Supplementary Table 1. Primers used for the PCR and qRT-PCR in this study

Primers	Primer sequences (5'-3')	Tm (°C)	GC (%)	Reference
phlG F'	ATGGAAGCGCGCGTAATGACACCTTTCACC	66.8	53.33	This study
phlG R'	CGCCGCGCCGCTGAACTGTGC	67.6	76.19	This study
*phlG*_qRT F'	GTCCGATGGCCTATGTGCAA	57.5	55.0	This study
*phlG*_qRT R'	GGGAACCACAGGGTATAGCG	59.5	60.0	This study
WRKY11 F'	CCACCGTCTAGTGTAACACTCGAT	60.4	50.0	Journot-Catalino et al. (2006)
WRKY11 R'	TGCAACGGAGCAGAAGCAAGGAA	60.2	52.17	Journot-Catalino et al. (2006)
LOX2 F'	GTCCAAACCTCAGAAGACGAT	55.9	47.62	Journot-Catalino et al. (2006)
LOX2 R'	CACCCATGACTCACATGTAA	53.4	45.0	Journot-Catalino et al. (2006)
EDS5 F'	CATCAGGTGATGGCTCAGAC	57.5	55.0	Wang et al. (2010)
EDS5 R'	ACTAATCCAAGCGTGGCTCC	57.5	55.0	Wang et al. (2010)
PDF 1.2 F'	TCATGGCTAAGTTTGCTTCC	53.4	45.0	Journot-Catalino et al. (2006)
PDF 1.2 R'	AATACACACGATTTAGCACC	51.3	40.0	Journot-Catalino et al. (2006)
WRKY70 F'	CGTCATCATGGTTCGTCCA	54.9	52.63	Journot-Catalino et al. (2006)
WRKY70 R'	CCACCTCCAAACACCATGAGAT	58.1	50.0	Journot-Catalino et al. (2006)
PR2 F'	GGAGCTACGCAGAACAACTAAGA	58.4	47.83	Journot-Catalino et al. (2006)
PR2 R'	CCCACGAGGATCATAGTTGCAACTGA	62.3	50.0	Journot-Catalino et al. (2006)
PR1 F'	CGGTACATCAACGTTGGAA	52.7	47.37	Journot-Catalino et al. (2006)
PR1 R'	GCGTAGTCTAGATGGATGTT	53.4	45.0	Journot-Catalino et al. (2006)
UBC F'	CTGCGACTCAGGGAATCTTCTAA	58.4	47.83	Czechowski et al. (2005)
UBC R'	TTGTGCCATTGAATTGAACCC	53.9	42.86	Czechowski et al. (2005)
SAND F'	AACTCTATGCAGCATTTGATCCACT	57.3	40.0	Czechowski et al. (2005)
SAND R'	TGATTGCATATCTTTATCGCCATC	55.3	37.5	Czechowski et al. (2005)

qRT-PCR, quantitative real time polymerase chain reaction.

References

Czechowski, T., Stitt, M., Altmann, T., Udvardi, M. K. and Scheible, W.-R. 2005. Genome-wide identification and testing of superior reference genes for transcript normalization in Arabidopsis. *Plant Physiol.* 139:5-17.

Journot-Catalino, N., Somssich, I. E., Roby, D. and Kroj, T. 2006. The transcription factors WRKY11 and WRKY17 act as negative regulators of basal resistance in *Arabidopsis thaliana. Plant Cell* 18:3289-3302.

Wang, C., Gao, F., Wu, J., Dai, J., Wei, C. and Li, Y. 2010. Arabidopsis putative deacetylase AtSRT2 regulates basal defense by suppressing PAD4, EDS5 and SID2 expression. *Plant Cell Physiol.* 51:1291-1299.

Supplementary Table 2. Confirmation of DAPG sensitivity in *Arabidopsis thaliana* Col-0 plants

DAPG	Germination (%)									
	Day 1	Day 2	Day 3	Day 4	Day 5	Day 6	Day 7	Day 8	Day 9	Day 10
Control	0 a	100 a	100 a	100 a	100 a	100 a	100 a	100 a	100 a	100 a
20 μM	0 a	11.32 b	97.16 a	98.74 a	100 a	100 a	100 a	100 a	100 a	100 a
40 μM	0 a	0 c	6.52 b	78.35 b	95.87 b	97.93 b	97.93 b	97.93 a	97.93 b	97.93 b
60 μM	0 a	0 c	0 c	7.84 c	30.81 c	43.13 c	43.13 c	55.46 b	59.66 c	61.62 c
80 μM	0 a	0 c	0 c	0 d	0 d	0 d	0 d	0 c	0 d	0 d
100 μM	0 a	0 c	0 c	0 d	0 d	0 d	0 d	0 c	0 d	0 d

Statistical analysis was performed with Tukey's HSD test ($P < 0.05$): differing letters within columns indicate mean values significantly different from one another among the 2,4-diacetylphloroglucinol (DAPG) groups.

