Table S 1

Comparison of priming efficiency of different generations of Ws and *ibs1* lines in response to inoculation with virulent *Pst* (based on data shown in Fig. 3A, B).

Lines	Priming-factor* in water-treated plants	Priming-factor* in response to BABA treatment
WsH / WsB	1.4	1.9
WsB / WsBB	1.4	1.6
WsBH / WsB	1.2	1.7
ibs1H / ibs1B	1.2	1.3
ibs1B / ibs1BB	1.1	1.1
*ibs1*BH / *ibs1*B	1.3	1.3

*The priming-factor was calculated by dividing the bacterial titer in plants of a given generation with the titer in their respective direct descendants. Bacterial titers were determined at 72 h post inoculation.

Table S2: Ct values for the trans-generational lines and treatments at time -48 h

PR1

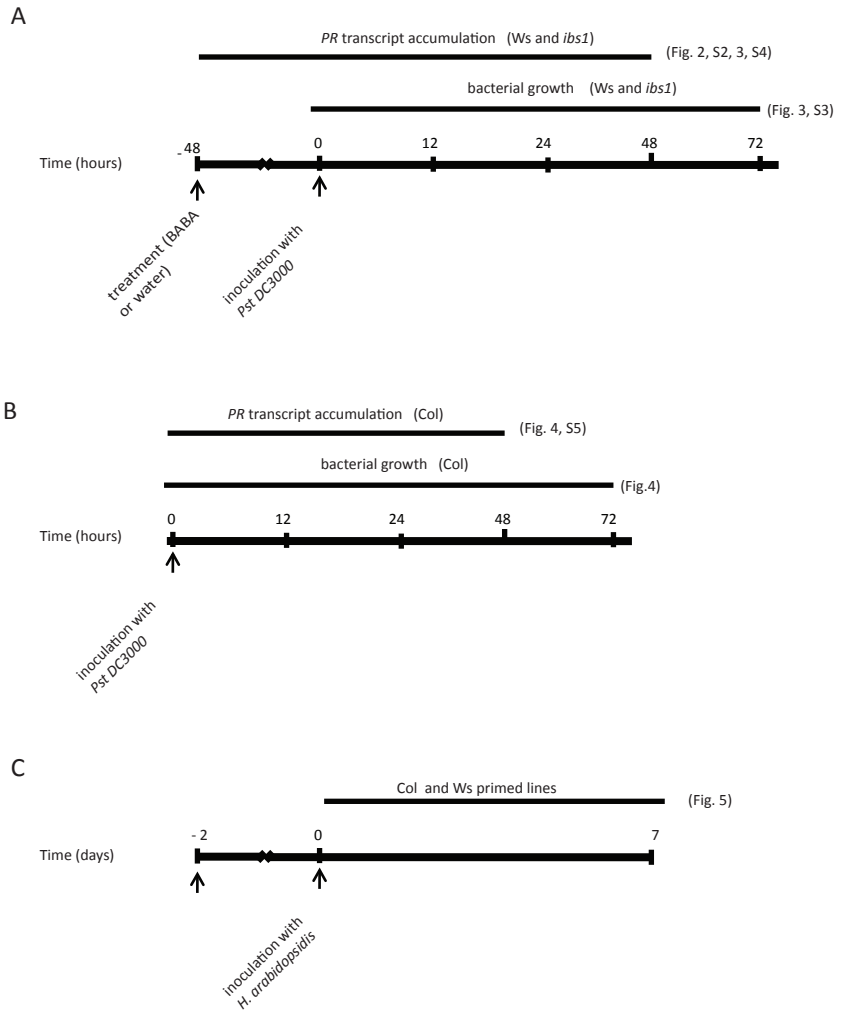
line/ treatment	Ct	± SD	line/ treatment	Ct	± SD
Ws BABA	19.20	0.490	*ibs1* BABA	18.41	1.10
WsB BABA	18.91	0.102	*ibs1*B BABA	17.97	0.21
WsBB BABA	17.88	0.015	*ibs1*BB BABA	18.45	1.13
WsBH BABA	19.42	0.028	*ibs1*BH BABA	19.67	0.14
Ws water	22.46	0.028	*ibs1* water	24.79	0.048
WsB water	25.43	0.007	*ibs1*B water	21.91	0.078
WsBB water	25.58	0.070	*ibs1*BB water	22.05	0.086
WsBH water	24.47	0.021	*ibs1*BH water	24.52	0.021

PR2

line/ treatment			line/ treatment		
Ws BABA	19.71	0.134	*ibs1* BABA	18.41	0.110
WsB BABA	19.30	0.093	*ibs1*B BABA	17.97	0.021
WsBB BABA	18.71	0.042	*ibs1*BB BABA	18.45	0.113
WsBH BABA	19.29	0.163	*ibs1*BH BABA	19.67	0.014
Ws water	25.40	0.078	*ibs1* water	24.79	0.049
WsB water	24.63	0.049	*ibs1*B water	21.99	0.078
WsBB water	24.68	0.255	*ibs1*BB water	22.05	0.096
WsBH water	25.44	0.064	*ibs1*BH water	24.52	0.021

