Supplementary Figure 1 : Responses of the allene oxide synthase mutant dde2-2 to *B. cinerea.*

(A) PR1 mRNA accumulation in WT Col-0 and dde2-2 plants infected with B. cinerea. The leaves from sixteen plants were harvested at the indicated time points after being sprayed with mock or B. cinerea. transcript levels were quantified by real-time PCR and normalized to the plant reference gene AT4G26410 transcript level (Czechowski et al., 2005). Data are expressed as normalized expression (no unit) and are the mean of duplicates. Experiment has been repeated twice.

(B) Diameter of lesions observed on WT Col-0 and dde2-2 plants after inoculation with B. cinerea. Plants were inoculated by depositing 6 µL of spore suspension on leaves and lesion diameters were measured 3 days after. The data represent the mean of 3 independent experiments. Significant difference from WT plants was determined by a t-test (* $P<0.01$).

Supplementary Figure 2 : Alignment of the genomic sequence of AT1G03850 to the cDNA of the three ATG1G03850 splice variants.

Alignment was made using dialign (Morgenstern, 1999) and displayed using Jalview2 (Waterhouse et al., 2009).

Waterhouse, A.M., Procter, J.B., Martin, D.M., Clamp, M. and Barton, G.J. (2009) Jalview Version2 - a multiple sequence alignment editor and analysis workbench. Bioinformatics, 25, 1189-1191.

Morgenstern, B. (1999) DIALIGN 2: improvement of the segment-to-segment approach to multiple sequence alignment. Bioinformatics, 15, 211-218.

Supplementary Figure 3: Phenotype of the grxs13 mutants infected with B. cinerea.

Lesion size distribution observed on WT Col and grxs13 mutants after inoculation with *B. cinerea*. Plants were inoculated and lesion diameters (LD) were measured 3 days after and grouped into three classes according to their sizes. The percentage of lesion distribution from 12 (grxs13-1) and 6 (grxs13-2) independent experiments is shown. Significant differences from WT plants were determined by a one-way ANOVA analysis followed by a multiple comparison with the Student-Newman-Keulsmethod (* $P<0.05$).

Supplementary Figure 4 : Histochemical detection of ROS accumulation by diaminobenzidine (DAB) staining in wild type Col plants and in plants overexpressing GRXS13 splice variants.

DAB staining was processed as described by Trouvelot *et al.* (2008) on 2 independant lines over-expressing ATGRXS13.1 (1.5 and 1.15), ATGRXS13.2 (2.7 and 2.8) and ATGRXS13.3 (3.8 and 3.18). The brown precipitate representative of hydrogen peroxide production was not observed neither in WT Col plants nor in plants over-expressing ATGRXS13 splice variants.The experiment was performed on 5-weeks old plants and was repeated twice with similar results.

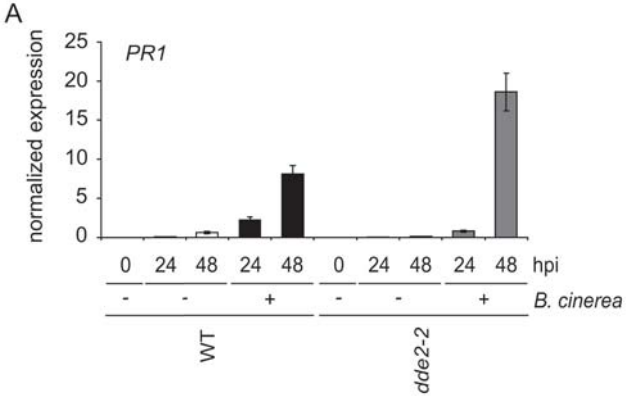
Trouvelot, S., Varnier, A.-L., Allègre, M., Mercier, L., Baillieul, F., Arnould, C., Gianinazzi-Pearson, V., Klarzynski, O., Joubert, J.-M., and Pugin, A. (2008) A β-1,3 glucan sulfate induces resistance in grapevine against Plasmopara viticola through priming of defense responses, including HR-like cell death. Mol. Plant-Microbe Interact. 21, 232-243.

