

Title: Tomato genomic regions and candidate genes linked to responses to a resistance inducer against *Phytophthora infestans*

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Supplementary Information (SI)

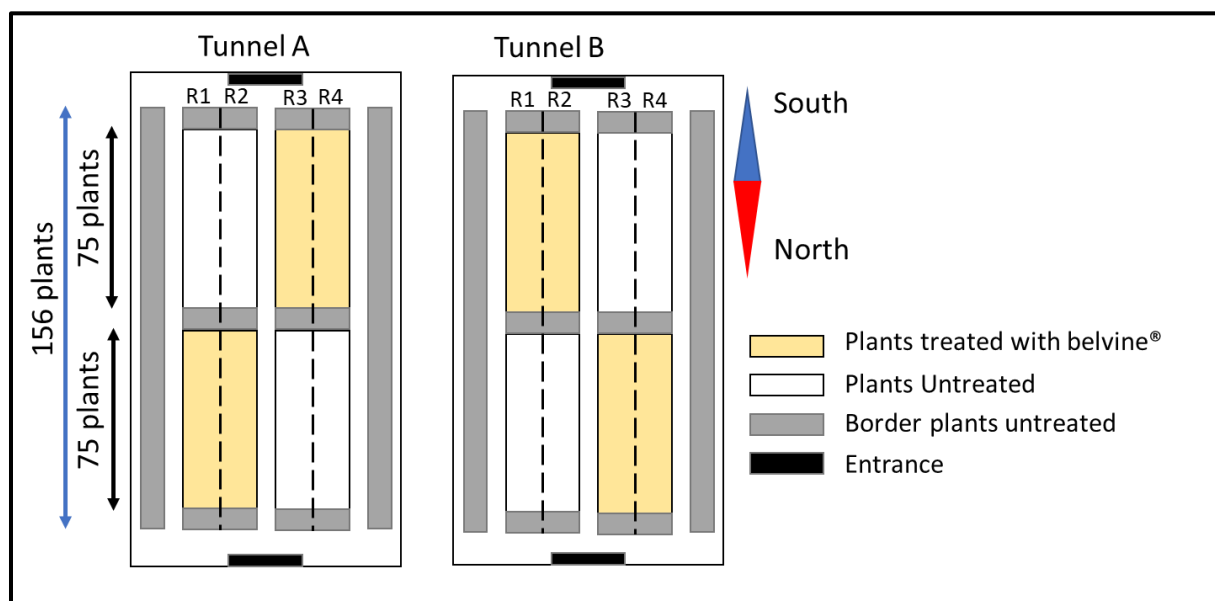


Fig. S1 Experimental design in trial 4. The design presented corresponds to the layout used in 2024. In 2025, the opposite layout was implemented. Each tunnel contained six rows: two single rows used as borders, and two double rows. Each double row was divided into two blocks corresponding to two modalities: one treated with Belvine®, and one untreated control. The two modalities were separated by two untreated Rose de Berne plants per row. Each block contained 150 tomato accessions, randomly assigned within its double row. The experiment was arranged so that each modality faced its opposite