PR5

line/ treatment			line/ treatment		
Ws BABA	20.11	0.021	*ibs1* BABA	24.60	0.049
WsB BABA	19.13	0.092	*ibs1*B BABA	24.79	0.064
WsBB BABA	19.47	0.021	*ibs1*BB BABA	23.96	0.015
WsBH BABA	19.94	0.021	*ibs1*BH BABA	23.32	0.074
Ws water	24.11	0.049	*ibs1* water	26.07	0.156
WsB water	25.19	0.004	*ibs1*B water	25.23	0.219
WsBB water	24.38	0.020	*ibs1*BB water	25.62	0.014
WsBH water	23.58	0.060	*ibs1*BH water	25.67	0.028


A
PR transcript accumulation (Ws and ibs1)
(Fig. 2, S2, 3, S4)
bacterial growth (Ws and ibs1)
(Fig. 3, S3)
Time (hours)
-48
0
12
24
48
72
treatment (BABA or water)
inoculation with Pst DC3000
B
PR transcript accumulation (Col)
(Fig. 4, S5)
bacterial growth (Col)
(Fig.4)
Time (hours)
0
12
24
48
72
inoculation with Pst DC3000
C
Col and Ws primed lines
(Fig. 5)
Time (days)
- 2
0
7
inoculation with H.arabidopsidis