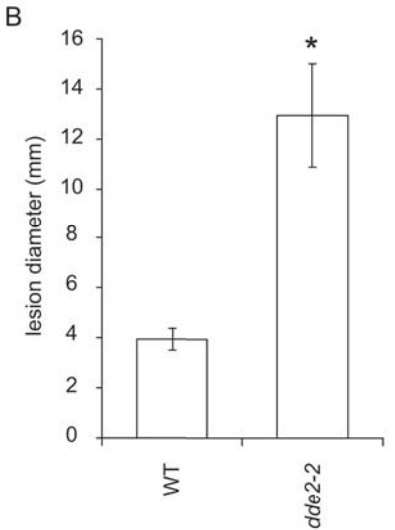
Supplementary Figure 5 : Sequence of the 1,500 bp upstream of the transcriptional starting site of ATGRXS13.

The surrounded TGACGTCA sequences correspond to the perfect binding site for TGA transcription factor dimers and the underlined sequences TGACG corresponds to the minimal TGA recognition element. Sequence in light gray correspond to the 5'-UTR of AT1G03850 that ends with the start codon ATG in capitals.

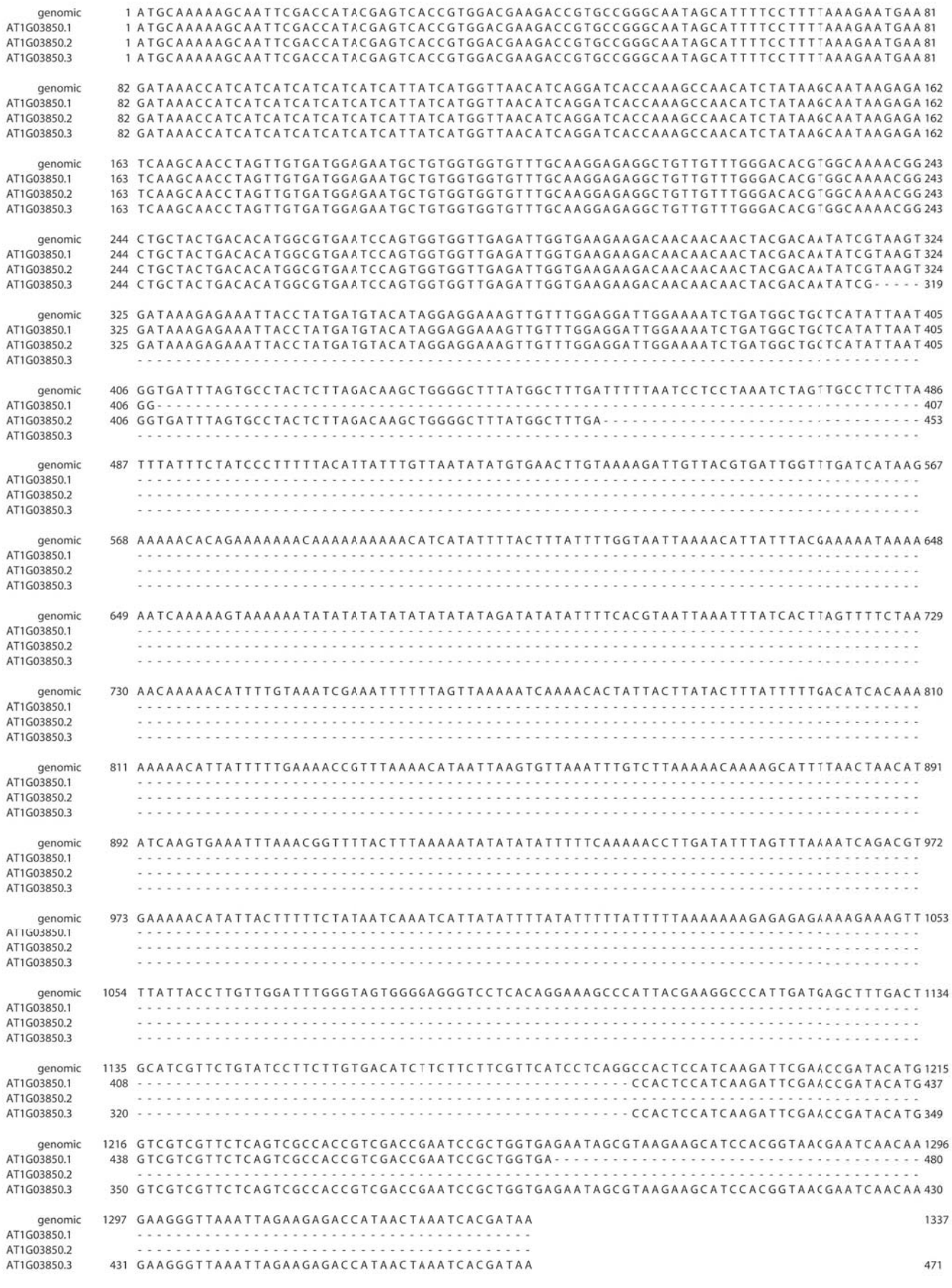
Supplementary Figure 6 : Role of ATGRXS13 in the accumulation of mRNA coding classical defense genes induced after *B. cinerea* infection and in the accumulation of the phytoalexin camalexin.

