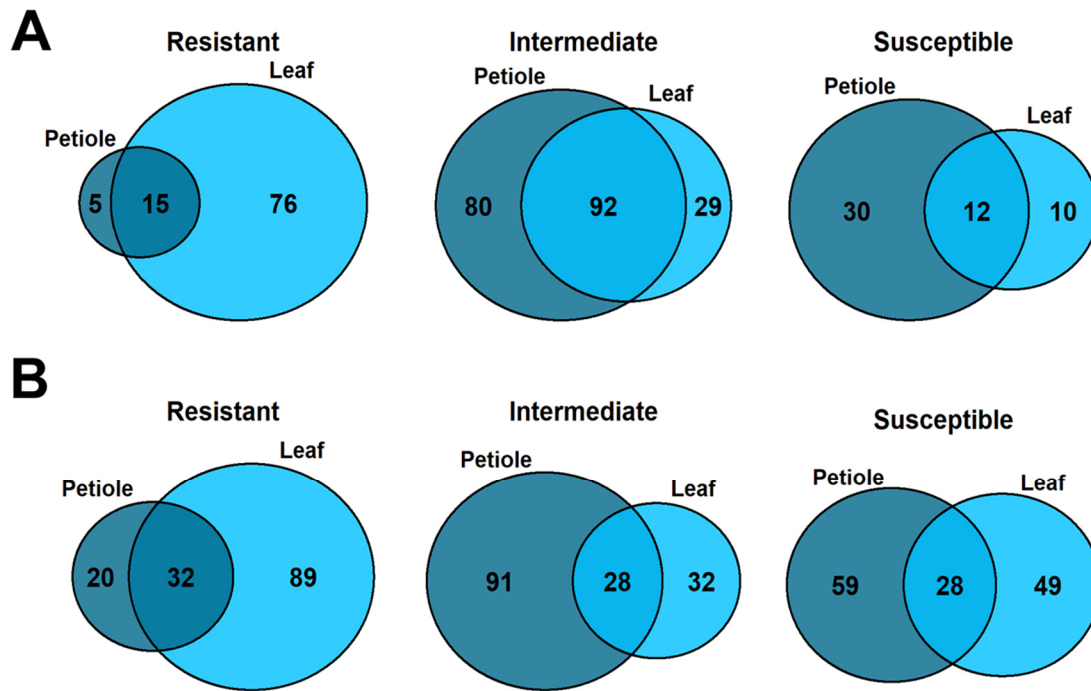
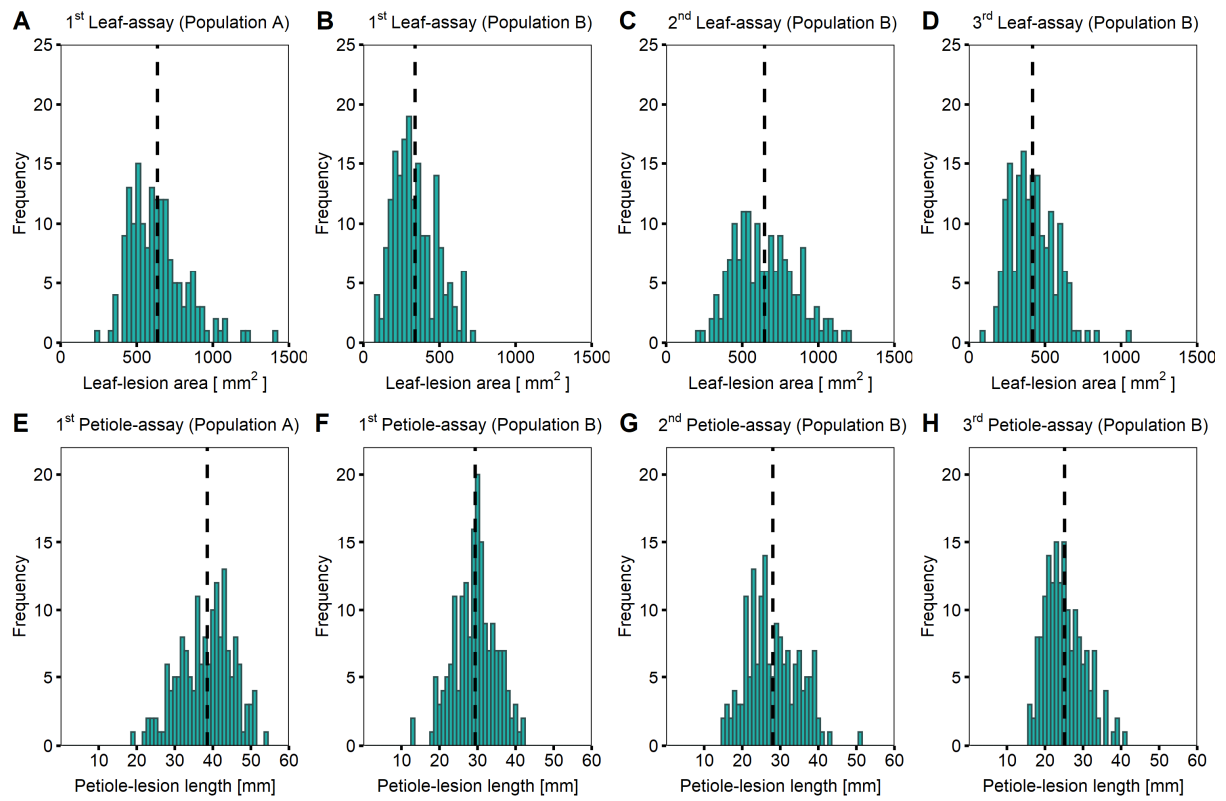