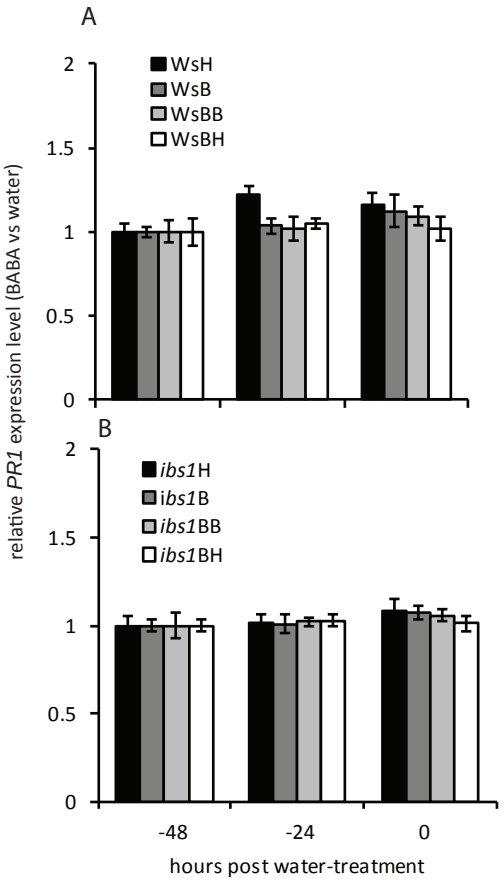
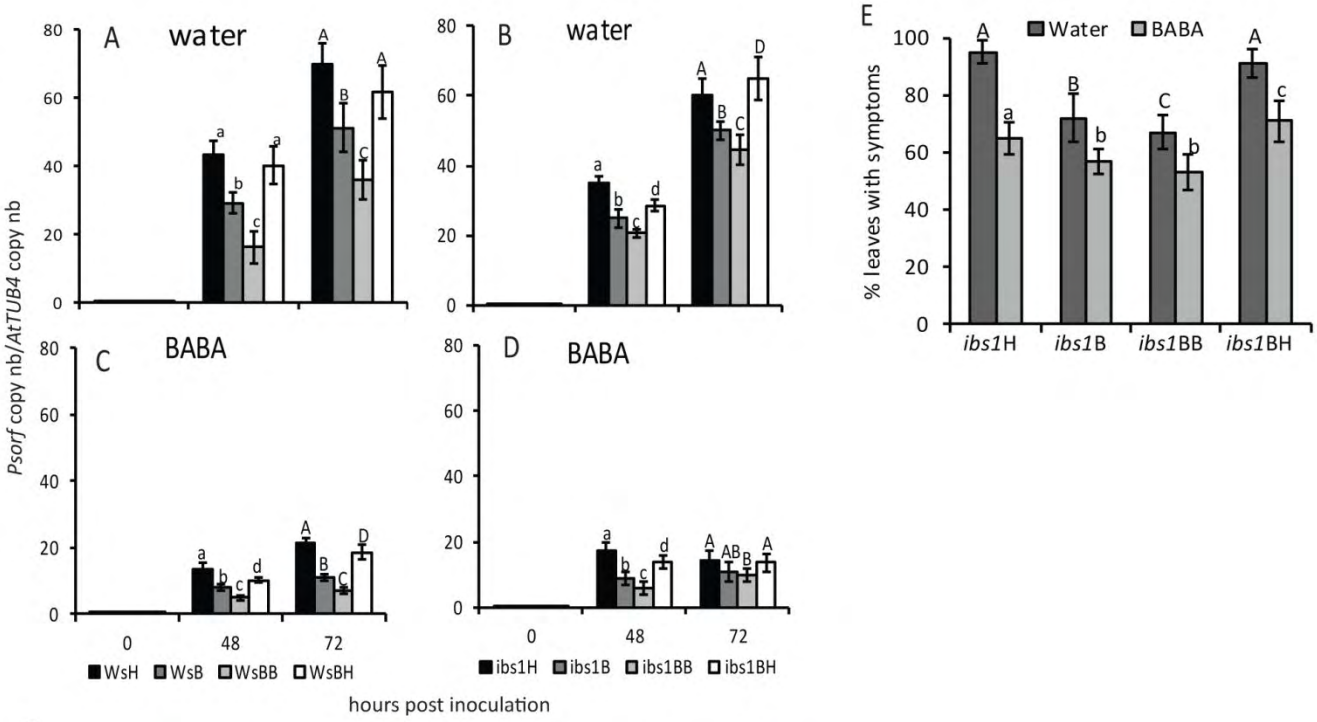
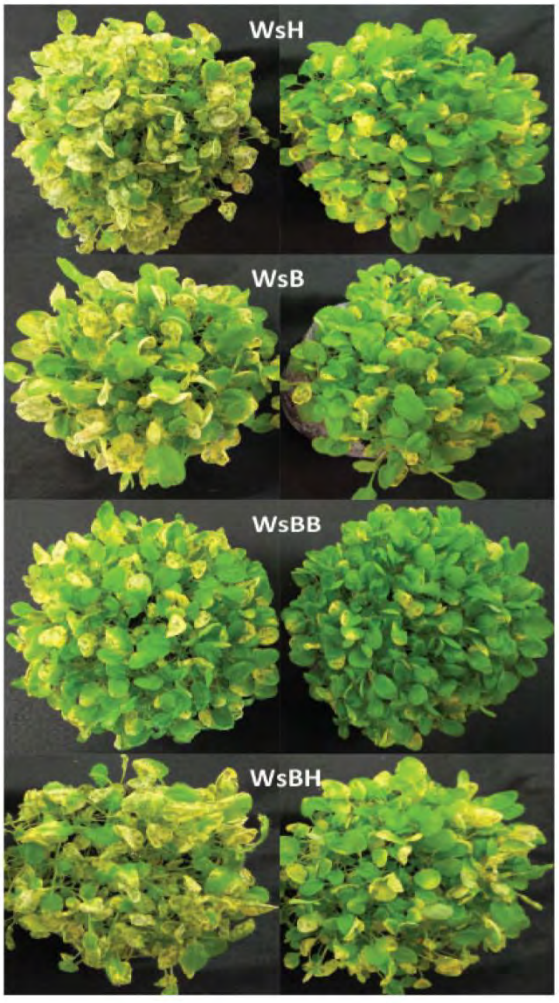


Figure S2. *PR1* expression levels in Ws-0 and *ibs1* lines control-treated with water. Four-wk-old plants were treated with water and *PR1* expression was analyzed by qRT-PCR. A, *PR1* expression in Ws-0 lines. B, *PR1* expression in *ibs1* lines. Expression was normalized to the values of WsH and *ibs1*H, respectively, at -48 h. Values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.


A water
B water
C BABA
D BABA
Psorf copy nb/AtTUB4 copy nb
0
20
40
60
80
0
48
72
hours post inoculation
WsH
WsB
WsBB
WsBH
ibs1H
ibs1B
ibs1BB
ibs1BH
E
Water
BABA
% leaves with symptoms
0
20
40
60
80
100
ibs1H
ibs1B
ibs1BB
ibs1BH


