Differential expression of genes involved in resistance to rhizomania

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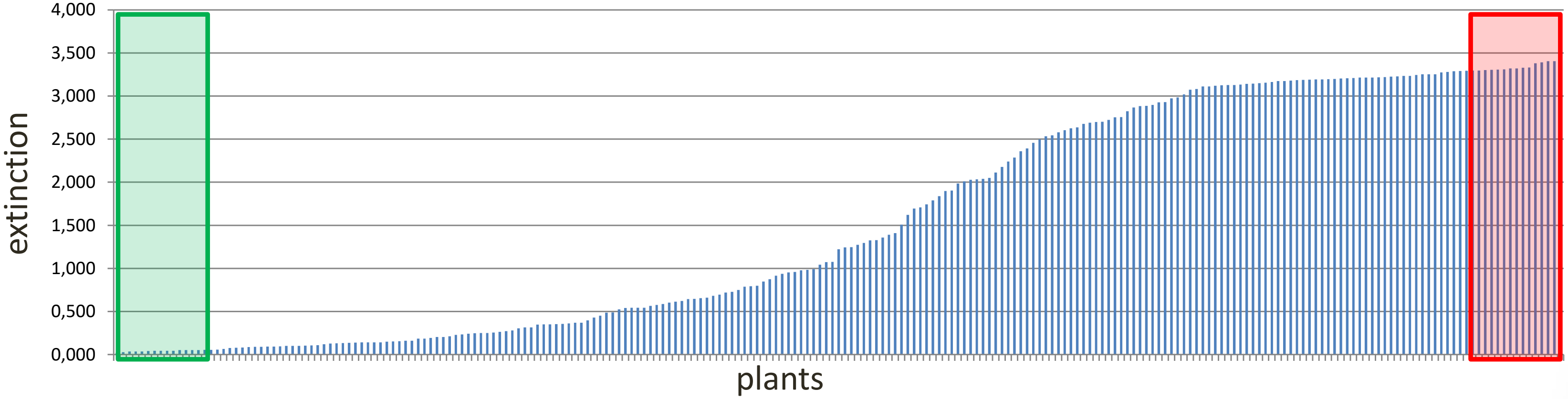
The aim of the experiment:

To identify genes involved in resistance to rhizomania governed by *Rz*1 by measuring changes in expression levels using comparative transcriptomics

Experimental layout

1. Plant materials: 231 plants from the *2SRhF114* 5 F2 population segregating with respect to *Rz*1
2. Standard pot assay for resistance to rhizomania and ELISA quantification of BNYVV



3. Selection of plants showing contrasting reaction to BNYVV:

5 resistant (ELISA: 0.05) / 5 susceptible (ELISA: 3,34)

4. Deep transcriptome sequencing with 5 biological replicates

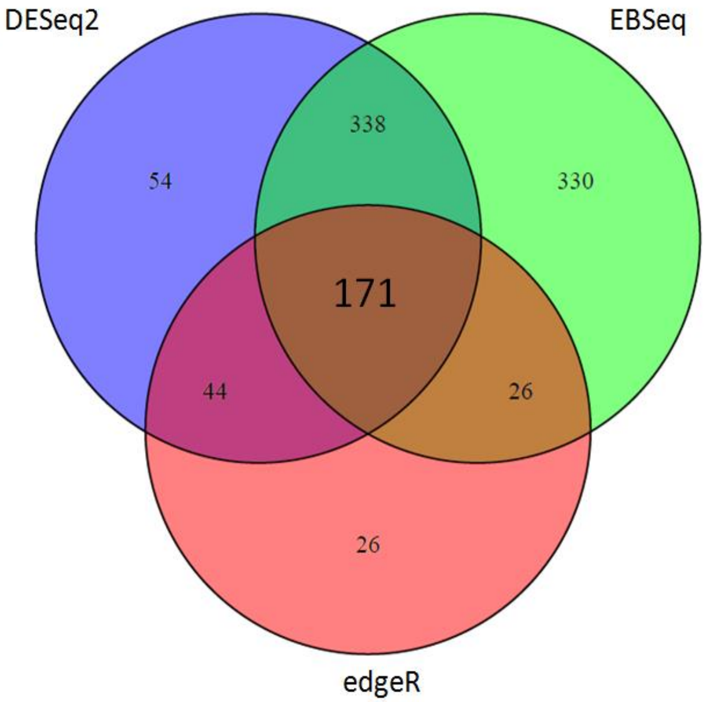
Sample	Read pairs	QC filtering	rRNA fraction	Mapping
R1	79,064,114	92.03 %	33.33 %	93.08 %
R2	68,054,557	90.49 %	18.72 %	93.82 %
R3	65,949,057	91.85 %	16.58 %	94.77 %
R4	74,479,986	91.94 %	19.36 %	94.78 %
R5	64,696,739	90.71 %	16.56 %	95.40 %
S1	83,059,647	93.45 %	19.03 %	95.06 %
S2	71,091,226	93.38 %	16.08 %	93.98 %
S3	67,851,847	91.86 %	14.61 %	95.20 %
S4	68,712,124	93.64 %	17.22 %	95.73 %
S5	69,509,092	93.29 %	15.21 %	93.48 %