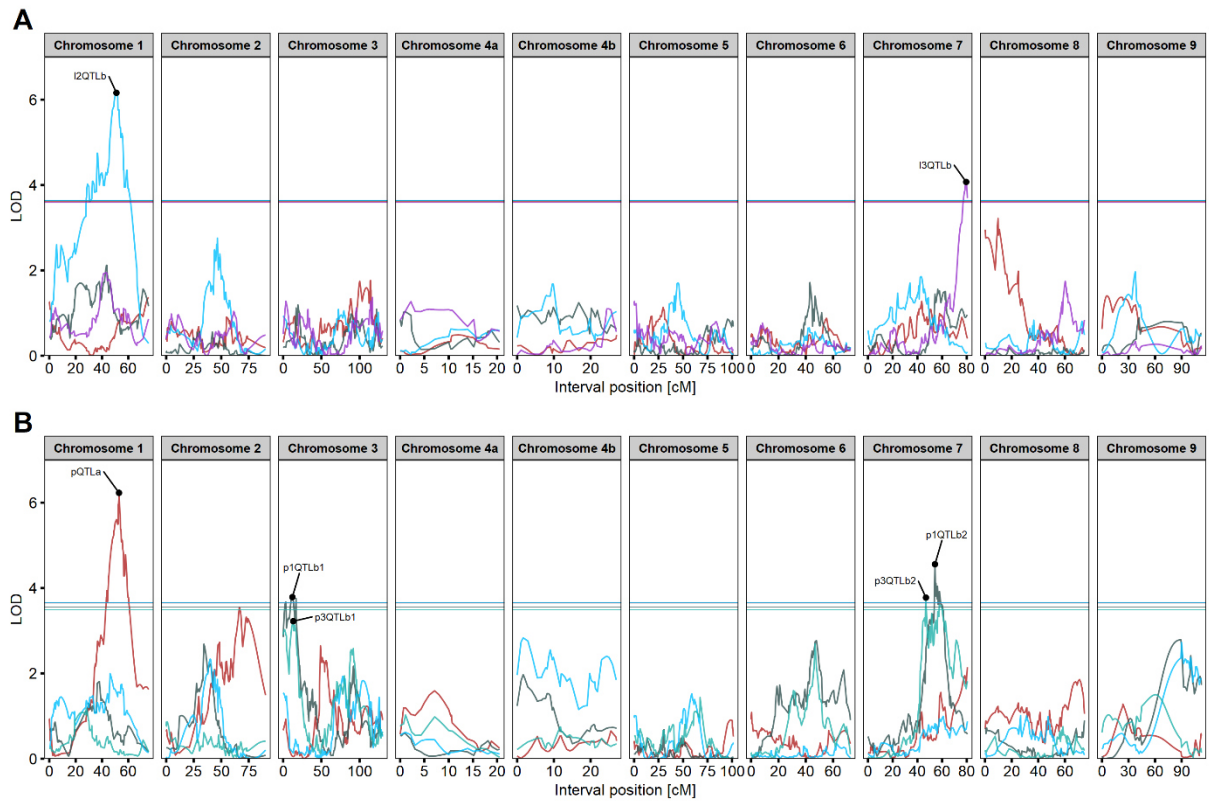
**Figure S1** Trypan blue staining of inoculated leaves of **A – B** *B. oleracea* (BRA1909) and **C – D** *B. villosa* (BRA1896). A dense and compact structural fungal growth mainly within necrotic tissue was observed in leaves of the susceptible *B. oleracea*. In the resistant *B. villosa*, fungal expansion appeared less structured and focused mainly on the leaf surface with no delimited junction between healthy and infected tissue.



