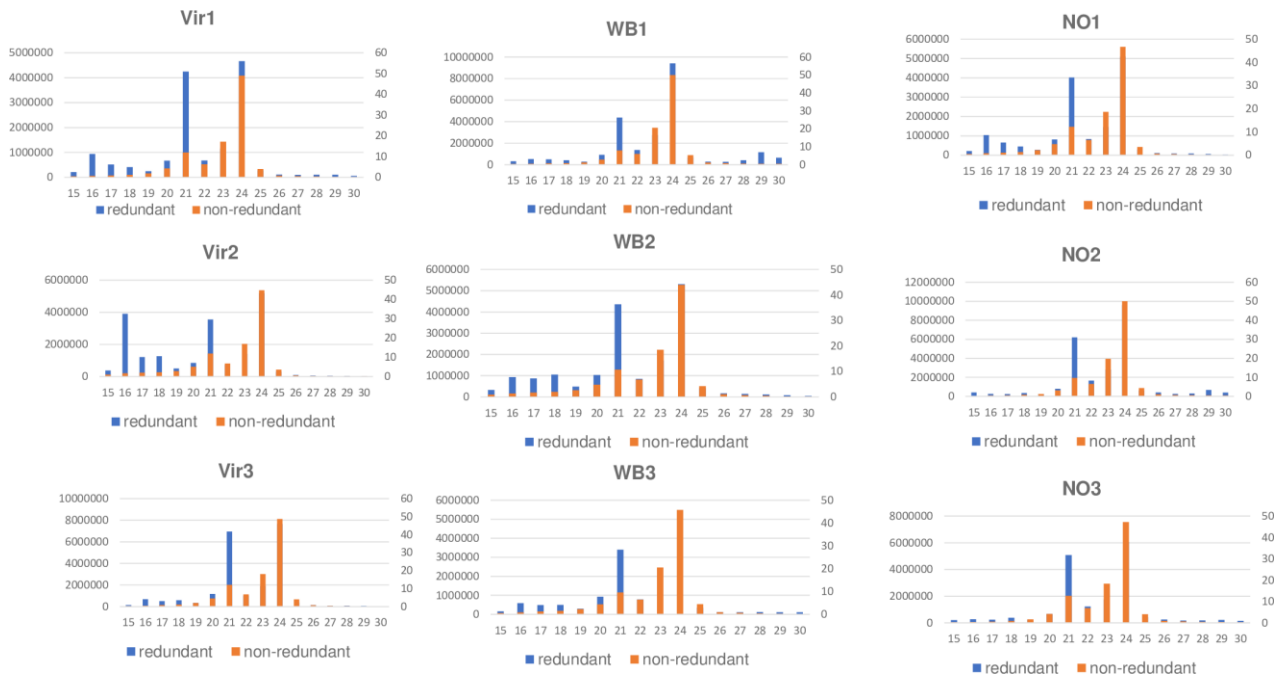


Figure S1: Photos about the groups of periwinkle plants used for small RNA HTS, showing different symptoms: virescence (Vir), witches' broom (WB) and asymptomatic (NO).

(a)



(b)