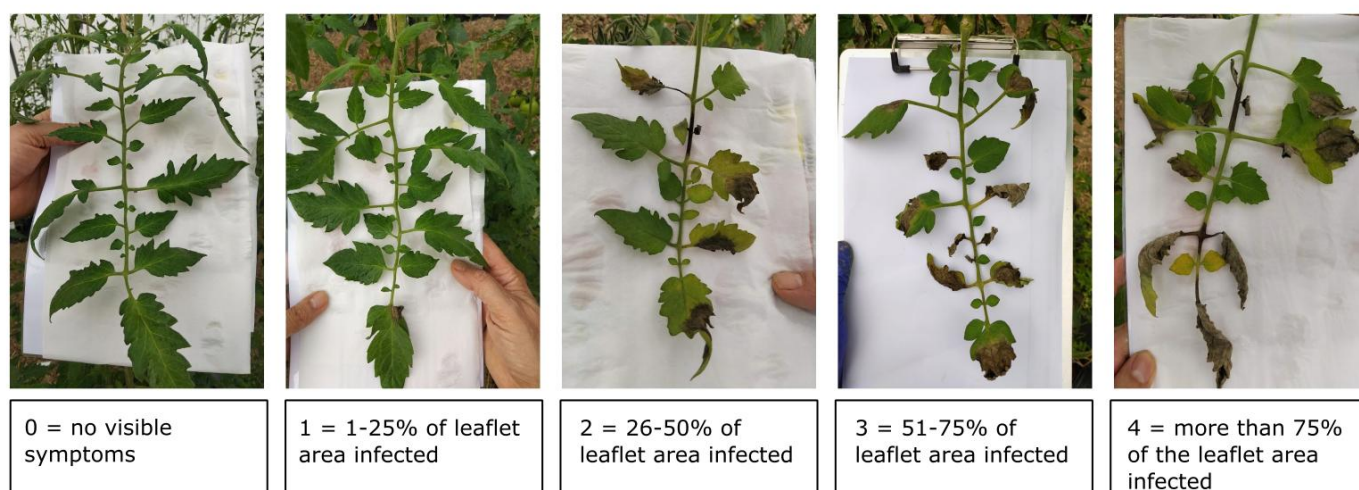


Fig. S2 Scale of disease severity on infected leaflets. Disease severity on infected leaflets was assessed using a 0-4 ordinal scale, where 0 = no visible symptoms; 1 = 1-25% of leaflet area infected; 2 = 26-50% of leaflet area infected; 3 = 51-75% of leaflet area infected; and 4 = more than 75% of the leaflet area infected

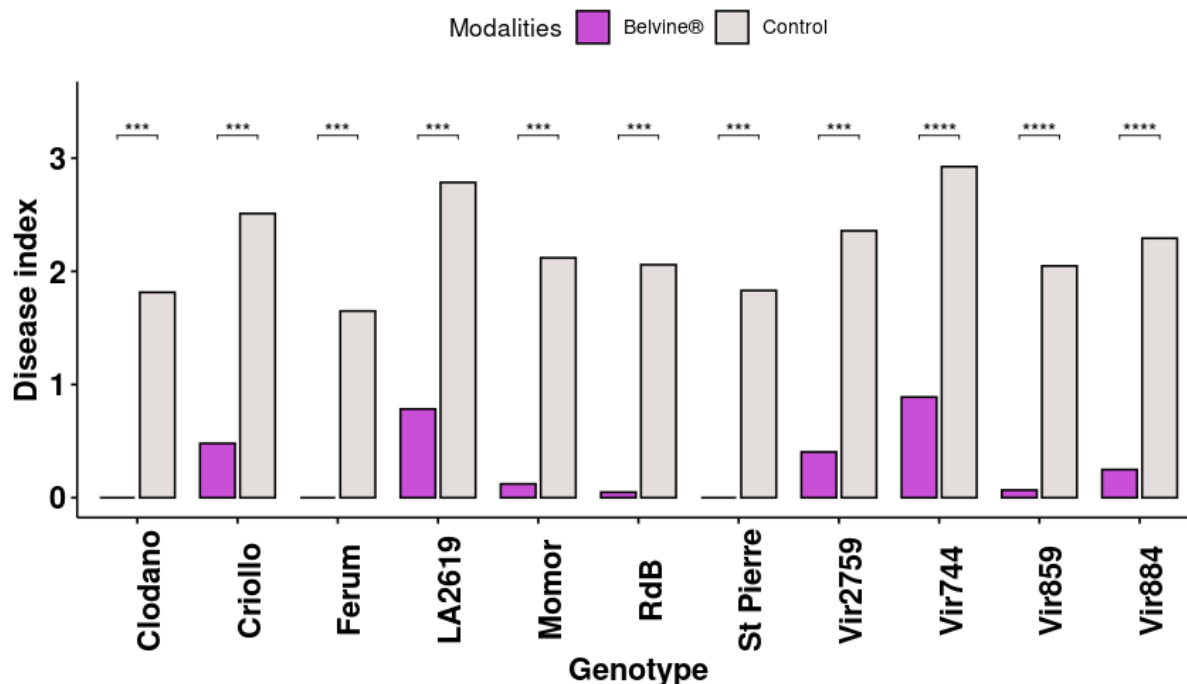


Fig. S3 Genotypic variation of Belvine® efficacy. Disease index of late blight calculated from four biological replicates for eleven tomato genotypes treated with Belvine® (purple), or untreated as controls (grey). Asterisks (*) indicate significant differences between treated and control modalities based on ANOVA.

