

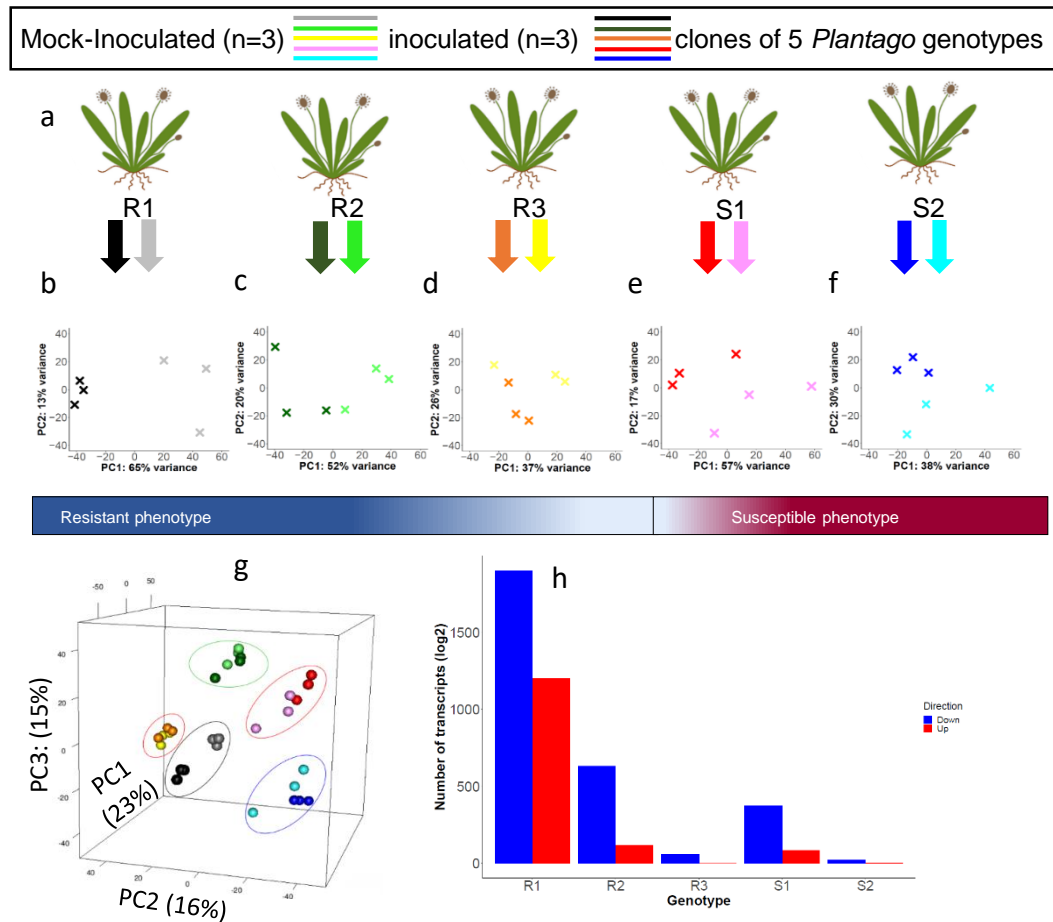
## Safdari et al. Tables & Figures

**Table 1. Differential gene expression (DE).** Number of differentially expressed transcripts (DE transcripts), the number of transcripts with large changes ( $|\log FC| > 1$ ), and the numbers of differentially expressed NLR transcripts (DE NLRs) and NLRs with large expression changes (DE NLRs  $|\log FC| > 1$ ) under inoculation vs. control. The numbers are reported for five genotypes separately, as well as the combined effect from two phenotypes susceptible (Sus) and resistant (Res), as well as their comparison (Res\_vs\_Sus).