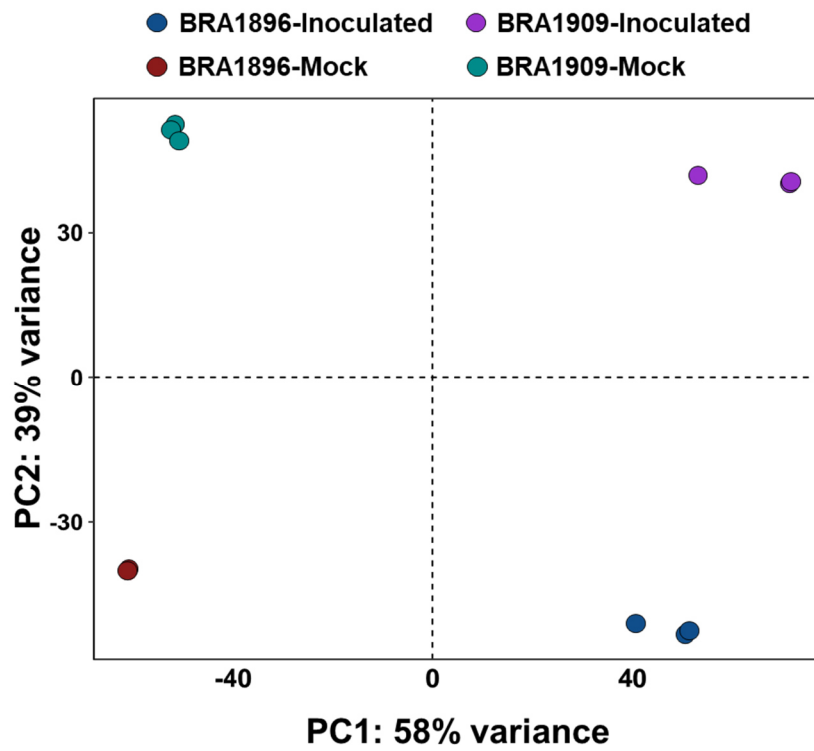
**Figure S2** Venn diagram showing the proportion of F<sub>2</sub> individuals in **A** Population A and **B** Population B which were commonly classified as resistant, intermediate, and susceptible in the leaf- and petiole-assay. The grouping is based on the comparison to the resistant *B. villosa* (BRA1896) and the susceptible *B. oleracea* (BRA1909) parents in each population, respectively.



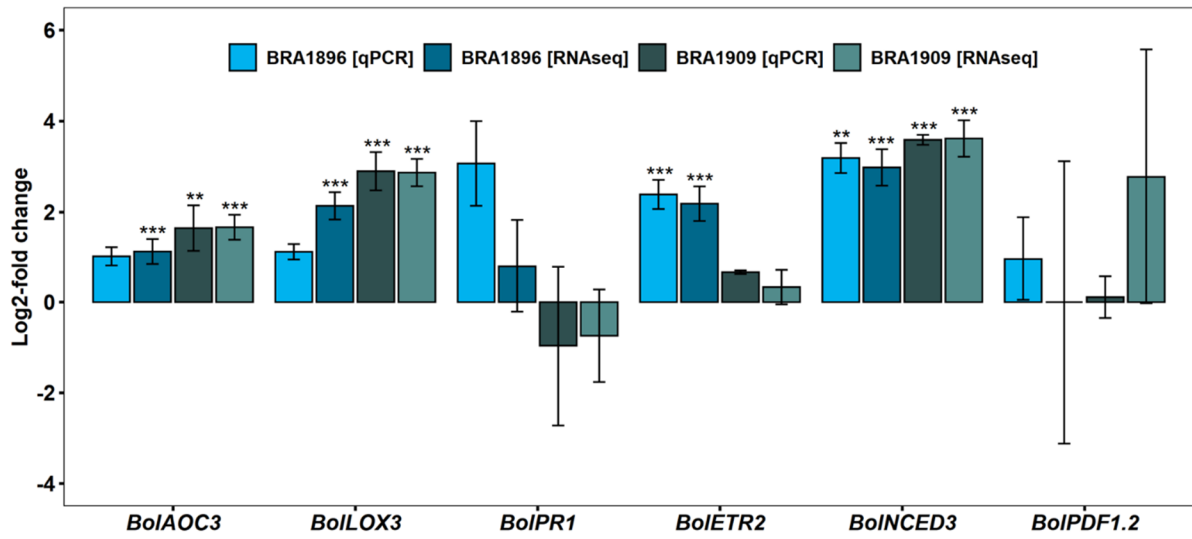
**Figure S3** Lesion size distributions of genotyped  $F_2$  plants. **A – D** Leaf-lesion size distributions of all genotyped  $F_2$  individuals in **A** Population A and **B – D** in Population B. **E – H** Petiole-lesion size distributions of all genotyped  $F_2$  individuals in **E** Population A and **F – H** in Population B.