PR1 (A), *PDF1.2* (B), *PAD3* (C) mRNA accumulation in WT Col and *grxs13-1* mutant plants infected with *B. cinerea*. The leaves from sixteen plants were harvested at the indicated time points after mock- or *B. cinerea* inoculation. Transcript level were quantified by real-time PCR. Data are expressed as normalized expression (no unit) +/- SD. Camalexin level (D) was quantified as described (see Material and method part). The leaves from sixteen plants harvested at the indicated time points after mock- or *B. cinerea* inoculation. The data are the mean of three independant biological experiments +/- SD. Different letters represent groups which are significantly different from one another as determined by a one-way ANOVA followed by a multiple comparison with the Student-Newman-Keuls method ($P<0.05$). FW : fresh weight.

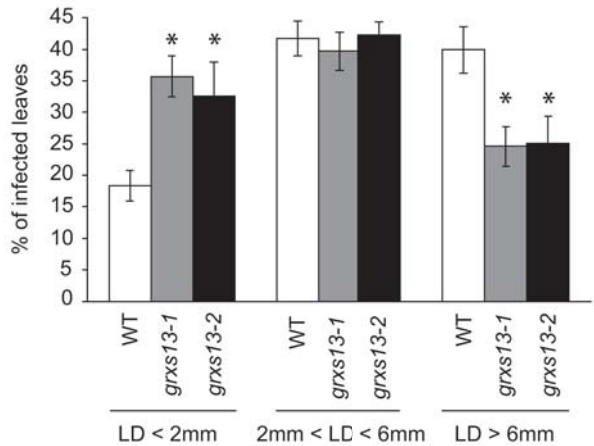




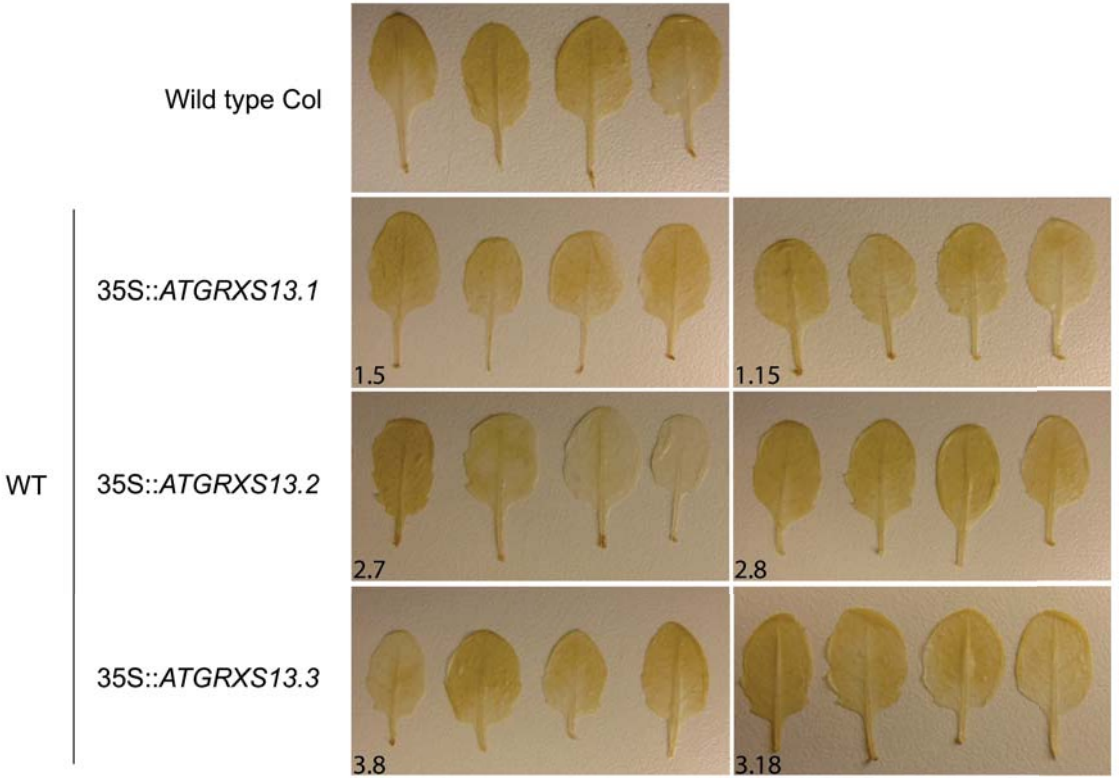
La Camera *et al.*, Supplementary Figure1



