Ji et al. Supplemental Materials

Supplemental Figures

Figure S1. All plate assay tracings for treatments with 0 µM and 1.5 µM ABA. A scale bar (1cm) is included with the first replicate of each treatment.

Figure S2. Plates traced for root length in Fig. 2H. These photos were taken four days after the tracings were made. Show here is the tenth replicate.

Figure S3. Expression of AtABCG17 and AtABCG18 in *abcg16* mutant relative to the wildtype background line (Col-0).

Figure S4. Images of 35S::GFP positive controls for root and leaf epidermus.

Figure S5. Gene tree of ABCG subfamily of ABC transporters in *Arabidopsis thaliana*.

Supplemental Tables

Table S1. Average log(cfu) of *Pst* DC3000 in RegMap panel lines at 0,1,4, and 7 days post inoculation from each of three independent experiments described previously (Atwell et al. 2010) sorted by average titer on day 4.

Table S2. Candidate genes from genome-wide association map for resistance to *Pst* DC3000. Sorted by Wilcoxon score. N/As represent genes found inside candidate loci but lacking SNPs inside the gene coding region.

Table S3. Base calls for SNP#s 118594 – 118611 for each of the 96 lines in the RegMap panel (Atwell et al. 2010). Corresponding base positions on Chromosome 3 are shown in Table S4.

Table S4. Single nucleotide polymorphisms with corresponding base position, gene, base call, Wilcoxon score, EMMA score, and nucleotide diversity score.

Table S5. Expression of all genes in the neighborhood of *ABCG16* (At3g55090) in response to bacterial infection and exogenous application of ABA, IAA, and SA.

Table S6. Primers used for RT-PCR, gene and promoter cloning.

Table S7. RT-PCR measuring AtABCG16 expression in T-DNA knockouts, RNAi knockdowns and overexpressors.

Table S8. Plate assay results for germination (%) of *abcg16-1* and *abcg16-2* knockouts relative to the CS60000 background in response to low (0-3 µM) or high (0-300 µM) range abscisic acid (ABA), indole-3-acetic acid (IAA), or salicylic acid (SA).

Table S9. Plate assay results for germination (%) on day 4, root length (cm) on day 10, and mortality (%) on day 30 of *abcg16-1* and *abcg16-2* knockouts relative to the CS60000 background in response to four concentrations of abscisic acid (ABA).

Table S10. Leaf bacterial titers at 18 days post infection (dpi) following surface spray inoculation of soil-grown plants with *Pst* DC3118 (COR- mutant) and *Pst* DC3000 (COR+ wildtype) at Day 36 of plant growth.

Table S11. Shoot dry biomass (mg) at Day 95 of plant growth following surface spray inoculation of soil-grown plants with *Pst* DC3118 (COR- mutant) and *Pst* DC3000 (COR+ wildtype) at Day 36 of plant growth.

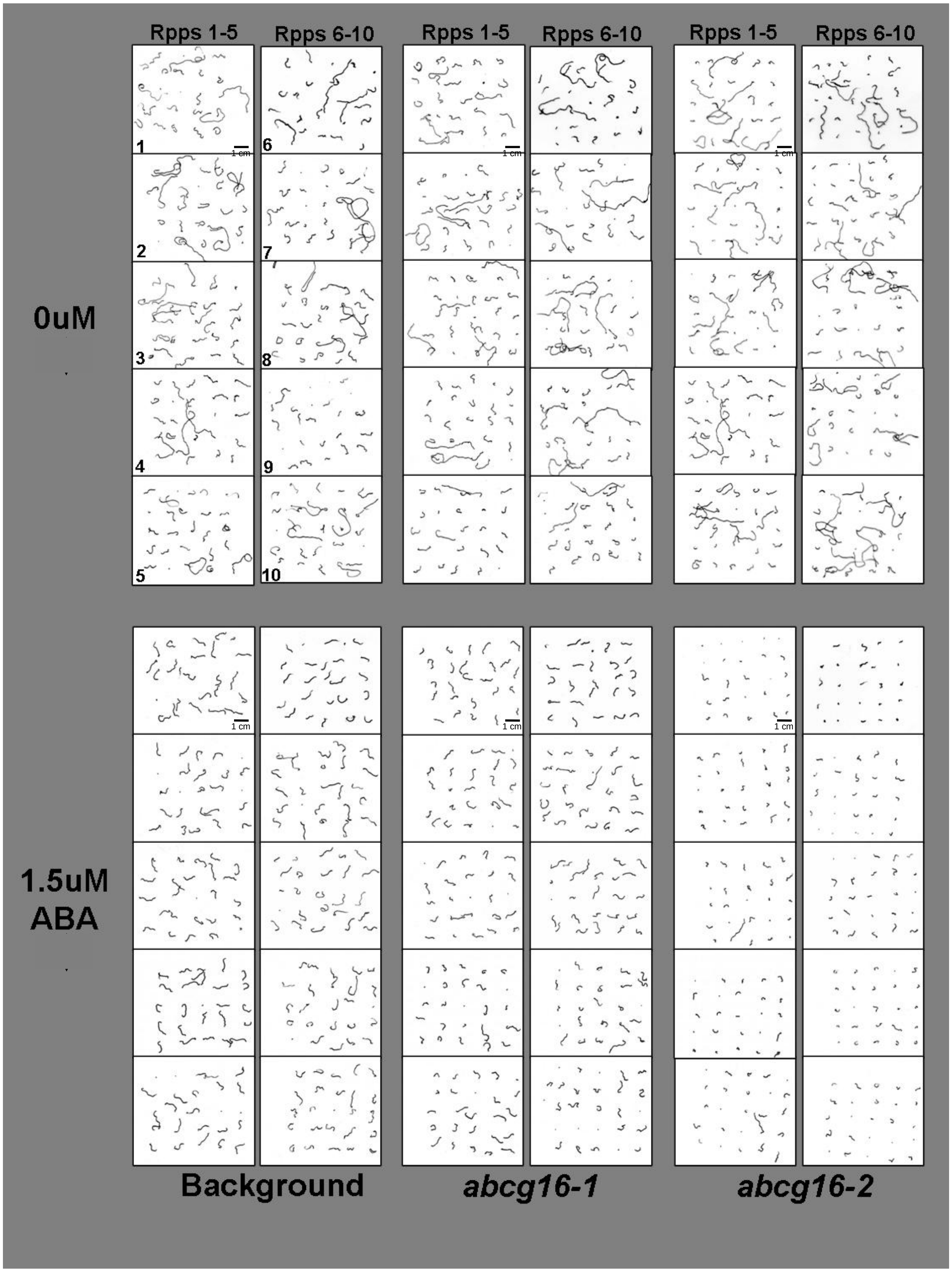


Figure S1. All plate assay tracings for treatments with 0 μM and 1.5 μM ABA. A scale bar (1cm) is included with the first replicate of each treatment.