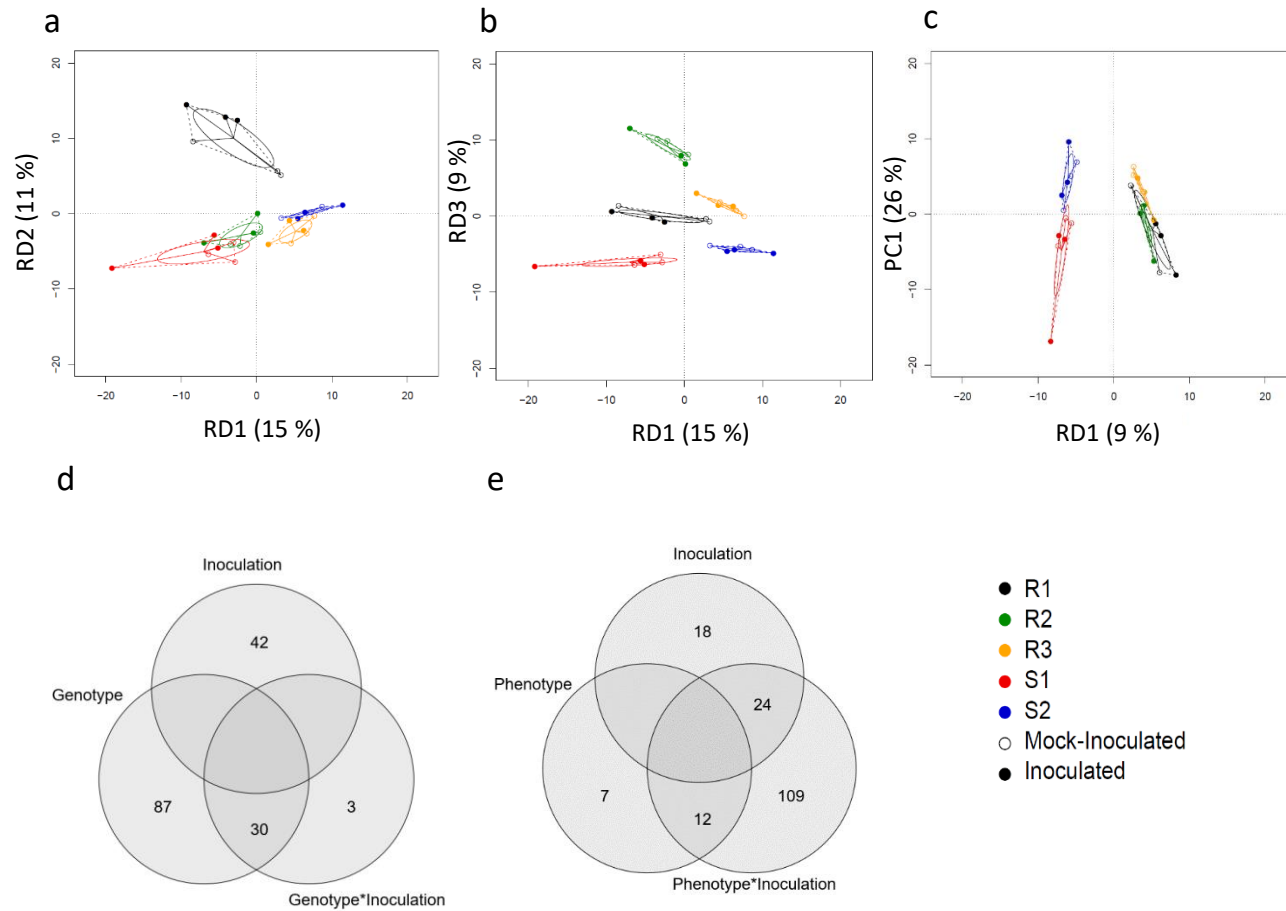
Sample	DE transcripts	$ \log FC  > 1$	DE NLRs	DE NLRs $ \log FC  > 1$
Sus1	791	166	10	3
Sus2	43	20	0	0
Res1	3803	1987	70	30
Res2	1180	412	17	4
Res3	111	7	1	0
Sus	3787	1212	104	54
Res	1108	143	13	0
Res_vs_Sus	3912	1325	107	45

**Table 2. A summary of the Redundancy Analysis (RDA).** *P*-values of RDA axes for Genotype, Phenotype and Inoculation treatment effects and their interactions, and the individual and overall percentage of variance explained by each of the RDA axes.

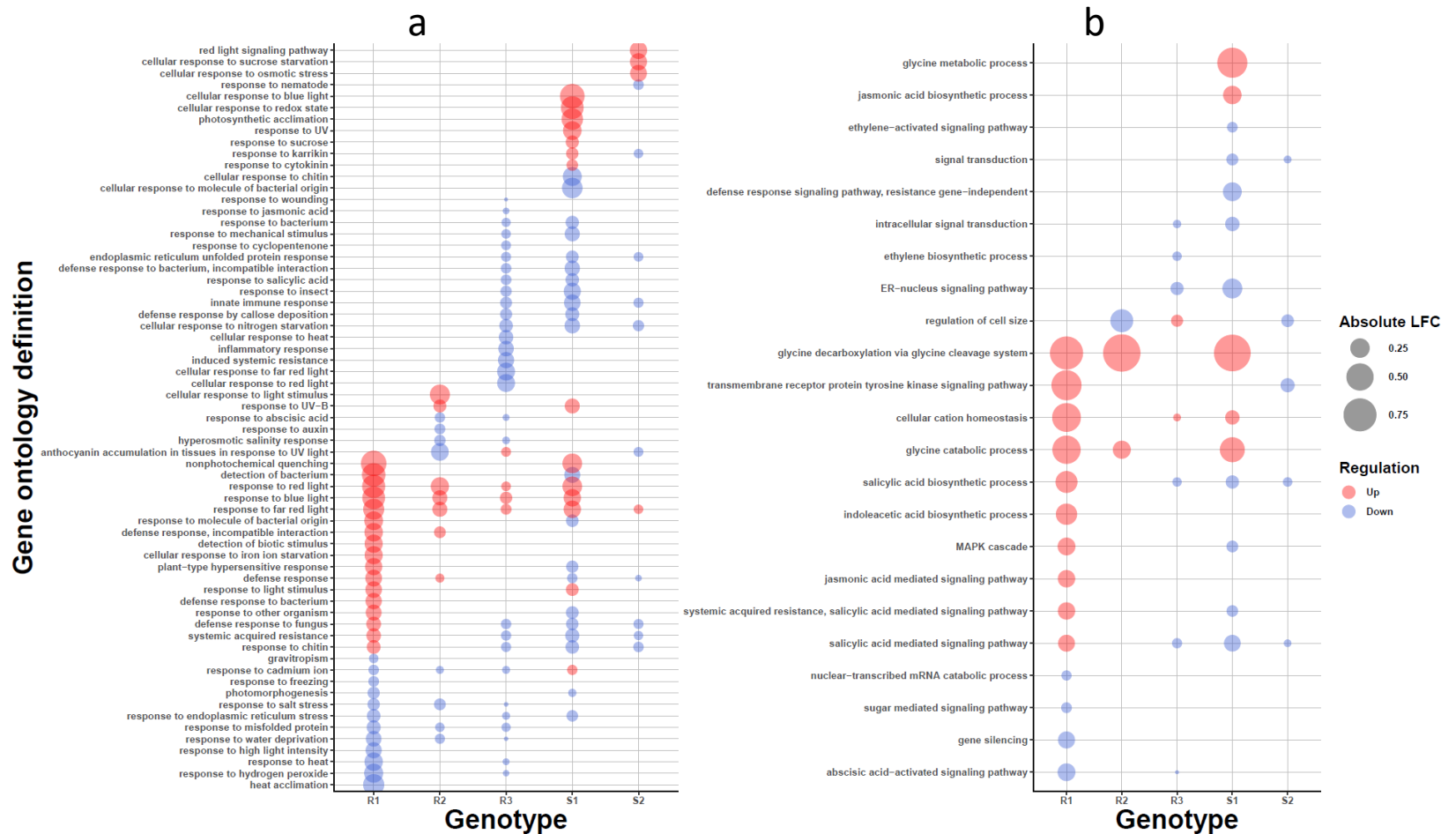
Source	P-value				Percentage of variation (%)				Total percentage of variation
	RDA1	RDA2	RDA3	RDA4	RDA1	RDA2	RDA3	RDA4	(%)
Genotype	0.001	0.001	0.001	0.002	15	11	9		35
Phenotype	0.004	NA	NA	NA	9	NA	NA	NA	9
Inoculation	0.238	NA	NA	NA	4	NA	NA	NA	4
Genotype x Inoculation	0.001	0.001	0.005	0.021	17	12	9	8	46
Phenotype x Inoculation	0.048	0.413	0.823	NA	9	4	2	NA	14