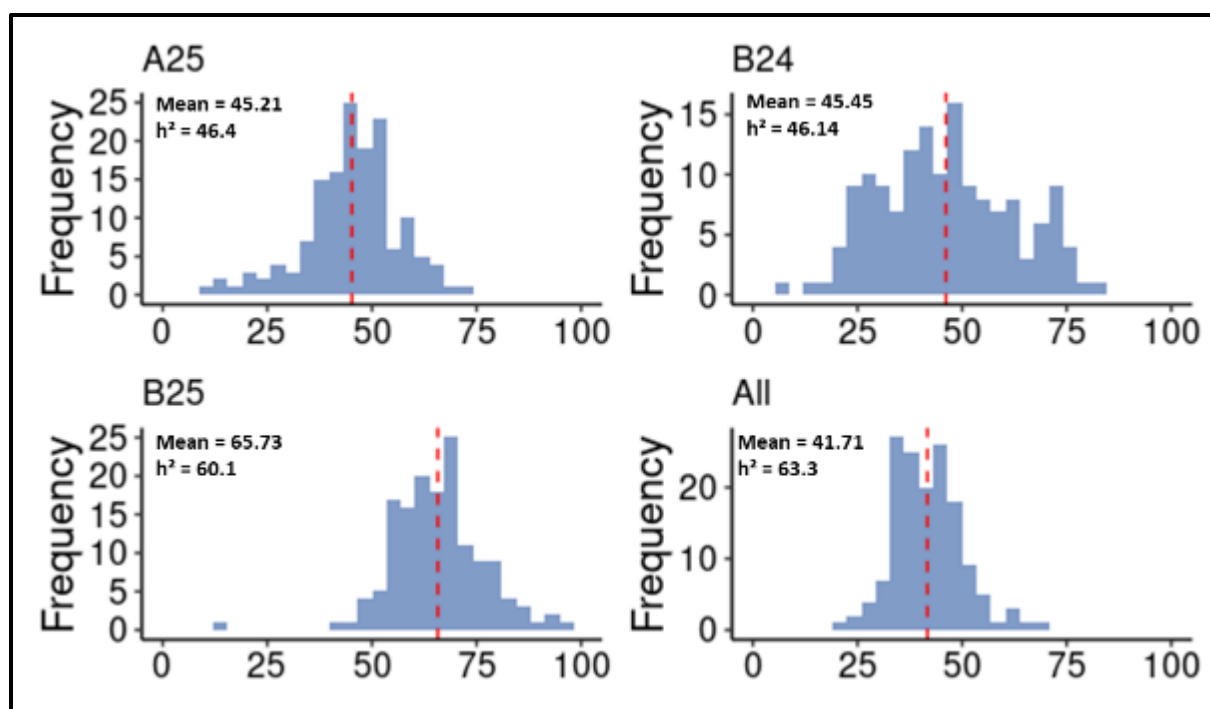
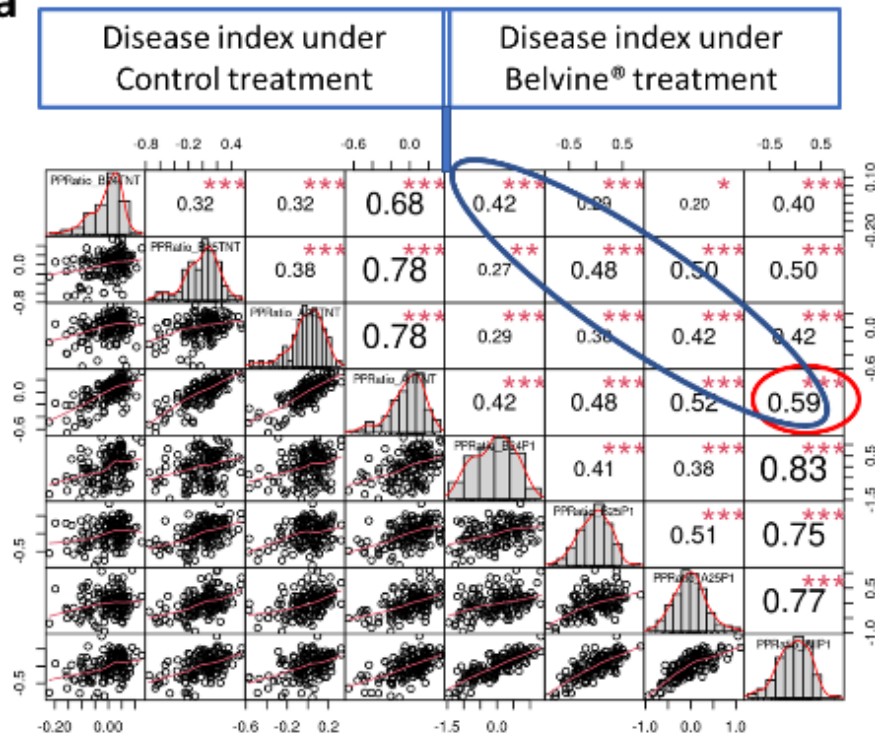