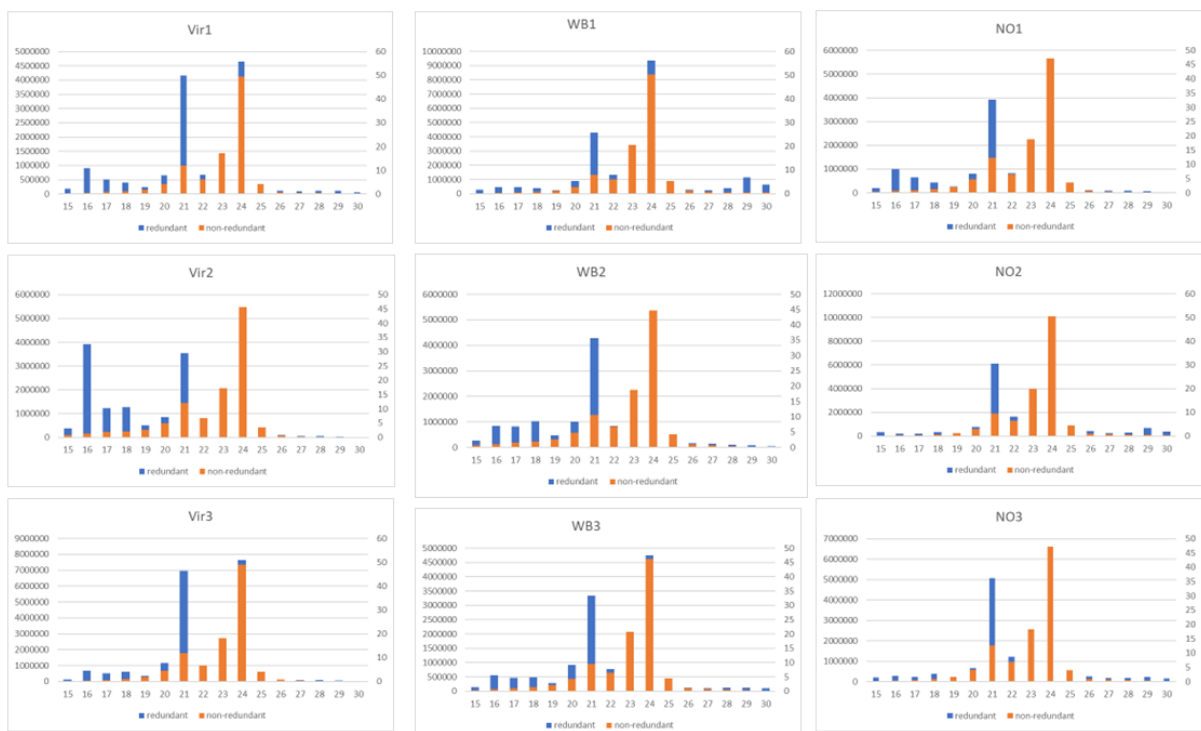


Figure S2. A column diagram of the size distribution of the sequenced and *C.roseus* genome mapped small RNA reads in the nine sequenced small RNA libraries (a) Column diagram of the size distribution of the sequenced small RNA reads in the nine sequenced small RNA libraries, showing number of redundant reads (blue) and percentage of the indicated size-class of non-redundant reads (orange). (b) Column diagram of the size distribution of the *C. roseus* mapped sequenced small RNA reads in the nine sequenced small RNA libraries, showing number of redundant reads (blue) and percentage of the indicated size-class of non-redundant reads (orange).

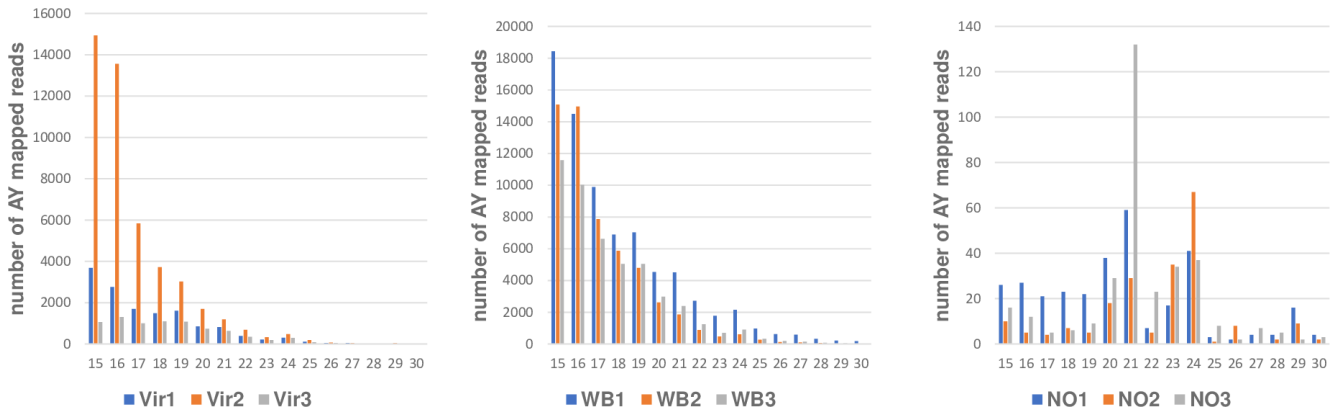


Figure S3. A column diagram of the size distribution of the AY-phytoplasma-mapped reads in the sequenced small RNA libraries .