La Camera *et al.*, Supplementary Figure 2

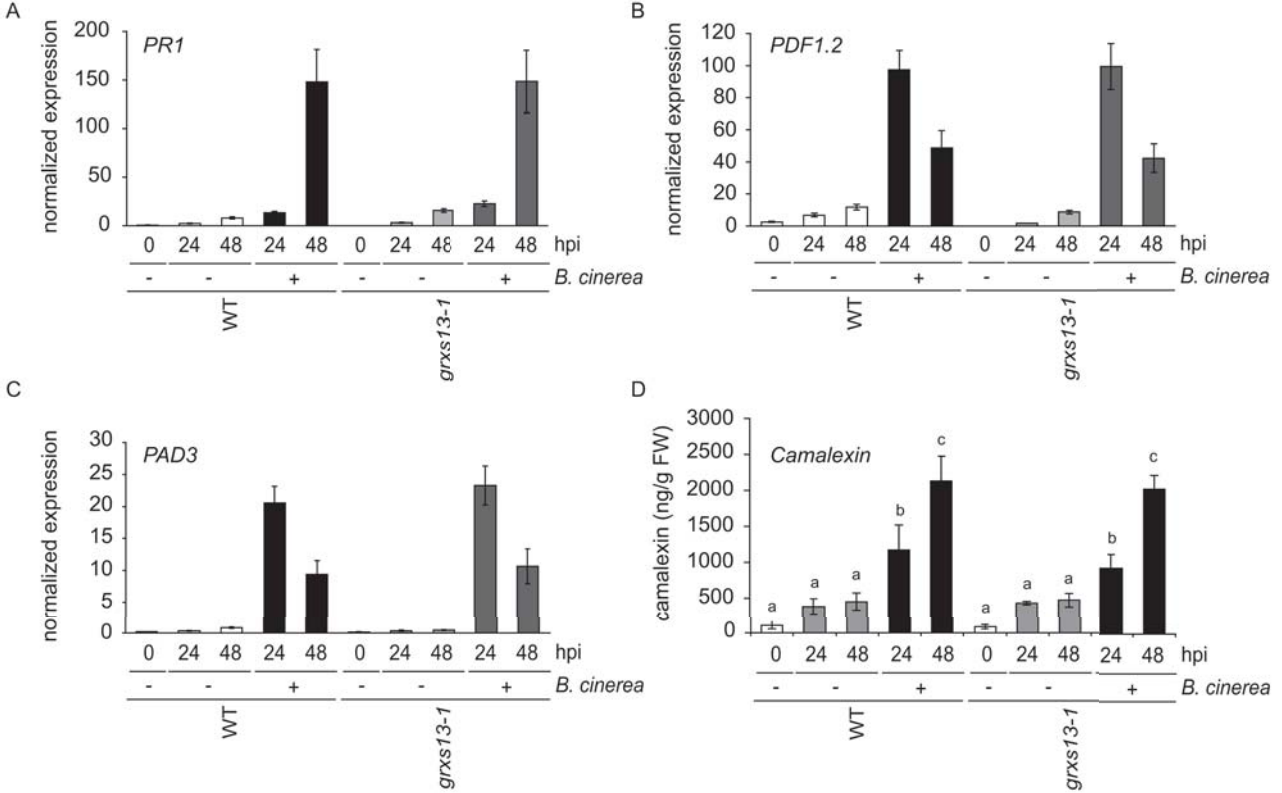


La Camera *et al.*, Supplementary Figure 3



La Camera *et al.*, Supplementary Figure 4

La Camera *et al.*, Supplementary Figure 5



La Camera *et al.*, Supplementary Figure 6

Supplementary data – TABLE SI 1 – list of primers used in La Camera *et al.*

primer name	Sequence	target sequence in Arabidopsis	reference
LBa1	TGGTTCACGTAGTGGGCCATCG	none	Science, 301: 653-657
S13-1 RP	AGGACGTGTACTGGGTAGTGG	*At1G03850*	this work
S13-1 LP	AAAATCAAAGCCATAAAGCCC	*At1G03850*	this work
S13-2 RP	ACGAACCCAACTACACAAGTC	*At1G03850*	this work
S13-2 LP	TTCATCTCAGAACCTATCCGT	*At1G03850*	this work
GRXS13promAttB4	GGGGACAACTTTGTATAGAAAAGTTGGTAAGATCCGTACCAATCCTTTCA	*promoter At1G03850*	this work
GRXS13promAttB1r	GGGGACTGCTTTTTTGTACAAACTTGCAATTGATGATAGAGAGACAAAGA	*promoter At1G03850*	this work
GRXS13Y2Hfor	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGCAAAAAGCAATTCGACC	*At1G03850.2*	this work
GRXS13Y2Hrev	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAGGAGGATTAAAAATCAAAGCC	*At1G03850.2*	this work
GRXS13fw1	CACCACGAACCCAACTACACAAGTC	*At1G03850.1, At1G03850.2, At1G03850.3*	this work
GRXS13rev1	TTCATCTCAGAACCTATCCGT	*At1G03850.1, At1G03850.3*	this work
