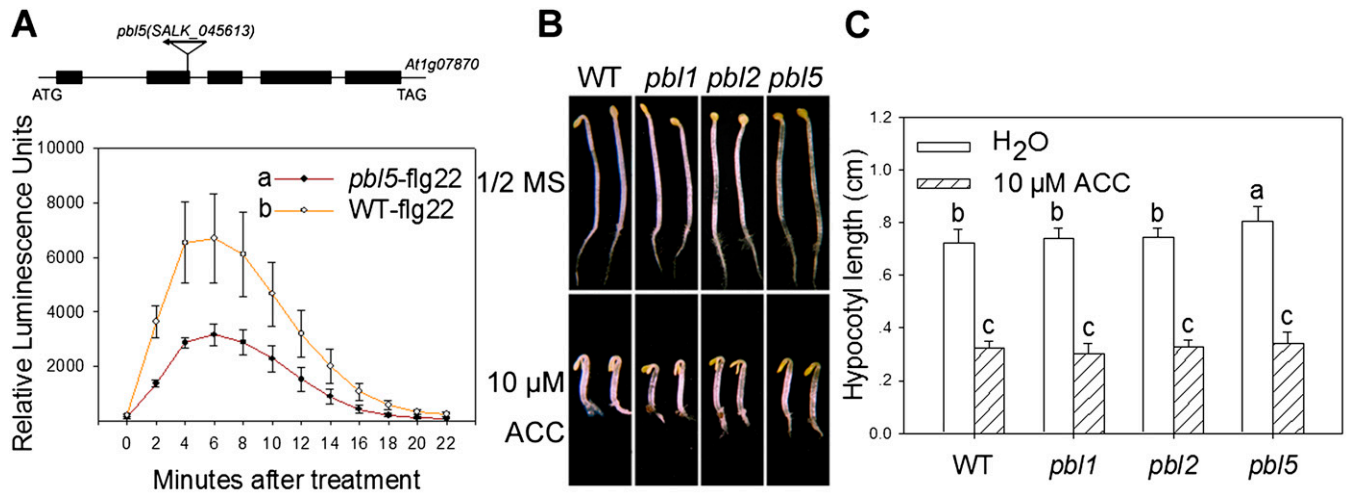
Liu et al. 10.1073/pnas.1215543110



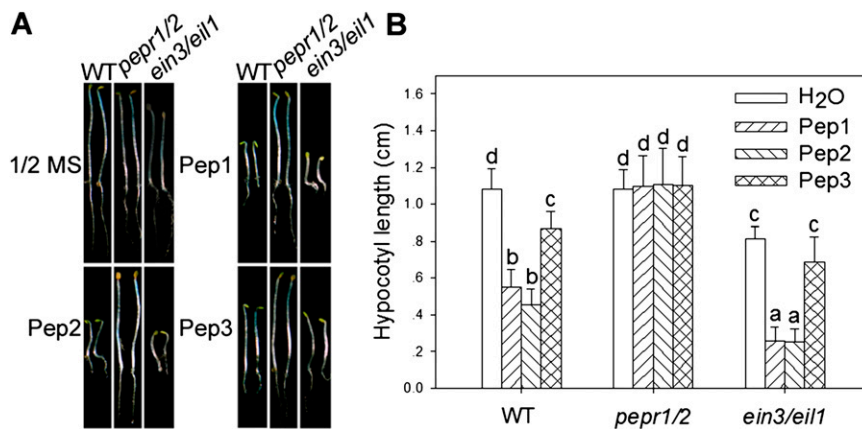
**Fig. S1.** *Botrytis*-induced kinase 1 (*bik1*) is compromised in Pep1-induced defenses. (A) H<sub>2</sub>O<sub>2</sub> production in leaf strips of *bik1*, *pepr1* receptor kinase 1/*pepr1* receptor kinase 2 (*pepr1/2*), and WT treated with 1 μM Pep1. Different letters indicate significant difference (mean ± SD; n ≥ 4; P < 0.01). (B) Callose deposition in *bik1*, *pepr1/pepr2* (*pepr1/2*), and WT leaves treated with 1.5 μM Pep1. Different letters indicate significant difference (mean + SD; n ≥ 16; P < 0.01).



**Fig. S2.** Interaction of PBL5-like proteins (PBLs) with PEPR1. The truncated PEPR1 KD (PEPR1-tKD) prey plasmid was cotransfected into yeast with different PBL bait plasmids and tested for *lacZ* and *His* reporter activity as described Fig. 1A.