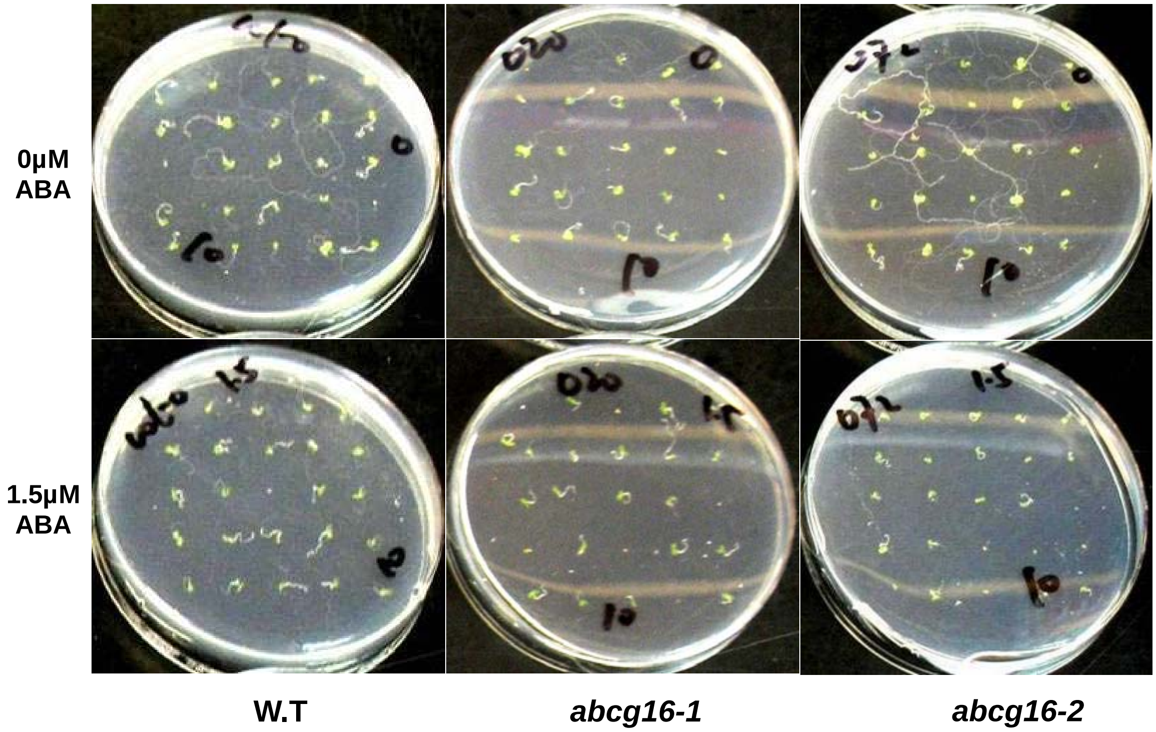


Figure S2. Plates traced for root length in Fig. 2H. These photos were taken four days after the tracings were made. Shown here is the tenth replicate.

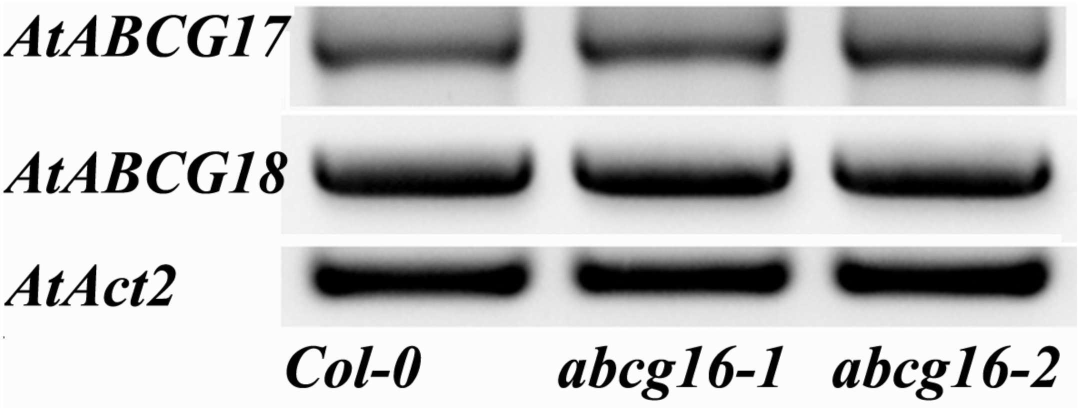


Figure S3. Expression of AtABCG17 and AtABCG18 in *abcg16* mutant relative to the wildtype background line (Col-0).

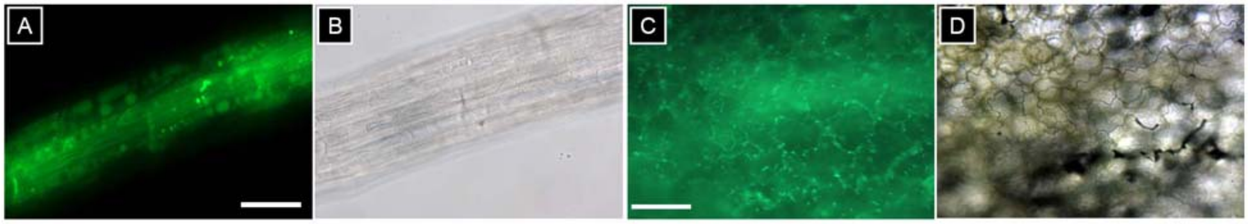


Figure S4. Images of 35S::GFP positive controls. Root tissue showing **(A)** fluorescence levels under GFP expression conditions and **(B)** under white light conditions. Epidermal tissue showing **(C)** fluorescence levels under GFP expression conditions and **(D)** under white light conditions.