GRXS13rev2	AAGGGATAGAAATAAATAAGAAGGCAAC	*At1G03850.2*	this work
AT1G03850.1qPCRfw	TGGAAAATCTGATGGCTGCTC	*At1G03850.1*	this work
AT1G03850.1qPCRrev	GATTTGAGCGGAGGAAAGCA	*At1G03850.1*	this work
AT1G03850.2qPCRfw	CAGGATCACCAAAGCCAACA	*At1G03850.2*	this work
AT1G03850.2qPCRrev	AAGGGATAGAAATAAATAAGAAGGCAAC	*At1G03850.2*	this work
AT1G03850.3qPCRfw	TGCAAAAAGCAATTCGACCA	*At1G03850.3*	this work
AT1G03850.3qPCRrev	TTGATGGAGTGGCGATATT	*At1G03850.3*	this work
PDF1.2qPCRfw	TTTGCTGCTTTCGACGCAC	*At5G44420*	Plant Cell, 17:2384-2396
PDF1.2qPCRrev	CGCAAACCCCTGACCATG	*At5G44420*	
PR1qPCRfw	AAGGGTTCACAACCAGGCAC	*At2G14610*	Plant Cell, 19:3266-3279
PR1qPCrev	CACTGCATGGGACCTACGC	*At2G14610*	
PAD3qPCRfw	TGCTCCCAAGACAGACAATG	*At3G26830*	Plant J., 55: 555-567
PAD3qPCRrev	GTTTTGGATCACGACCCATC	*At3G26830*	
AT4G26410qPCRfw	GAGCTGAAGTGGCTTCCATGAC	*At4G26410*	Plant Physiol., 139: 5-17
AT4G26410qPCRrev	GGTCCGACATACCCATGATCC	*At4G26410*	

Primer combination	PCR amplification of :
GRXS13fw1 + GRXS13rev1	*At1G03850.1, At1G03850.3*
GRXS13fw1 + GRXS13rev2	*At1G03850.2*
GRXS13promAttB4 + GRXS13promAttB1r	*AT1G03850* promoter
GRXS13Y2Hfor + GRXS13Y2Hrev	*At1G03850.2* for yeast two hybrid experiment