F
WsH
WsB
WsBB
WsBH
water
BABA

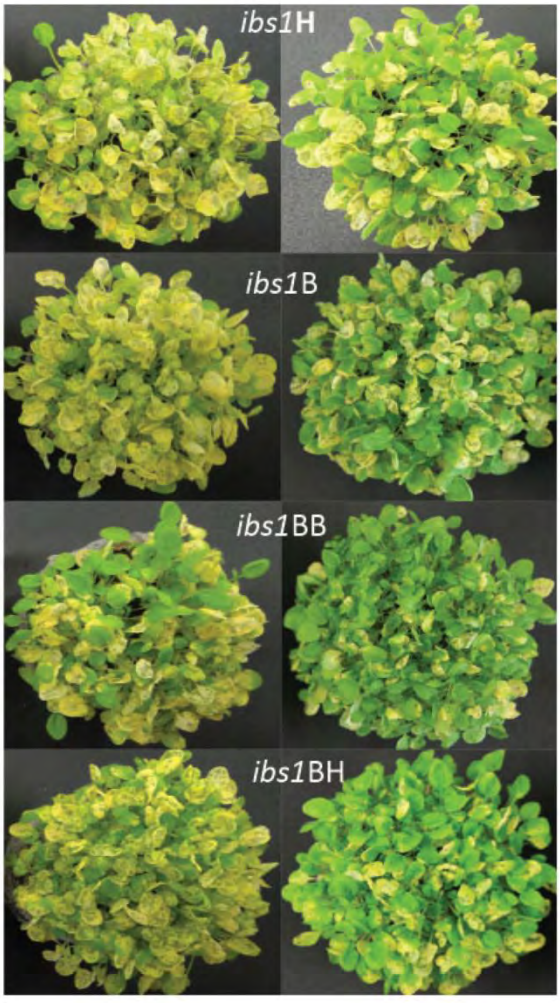

G
ibs1H
ibs1B
ibs1BB
ibs1BH
water
BABA

Figure S3. Descendants of BABA-treated Ws-0 plants are more resistant to virulent *Pseudomonas syringae*. Three-wk-old plants were treated with BABA (25 ppm final concentration in the soil) or water 2 days prior to inoculation with *Pst* DC3000 (OD_{600} = 0.08). A, Growth of *Pst* DC3000 in the water-treated Ws-0 lines (WsH, WsB, WsBB and WsBH).B, *ibs1* lines (*ibs1*H, *ibs1*B, *ibs1*BB and *ibs1*BH) at 0, 48 and 72pih. C, Growth of *Pst* DC3000 in BABA-treated Ws-0 lines compared to that in D, *ibs1* lines at 0, 48 and 72 hpi. Bacterial growth was quantified by qRT-PCR as transcript levels of *Psorf* normalized to the transcript level of the Arabidopsis gene *AtTUB4*. Capital letters indicate statistically significant bacterial growth at 72 h (ANOVA, Student-Newman-Keuls, n = 3, $P < 0.05$). Small letters indicate statistically significant bacterial growth at 48 h (ANOVA, Student-Newman-Keuls, n = 3, $P < 0.05$). E, Disease response of the BABA- or water-treated of *ibs1* lines at 5 days post-inoculation. Small and capital letters above error bars indicate statistically significant differences in the percentage of leaves with symptoms in BABA- and water-treated lines, respectively (ANOVA, Student-Newman-Keuls, n = 30, $P < 0.001$). F, Visible disease phenotype in the Ws-0 lines. G, Visible disease phenotype in the *ibs1* lines.