Fig. S4 Phenotypic distribution of the percentage of protection (PP) of 148 tomato accessions for each tunnel and the combined dataset (All). Combined PP represents the average of the three tunnels. PP = BLUP + mean. Blups are from spatial correction with statgenHTP Rpackage. Vertical lines in red indicate the average (mean) of PP. h^2 is the GBLUP calculated genomic heritability

a



b

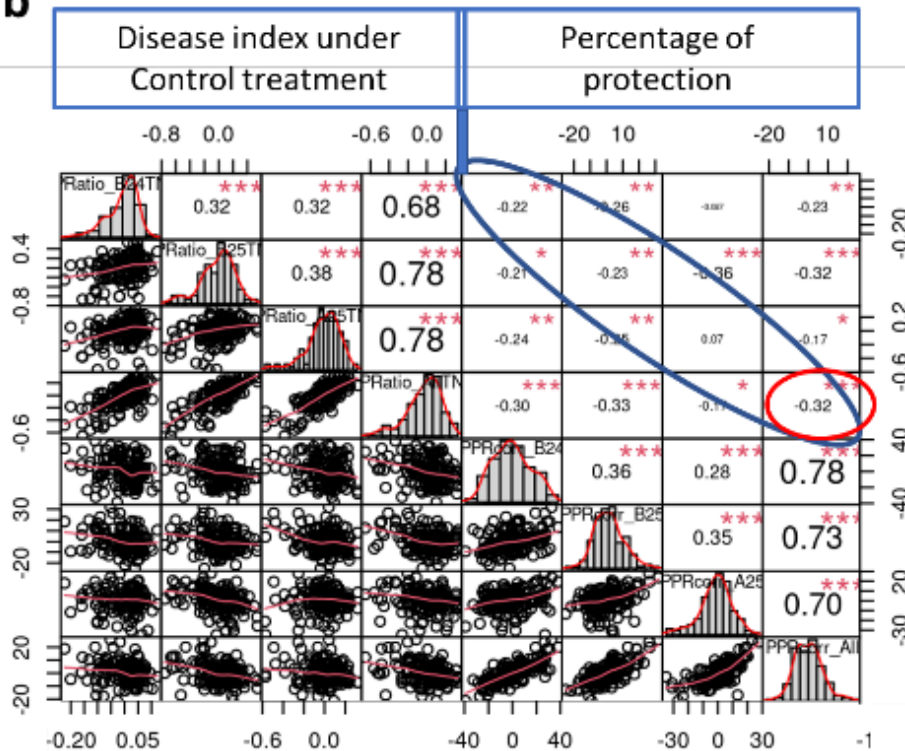


Fig. S5 Pairwise data correlation. a) between the disease index under control and Belvine® treatments. b) between the disease index under control treatment and the percentage of protection. Blue ellipses show the pairwise correlation coefficients within the tunnels, red ellipses emphasizes correlation coefficient with