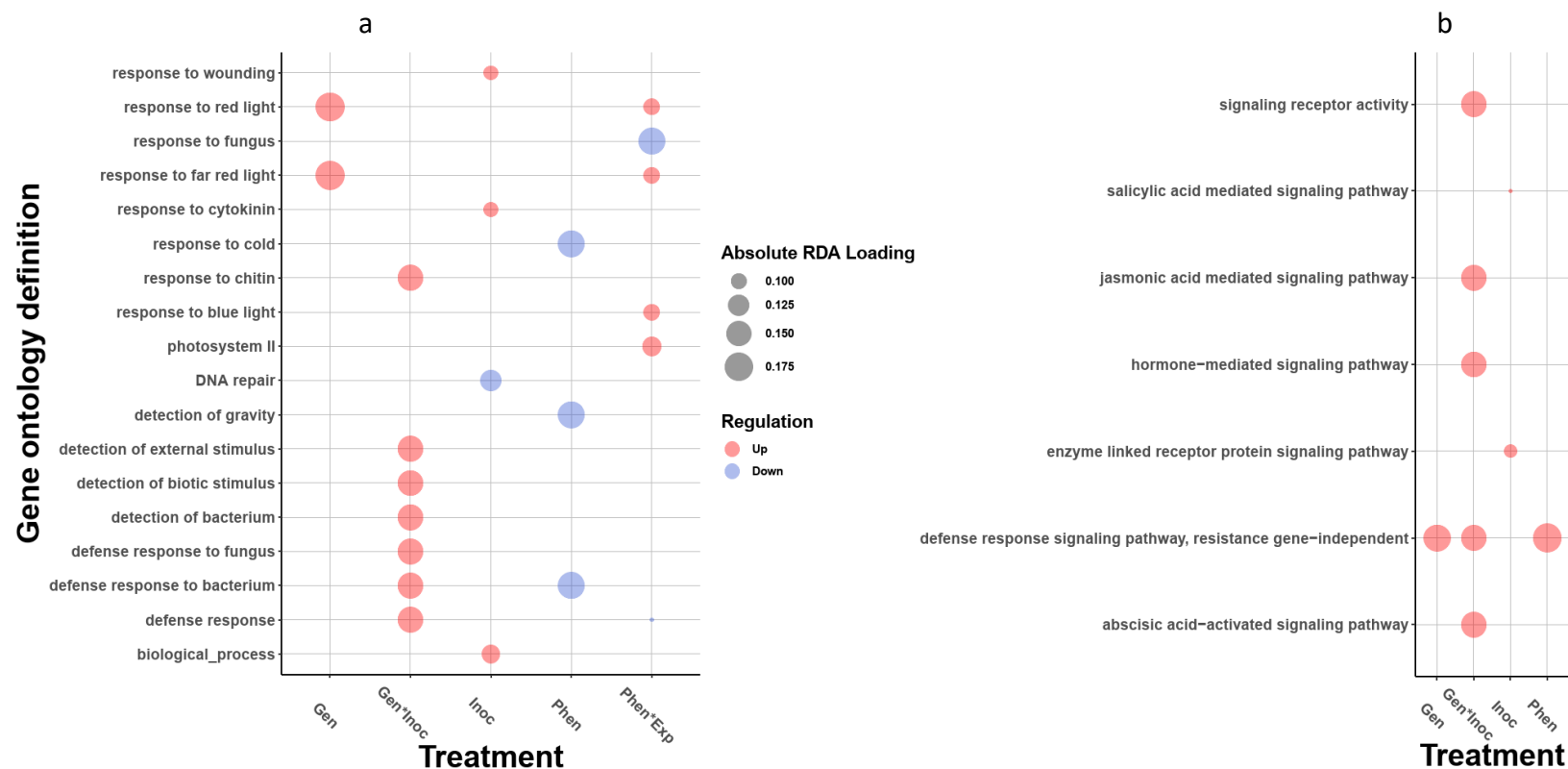
**Figure 1. The Experimental design of the inoculation experiment and resulting differential gene expression in five *Plantago lanceolata* genotypes.** (a) Three clones of five *P. lanceolata* genotypes were inoculated with a strain of *Podosphaera plantaginis*, while three were mock-inoculated as control. RNA was extracted at 72 hours post inoculation for RNA-Seq, and the phenotypes (resistant-susceptible) were scored at day 14 post inoculation. (b-f) The effect of the inoculation treatment within each genotype is illustrated with Principal Component Analysis (PCA) where the first two axes PC1 and PC2 explain between 37-65% and 13-30 percent of the variation, and are associated with the treatment effect. (g) When analyzed together, the genotypes separate in their gene expression in PCA along PC1, PC2 and PC3 axes, which explain 23, 16 and 15 percent of the variation, respectively. (h) Within genotypes, R1-3 and S1-2 showed varying numbers of significantly up (red) and down (blue) regulated genes in response to the inoculation treatment.