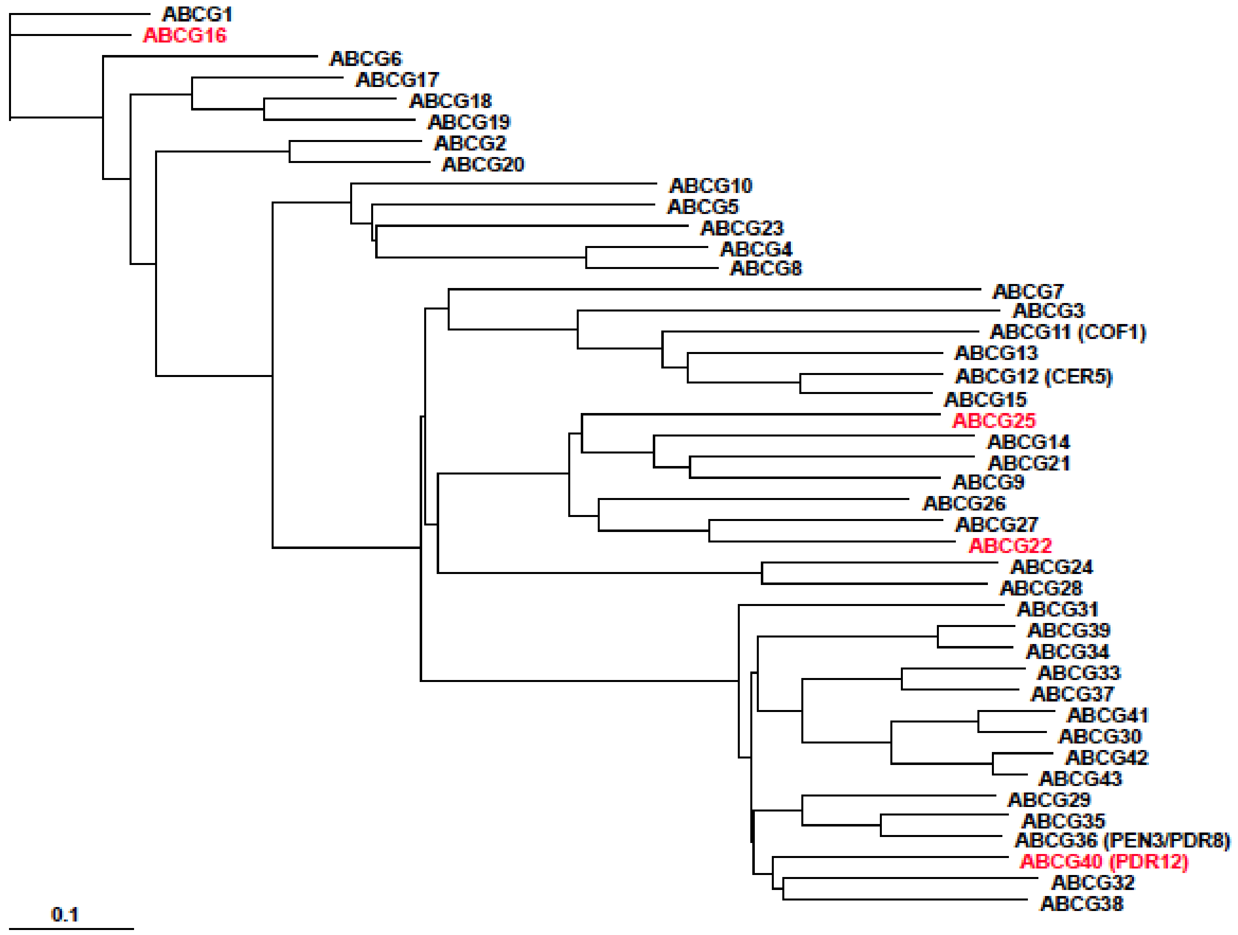
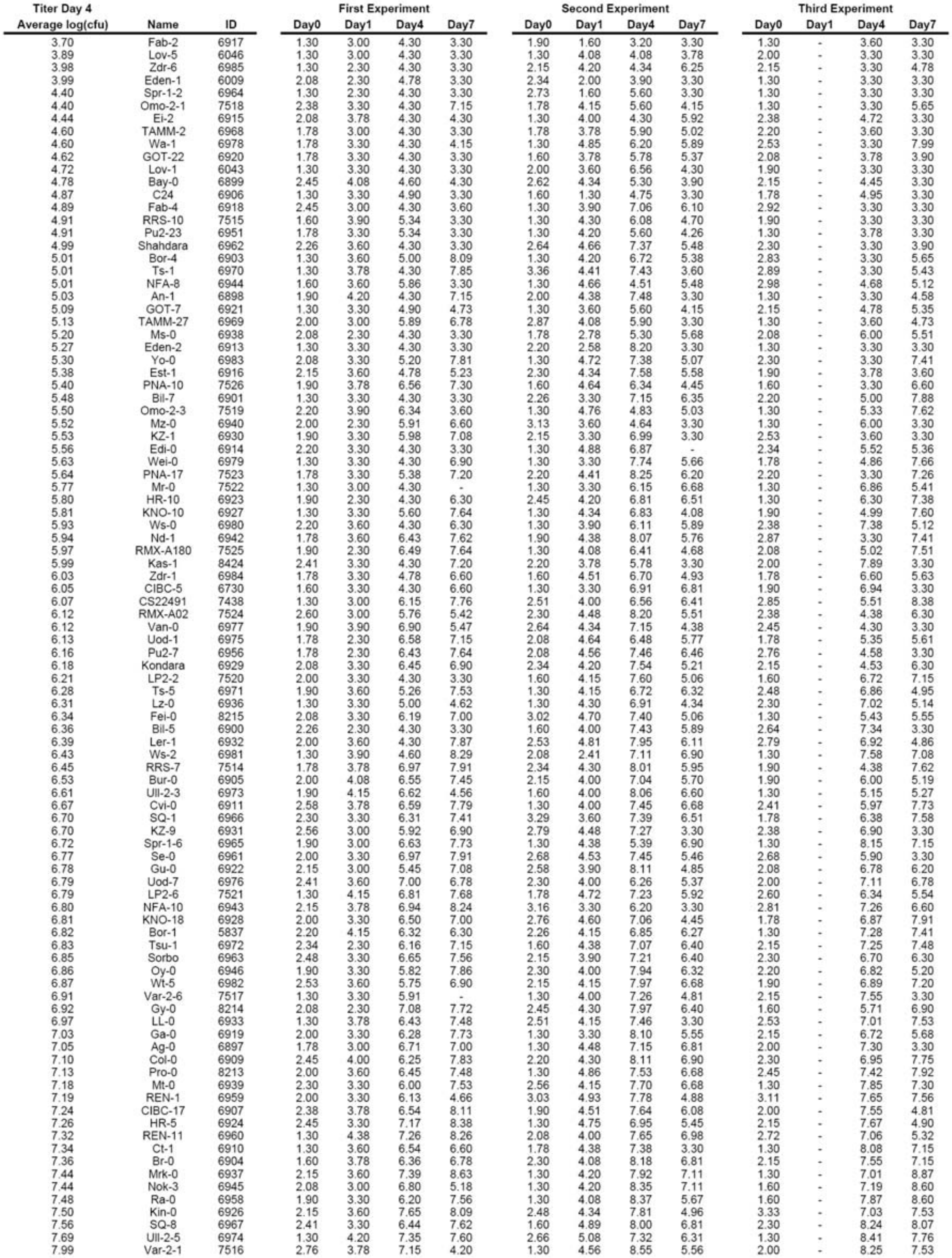


Figure S5. Gene tree of ABCG subfamily of ABC transporters in Arabidopsis. Phylogenetic analysis following prior analyses (Ukitsu et al., 2007; Kuromori et al., 2011). Nucleotide sequences are from TAIR (http://www.arabidopsis.org/servlets/Search). Sequence alignment and phylogeny tree construction were performed in Clustal X. Proteins implicated in ABA transport are indicated in red.

Table S1. Average log(cfu) of *Pst* DC3000 in RegMap panel lines at 0,1,4, and 7 days post inoculation from each of three independent experiments described previously (Atwell et al. 2010) sorted by average titer on day 4.