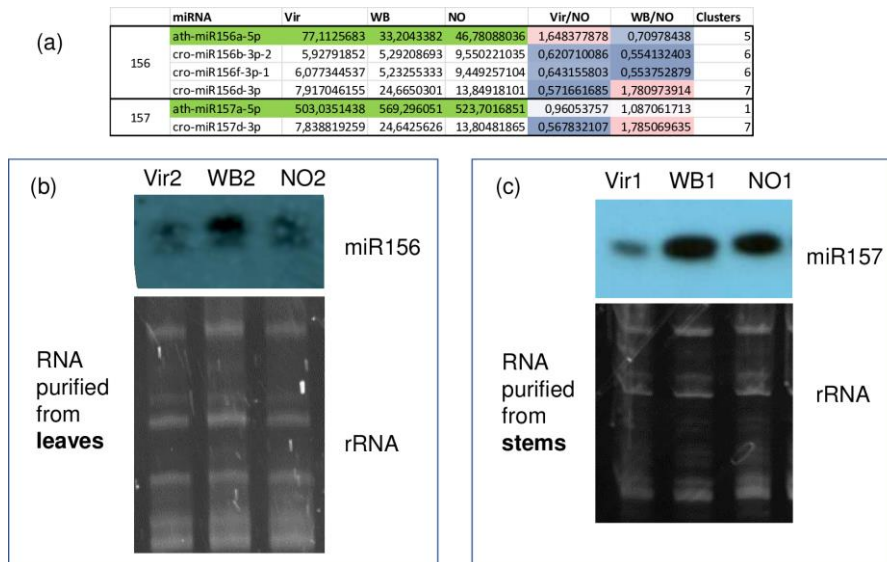


Figure S4. Summarized data (a) and Northern-blot-based validation of the miR156 (b) and miR157 (c) expressions (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three different libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. The intensity of the colour is proportional to the intensity of the change. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control.