the combined dataset. (*) denotes significance at a P-value of 0.05, (**) denotes significance at a P-value of 0.01, (***) denotes significance at a P-value of 0.001. no Asterisk indicated the correlation coefficient is not statistically significant

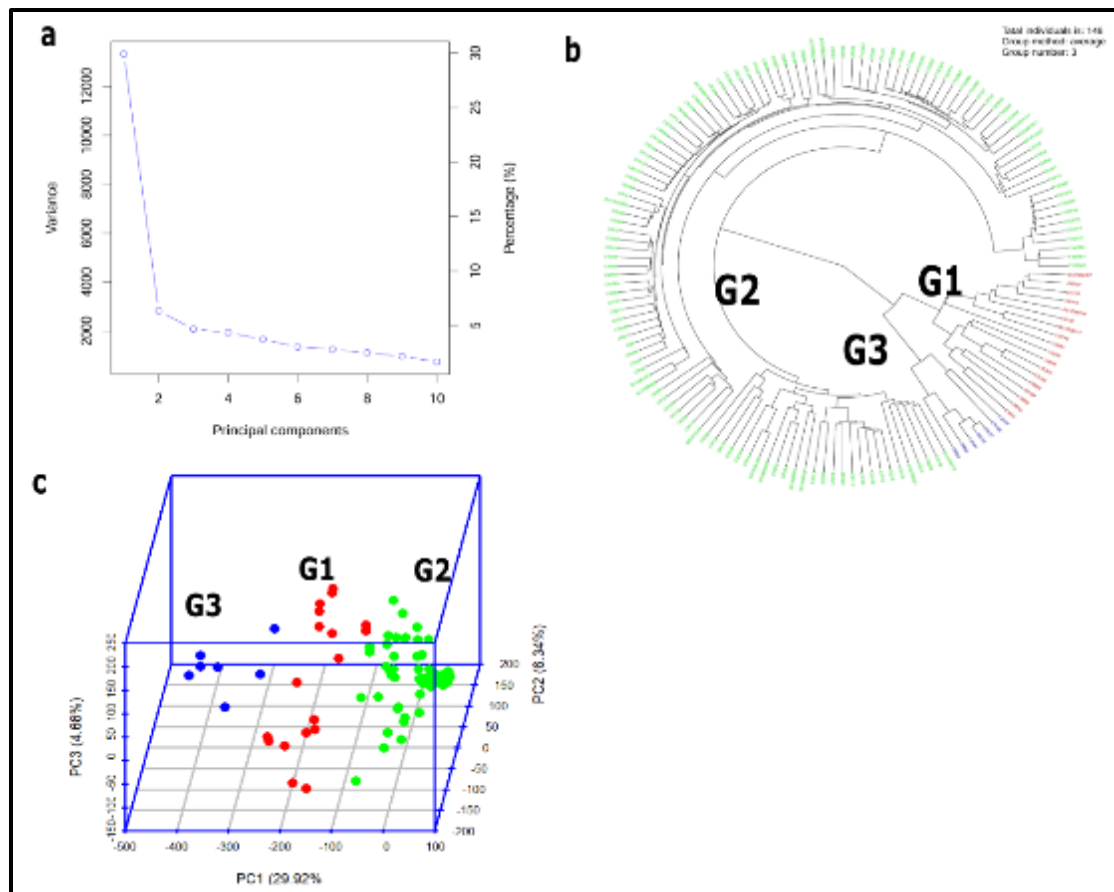


Fig. S6 Population genetic diversity analysis of the 148 tomato accessions. **a)** PCA eigenvalue plot generated using GAPIT 3, showing that the top three principal components (PCA = 3) explain majority of the variation among the 148 individuals; **b)** Phylogenetic tree constructed using the neighbor-joining (NJ) method, showing three subpopulations; and **c)** 3D graphical plot of principal component analysis (PCA), illustrating the three subpopulations