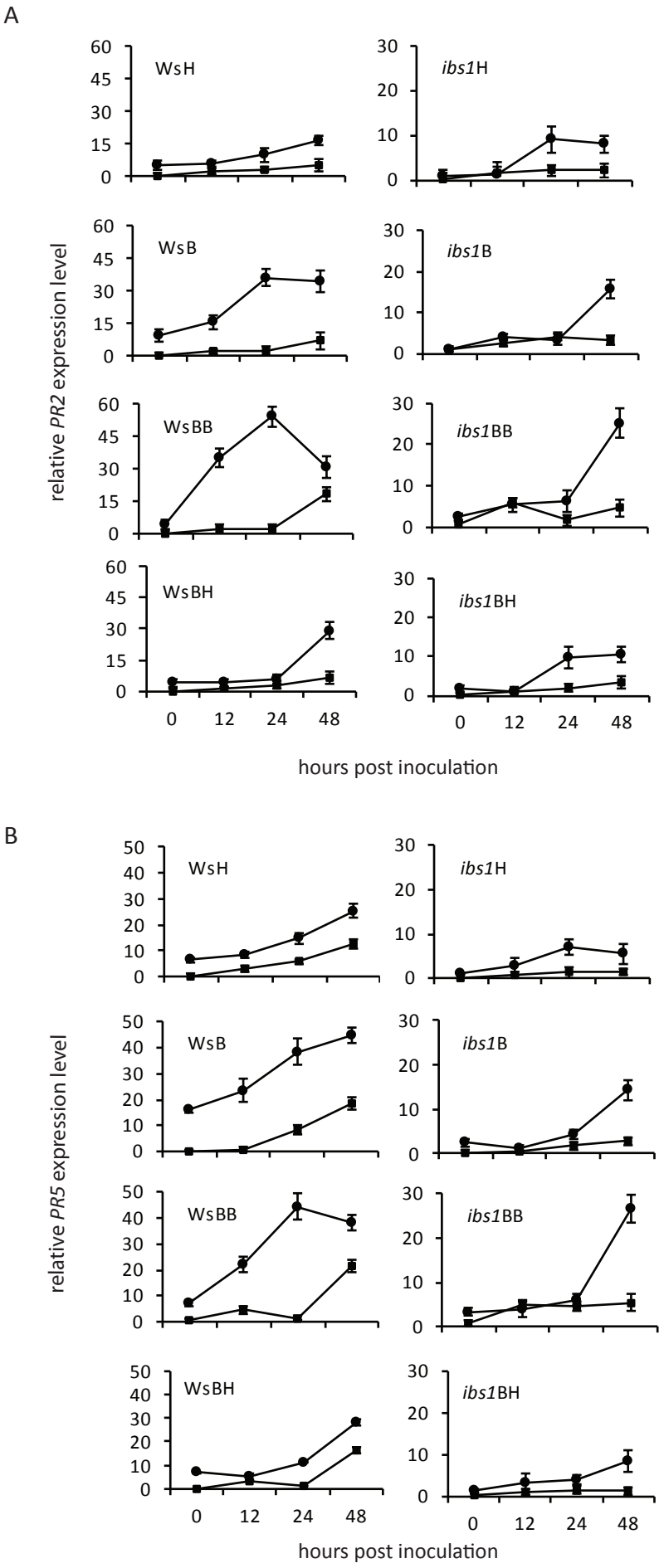


Figure S4. qRT-PCR analysis of *PR2* and *PR5* transcript levels in Ws -0 and *ibs1* lines upon inoculation with virulent *Pst*. Expression levels of PR2 (A) and PR5 (B) in BABA -treated (circles) and water -treated (squares) Ws -0 and *ibs1* lines. Expression was normalized to the corresponding sample treated with water at 0 h. The values represent means +/- SD of three replicates. Similar results were obtained in three indepe ndent experiments.

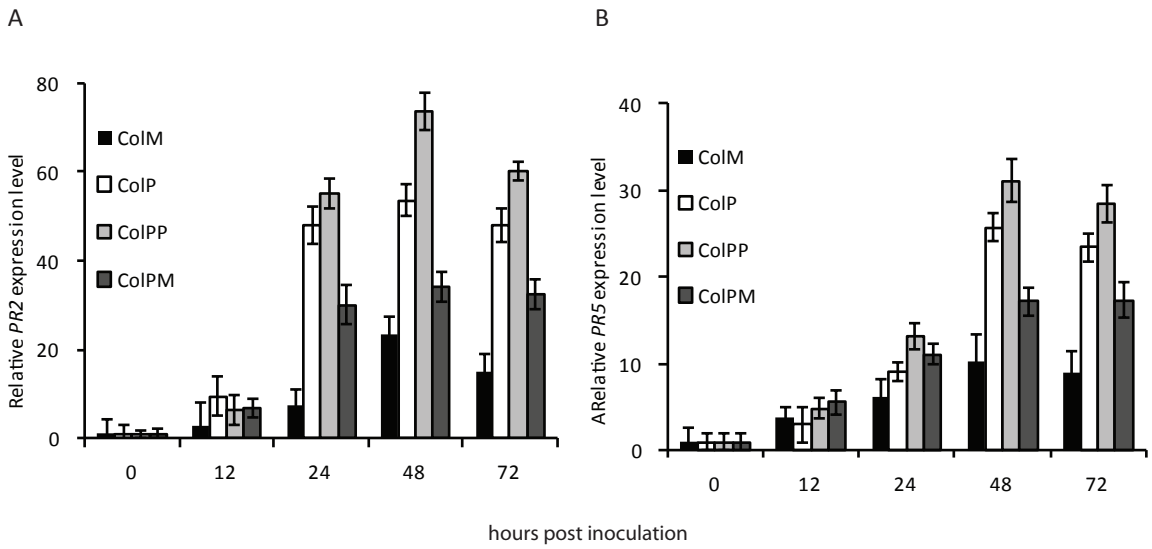


Figure S5. qRT-PCR analysis of *PR2* and *PR5* transcript levels in Col -0 lines upon inoculation with virulent *Pst*. Expression levels of *PR2* (A) and *PR5* (B). Expression was normalized to the corresponding sample at 0 h. The values represen t means +/- SD of three replicates. Similar results were obtained in three independent experiments.