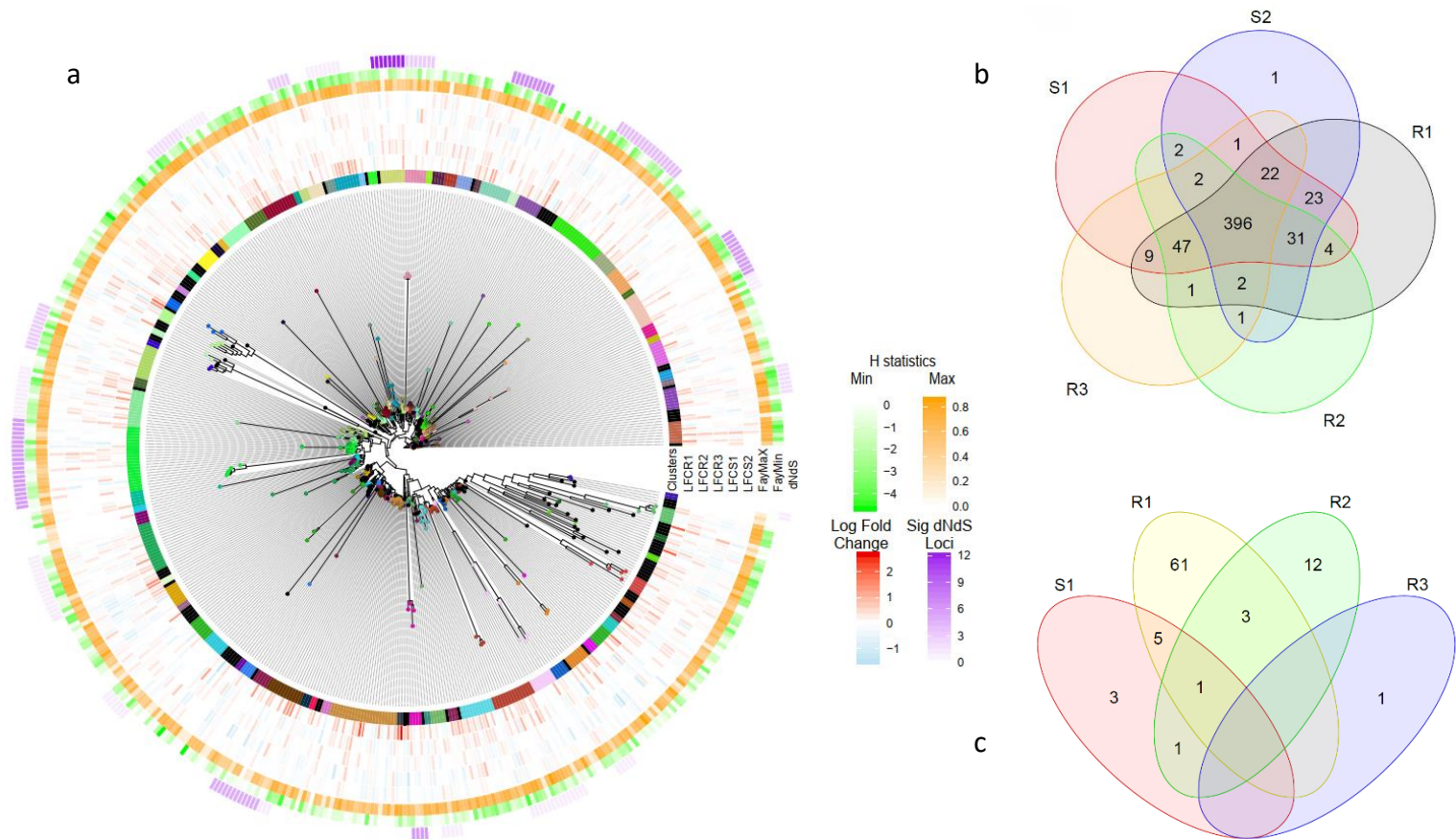
**Figure 2. Redundancy analysis (RDA) of RNASeq data. (A-B)** *Plantago lanceolata* genotypes separate according to RDA1, RDA2 and RDA3 which explain 15, 11, and 9 percent of the variation, respectively. **(C)** The phenotypes separate according to RDA1 which explains 9% of the variation. Results are displayed along PC1 as there is only one DRA axis for phenotype (resistant-susceptible). **(D)** The number of genes that contribute significantly to variation in genotype, inoculation treatment and genotype-by-inoculation interaction. **(E)** The number of genes that contribute significantly to variation in phenotype, inoculation treatment and phenotype-by-inoculation interaction.