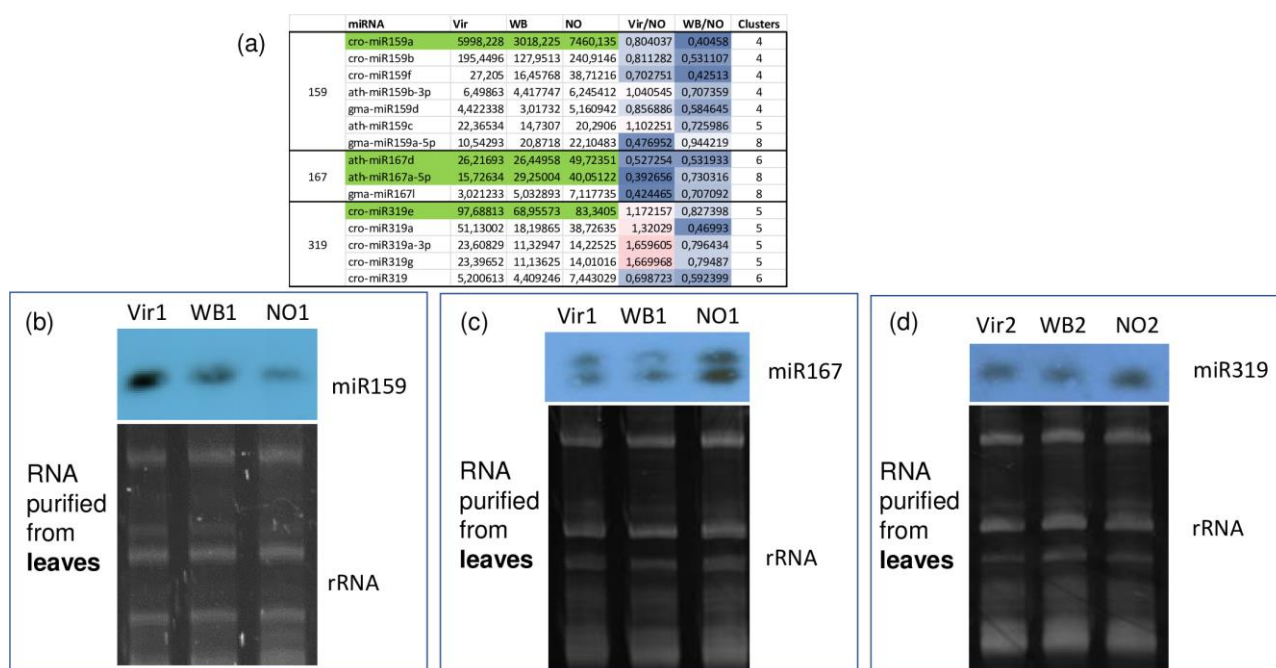


Figure S5. Summarized data (a) and Northern-blot-based validation of the miR159 (b), miR167 (c), and miR319 (d) expressions (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control.

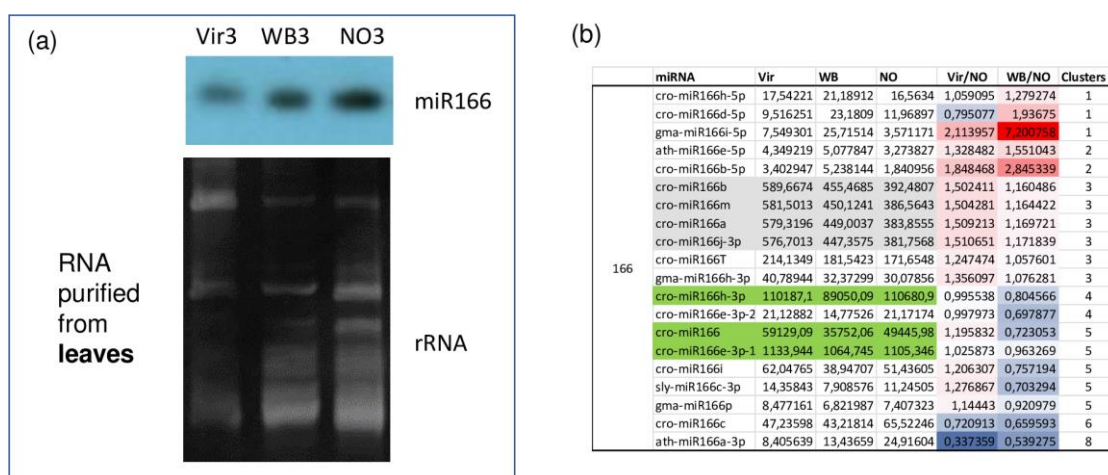


Figure S6. Northern-blot-based validation (a) of the expression changes (b) in the miR166 family (a) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control. (b) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. MiRNA forms indicated with grey have identical sequences. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour.