Titer Day 4			First Experiment				Second Experiment				Third Experiment			
Average log(cfu)	Name	ID	Day0	Day1	Day4	Day7	Day0	Day1	Day4	Day7	Day0	Day1	Day4	Day7
3.70	Fab-2	6917	1.30	3.00	4.30	3.30	1.90	1.60	3.20	3.30	1.30	-	3.60	3.30
3.89	Lov-5	6046	1.30	3.00	4.30	3.30	1.30	4.08	4.08	3.78	2.00	-	3.30	3.30
3.98	Zdr-6	6985	1.30	2.30	4.30	3.30	2.15	4.20	4.34	6.25	2.15	-	3.30	4.78
3.99	Eden-1	6009	2.08	2.30	4.78	3.30	2.34	2.00	3.90	3.30	1.30	-	3.30	3.30
4.40	Spr-1-2	6964	1.30	2.30	4.30	3.30	2.73	1.60	5.60	3.30	1.30	-	3.30	3.30
4.40	Omo-2-1	7518	2.38	3.30	4.30	7.15	1.78	4.15	5.60	4.15	1.30	-	3.30	5.65
4.44	Ei-2	6915	2.08	3.78	4.30	4.30	1.30	4.00	4.30	5.92	2.38	-	4.72	3.30
4.60	TAMM-2	6968	1.78	3.00	4.30	3.30	1.78	3.78	5.90	5.02	2.20	-	3.60	3.30
4.60	Wa-1	6978	1.78	3.30	4.30	4.15	1.30	4.85	6.20	5.89	2.53	-	3.30	7.99
4.62	GOT-22	6920	1.78	3.30	4.30	3.30	1.60	3.78	5.78	5.37	2.08	-	3.78	3.90
4.72	Lov-1	6043	1.30	3.30	4.30	3.30	2.00	3.60	6.56	4.30	1.90	-	3.30	3.30
4.78	Bay-0	6899	2.45	4.08	4.60	4.30	2.62	4.34	5.30	3.90	2.15	-	4.45	3.30
4.87	C24	6906	1.30	3.30	4.90	3.30	1.60	1.30	4.75	3.30	1.78	-	4.95	3.30
4.89	Fab-4	6918	2.45	3.00	4.30	3.60	1.30	3.90	7.06	6.10	2.92	-	3.30	3.30
4.91	RRS-10	7515	1.60	3.90	5.34	3.30	1.30	4.30	6.08	4.70	1.90	-	3.30	3.30
4.91	Pu2-23	6951	1.78	3.30	5.34	3.30	1.30	4.20	5.60	4.26	1.30	-	3.78	3.30
4.99	Shahdara	6962	2.26	3.60	4.30	3.30	2.64	4.66	7.37	5.48	2.30	-	3.30	3.90
5.01	Bor-4	6903	1.30	3.60	5.00	8.09	1.30	4.20	6.72	5.38	2.83	-	3.30	5.65
5.01	Ts-1	6970	1.30	3.78	4.30	7.85	3.36	4.41	7.43	3.60	2.89	-	3.30	5.43
5.01	NFA-8	6944	1.60	3.60	5.86	3.30	1.30	4.66	4.51	5.48	2.98	-	4.68	5.12
5.03	An-1	6898	1.90	4.20	4.30	7.15	2.00	4.38	7.48	3.30	1.30	-	3.30	4.58
5.09	GOT-7	6921	1.30	3.30	4.90	4.73	1.30	3.60	5.60	4.15	2.15	-	4.78	5.35
5.13	TAMM-27	6969	2.00	3.00	5.89	6.78	2.87	4.08	5.90	3.30	1.30	-	3.60	4.73
5.20	Ms-0	6938	2.08	2.30	4.30	3.30	1.78	2.78	5.30	5.68	2.08	-	6.00	5.51
5.27	Eden-2	6913	1.30	3.30	4.30	3.30	2.20	2.58	8.20	3.30	1.30	-	3.30	3.30
5.30	Yo-0	6983	2.08	3.30	5.20	7.81	1.30	4.72	7.38	5.07	2.30	-	3.30	7.41
5.38	Est-1	6916	2.15	3.60	4.78	5.23	2.30	4.34	7.58	5.58	1.90	-	3.78	3.60
5.40	PNA-10	7526	1.90	3.78	6.56	7.30	1.60	4.64	6.34	4.45	1.60	-	3.30	6.60
5.48	Bil-7	6901	1.30	3.30	4.30	3.30	2.26	3.30	7.15	6.35	2.20	-	5.00	7.88
5.50	Omo-2-3	7519	2.20	3.90	6.34	3.60	1.30	4.76	4.83	5.03	1.30	-	5.33	7.62
5.52	Mz-0	6940	2.00	2.30	5.91	6.60	3.13	3.60	4.64	3.30	1.30	-	6.00	3.30
5.53	KZ-1	6930	1.90	3.30	5.98	7.08	2.15	3.30	6.99	3.30	2.53	-	3.60	3.30
5.56	Edi-0	6914	2.20	3.30	4.30	3.30	1.30	4.88	6.87	-	2.34	-	5.52	5.36
5.63	Wei-0	6979	1.30	3.30	4.30	6.90	1.30	3.30	7.74	5.66	1.78	-	4.86	7.66
5.64	PNA-17	7523	1.78	3.30	5.38	7.20	2.20	4.41	8.25	6.20	2.20	-	3.30	7.26
5.77	Mr-0	7522	1.30	3.00	4.30	-	1.30	3.30	6.15	6.68	1.30	-	6.86	5.41
5.80	HR-10	6923	1.90	2.30	4.30	6.30	2.45	4.20	6.81	6.51	1.30	-	6.30	7.38
5.81	KNO-10	6927	1.30	3.30	5.60	7.64	1.30	4.34	6.83	4.08	1.90	-	4.99	7.60
5.93	Ws-0	6980	2.20	3.60	4.30	6.30	1.30	3.90	6.11	5.89	2.38	-	7.38	5.12
5.94	Nd-1	6942	1.78	3.60	6.43	7.62	1.90	4.38	8.07	5.76	2.87	-	3.30	7.41
5.97	RMX-A180	7525	1.90	2.30	6.49	7.64	1.30	4.08	6.41	4.68	2.08	-	5.02	7.51
5.99	Kas-1	8424	2.41	3.30	4.30	7.20	2.20	3.78	5.78	3.30	2.00	-	7.89	3.30
6.03	Zdr-1	6984	1.78	3.30	4.78	6.60	1.60	4.51	6.70	4.93	1.78	-	6.60	5.63
6.05	CIBC-5	6730	1.60	3.30	4.30	6.60	1.30	3.30	6.91	6.81	1.90	-	6.94	3.30
6.07	CS22491	7438	1.30	3.00	6.15	7.76	2.51	4.00	6.56	6.41	2.85	-	5.51	8.38
6.12	RMX-A02	7524	2.60	3.00	5.76	5.42	2.30	4.48	8.20	5.51	2.38	-	4.38	6.30
6.12	Van-0	6977	1.90	3.90	6.90	5.47	2.64	4.34	7.15	4.38	2.45	-	4.30	3.30
6.13	Uod-1	6975	1.78	2.30	6.58	7.15	2.08	4.64	6.48	5.77	1.78	-	5.35	5.61
6.16	Pu2-7	6956	1.78	2.30	6.43	7.64	2.08	4.56	7.46	6.46	2.76	-	4.58	3.30
6.18	Kondara	6929	2.08	3.30	6.45	6.90	2.34	4.20	7.54	5.21	2.15	-	4.53	6.30
6.21	LP2-2	7520	2.00	3.30	4.30	3.30	1.60	4.15	7.60	5.06	1.60	-	6.72	7.15
6.28	Ts-5	6971	1.90	3.60	5.26	7.53	1.30	4.15	6.72	6.32	2.48	-	6.86	4.95
6.31	Lz-0	6936	1.30	3.30	5.00	4.62	1.30	4.30	6.91	4.34	2.30	-	7.02	5.14
6.34	Fei-0	8215	2.08	3.30	6.19	7.00	3.02	4.70	7.40	5.06	1.30	-	5.43	5.55
6.36	Bil-5	6900	2.26	2.30	4.30	3.30	1.60	4.00	7.43	5.89	2.64	-	7.34	3.30
6.39	Ler-1	6932	2.00	3.60	4.30	7.87	2.53	4.81	7.95	6.11	2.79	-	6.92	4.86
6.43	Ws-2	6981	1.30	3.90	4.60	8.29	2.08	2.41	7.11	6.90	1.30	-	7.58	7.08
6.45	RRS-7	7514	1.78	3.78	6.97	7.91	2.34	4.30	8.01	5.95	1.90	-	4.38	7.62
6.53	Bur-0	6905	2.00	4.08	6.55	7.45	2.15	4.00	7.04	5.70	1.90	-	6.00	5.19
6.61	Ull-2-3	6973	1.90	4.15	6.62	4.56	1.60	4.00	8.06	6.60	1.30	-	5.15	5.27
6.67	Cvi-0	6911	2.58	3.78	6.59	7.79	1.30	4.00	7.45	6.68	2.41	-	5.97	7.73
6.70	SQ-1	6966	2.30	3.30	6.31	7.41	3.29	3.60	7.39	6.51	1.78	-	6.38	7.58
6.70	KZ-9	6931	2.56	3.00	5.92	6.90	2.79	4.48	7.27	3.30	2.38	-	6.90	3.30
6.72	Spr-1-6	6965	1.90	3.00	6.63	7.73	1.30	4.38	5.39	6.90	1.30	-	8.15	7.15
6.77	Se-0	6961	2.00	3.30	6.97	7.91	2.68	4.53	7.45	5.46	2.68	-	5.90	3.30
6.78	Gu-0	6922	2.15	3.00	5.45	7.08	2.58	3.90	8.11	4.85	2.08	-	6.78	6.20
6.79	Uod-7	6976	2.41	3.60	7.00	6.78	2.30	4.00	6.26	5.37	2.00	-	7.11	6.78
6.79	LP2-6	7521	1.30	4.15	6.81	7.68	1.78	4.72	7.23	5.92	2.60	-	6.34	5.54
6.80	NFA-10	6943	2.15	3.78	6.94	8.24	3.16	3.30	6.20	3.30	2.81	-	7.26	6.60
6.81	KNO-18	6928	2.00	3.30	6.50	7.00	2.76	4.60	7.06	4.45	1.78	-	6.87	7.91
6.82	Bor-1	5837	2.20	4.15	6.32	6.30	2.26	4.15	6.85	6.27	1.30	-	7.28	7.41
6.83	Tsu-1	6972	2.34	2.30	6.16	7.15	1.60	4.38	7.07	6.40	2.15	-	7.25	7.48
6.85	Sorbo	6963	2.48	3.30	6.65	7.56	2.15	3.90	7.21	6.40	2.30	-	6.70	6.30
6.86	Oy-0	6946	1.90	3.30	5.82	7.86	2.30	4.00	7.94	6.32	2.20	-	6.82	5.20
6.87	Wt-5	6982	2.53	3.60	5.75	6.90	2.15	4.15	7.97	6.68	1.90	-	6.89	7.20
6.91	Var-2-6	7517	1.30	3.30	5.91	-	1.30	4.00	7.26	4.81	2.15	-	7.55	3.30
6.92	Gy-0	8214	2.08	2.30	7.08	7.72	2.45	4.30	7.97	6.40	1.60	-	5.71	6.90
6.97	LL-0	6933	1.30	3.78	6.43	7.48	2.51	4.15	7.46	3.30	2.53	-	7.01	7.53
7.03	Ga-0	6919	2.00	3.30	6.28	7.73	1.30	3.30	8.10	5.55	2.15	-	6.72	5.68
7.05	Ag-0	6897	1.78	3.00	6.71	7.00	1.30	4.48	7.15	6.81	2.00	-	7.30	3.30
7.10	Col-0	6909	2.45	4.00	6.25	7.83	2.20	4.30	8.11	6.90	2.30	-	6.95	7.75
7.13	Pro-0	8213	2.00	3.60	6.45	7.48	1.30	4.86	7.53	6.68	2.45	-	7.42	7.92
7.18	Mt-0	6939	2.30	3.30	6.00	7.53	2.56	4.15	7.70	6.68	1.30	-	7.85	7.30
7.19	REN-1	6959	2.00	3.30	6.13	4.66	3.03	4.93	7.78	4.88	3.11	-	7.65	7.56
7.24	CIBC-17	6907	2.38	3.78	6.54	8.11	1.90	4.51	7.64	6.08	2.00	-	7.55	4.81
7.26	HR-5	6924	2.45	3.30	7.17	8.38	1.30	4.75	6.95	5.45	2.15	-	7.67	4.90
7.32	REN-11	6960	1.30	4.38	7.26	8.26	2.08	4.00	7.65	6.98	2.72	-	7.06	5.32
7.34	Ct-1	6910	1.30	3.60	6.54	6.60	1.78	4.38	7.38	3.30	1.30	-	8.08	7.15
7.36	Br-0	6904	1.60	3.78	6.36	6.78	2.30	4.08	8.18	6.81	2.15	-	7.55	7.15
7.44	Mrk-0	6937	2.15	3.60	7.39	8.63	1.30	4.20	7.92	7.11	1.30	-	7.01	8.87
7.44	Nok-3	6945	2.08	3.00	6.80	5.18	1.30	4.20	8.35	7.11	1.60	-	7.19	8.60
7.48	Ra-0	6958	1.90	3.30	6.20	7.56	1.30	4.08	8.37	5.67	1.60	-	7.87	8.60
7.50	Kin-0	6926	2.15	3.60	7.65	8.09	2.48	4.34	7.81	4.96	3.33	-	7.03	7.53
7.56	SQ-8	6967	2.41	3.30	6.44	7.62	1.60	4.89	8.00	6.81	2.30	-	8.24	8.07
7.69	Ull-2-5	6974	1.30	4.20	7.35	7.60	2.66	5.08	7.32	6.31	1.30	-	8.41	7.76
7.99	Var-2-1	7516	2.76	3.78	7.15	4.20	1.30	4.56	8.55	5.56	2.00	-	8.25	7.53