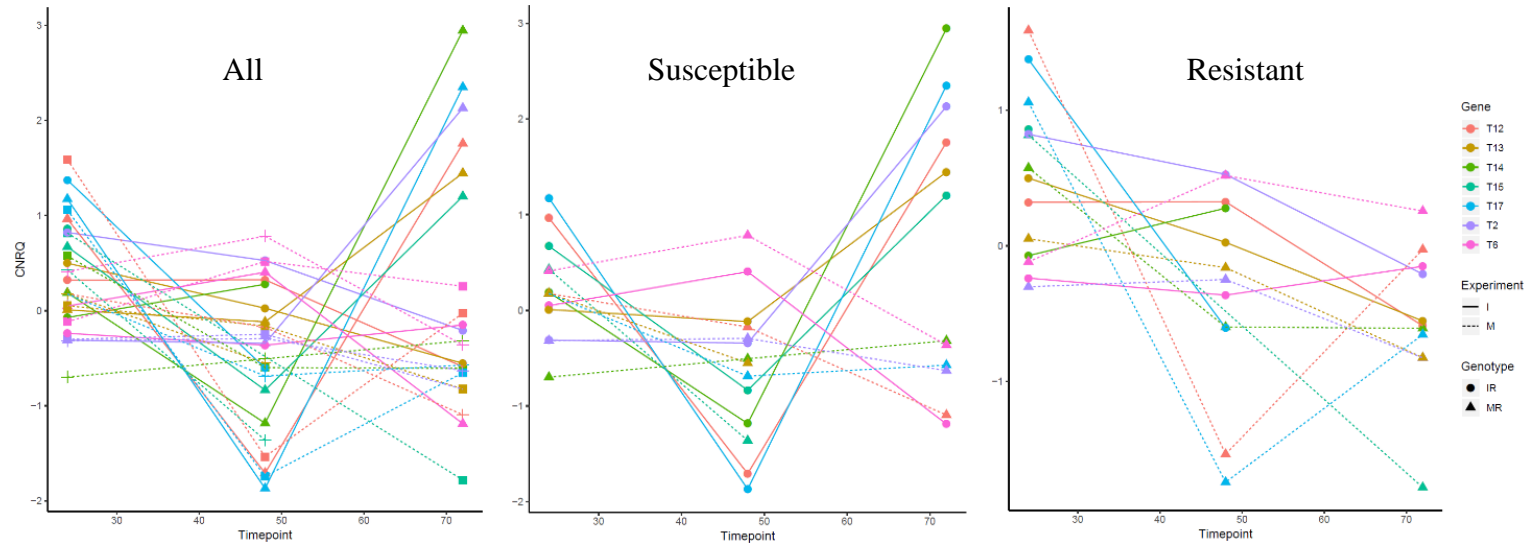
**Figure 3. Gene Ontology (GO) enrichments of the Differentially Expressed (DE) transcripts in the different genotypes R1-3,S1-2.** The GO enrichment of the DE transcripts for responses GO categories (a) and signalling hierarchies (b). The size of the bubble is proportional to the mean fold change of the genes assigned to the GO category and the colour describes the direction, upregulation (red) or downregulation (blue).



**Figure 4. Gene Ontology (GO) enrichments of the genes contributing to the separation at treatment, genotype and phenotype levels in Redundancy analysis.** Enrichment test was carried with gene loadings along RDA axes, see Methods. The bubble plot depicts (a) the GO enrichment responses GO hierarchies, and (b) enrichment limited to signaling hierarchies, the size of the bubble is proportional to the mean fold change of the genes assigned to the GO category and the color describes the direction, upregulation (red) or downregulation (blue).