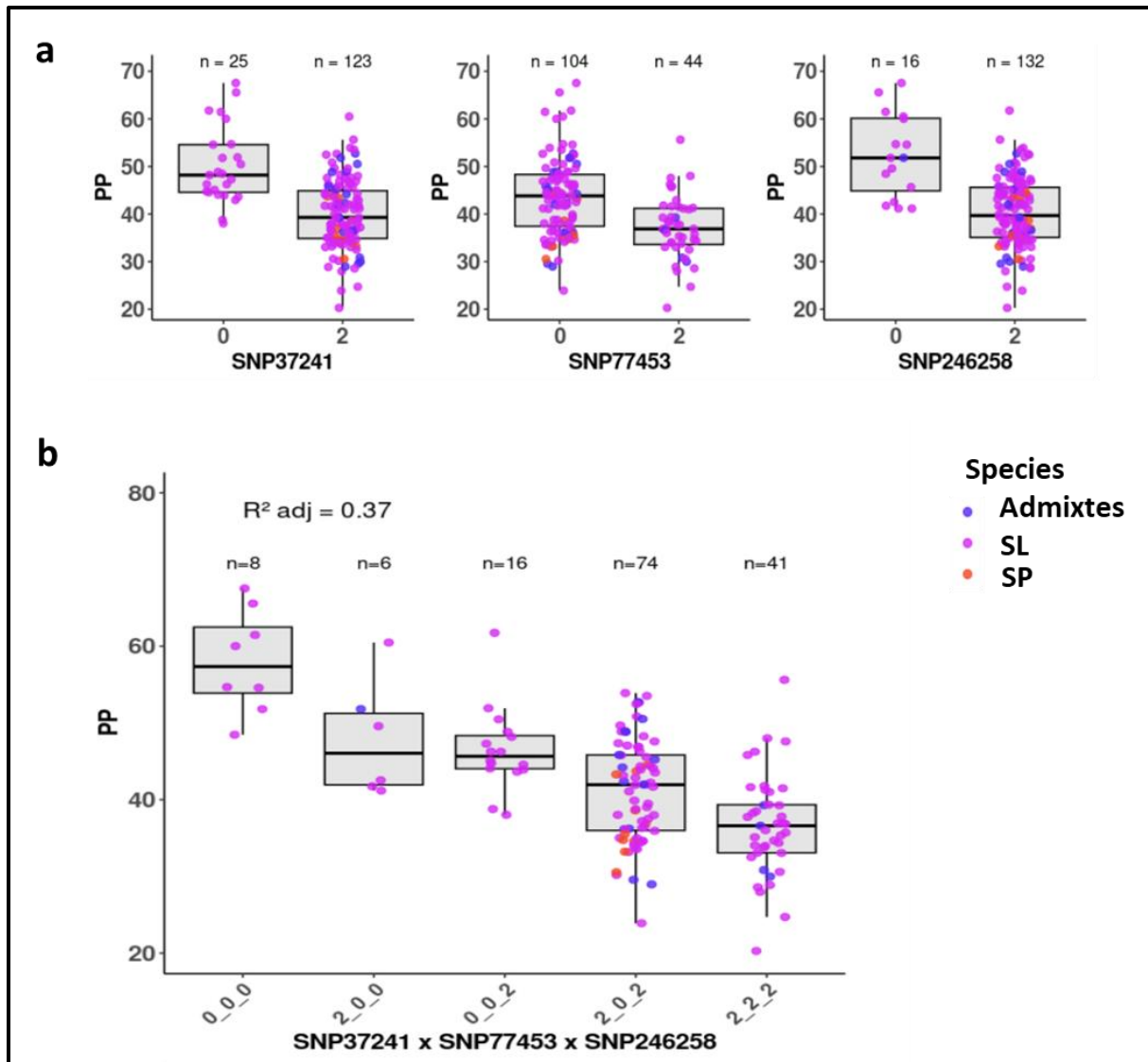


Fig. S7 Phenotypic differences of plant responses among the significant SNPs detected. a) phenotypic differences between the genotypes of the significant SNPs found with combined dataset. b) interaction plot of the three SNPs found with the combination of the data of the three tunnels. Difference point colors represent the species of the plant: SP for *Solanum pimpinellifolium* (red), SL for *Solanum lycopersicum*, including cerasiforme and large-fruited tomato (pink), and admixture for the admixtes of *Solanum lycopersicum* var. *cerasiforme* and *Solanum pimpinellifolium*. The text above the boxplot indicates the number of individuals in the genotypic class