Supplementary Table 3. The *phlG* transgenic *Arabidopsis thaliana* (T_1) selection

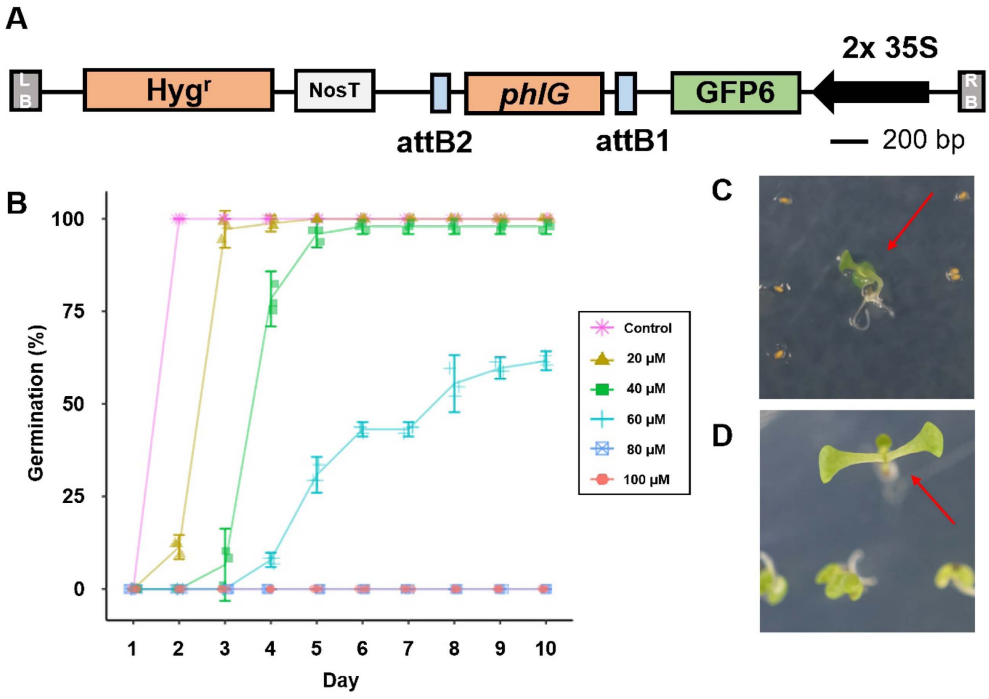
Selective agent	Concentration (μM)	Seeds sowed	No. of resistant seedlings	Total
Hygromycin	57	4,100	7	7
DAPG	80	2,000	19	26
	100	2,000	7	

DAPG, 2,4-diacetylphloroglucinol.

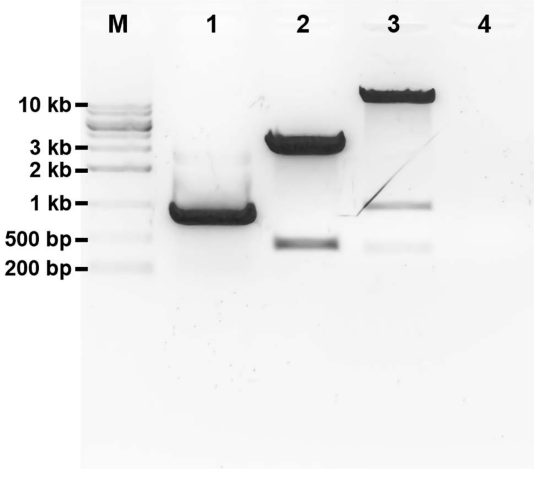
Supplementary Table 4. The *phlG* transgenic *Arabidopsis thaliana* (T_2) segregation test

Line name	DAPG media (100 μM)		Hygromycin media (57 μM)	
	Resistant seeds	Non-resistant seeds	Resistant seeds	Non-resistant seeds
WT	0	186	0	151
D16	144	45	178	58
H2	132	50	90	31
H3	120	32	0	142
H4	26	120	0	140
Other lines	0	All seeds	0	All seeds