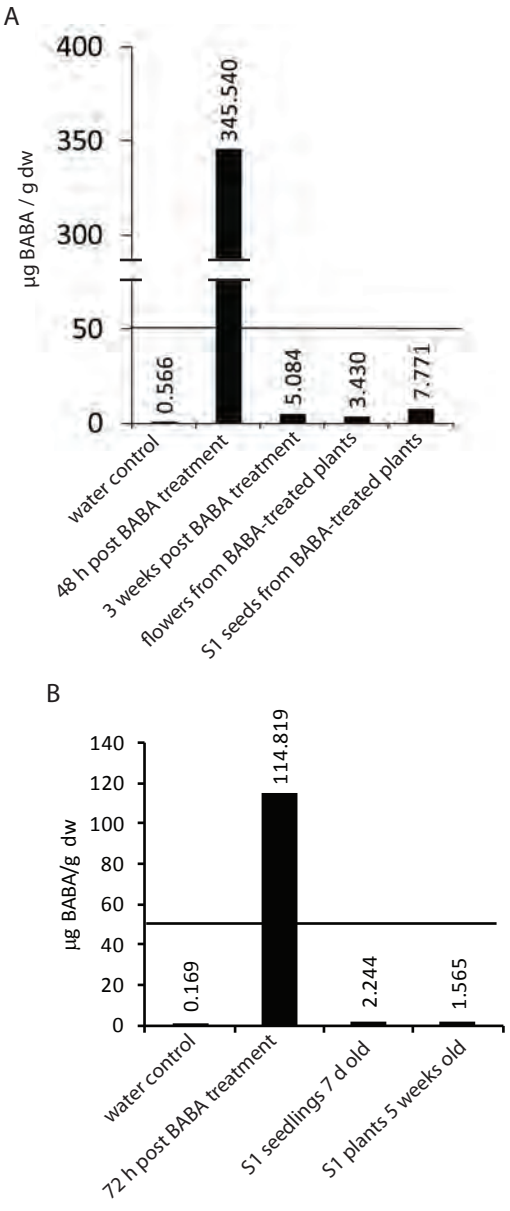
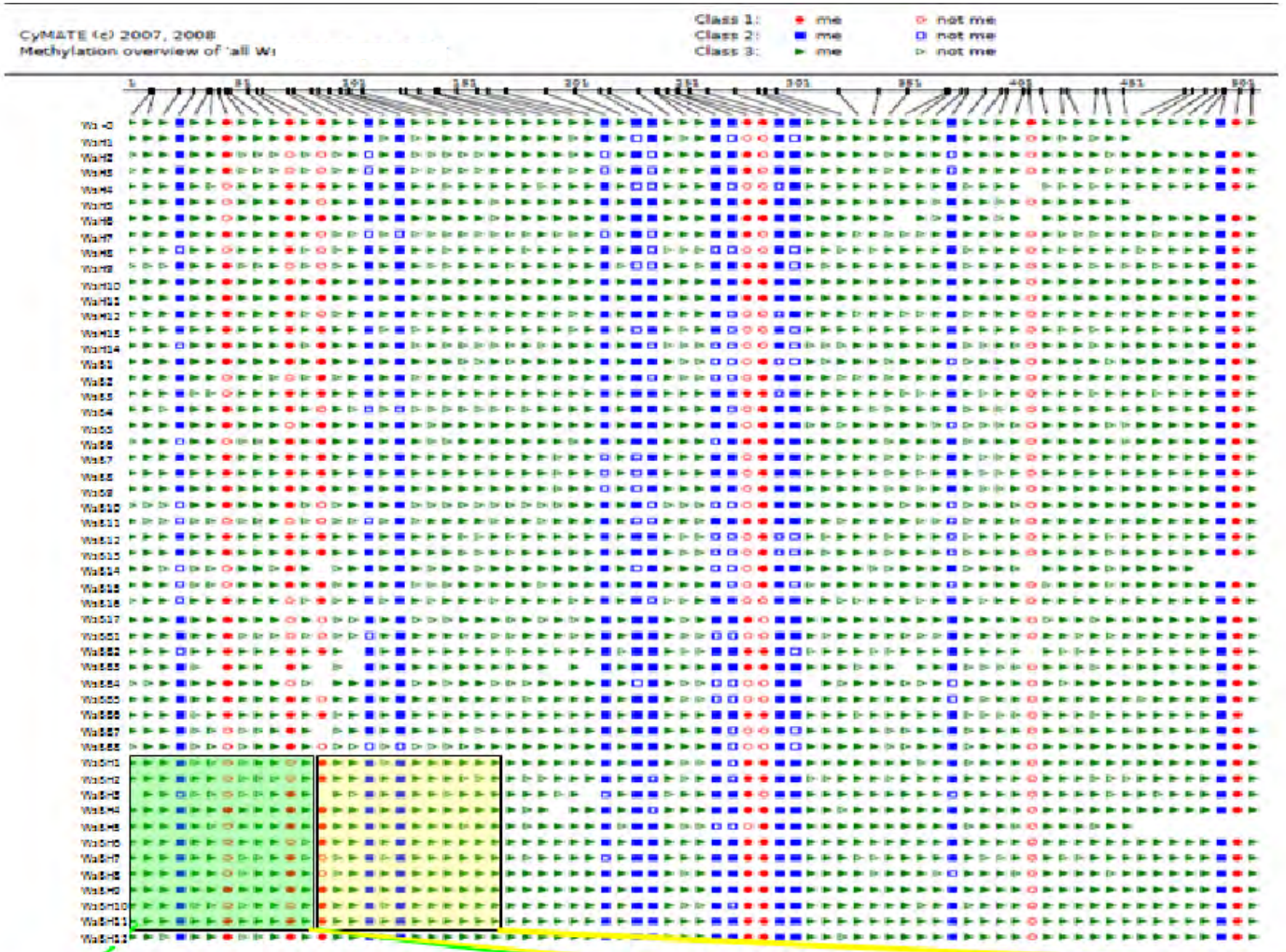