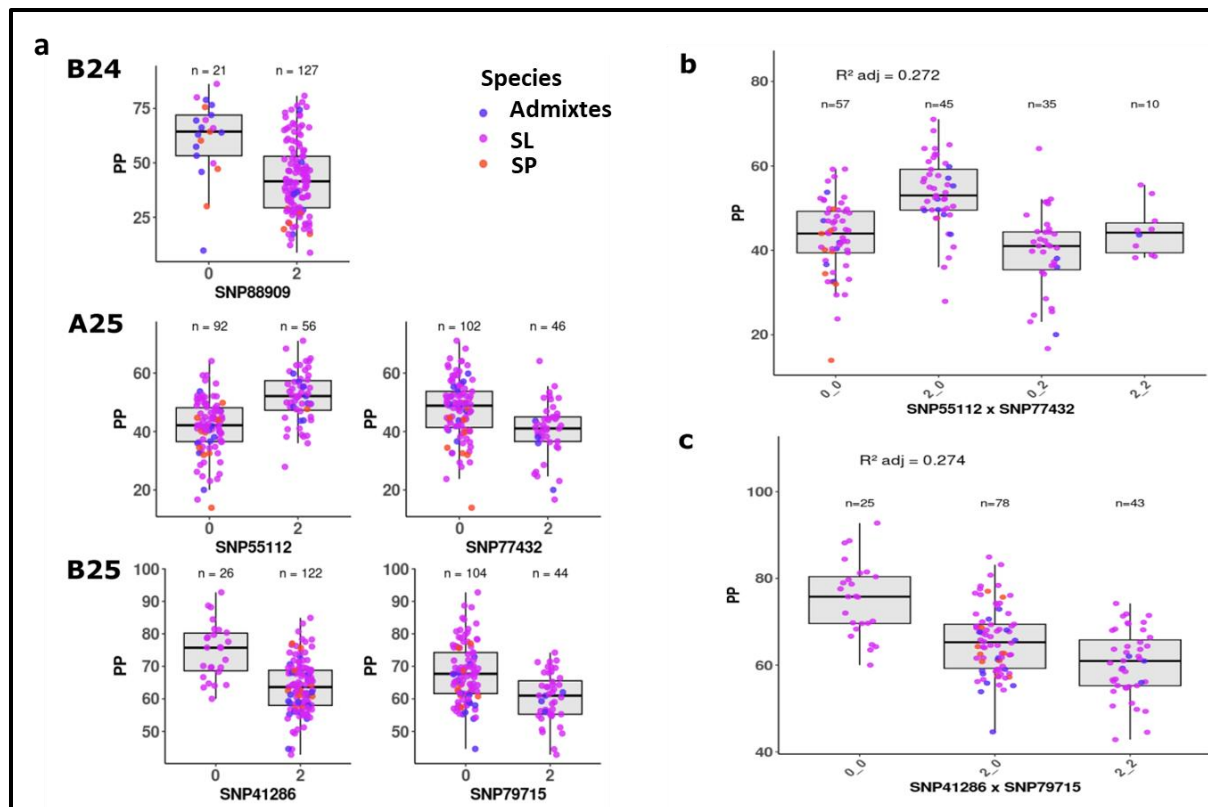


Fig. S8 Phenotypic differences of plant responses among the significant SNP detected. a) phenotypic differences between the genotypes of the significant SNPs found in tunnels B24, A25 and B25. b) phenotypic differences between the genotypic combination of the significant SNP. b) interaction plot of the two SNPs found in tunnel A25. c) interaction plot of the three SNPs found in tunnel B25; The text above the boxplot indicate the number of individuals in the genotypic class. Difference point colors represent the species of the plant: SP for *Solanum pimpinellifolium* (red), SL for *Solanum lycopersicum*, including cerasiforme and large-fruited tomato (pink), and mixture for the admixtures of SLC and SP