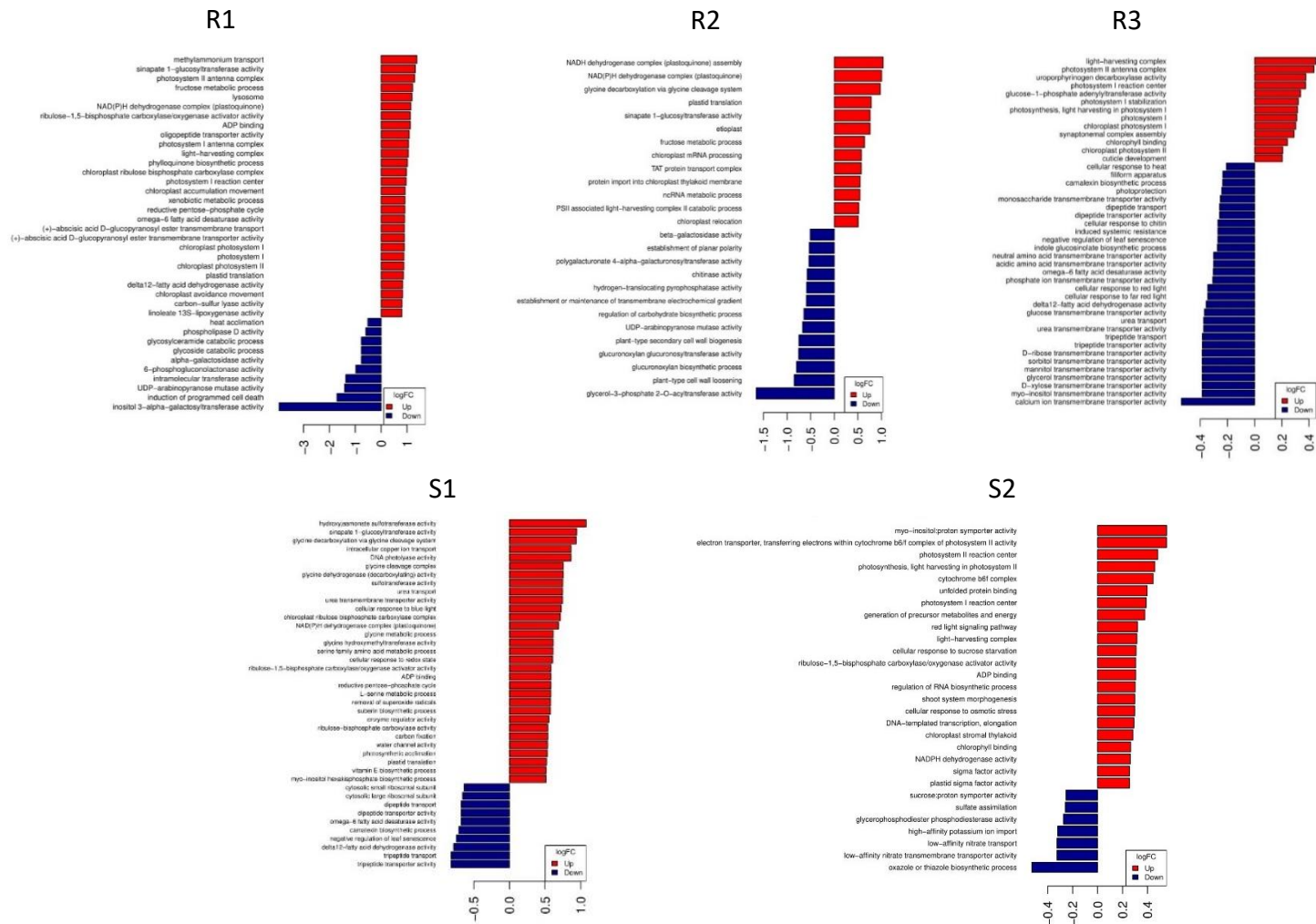


**Figure 5. NLR transcripts: clustering, differential expression, dN/dS and Fay H statistic. Panel a:** The phylogenetic tree of NLR transcripts. The different colors in the innermost circle illustrates clusters (denoted as Clusters in the plot), the next five circles show the log fold change of the transcript in each of the genotypes (LFCR1-3, LFCS1-2), FayMax and FayMin show minimum and maximum value of H statistic. Finally, dN/dS illustrates the number of loci with significant dN/dS value in each cluster, the color is proportional to the number. Panels b and C: Venn diagrams illustrating the number of expressed (b) and differentially expressed (c) NLR transcripts in each genotype.