Figure S6. Priming of the progeny of BABA -treated lines is not due to direct transfer of BABA to the next generation. BABA concentrations were determined in u ntreated plants and in plants soil-drenched with BABA, respectively. A,BABA 40 ppm and B,BABA 25 ppm. S_1 = first generation selfed progeny. The horizontal lines at 50 µg BABA/g dw show the threshold concentration for resistance induction.

A


CyMATE (c) 2007, 2008
Methylation overview of 'all W1
Class 1: me not me
Class 2: me not me
Class 3: me not me

B


ruler
L54 (WRKY)
L55 (TGA)
L57 (TGA)
L58 (ERF)
L59 (PR-00B)
L510 (NF-κB)

Figure S7. Graphical output generated by CyMate of the Ws transgenerational lines.

A) Methylation analysis of a 503 bp fragment of the *PR1* promotor of Ws and descendants. The location of the cytosines within the sequenced fragment is shown in the ruler at the top of the Figure. Beneath the ruler, the filled symbols represent methylated cytosine residues, whereas the open symbols represent cytosine residues lacking methylation. The red circles stand for ^{m}CGN, the blue squares represent ^{m}CHG and the green triangles represent ^{m}CHH.. The uppermost sequence (Ws-0) corresponds to consensus sequence and is followed by individual clones obtained by polymerase chain reaction amplification of bisulfite-treated DNA. The order of the individual sequences is shown on the left.

B) Zoom-in view of the *PR1* promotor fragment showing the different motives (WRKY, TGA, ERF, PR-box and NFκB) identified on the promotor.