Table S2. Candidate genes from genome-wide association map for resistance to *Pst* DC3000. Sorted by Wilcoxon score. N/As represent genes found inside candidate loci but lacking SNPs inside the gene coding region.

Rank	Wilcoxon.DC3000	Locus	Gene	Name	Description
1	5.42	3	AT2G21910	CYP96A5	CYTOCHROME P450
2	4.97	7	AT2G44581	Unknown	RING/U-box superfamily protein
3	4.93	8	AT2G45850	Unknown	AT hook motif DNA-binding family protein
3	4.93	8	AT2G45890	RHS11	Kinase partner family protein
3	4.93	8	AT2G45900	Unknown	Phosphatidylinositol N-acetyglucosaminlytransferase subuni
6	4.91	7	AT2G44570	GH9B12	Glycosyl hydrolase 9B12,hydrolase activity
6	4.91	7	AT2G44590	DL1D	DYNAMIN-like 1D,GTPase activity
8	4.89	8	AT2G45870	Unknown	Bestrophin-like protein
9	4.77	12	AT4G32970	Unknown	Unknown
10	4.74	8	AT2G45860	Unknown	Unknown
11	4.58	4	AT2G22950	Unknown	Cation transporter/ E1-E2 ATPase family protein
12	4.54	10	AT3G55070	Unknown	LisH/CRA/RING-U-box domains-containing protein
13	4.53	12	AT4G32960	Unknown	Unknown
14	4.42	12	AT4G32980	ATH1	Transcription factor involved in photomorphogenesis
15	4.29	2	AT2G17580	Unknown	Undecaprenyl pyrophosphate synthetase family protein
16	4.25	6	AT2G43850	Unknown	Integrin-linked protein kinase family
17	4.17	8	AT2G45830	DTA2	Downstream target of AGL15, post-germinative developmen
18	4.16	1	AT1G78660	GGH1	Gamma-glutamyl hydrolase cleaving pentaglutamates
19	4.14	10	AT3G55080	Unknown	SET domain-containing protein
19	4.14	10	AT3G55090	ABCG16	ABC-2 type transporter family protein
21	3.86	2	AT2G17560	Unknown	HMGB (high mobility group B) protein
22	3.82	2	AT2G17570	Unknown	Undecaprenyl pyrophosphate synthetase family protein
23	3.81	6	AT2G43820	SAGT1	Induced by Salicylic acid, virus, fungus and bacteria
24	3.79	6	AT2G43840	UGT74F1	Transfers UDP:glucose to salicylic acid (forming a glucoside
25	3.57	12	AT4G32950	Unknown	Protein phosphatase 2C family protein
26	3.55	9	AT3G03060	Unknown	P-loop containing nucleoside triphosphate hydrolase
27	3.51	4	AT2G22970	SCPL11	Serine-type carboxypeptidase activity
28	3.48	11	AT4G15180	SDG2	SET domain protein 2
29	3.37	5	AT2G27600	SKD1	Suppressor of K+ Transport Growth Defect1
29	3.37	5	AT2G27610	Unknown	Tetratricopeptide repeat (TPR)-like superfamily protein
29	3.37	5	AT2G27630	Unknown	Ubiquitin carboxyl-terminal hydrolase-related protein
32	3.34	1	AT1G78650	POLD3	Similar to DNA polymerase delta
33	2.95	9	AT3G03050	RHD7	Root hair development
34	2.90	9	AT3G03070	Unknown	NADH-ubiquinone oxidoreductase-related
35	2.68	4	AT2G22960	Unknown	Alpha/beta-Hydrolases superfamily protein
N/A	N/A	2	AT2G17556	Unknown	Unknown
N/A	N/A	2	AT2G17590	Unknown	Cysteine/Histidine-rich C1 domain family protein
N/A	N/A	3	AT2G21905	Unknown	Pseudogene
N/A	N/A	3	AT2G21920	Unknown	F-box associated ubiquitination effector family protein
N/A	N/A	4	AT2G22942	Unknown	Growth factors
N/A	N/A	4	AT2G22955	Unknown	Potential natural antisense gene
N/A	N/A	4	AT2G22980	SCPL13	Serine carboxypeptidase-like 13
N/A	N/A	5	AT2G27650	Unknown	Ubiquitin carboxyl-terminal hydrolase-related protein
N/A	N/A	6	AT2G43830	Unknown	Pseudogene
N/A	N/A	6	AT2G43860	Unknown	Pectin lyase-like superfamily protein
N/A	N/A	7	AT2G44578	Unknown	RING/U-box superfamily protein
N/A	N/A	7	AT2G44580	Unknown	Zinc ion binding
N/A	N/A	8	AT2G45840	Unknown	InterPro DOMAIN/s
N/A	N/A	8	AT2G45880	BAM7	Encodes a beta-amylase-like protein
N/A	N/A	10	AT3G55060	Unknown	Unknown
N/A	N/A	11	AT4G15165	Unknown	N-terminal nucleophile aminohydrolases
N/A	N/A	13	AT5G25310	Unknown	Exostosin family protein
N/A	N/A	13	AT5G25320	Unknown	ACT-like superfamily protein
N/A	N/A	13	AT5G25330	Unknown	Acetylglucosaminyltransferase family protein

Table S3. Base calls for SNP#s 118594 – 118611 for each of the 96 lines in the RegMap panel (Atwell et al. 2010). Corresponding base positions on Chromosome 3 are shown in Table S4.