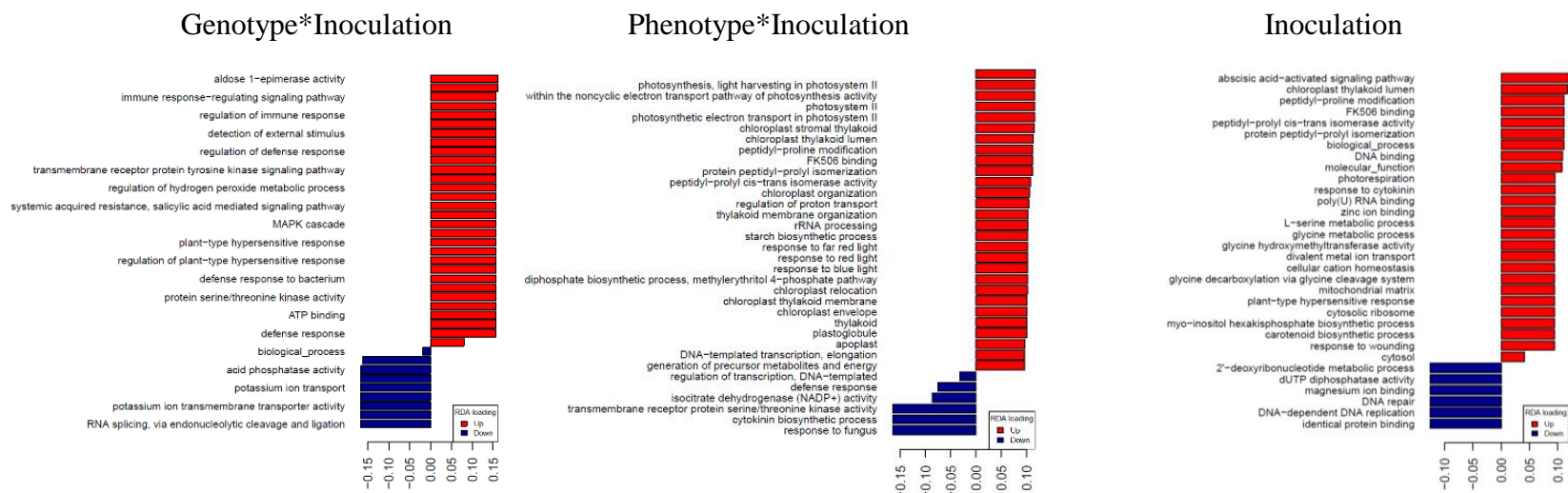


**Supplementary Figure 1. Inoculation experiment and qPCR.** Calibrated normalized relative quantities (CNRQ) for seven putative disease induced genes of two plant genotypes (resistant 193\_2.1 and susceptible 1553\_5.1) at three time points (24, 48 and 72 h post inoculation). The solid lines are inoculated and dashed lines are mock-inoculated samples (control). The result illustrates expression differences between resistance and susceptible genotypes at 72 hpi.