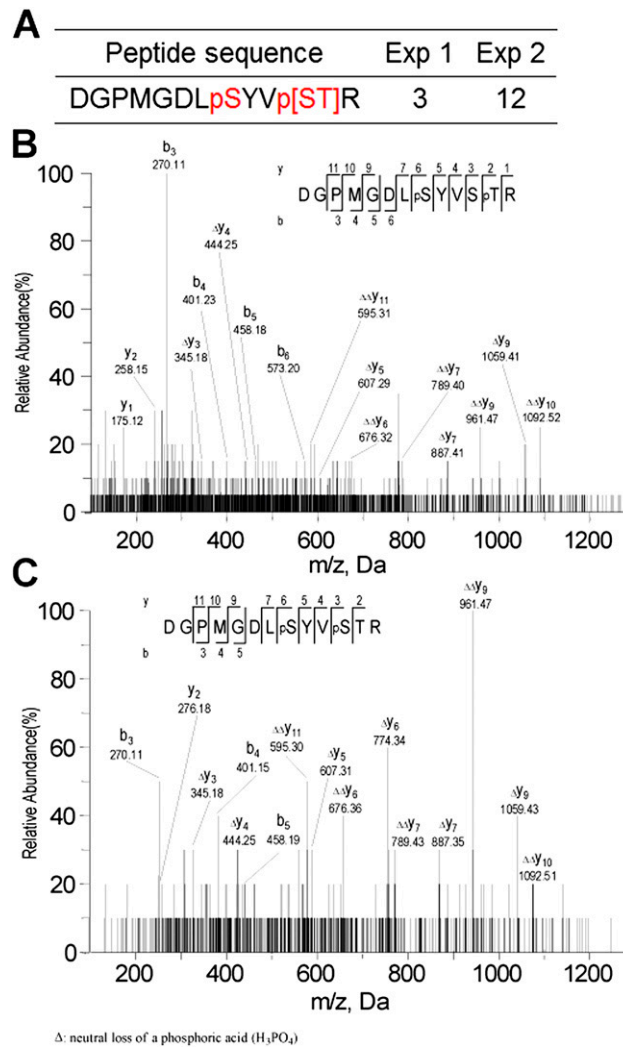


**Fig. 53.** (A) The *pbl5* mutant is compromised in flg22-induced H<sub>2</sub>O<sub>2</sub> accumulation. (Upper) Schematic representation of T-DNA insertion in the *PBL5* gene. Black boxes denote annotated exons from TAIR. The triangle and arrowhead indicate position and direction of T-DNA insertion, respectively. (Lower) *pbl5* plants are compromised in flg22-induced oxidative burst. Different letters denote significant difference (mean  $\pm$  SD;  $n \geq 4$ ;  $P < 0.01$ ). (B and C) *pbl1*, *pbl2*, and *pbl5* mutants display normal triple response. (B) Photograph of 5-d-old WT, *pbl1*, *pbl2*, and *pbl5* etiolated seedlings germinated on 1/2 MS medium with or without 10  $\mu$ M 1-aminocyclopropane-1-carboxylate (ACC). (C) Hypocotyl length of the seedlings (mean  $\pm$  SD;  $n \geq 12$ ;  $P < 0.01$ ).

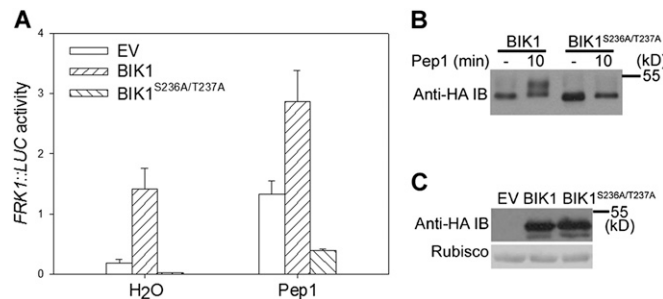


**Fig. 54.** Pep1-3 inhibits hypocotyl and root growth. (A) Photograph of 5-d-old etiolated seedlings grown in the presence of 10  $\mu$ M Pep1, Pep2, and Pep3. (B) Hypocotyl length. Different letters denote significant difference (mean  $\pm$  SD;  $n \geq 17$ ;  $P < 0.01$ ).





**Fig. S8.** Identification of BIK1 amino acids phosphorylated by PEPR1 KD. The GST-BIK1<sup>K105E</sup> protein, coexpressed with PEPR1-KD-His in *Escherichia coli*, was isolated and subjected to LC-MS/MS analysis. (A) Number of phosphorylated peptides corresponding to the activation loop identified in two independent experiments. Parenthesis indicates that the phosphorylation on serine 236 or threonine 237 cannot be easily distinguished. (B and C) Representative collision-induced dissociation (CID) spectra of the phosphopeptide DGPMGDLpSYVp[ST]R. The major b- and y-type ions are indicated in the mass graphs. Δ, neutral loss of a phosphoric acid.



**Fig. S9.** Serine 236 and threonine 237 are required for Pep1-induced BIK1 phosphorylation and signaling. (A) Ala substitution of Ser-236 and Thr-237 in BIK1 blocks Pep1-induced *FRK1* reporter expression in protoplasts. Empty vector (EV), WT BIK1, and BIK1<sup>S236A/T237A</sup> plasmids were transfected into WT protoplasts along with *35S::R-LUC* and *FRK1::LUC*, treated with H<sub>2</sub>O or 1 μM Pep1 for 3 h, and the *FRK1::LUC* activity was determined. (B) The BIK1<sup>S236A/T237A</sup> mutant is not phosphorylated upon Pep1 treatment. (C) BIK1 and BIK1<sup>S236A/T237A</sup> protein accumulation in A.