logcfu	Name	Line	118594	118595	118596	118597	118598	118599	118600	118601	118602	118603	118604	118605	118606	118607	118608	118609	118610	118611
3.70	Fab.2	6917	G	G	C	A	A	T	A	G	C	T	T	G	A	C	G	T	A	G
3.89	Lov.5	6046	G	G	C	A	A	T	A	G	C	T	T	G	A	C	G	T	A	G
3.98	Zdr.6	6985	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
3.99	Eden.1	6009	G	G	C	A	A	T	A	G	C	T	T	G	A	C	G	T	A	G
4.40	Spr.1.2	6964	A	A	T	G	A	C	T	A	C	C	A	A	A	C	G	G	C	A
4.40	Omo.2.1	7518	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
4.44	Ei.2	6915	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
4.60	TAMM.2	6968	G	G	C	A	G	T	A	G	C	T	T	G	A	C	G	T	A	G
4.60	Wa.1	6978	A	A	T	G	A	C	T	A	C	C	A	A	A	C	G	G	C	A
4.62	GOT.22	6920	A	A	T	G	A	T	T	G	C	C	A	A	A	C	G	G	C	A
4.72	Lov.1	6043	G	G	C	A	A	T	A	G	C	T	T	G	A	C	G	T	A	G
4.78	Bay.0	6899	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
4.87	C24	6906	A	A	T	G	A	T	T	G	C	C	A	A	G	C	G	G	C	A
4.89	Fab.4	6918	G	G	C	A	G	T	A	G	C	T	T	G	A	C	G	T	A	G
4.91	Pu2.23	6951	A	A	T	A	A	C	T	A	C	C	A	A	A	C	G	G	C	A
4.91	RRS.10	7515	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
4.99	Shahdara	6962	A	A	T	G	A	C	T	A	C	C	A	A	A	C	G	G	C	A
5.01	Bor.4	6903	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.01	NFA.8	6944	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
5.01	Ts.1	6970	A	A	T	G	A	T	T	G	C	C	A	A	A	C	G	G	C	A
5.03	An.1	6898	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.09	GOT.7	6921	A	A	T	G	G	T	T	G	C	C	A	A	A	C	G	G	C	A
5.13	TAMM.27	6969	G	G	C	A	A	T	A	A	C	T	T	G	A	C	G	T	A	G
5.20	Ms.0	6938	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.27	Eden.2	6913	G	G	C	A	A	T	A	G	C	T	T	G	A	C	G	T	A	G
5.30	Yo.0	6983	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.38	Est.1	6916	A	A	T	G	A	T	T	G	C	C	A	A	A	C	G	G	C	A
5.40	PNA.10	7526	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.48	Bil.7	6901	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
5.50	Omo.2.3	7519	A	A	T	G	A	T	T	G	C	C	A	A	G	C	G	G	C	A
5.52	Mz.0	6940	A	A	T	G	G	T	T	G	C	C	A	A	A	C	G	G	C	A
5.53	KZ.1	6930	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.56	Edi.0	6914	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
5.63	Wei.0	6979	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.64	PNA.17	7523	A	A	C	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.77	Mr.0	7522	A	A	C	G	A	T	T	G	C	C	A	A	A	C	G	T	C	A
5.80	HR.10	6923	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
5.81	KNO.10	6927	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.93	Ws.0	6980	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
5.94	Nd.1	6942	A	A	T	G	G	T	T	G	C	C	A	A	A	C	G	G	C	A
5.97	RMX.A180	7525	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
5.99	Kas.1	8424	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.03	Zdr.1	6984	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.05	CIBC.5	6730	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.07	CS22491	7438	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.12	Van.0	6977	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.12	RMX.A02	7524	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.13	Uod.1	6975	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.16	Pu2.7	6956	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.18	Kondara	6929	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.21	LP2.2	7520	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.28	Ts.5	6971	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.31	Lz.0	6936	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.34	Fei.0	8215	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.36	Bil.5	6900	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.39	Ler.1	6932	A	A	T	G	A	C	T	A	C	C	A	A	A	C	G	G	C	A
6.43	Ws.2	6981	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
6.45	RRS.7	7514	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.53	Bur.0	6905	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.61	Ull.2.3	6973	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.67	Cvi.0	6911	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
6.70	KZ.9	6931	A	A	T	G	A	T	T	G	C	C	A	A	G	C	G	G	C	A
6.70	SQ.1	6966	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.72	Spr.1.6	6965	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.77	Se.0	6961	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.78	Gu.0	6922	A	A	T	G	A	T	T	G	C	C	A	A	G	C	G	G	C	A
6.79	Uod.7	6976	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
6.79	LP2.6	7521	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.80	NFA.10	6943	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.81	KNO.18	6928	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.82	Bor.1	5837	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.83	Tsu.1	6972	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.85	Sorbo	6963	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.86	Oy.0	6946	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.87	Wt.5	6982	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
6.91	Var.2.6	7517	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.92	Gy.0	8214	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
6.97	LL.0	6933	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.03	Ga.0	6919	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.05	Ag.0	6897	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.10	Col.0	6909	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.13	Pro.0	8213	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.18	Mt.0	6939	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.19	REN.1	6959	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
7.24	CIBC.17	6907	A	A	T	G	G	T	T	G	C	C	A	A	G	C	G	G	C	G
7.26	HR.5	6924	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
7.32	REN.11	6960	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
7.34	Ct.1	6910	A	A	T	G	A	T	T	A	A	C	A	A	A	A	G	G	C	A
7.36	Br.0	6904	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.44	Mrk.0	6937	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.44	Nok.3	6945	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.48	Ra.0	6958	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.50	Kin.0	6926	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.56	SQ.8	6967	A	A	T	G	A	T	T	A	A	C	A	A	G	A	G	G	C	A
7.69	Ull.2.5	6974	A	A	T	G	A	T	T	G	C	C	A	A	A	C	T	G	C	A
7.99	Var.2.1	7516	A	A	T	G	A	T	T	G	C	C	A	A	A	C	G	G	C	A

Table S4. Single nucleotide polymorphisms with corresponding base position, gene, base call, Wilcoxon score, EMMA score, and nucleotide diversity score.

SNP#	Chr	Base	Gene	1	2	Wilcoxon	EMMA	Diversity
118594	3	20409100	AT3G55070	A	G	4.14	2.64	0.287
118595	3	20409187	AT3G55070	A	G	4.14	2.64	0.287
118596	3	20409475	AT3G55070	C	T	4.02	2.18	0.334
118597	3	20409973	AT3G55070	A	G	4.53	3.09	0.311
118598	3	20410063	AT3G55070	A	G	0.15	0.03	0.433
118599	3	20410101	AT3G55070	C	T	1.68	2.01	0.205
118600	3	20410893	AT3G55070	A	T	4.14	2.64	0.287
118601	3	20411394	NA	A	G	0.67	0.34	0.675
118602	3	20411685	AT3G55080	A	C	1.83	1.26	0.691
118603	3	20411760	AT3G55080	C	T	4.14	2.64	0.287
118604	3	20412188	AT3G55080	A	T	4.14	2.64	0.287
118605	3	20414398	AT3G55080	A	G	4.14	2.64	0.287
118606	3	20415389	AT3G55080	A	G	2.28	1.48	0.637
118607	3	20415801	AT3G55080	A	C	1.83	1.26	0.691
118608	3	20417220	AT3G55090	G	T	1.11	0.61	0.334
118609	3	20417245	AT3G55090	G	T	4.06	2.37	0.311
118610	3	20418355	AT3G55090	A	C	4.14	2.64	0.287
118611	3	20418626	NA	A	G	1.31	0.35	0.483

Table S5. Expression of all genes in the neighborhood of *ABCG16* (At3g55090) in response to bacterial infection and exogenous application of ABA, IAA, and SA.