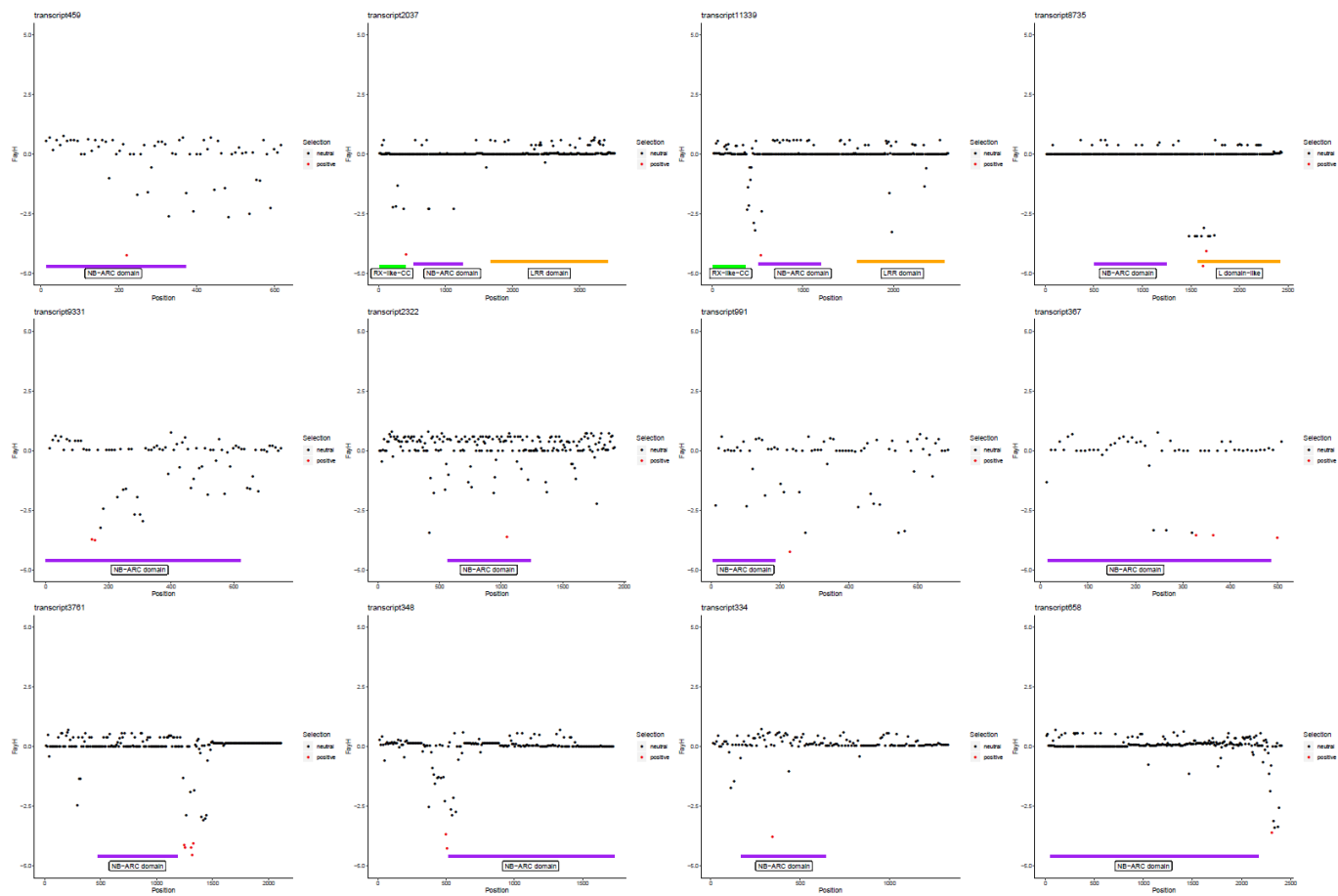


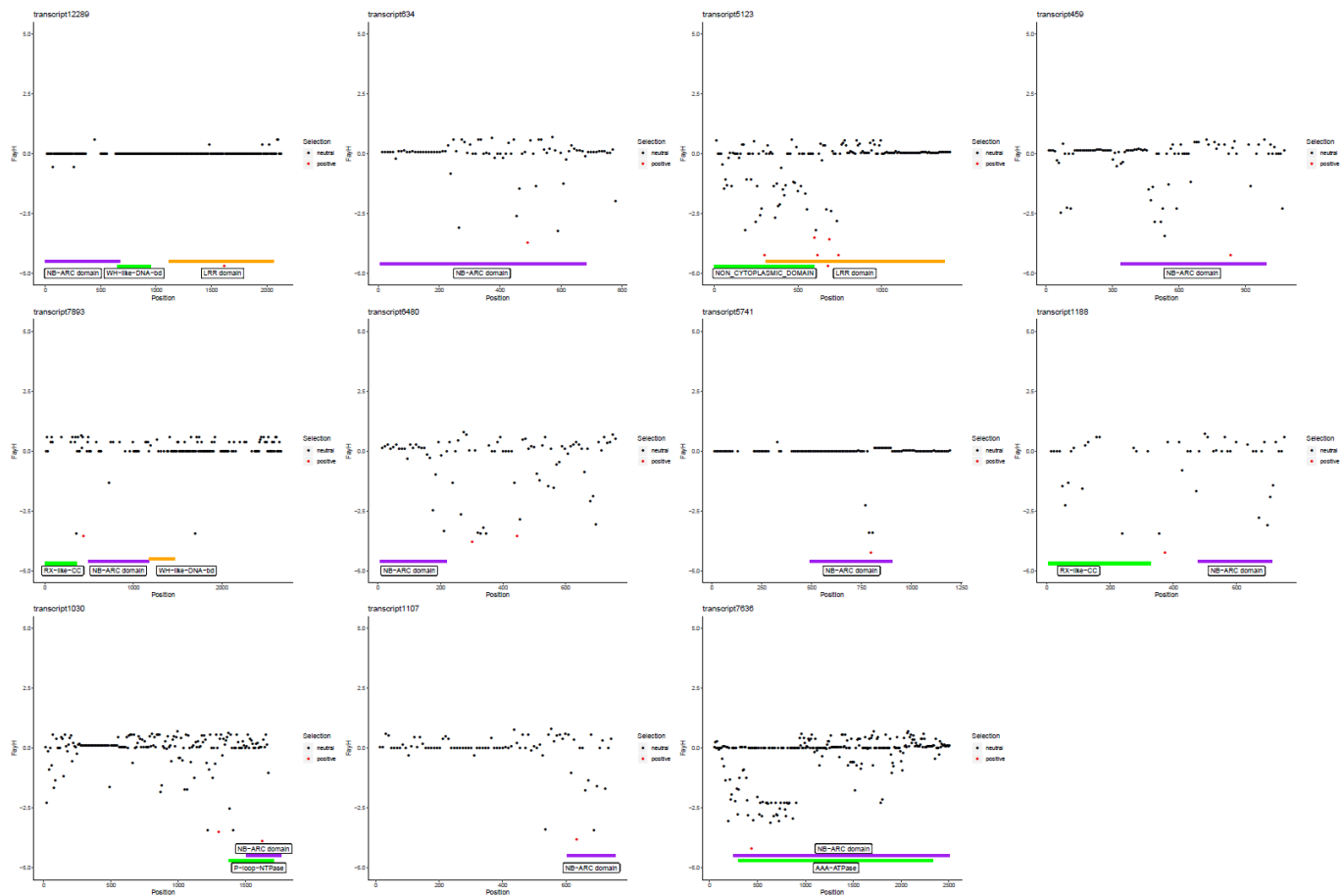


**Supplementary Figure 2. Gene Ontology (GO) enrichments of the Differentially Expressed (DE) transcripts in each of the genotypes.** GO categories of DE transcripts with elevated or lowered expressions per genotype. Decreased average expression levels of tripeptide transporter and fatty acids may be indications of failed defense in susceptible genotypes S1 and S2. Increased expression levels of glucosyltransferase, NADH dehydrogenase and photosynthesis relate genes are an indication of successful defense and signaling in resistant genotypes.



**Supplementary Figure 3. Gene Ontology (GO) enrichments of the genes contributing to the differences in Redundancy Analysis.** The panels illustrate the GO categories of the genes with the most contributing to the RDA axes. The response GO hierarchies such as immune and defence responses are regulated in genotype by experiment. Photosynthesis and photosynthesis related hierarchies are regulated in phenotype by experiment. Defence related metabolic process and signalling such as jasmonic acid biosynthesis and defence response signalling are regulated in Inoculation.





**Supplementary Figure 4. Neutrality test dN/dS and Fay H statistics.** The Y-axis shows the Fay H values of NLR transcript averaged through a window of 9 basepairs, and X-axis shows the position in the transcript. NLR transcripts with negative Fay H values less than 3.5 were used as indication of positive selection pressure (highlighted with red dots). The colored bars along X-axis illustrate the functional domains within the transcripts.