5. Differential gene expression analysis, functional classification

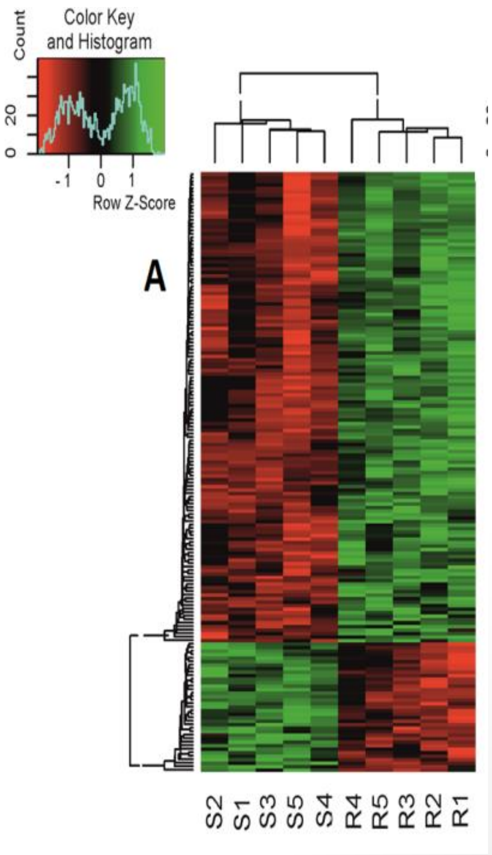
Results

A pipeline combining three algorithms for the identification of differentially expressed genes (DEGs) was used:

171 DEGs in common



FDR≤0.001

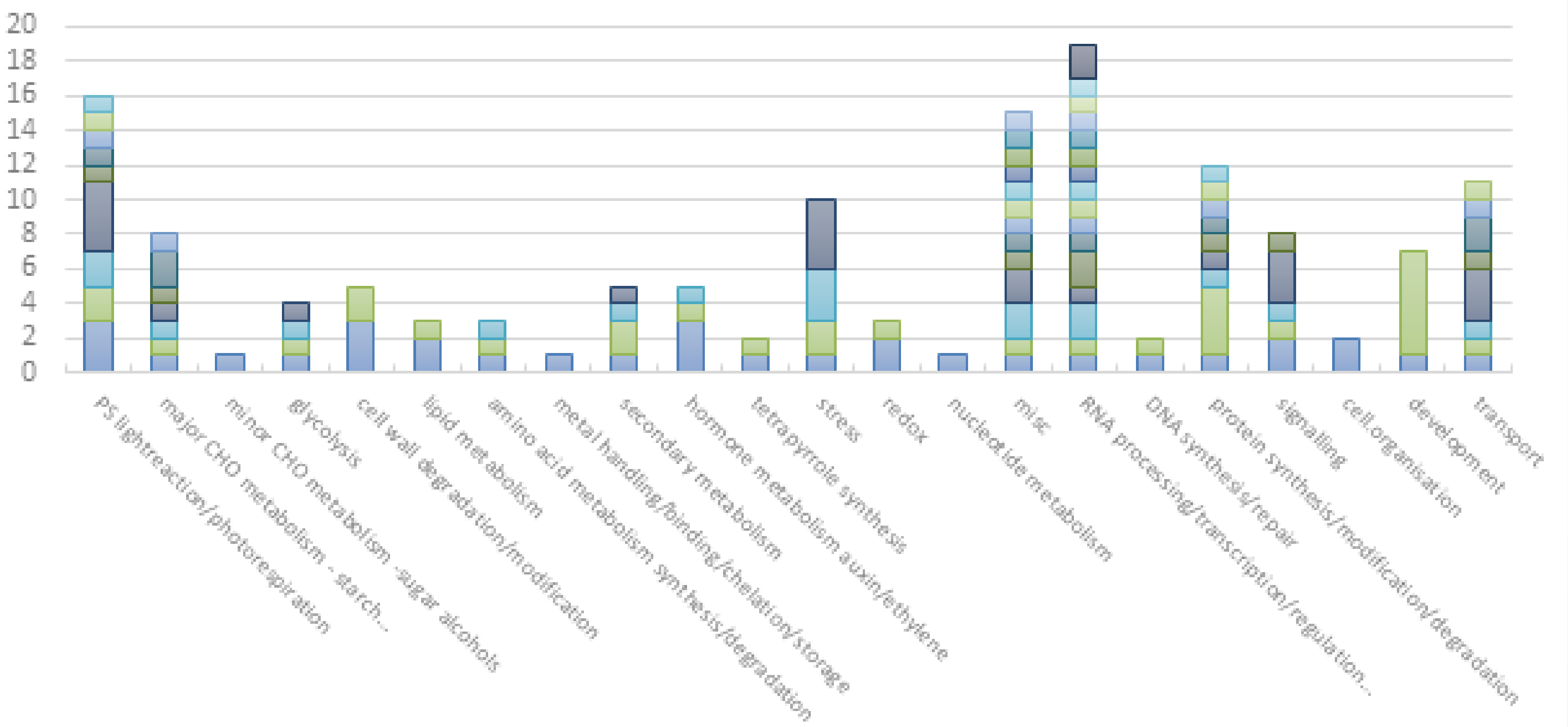


132 DEGs **up-regulated** in resistant plants

39 DEGs **down-regulated** in resistant plants

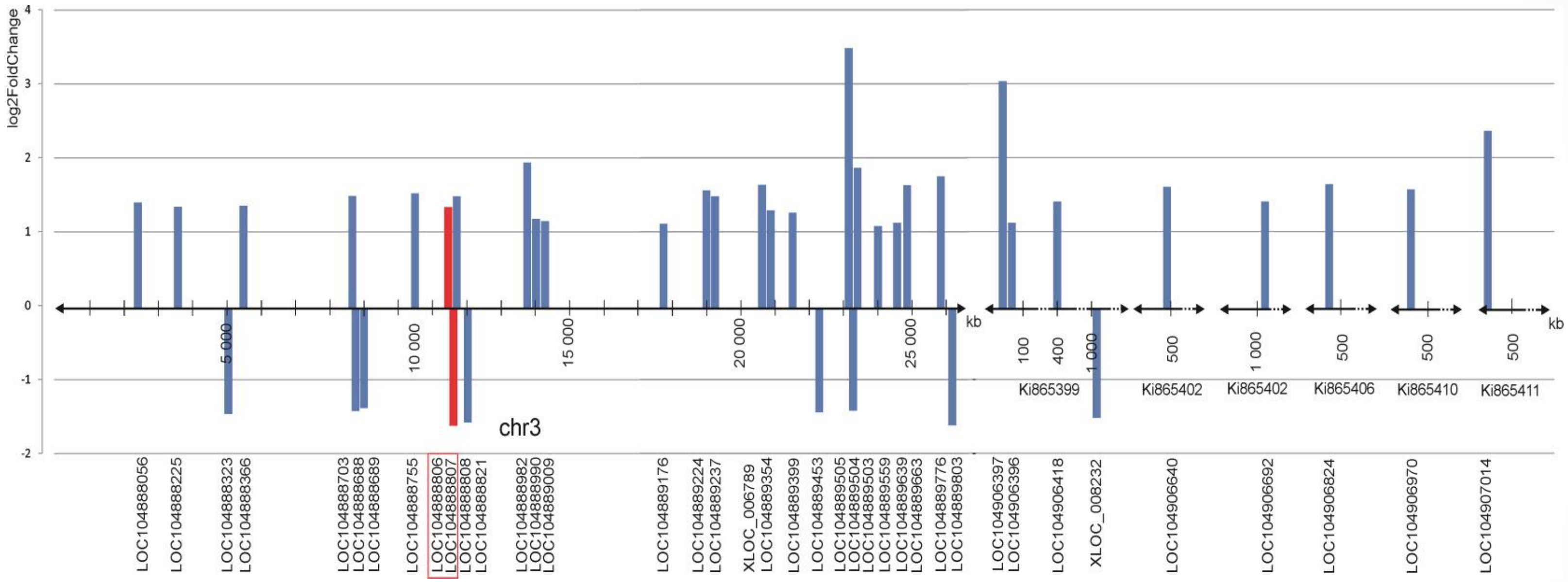
Results

Functional classification of DEGs