		NASCArray-120		NASCArray-176			NASCArray-175			NASCArray-192	
Gene	Descroption	Mock	*Pst* DC3000 2hr	Mock	ABA 1hr	ABA 3hr	Mock	IAA 1hr	IAA 3hr	Mock	SA 3hr
AT3G54750	putative protein	63	0.9	160	1.0	0.9	169	1.1	1.2	158	0.9
AT3G54770	RNA binding protein	4	0.8	78	0.5	0.4	70	0.4	0.5	83	0.6
AT3G54790	putative protein	230	0.9	97	1.0	0.6	103	1.1	1.1	125	0.9
AT3G54800	putative protein	15	1.1	13	1.0	0.4	8	**1.8**	0.7	14	0.5
AT3G54810	GATA transcription factor 3	152	1.0	128	0.9	0.8	138	1.2	1.1	123	1.0
AT3G54820	aquaporin	37	2.3	51	1.2	1.6	34	0.9	0.5	42	0.6
AT3G54840	small GTP-binding protein	257	1.1	208	1.0	1.3	195	1.0	1.0	256	0.9
AT3G54850	putative protein	80	1.4	38	0.9	1.4	41	1.2	0.9	42	1.1
AT3G54860	vacuolar sorting protein	153	0.9	118	1.1	0.9	107	1.2	1.0	109	1.0
AT3G54870	kinesin-like protein	8	1.0	38	1.1	0.9	34	0.9	1.1	26	0.7
AT3G54890	chlorophyll a/b-binding protein	4061	0.8	2721	0.7	0.7	2074	1.3	0.9	1858	1.1
AT3G54900	thioredoxin-like protein	917	0.7	681	0.9	0.7	646	1.0	0.9	540	0.9
AT3G54920	pectate lyase	91	0.6	175	0.6	0.3	190	1.1	0.9	164	0.5
AT3G54930	protein phosphatase	16	1.7	32	1.5	0.7	22	1.0	0.9	31	0.6
AT3G54940	cysteine proteinase	3	1.2	8	**2.9**	1.1	5	0.7	0.3	17	0.4
AT3G54950	putative protein patatin	43	1.1	23	1.2	1.3	39	**1.9**	**2.3**	30	**1.9**
AT3G54960	disulphide isomerase	172	2.5	299	0.9	1.1	296	0.9	1.0	245	1.2
AT3G54970	hypothetical protein	33	1.1	28	1.0	0.8	31	1.1	1.2	25	1.0
AT3G54980	putative protein CRP1	48	1.0	37	0.8	0.8	56	1.4	1.2	40	1.3
AT3G54990	APETALA2 - like protein	12	0.5	43	1.0	0.9	29	0.7	0.7	71	0.5
AT3G55000	Expressed protein	79	1.3	100	0.6	0.9	105	0.9	1.2	90	0.9
AT3G55005	Expressed protein	41	1.0	65	1.1	1.0	47	1.2	0.9	53	0.8
AT3G55010	cyclo-ligase precursor	126	0.8	220	0.9	0.6	214	1.0	1.1	190	0.9
AT3G55020	putative protein	106	1.1	74	1.0	1.1	67	1.0	1.0	63	0.7
AT3G55030	phosphatidylglycerophosphate synthase	137	1.0	109	1.2	1.3	137	1.1	1.2	105	0.9
AT3G55040	putative protein	402	0.8	201	0.9	0.8	224	0.9	0.9	210	1.0
AT3G55050	protein phosphatase	120	1.0	119	1.0	1.1	119	1.1	1.0	135	0.9
AT3G55060	centromere protein	18	1.4	22	1.8	0.4	18	1.6	1.0	21	0.8
AT3G55070	putative protein	78	1.1	81	1.3	1.4	60	1.2	0.7	68	1.0
AT3G55080	putative protein	89	1.0	77	0.8	0.8	74	0.9	1.0	83	1.0
AT3G55090	ABC transporter	14	**2.8**	8	**4.3**	**38.1**	17	0.9	**3.5**	15	**3.8**
AT3G55100	ABC transporter	5	2.4	8	1.2	0.8	6	0.4	0.4	5	1.2
AT3G55110	ABC transporter	46	1.1	52	1.1	0.7	42	0.9	0.7	46	0.8
AT3G55120	chalcone isomerase	81	0.8	184	1.0	1.2	185	0.9	0.7	173	1.2
AT3G55130	ABC transporter	154	0.8	62	1.2	0.7	64	0.9	1.3	60	1.0
AT3G55140	pectate lyase	121	1.0	84	1.0	0.9	72	1.2	1.1	77	1.0
AT3G55150	leucine zipper-containing	25	**6.0**	43	0.7	0.6	34	0.9	0.8	42	1.0
AT3G55160	putative protein	46	0.8	48	0.8	0.9	44	0.8	1.0	42	0.8
AT3G55170	ribosomal L35	45	0.6	96	1.4	1.0	76	0.8	1.1	66	0.6
AT3G55180	lipase	8	1.3	13	**2.8**	0.5	7	**7.6**	0.5	6	1.0
AT3G55190	lipase	10	0.7	6	0.9	1.0	4	1.2	**2.1**	10	0.9
AT3G55250	pectate-lyase	698	0.7	737	1.0	1.0	624	0.9	0.9	505	1.0
AT3G55260	beta-N-acetylhexosaminidas	163	0.6	118	1.1	0.8	126	0.9	0.9	100	1.6
AT3G55270	phosphatase	65	1.3	45	0.9	1.1	42	1.0	1.2	41	0.9
AT3G55280	ribosomal L23a	366	0.9	696	0.9	0.6	729	1.0	1.0	550	1.0
AT3G55300	putative protein	9	0.9	12	0.4	0.6	4	0.7	0.6	10	0.7
AT3G55320	P-glycoprotein	71	1.1	51	1.0	**1.7**	61	0.9	1.0	44	1.0
AT3G55330	psbP	904	0.8	560	0.9	0.7	634	1.0	0.9	864	0.8
AT3G55350	putative protein	17	0.4	30	0.9	0.8	33	1.0	0.9	30	0.9
AT3G55360	glycoprotein SC2	576	0.7	646	0.9	1.4	678	0.9	1.0	707	1.2
AT3G55370	zinc finger protein OBP3	6	1.3	10	0.9	1.3	5	0.6	1.1	9	0.5
AT3G55380	E2, ubiquitin-conjugating	123	1.3	154	0.8	0.8	159	0.9	1.0	173	1.0
AT3G55390	putative protein MtN24	55	1.1	66	0.9	0.4	43	0.8	0.8	40	1.1
AT3G55400	methionyl-tRNA synthetase	160	0.7	165	1.0	1.0	226	0.9	1.0	213	0.9
AT3G55410	2-oxoglutarate dehydrogenase	325	1.3	335	1.0	0.8	384	1.0	1.2	278	1.2
AT3G55420	putative protein	51	0.8	71	0.8	0.8	53	1.0	0.8	56	0.8
AT3G55430	beta-1,3-glucanase	161	0.7	140	1.8	**4.9**	149	1.0	1.2	118	1.5
AT3G55440	cytosolic triosephosphatisomerase	1754	0.9	2573	0.8	0.8	1996	1.1	1.0	1829	1.1
AT3G55450	serine/threonine protein kinase	177	1.4	95	0.9	0.3	102	1.2	1.2	112	1.2
AT3G55460	putative RNA binding protein	253	1.1	219	0.9	1.0	227	0.9	0.9	177	1.3
AT3G55470	FIERG2 protein	20	**3.2**	26	0.8	0.6	23	1.3	1.0	36	**2.4**

Table S6. Primers list for RT-PCR, gene and promoter cloning.