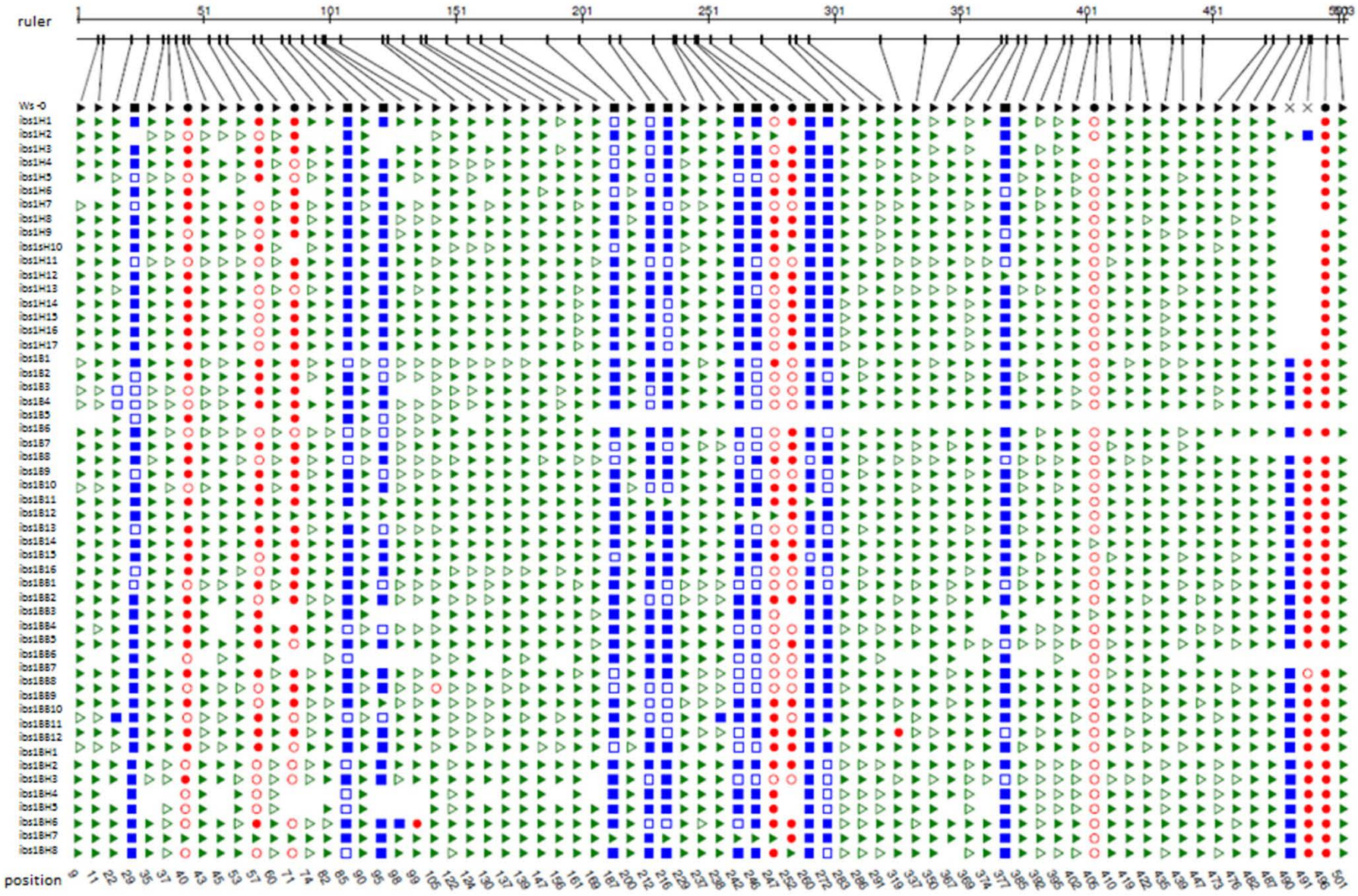

ruler
1
51
101
151
201
251
301
351
401
451
503
Ws-0
Ibs1H1
Ibs1H2
Ibs1H3
Ibs1H4
Ibs1H5
Ibs1H6
Ibs1H7
Ibs1H8
Ibs1H9
Ibs1sH10
Ibs1H11
Ibs1H12
Ibs1H13
Ibs1H14
Ibs1H15
Ibs1H16
Ibs1H17
Ibs1B1
Ibs1B2
Ibs1B3
Ibs1B4
Ibs1B5
Ibs1B6
Ibs1B7
Ibs1B8
Ibs1B9
Ibs1B10
Ibs1B11
Ibs1B12
Ibs1B13
Ibs1B14
Ibs1B15
Ibs1B16
Ibs1BB1
Ibs1BB2
Ibs1BB3
Ibs1BB4
Ibs1BB5
Ibs1BB6
Ibs1BB7
Ibs1BB8
Ibs1BB9
Ibs1BB10
Ibs1BB11
Ibs1BB12
Ibs1BH1
Ibs1BH2
Ibs1BH3
Ibs1BH4
Ibs1BH5
Ibs1BH6
Ibs1BH7
Ibs1BH8
position

Figure S8. Graphical output generated by CyMate of the *ibs1* trans-generational lines. Methylation analysis of 503 bp fragment of *PR1* promotor of *ibs1* and descendants.Filled symbols represent cytosine methylation, wheras open symbols represent lack of methylation. Circles represent ^{m}CG, squares represent ^{m}CHG and triangles represent ^{m}CHH. The order of the individual sequences is shown on the left.

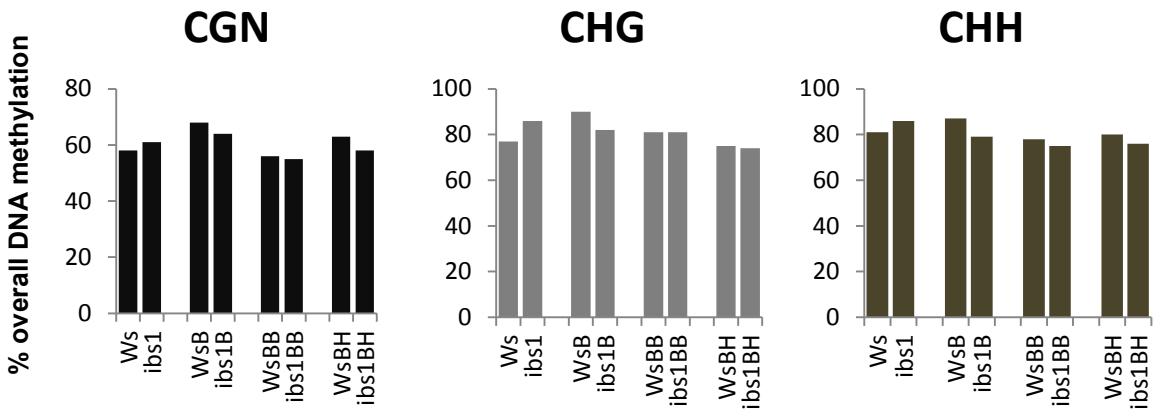


Fig. S9: Bilsulfite sequencing data showing percentage of CGN, CHG and CHH methylation, as computed by the CyMate program, in a 503-bp region of the *PR1* promotor of Ws-0 and descendants and *ibs1* and descendants, respectively.