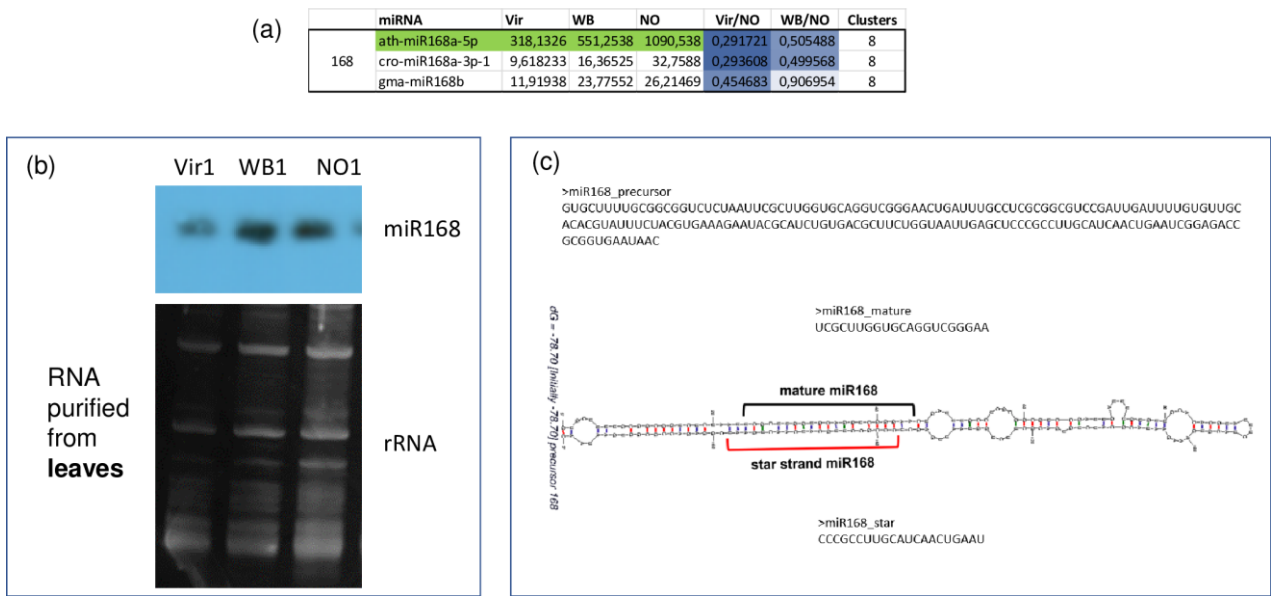


Figure S7. Northern-blot-based validation (b) of the expression changes (a) in miR168. (c) The revised annotation of the *C. roseus* miR168 and its precursor (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control. (c) Proper sequence of the miR168 precursor and the mature miR168 miRNA, together with the schematic draw of the stem-loop structure of the miR168 precursor.

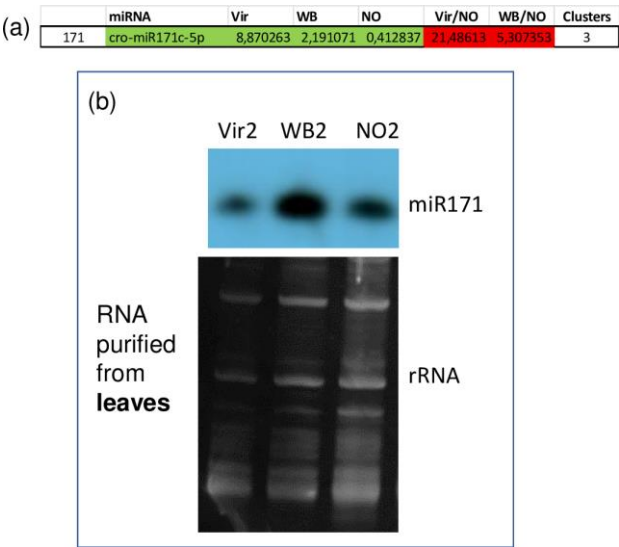


Figure S8. Northern-blot-based validation of the expression changes (a) in miR171 (b). (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control.

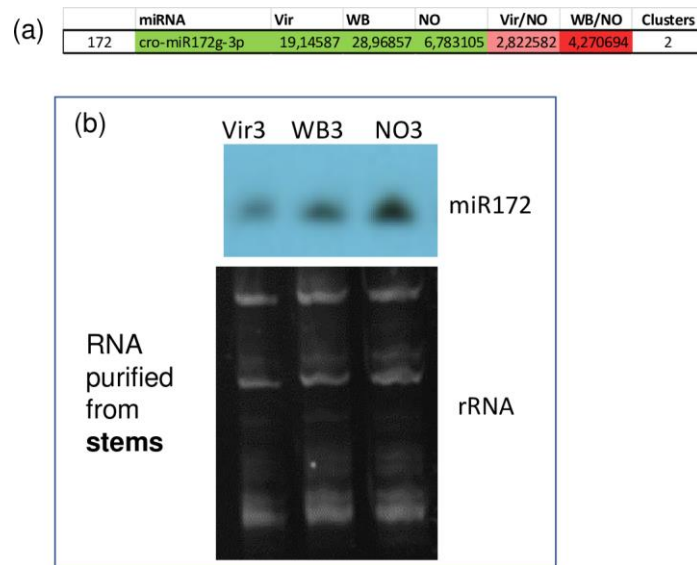


Figure S9. Northern-blot-based validation of expression changes (a) in miR172 (b). (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control.