Name	**sequences**	**Note**
RT-ABCG16F	CCTCAGTATTGGATTTGGTTTC	RT-PCR 296 bp
RT-ABCG16R	CCTACCGTGATAAGCAAGCAGT	
AtAct2F	CTCTCCCGCTATGTATGTCGC	RT-PCR 178 bp
AtAct2R	GTAAGGTCACGTCCAGCAAGG	
ABCG16F	CACCATGTCTCGCATACTAGTAGAAG	Cloning 2215 bp
ABCG16F	TCACCTCCTCTTGTTTTTGCTCCC	
pABCG16F	GTGCGTGTGAGCTATATGCCATC	Promoter 1388 bp
pABCG16R	CTCTGTTTTGCTAGTATCTGTGTA	
Primer A	GAATTCCTGCAGCCCcaaacac	AmiRNAi 699 bp
Primer B	GGATCCCCCcatggcgatgcc	
ABCG16I	gaTACTAAGCTGTGTCACTGCTTtctctcttttgtattcc	
ABCG16II	gaAAGCAGTGACACAGCTTAGTAtcaaagagaatcaatga	
ABCG16III	gaAAACAGTGACACACCTTAGTTtcacaggtcgtgatatg	
ABCG16IV	gaAACTAAGGTGTGTCACTGTTTtctacatatatattcct	

Table S7. RT-PCR measuring AtABCG16 expression in the two T-DNA insertion knockouts, *abcg16-1* and *abcg16-2*, relative to the Col-0 wildtype line (CS60000).

SALK Knockouts

	WT	***abcg16-1***	***abcg16-2***
Related to ACT2 rpp1	0.00044	0.00004	0.00010
Related to ACT2 rpp2	0.00051	0.00005	0.00012
Related to ACT2 rpp3	0.00085	0.00005	0.00007
Average	0.00060	0.00005	0.00010
Ratio	1	0.07749	0.16058
STDEV		0.01577	0.03776

Table S8. Plate assay results for germination (%) of *abcg16-1* and *abcg16-2* knockouts relative to the CS60000 background in response to low (0-3 µM) or high (0-300 µM) range abscisic acid (ABA), indole-3-acetic acid (IAA), or salicylic acid (SA).

Experiment	Trt	Line	No. plates	No. Seeds per plate	Germination Average (%)	+/- SE
Low Range	Control	Background	6	25	92.7	0.7
		abcg16-1	6	25	89.3	2.2
		abcg16-2	6	25	91.3	3.0
	ABA 1uM	Background	6	25	94.0	2.3
		abcg16-1	6	25	88.0	2.1
		abcg16-2	6	25	78.0	4.5
	ABA 3uM	Background	6	25	52.0	5.4
		abcg16-1	6	25	2.7	1.3
		abcg16-2	6	25	29.3	4.2
	IAA 1uM	Background	6	25	92.7	1.6
		abcg16-1	6	25	88.7	3.5
		abcg16-2	6	25	78.7	2.0
	IAA 3uM	Background	6	25	93.3	2.2
		abcg16-1	6	25	88.7	2.8
		abcg16-2	6	25	82.0	4.6
	SA 1uM	Background	6	25	94.0	3.2
		abcg16-1	6	25	88.0	4.5
		abcg16-2	6	25	86.7	3.2
	SA 3uM	Background	6	25	93.3	1.3
		abcg16-1	6	25	92.0	2.7
		abcg16-2	6	25	85.3	4.3
High Range	Control	Background	5	25	93.6	2.4
		abcg16-1	5	25	95.2	3.2
		abcg16-2	5	25	94.4	3.0
	ABA 100uM	Background	5	25	0.0	0.0
		abcg16-1	5	25	0.0	0.0
		abcg16-2	5	25	0.0	0.0
	ABA 300uM	Background	5	25	0.0	0.0
		abcg16-1	5	25	0.0	0.0
		abcg16-2	5	25	0.0	0.0
	IAA 100uM	Background	5	25	89.6	1.6
		abcg16-1	5	25	92.0	2.2
		abcg16-2	5	25	91.2	4.8
	IAA 300uM	Background	5	25	91.2	3.9
		abcg16-1	5	25	88.8	2.0
		abcg16-2	5	25	94.4	1.6
	SA 100uM	Background	5	25	87.2	5.0
		abcg16-1	5	25	89.6	3.5
		abcg16-2	5	25	96.0	1.8
	SA 300uM	Background	5	25	0.0	0.0
		abcg16-1	5	25	0.8	0.8
		abcg16-2	5	25	2.4	1.6

Table S9. Plate assay results for germination (%) on day 4, root length (cm) on day 10, and mortality (%) on day 30 of *abcg16-1* and *abcg16-2* knockouts relative to the CS60000 background in response to four concentrations of abscisic acid (ABA).

				Germination (%)		Root Length (cm)		Mortality (%)	
Treatment	**Line**	**No. Plates**	**No. Seeds / Plate**	**Average**	**+/- SE**	**Average**	**+/- SE**	**Average**	**+/- SE**
Control	Background	10	25	91.2	2.2	1.25	0.07	0.9	0.9
	abcg16-1	10	25	88.8	2.0	1.19	0.07	1.3	0.7
	abcg16-2	10	25	94.8	1.0	1.25	0.09	2.1	1.3
0.5uM ABA	Background	10	25	92.8	1.8	1.11	0.04	22.3	5.6
	abcg16-1	10	25	83.6	2.7	1.08	0.06	25.9	6.6
	abcg16-2	10	25	87.2	2.3	0.72	0.05	45.1	4.5
1.0uM ABA	Background	10	25	93.2	1.5	1.02	0.04	33.5	2.0
	abcg16-1	10	25	78.4	2.2	0.80	0.04	57.4	3.8
	abcg16-2	10	25	84.0	2.1	0.65	0.03	66.2	3.3
1.5uM ABA	Background	10	25	90.4	1.6	0.99	0.04	70.5	7.1
	abcg16-1	10	25	74.0	4.7	0.82	0.03	61.0	5.9
	abcg16-2	10	25	72.4	2.9	0.40	0.02	75.1	3.5

Table S10. Leaf bacterial titers at 18 days post infection (dpi) following surface spray inoculation of soil-grown plants with *Pst* DC3118 (COR- mutant) and *Pst* DC3000 (COR+ wildtype) at Day 36 of plant growth. Six independent plants of Col-0 (background) and two T-DNA insertion knockouts of *ABCG16* (*abcg16-1*, *abcg16-2*) were sampled for each bacterial strain, for a total of 36 plants.

Bacterial Strain	PlantLine	Plant	Disk Area(cm^2)	Log(cfu/cm^2)	Average Log(cfu/cm^2)
Pst DC3000	Col-0	1	0.282	5.61	5.60
		2	0.282	5.47	
		3	0.282	5.86	
		4	0.282	5.31	
		5	0.282	5.55	
		6	0.282	5.77	
	abcg16-1	1	0.282	5.44	5.58
		2	0.282	5.44	
		3	0.282	5.55	
		4	0.282	5.54	
		5	0.282	5.92	
		6	0.282	5.58	
	abcg16-2	1	0.282	6.19	5.78
		2	0.282	5.46	
		3	0.282	5.64	
		4	0.282	5.61	
		5	0.282	5.77	
		6	0.282	6.02	
Pst DC3118	Col-0	1	0.282	5.08	5.23
		2	0.282	5.01	
		3	0.282	5.19	
		4	0.282	5.34	
		5	0.282	5.08	
		6	0.282	5.66	
	abcg16-1	1	0.282	5.45	5.47
		2	0.282	5.48	
		3	0.282	5.49	
		4	0.282	5.31	
		5	0.282	5.65	
		6	0.282	5.44	
	abcg16-2	1	0.282	5.74	5.54
		2	0.282	5.42	
		3	0.282	5.51	
		4	0.282	5.55	
		5	0.282	5.44	
		6	0.282	5.57	

Table S11. Shoot dry biomass (mg) at Day 95 of plant growth following surface spray inoculation of soil-grown plants with *Pst* DC3118 (COR- mutant) and *Pst* DC3000 (COR+ wildtype) at Day 36 of plant growth. Twelve independent plants of Col-0 (background) and two T- DNA insertion knockouts of *ABCG16* (*abcg16-1*, *abcg16-2*) were harvested from each treatment, for a total of 72 plants.

Bacterial Strain	Plant Line	No. Plants	Average Shoot Dry Mass(mg)	+/- SE
Pst DC3118	Background	12	34.3	4.1
	abcg16-1	12	36.1	4.3
	abcg16-2	12	29.0	3.3
Pst DC3000	Background	12	36.9	3.9
	abcg16-1	12	19.4	3.0
	abcg16-2	12	23.5	2.4