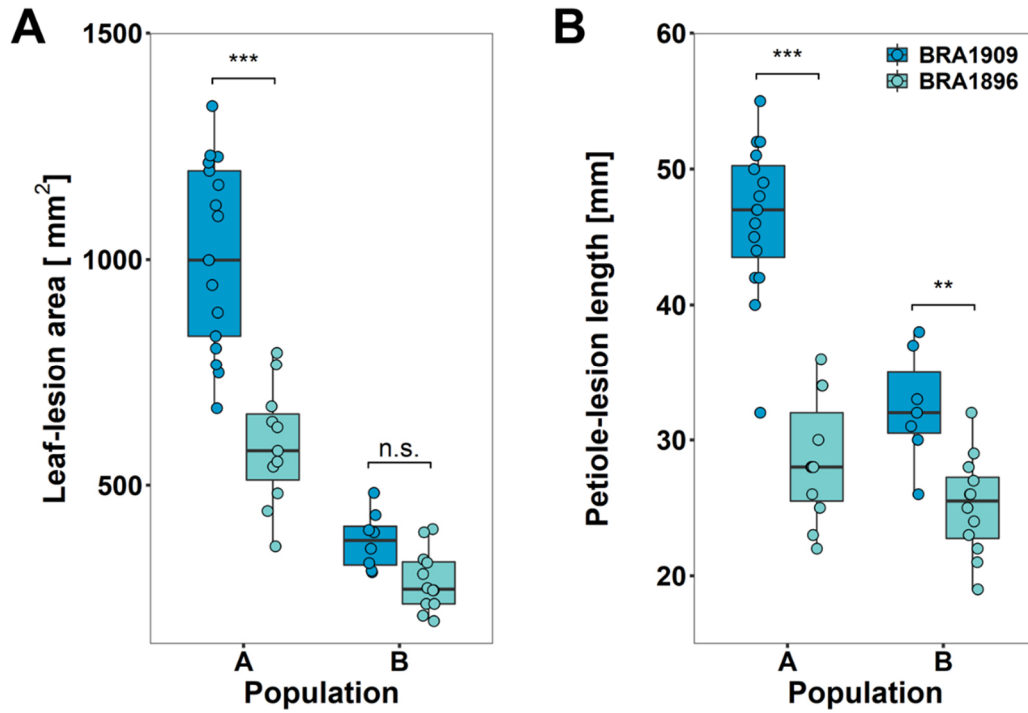
**Figure S4** Logarithm of the odds (LOD) profiles in both mapping populations. Horizontal lines indicate the threshold for significance. Different assays are highlighted by different colors.



**Figure S5** Principal component analysis (PCA) of RNAseq samples of *B. villosa* (BRA1896) and *B. oleracea* (BRA1909) after regularized log-transformation of the count matrix in DESeq2. Biological replications are highlighted by identical colors. PC1: variance between samples caused by species, PC2: variance between samples caused by the treatment.



**Figure S6** Marker gene expression comparison of reverse-transcribed quantitative PCR (RT-qPCR) and RNAseq data of resistant (BRA1896) and susceptible (BRA1909) petioles at 8 hours post inoculation (hpi) with *Sclerotinia*. Asterisks indicate a significant induction compared to the control sample. BRA1896 = *B. villosa*, BRA1909 = *B. oleracea*. RT-qPCR expression was log<sub>2</sub>-transformed for a better comparison to the RNAseq. Genes in the RNAseq were as follows: *BoIETR2* = Unigene.2465, *BoIAOC3* = Bo9g075870, *BoILOX3* = Bo8g067210, *BoIPDF1.2* = Bo2g086460, *BoINCED3* = Bo5g130280, *BoIPR1* = Bo3g088360. Primers for RT-qPCR analysis are listed in Supplementary Table S1.



**Figure S7** Lesion size comparison of the parental accessions in the two populations via the detached **A** leaf- and **B** petiole-assay at 2 days after *Sclerotinia*-inoculation under greenhouse conditions. Parental lesions in each population were compared with a linear model and multiple contrast tests. \*\*P value < 0.01, \*\*\*P value < 0.001.