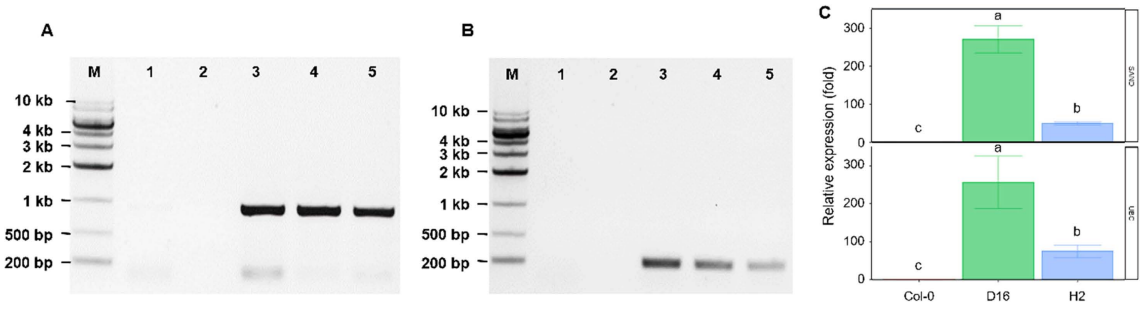
The T_2 generation of *Arabidopsis* independent lines, selected using the *phlG/HptII* system, were sown and germinated in 2,4-diacetylphloroglucinol (DAPG, 100 μM) or hygromycin (57 μM) media. After 10 days of germination, the number of resistant and non-resistant seedlings were determined and evaluated with the chi-square test ($P < 0.05$).



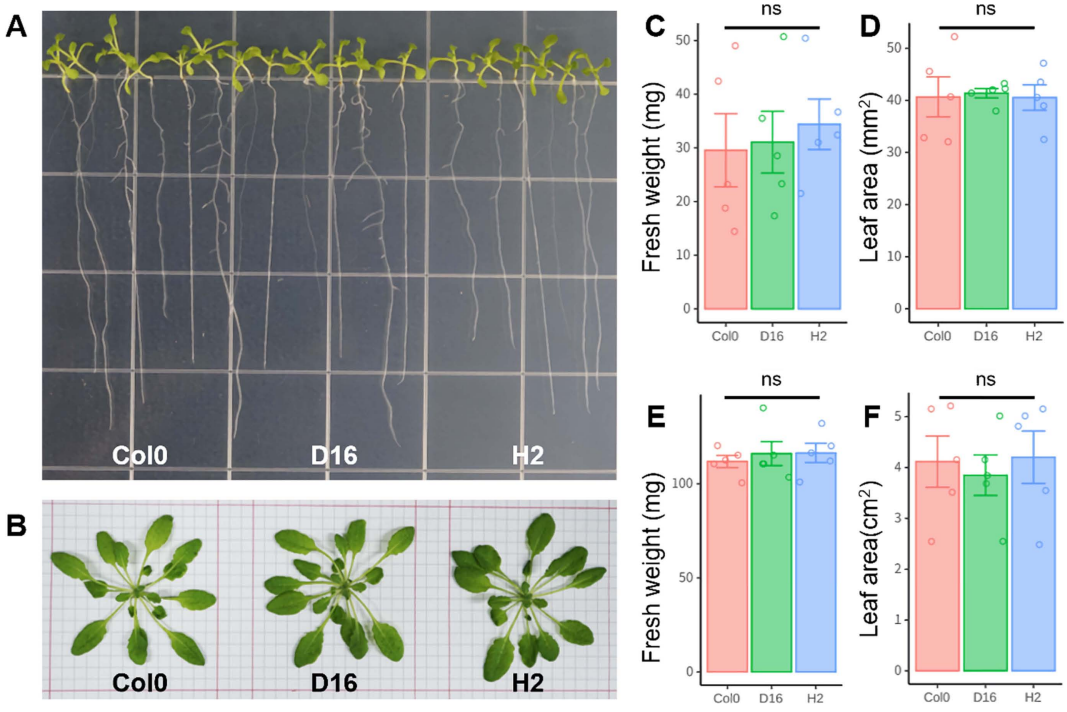
Supplementary Fig. 1. Screening of the *phlG* transgenic plants. (A) Physical map of the *phlG* gene containing the binary vector. (B) Identification of 2,4-diacetylphloroglucinol (DAPG) sensitivity in *Arabidopsis thaliana* Col-0. The number of ruptured seeds per total was confirmed by using MS agar media containing various DAPG concentrations (20, 40, 60, 80, or 100 μM) for 10 days. Values are the mean and the bars are the standard deviation from three biological replicates. Statistical analysis was conducted using Tukey's honestly significant difference test ($P < 0.05$), shown in Supplementary Table 2. (C) Germination of *phlG* transgenic Arabidopsis (T_1) in Murashige and Skoog (MS) agar medium containing DAPG (100 μM). (D) Selection of *phlG* transgenic Arabidopsis (T_1) in hygromycin (57 μM) MS medium.



