

Supplementary Figures:

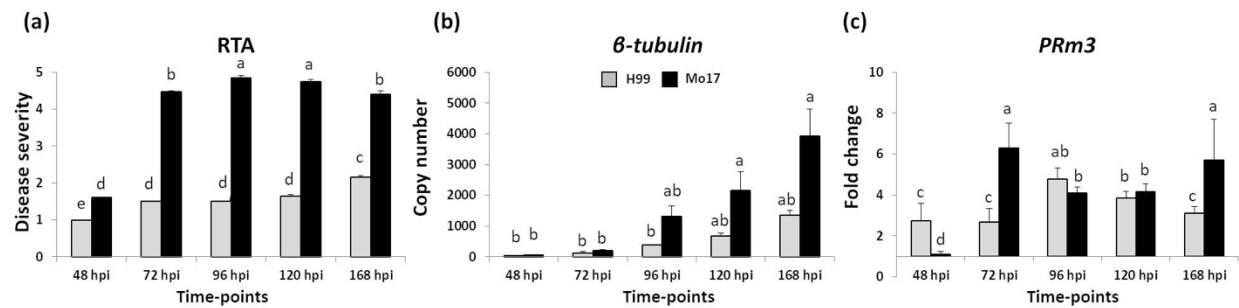


Fig. S1. Evaluation of *F. verticillioides* inoculation steps in a time-course experiments (48-168 hpi) in the highly susceptible Mo17 and in the highly resistant H99 MM founder lines. **(a)** FSR disease severity score was evaluated in seedlings by the Rolled Towel Assay (RTA). A score was assigned according to the level of infection ranging from 1 to 5 (Septiani *et al.*, 2019), where score 1 indicates minimum or no effects (resistant phenotype), while score 5 means that the seed is severely affected (susceptible phenotype). **(b)** Copy number of transcripts for the constitutive *F. verticillioides* β -tubulin gene quantified by RT-qPCR. **(c)** Relative quantification of the expression of maize *PRm3* gene measured by RT-qPCR. On panels (a), (b) and (c), standard deviations (SD) of the mean are indicated by vertical bars (n = 3). Letters on the bars are significantly different at $p < 0.05$ in the LSD test.

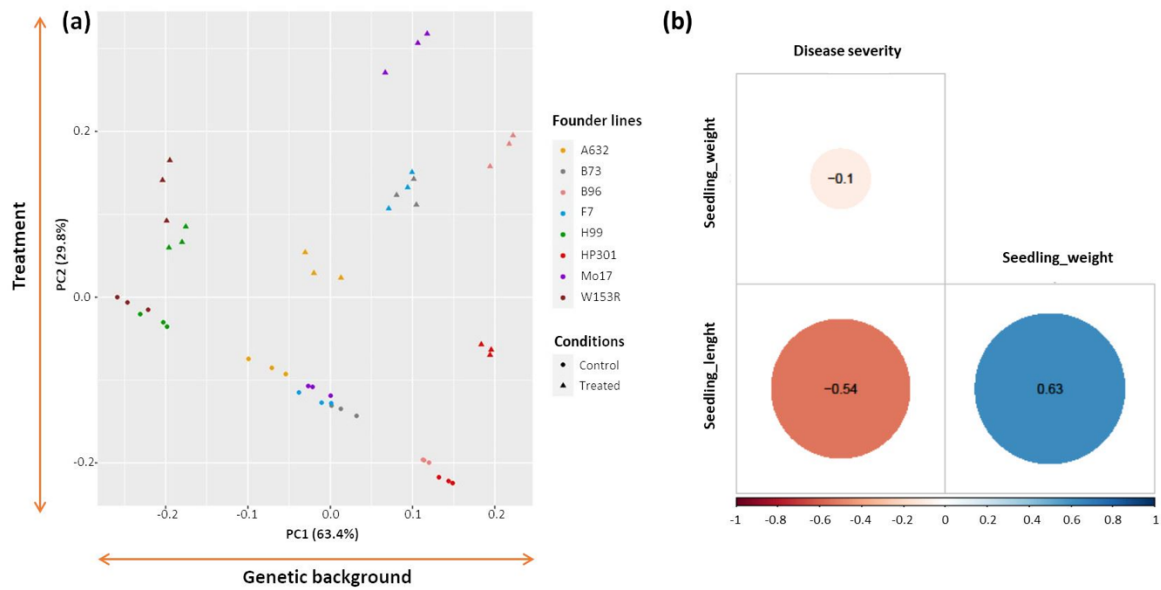
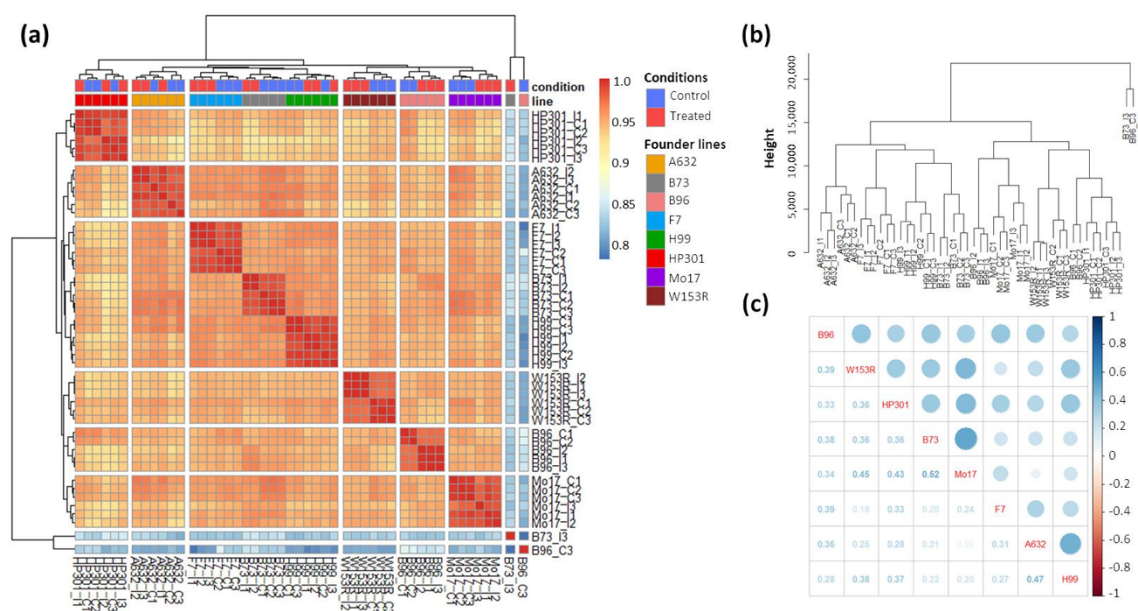


Fig. S2. Phenotype analysis of traits measured by the Rolled Towel Assay. **(a)** Principal Component Analysis of the traits for each biological replicate (seedling length, seedling weight, and FSR disease severity). **(b)** Correlation analysis between phenotypes among all samples.



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 18 **Fig. S3.** Transcriptomic data exploration for outlier removal. **(a)** Correlation of Count Per Million (CPM)
 19 measurements among biological replicates without removing outliers. **(b)** Unsorted dendrogram of CPM
 20 data calculated for each biological replicate. **(c)** Correlation of normalized expression data among the eight
 21 MM founder lines.