Table S1 List of tomato defense genes targeted for gene expression analysis

Gene	Name	Pathway or functions
<i>PR-1</i>	Pathogenesis-related protein 1	PR-protein
<i>PR-2</i>	Pathogenesis-related protein 2 (glucanases)	PR-protein
<i>PR-4</i>	Pathogenesis-related protein 4 (hevein-like)	PR-protein
<i>PR-5</i>	Pathogenesis-related protein 5 (thaumatin-like, osmotin)	PR-protein
<i>PR-8</i>	Pathogenesis-related protein 8 (class III chitinase)	PR-protein
<i>PR-14</i>	Pathogenesis-related protein 14 (lipid transfer protein)	PR-protein
<i>PR-15</i>	Pathogenesis-related protein 15 (oxalate oxidase)	PR-protein
<i>PAL</i>	Phenylalanine ammonia-lyase	Phenylpropanoid pathway
<i>CHS</i>	Chalcone synthase	Phenylpropanoid pathway
<i>DFR</i>	Dihydroflavonol reductase	Phenylpropanoid pathway
<i>ANS</i>	Anthocyanidin synthase	Phenylpropanoid pathway
<i>PPO</i>	Polyphenol oxidase	Phenylpropanoid pathway
<i>HMGR</i>	Hydroxymethyl glutarate-CoA reductase	Isoprenoid pathway
<i>FPPS</i>	Farnesyl pyrophosphate synthase	Isoprenoid pathway
<i>Far</i>	(E,E)-alpha-farnesene synthase	Isoprenoid pathway
<i>CSL</i>	Cystéine sulfoxide lyase	Cysteine sulfoxid pathway
<i>APOX</i>	Ascorbate peroxidase	Oxidative stress
<i>GST</i>	Glutathion S-transférase	Oxidative stress
<i>POX</i>	Peroxidase	Oxidative stress
<i>CalS</i>	Callose synthase	Cell wall modification
<i>Pect</i>	Pectin methyl esterase	Cell wall modification
<i>CAD</i>	Cinnamyl alcohol dehydrogenase	Cell wall modification
<i>EDS1</i>	Disease resistance protein EDS1	Salicylic acid pathway
<i>WRKY</i>	WRKY transcription factor 30	Salicylic acid pathway
<i>LOX2</i>	Lipoxygenase AtLOX2	Jasmonic acid pathway
<i>JAR</i>	Jasmonate resistant 1	Jasmonic acid pathway
<i>ACCO</i>	1-aminocyclopropane-1-carboxylate oxidase	Ethylene pathway
<i>EIN3</i>	EIN3-BINDING F-BOX PROTEIN 1	Ethylene pathway
<i>TuA</i>	Tubulin alpha-1 chain	Reference gene
<i>Actin</i>	Actin 7	Reference gene
<i>GAPDH</i>	Glyceraldehyde-3-phosphate dehydrogenase	Reference gene

Table S2 Linkage disequilibrium between SNPs detected on chromosomes 2 and 4

CHR SNP1	Position SNP1	SNP1	CHR SNP2	Position SNP2	SNP2	R²
2	740878	SNP37241	2	11610659	SNP41286	0.696259
4	7955113	SNP77432	4	7963272	SNP77453	0.818462
4	7955113	SNP77432	4	11286270	SNP79715	0.603616
4	7963272	SNP77453	4	11286270	SNP79715	0.598459
4	11286270	SNP79715	4	31269345	SNP88909	0.0699576