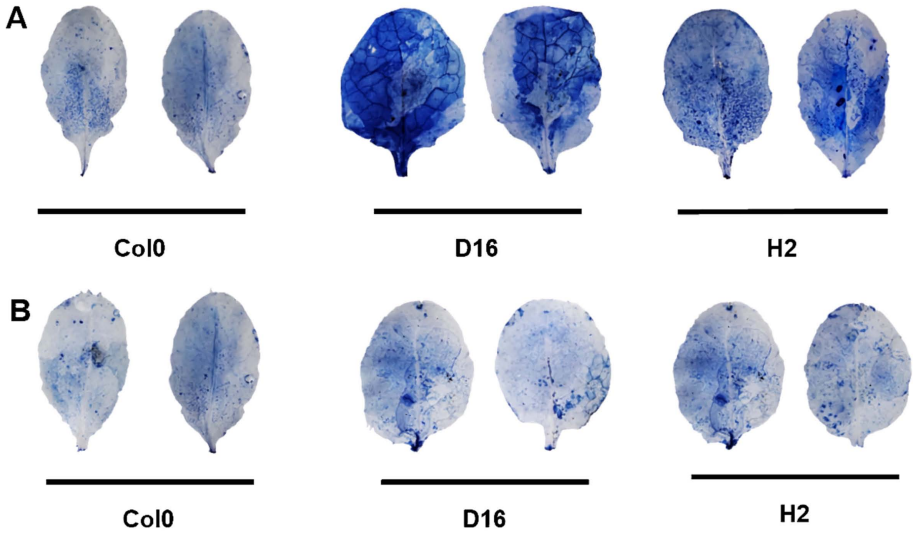
Supplementary Fig. 2. Cloning *phlG* in the Gateway vector system. Lane M, the 1-kb DNA ladder; lane 1, PCR product of *phlG* from *Pseudomonas fluorescens* Q2-87; lane 2, product of restriction digestion by *Eco*RV to the entry vector; lane 3, product of restriction digestion by *Eco*RI to the binary vector; lane 4, the negative control (ddH_2O). The electrophoresis gel contained 1% agarose.



Supplementary Fig. 3. Confirmation of the *phlG* gene in transgenic plants. (A) *phlG* gene detection by PCR using the genomic DNA sample. Lane 1, WT (Col-0); lane 2, ddH_2O; lane 3, genomic DNA of *Pseudomonas flourescens* Q2-87; lanes 4 and 5, D16, H2 genomic DNA. (B) The *phlG* gene detection by qRT-PCR with cDNA. Line numbers are presented as in (A). (C) Relative expression of the *phlG* gene compared to the housekeeping genes (by qRT-PCR) *ubc* (Ubiquitin C) and *sand* (SAND family). Total RNA was isolated from 10-day-old wild-type plants and the *phlG* transgenic Arabidopsis seedlings (D16, H2). Bar with different letters are significantly different ($P < 0.05$) according to Duncan's new multiple range test based on ANOVA analysis. Values are the mean and the bar are the standard deviation from three biological replicates.



Supplementary Fig. 4. Plant phenotype identification of *Arabidopsis thaliana* Col0 and the *phlG* transgenic line (T_3). (A) Fifteen days after seedling (15 days). (B) Twenty-one days after seedling (21 days). (C) Fresh weight of Col-0, D16, and H2 (15 days). (D) Primary root lengths of Col-0, D16, and H2 (15 days). (E) Fresh weight of Col-0, D16, and H2 (21 days). (F) Leaf area of Col-0, D16, and H2 (21 days). Statistical analysis was performed using Tukey's HSD test ($P < 0.05$); 'ns' denotes no statistical significance. The bar represents the standard error from five biological replicates.



Supplementary Fig. 5. Trypan blue (10 mg/ml) staining of DAPG-primed *Arabidopsis thaliana* Col-0, D16, and H2 plants. (A) *Botrytis cinerea* (1×10^5 cfu/ml). (B) *Pst* DC3000 (1×10^8 cfu/ml) were applied to 21-day-old plants. Each photograph shown was taken at 4 days post-inoculation (4 dpi) with the pathogen(s).