SUPPLEMENTAL FIGURE LEGENDS AND TABLES I-III

Supplementary Figure 1: Alignment of Farnesyltransferases from different plant species. Amino acid sequences were aligned using clustalW (http://www.ebi.ac.uk/clustalw/) and shaded using boxshade (http://www.ch.embnet.org/software/BOX_form.html). Conserved residues are shaded in black and similar residues are shaded in grey. The newly predicted start codon is indicated with a red *. At_ERA1 *Arabidopsis thaliana* (accession NP_198844); Le_FTaseB *Lycopersicon esculentum* (tomato, accession AB69757); Cr_FTase B: *Catharanthus roseus* (Madagascar periwinkle, accession AAQ02809); Os_FTaseB *Oryza sativa* japonica cultivar-group (rice, accession NP_001044183); Ps_FTaseB: *Pisum sativum* (pea, accession Q04903).

Supplementary Figure 2: Response of *era1* alleles to flg22.
Following procedures described in Gomez-Gomez *et al*., 1999, seedlings grown for ten days on MS agar plates were transferred to liquid MS or liquid MS supplemented with 30 μM flg22. The fresh weight of 20 plants from each treatment was analyzed 10 days later by weighing. Errar bars represent standard deviation, and the experiment was repeated once with similar results. (a) Data presented as bar format. (b) Pictures of representing seedlings. In each panel, the left two plants are the ones soaked in MS supplemented with flg22, while the right two seedlings are the control plants soaked in MS alone.

Supplementary Figure 3: Levels of ABA and its metabolites in leaves of Col and *snc1*.

DPA X 0.1, dihydrophaseic acid; PA phaseic acid; n-PA neophaseic acid. n=3.The experiment was repeated once with similar results.

Supplementary Figure 4: Contribution of ABA in *era1*-mediated enhanced pathogen susceptibility.
(a) Plants were infected with avirulent *P.s.t.* DC3000 carrying *AvrRPM1*.
(b) Plants were infected with avirulent *P.s.t.* DC3000 carrying *AvrRPS4*.
(d) Plants were infected with avirulent *H.p.* Cala2 carrying *AvrRPP2*.
Bacterial growth was determined as colony forming units dpi. Experiments were repeated at least once with similar results. Bars represent the average of six biological replicates, error bars indicate standard deviation.

Supplemental Table 1: Allelism test between several *era1*-alleles and *mos8 snc1 npr1-1.*

cross[1)]	F_1 morphology[2)]	F_2 phenotypic segregation [3)] total	wt-like	*snc1*-like	*era1*-like
era1-8 X *mos8 snc1 npr1-1*	*era1*-like	197	0	0	197
mos8 snc1 npr1-1 X *era1-5*	*era1*-like	150	0	0	150
mos8 snc1 npr1-1 X *era1-6*	*era1*-like	125	0	0	125
era1-2 X *era1-7*	*era1*-like	205	0	0	205

[1)] The crosses are indicated with the female parent first, the male parent second. *era1-4,5,6* are in Ler ecotype, *era1-2,8* are in Col ecotype.
[2)] F_1 phenotypes were scored for seedlings sown on MS-plates and transferred to soil, based on flowering time and morphology.
[3)] F_2 phenotypes were scored for seedlings stratified for seven days and sown directly on soil. wt, wild type.

Supplemental Table 2: Multiple *era1* alleles suppress *snc1.*

cross[1)]	F_1 morphology [2)]	F_2 phenotypic segregation [3)] total	wt-like	*snc1*-like	*era1*-like	hypothesis[4)]	χ^2	P
snc1 X *era1-4*	wt-like	142	80	28	34	9 : 3 : 4	0.1346	0.93
era1-5 X *snc1*	wt-like	104	61	20	23	9 : 3 : 4	0.4658	0.79
snc1 X *era1-6*	wt-like	168	92	35	41	9 : 3 : 4	0.4788	0.79
era1-8 X *snc1*	wt-like	327	175	66	86	9 : 3 : 4	1.0136	0.60
era1-2 X *snc1*	wt-like	206	118	41	47	9 : 3 : 4	0.5782	0.75

[1)] The crosses are indicated with the female parent first, the male parent second. *era1-4,5,6* are in Ler ecotype, *era1-2,8* are in Col ecotype.
[2)] F_1 phenotypes were scored for seedlings sown on MS-plates and transferred to soil, based on flowering time and morphology. wt, wild type.
[3)] F_2 phenotypes were scored for seedlings stratified for seven days and sown directly on soil.
[4)] The hypothesis for suppression of *snc1* in the F_2 is 9 wild type : 3 *snc1*-like : 4 *era1*-like.