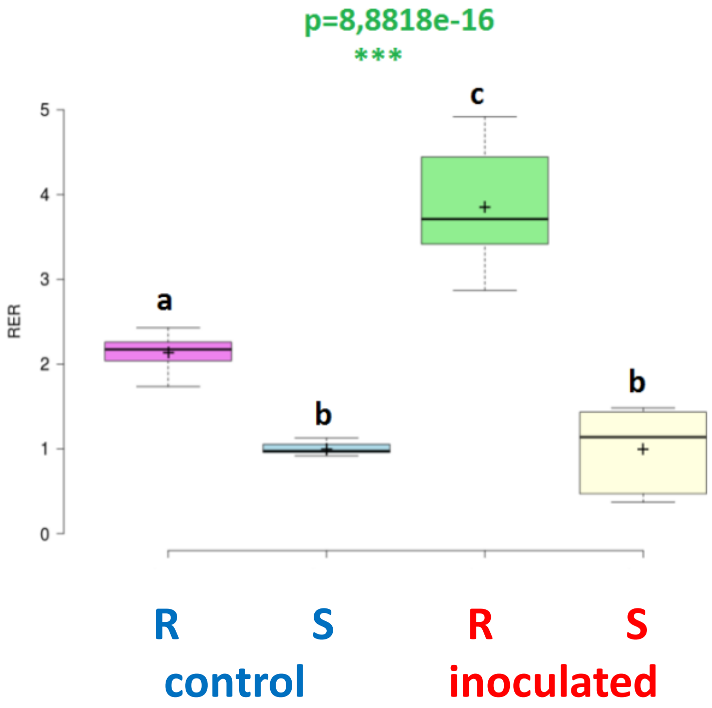


Results

Expression levels (*log2 Fold Change*) of DEGs mapped to **chromosome 3**

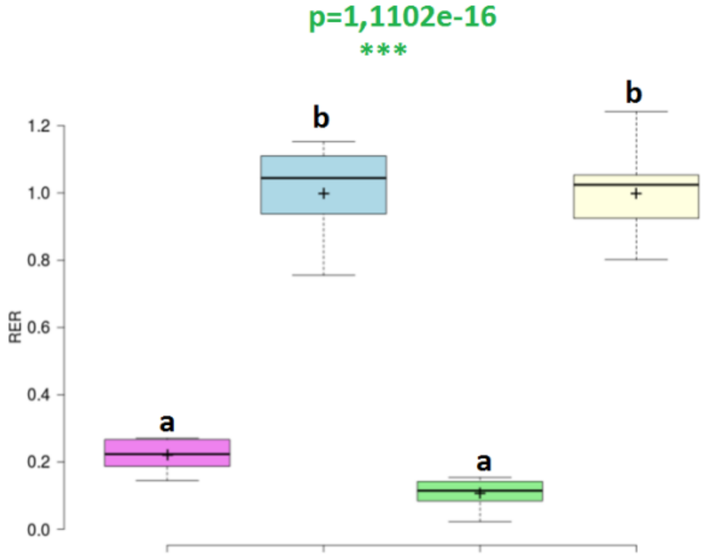


putative *Rz*1 locus



LOC104888806

CC/NBS/LRR



LOC104888807

HSF/LRR

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