Supplemental Table 3: Putative ERA1-targets tested in this study.

Gene ID	Putative function/homology	CAAX[1)]	T-DNA lines tested[2)]	location of T-DNA insert[3)]
At1g18760	Zinc finger (C3HC4-type RING finger) family protein	CEDQ	SALK_109030	300-UTR5
At1g22790	Expressed protein	CVIM	SALK_141943	300-UTR5
At1g23000	Heavy-metal-associated domain-containing protein	CNIM	SALK_114825	Exon
At1g27850	Similar to En/Spm-like transposon protein	CSIM	SALK_005882	300-UTR3
At1g28550	Putative Ras-related GTP-binding protein	CCSA	SAIL_218_C11	Exon
At1g33480	Zinc finger (C3HC4-type RING finger) family protein	CRMQ	SALK_108072	300-UTR3
At1g49420	Heavy-metal-associated domain-containing protein	CSIM	SALK_042250	Intron
At1g51580	Protein with KH domain/RNA binding protein	CGQS	SAIL_1285_H03	Exon
At1g67830	alpha-fucosidase 1	CKRQ	SALK_140323	300-UTR5
At1g74530	EscC (*E. coli*) Type III secretion system component	CAKS	SALK_110280	Intron
At2g47950	Hypothetical endomembrane protein	CLAS	SALK_142871	Exon
At3g04900	Heavy-metal-associated domain-containing protein	CSIM	SALK_037340	300-UTR5
At3g06300	Prolyl-4 hydroxylase	CKAC	SALK_034891	300-UTR3
At3g07600	Heavy-metal-associated domain-containing protein	CRIM	SAIL_118_F05	Intron
At3g13140	Hydroxyproline-rich glycoprotein family protein	CVIM	SALK_001636	300-UTR5
At3g21490	Copper-binding family protein	CSIS	SALK_101142	Intron
At3g26380	Glycosyl hydrolase family protein 27	CSNA	SALK_016141, SALK_117663	300-UTR5
At3g26980	Ubiquitin domain containing protein	CTIM	SALK_045794	Promoter
At3g44630	Disease resistance protein RPP1-WsB-like	CVSS	SALK_144159	Exon
At3g55260	Glycosyl hydrolase family protein 20	CYAQ	SALK_026094	Exon

Homozygous T-DNA insertion lines were tested for disease phenotypes after inoculation with *H. parasitica* and/or *P.s.m.* ES4326 (see Methods). Among all, none showed significant difference in resistance/susceptibility compared to simultaneously inoculated wild type plants.

continued on next page.

Gene ID	Putative function/homology	CAAX[1)]	T-DNA lines tested[2)]	Location of T-DNA insert[3)]
At4g32780	Expressed protein	CFLA	SALK_011990	300-UTR5
At5g03380	Heavy-metal-associated domain-containing protein	CSVM	SALK_111020	Exon
At5g08310	Pentatricopeptide (PPR) repeat-containing protein	CFCS	SALK_110420	Exon
At5g17450	Heavy-metal-associated domain-containing protein	CSIM	SALK_092415	Intron
At5g33335	Defensin-like family protein	CYKS	SAIL_667_C08	Exon
At5g42440	Protein kinase	CRFM	SALK_134111	Exon
At5g44880	Hypothetical protein	CRRC	SALK_122906	Exon
At5g52740	Heavy-metal-associated domain-containing protein	CVTS	SALK_082835, SALK_012334	300-UTR3, 300-UTR5
At5g63530	Copper chaperone (CCH)-related	CTVM	SALK_082835	300-UTR3
At5g66110	Heavy-metal-associated domain-containing protein	CTIM	SALK_051332	300-UTR5

Supplemental Table 3 continued.

[1)] CAAX-box denoting the farnesyltransferase recognition consensus at the C-terminus of putative targets.
[2)] T-DNA lines were obtained from ABRC and tested for homozygosity by PCR using a combination of T-DNA and gene specific primers.
[3)]Location of T-DNA insert. Over 50% of tested Salk-lines carry the T-DNA inside the gene (37.5% in exon, 15.625% in intron), while the remainder remaining lines have the T-DNA in the promoter (3.125%) or untranslated regions (28.125% 5'UTR, 15.625% 3'UTR)