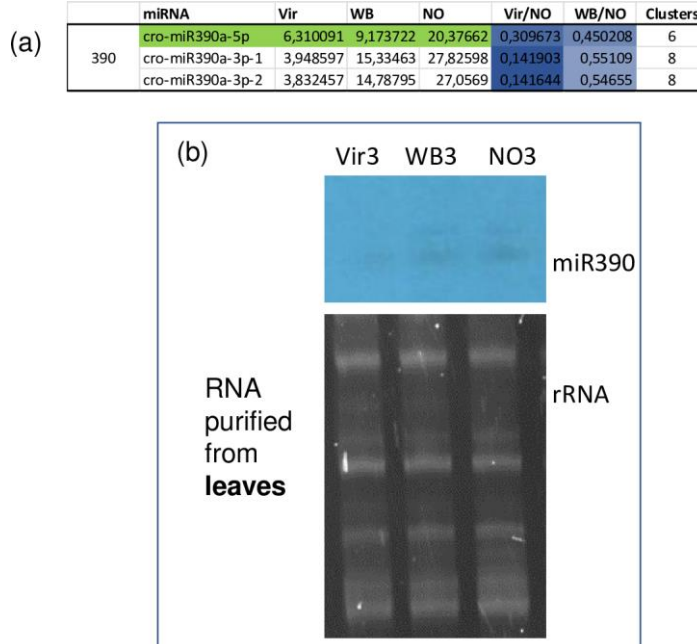


Figure S10. Northern-blot-based validation of the expression changes (a) of miR390 (b). (a) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour. (b) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control.

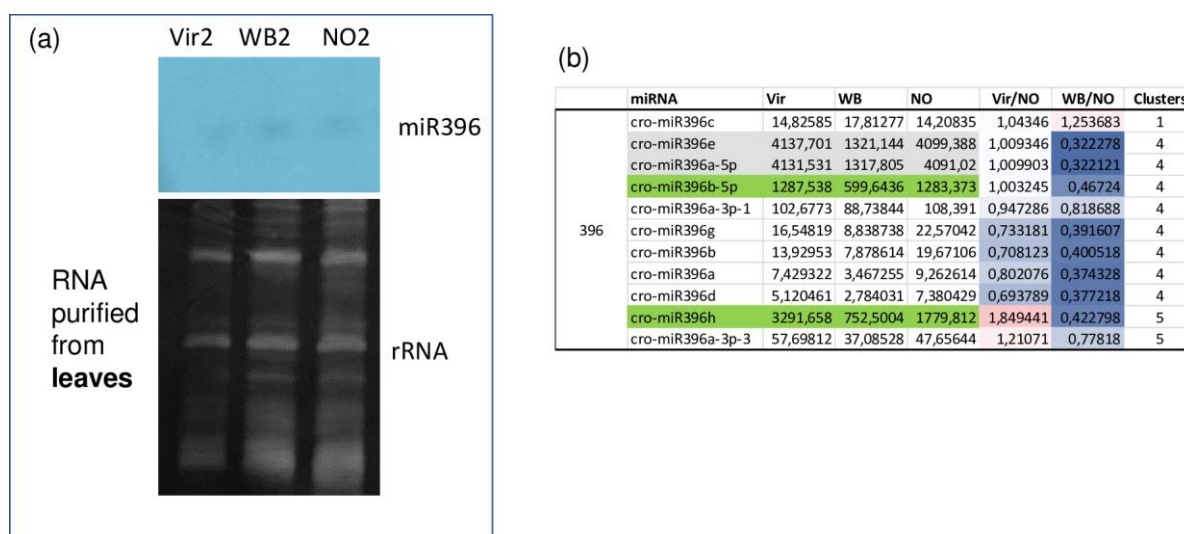


Figure S11. Northern-blot-based validation (a) of the expression changes (b) in miR396. (a) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control. (b) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. MiRNA forms indicated with grey have identical sequences. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour.

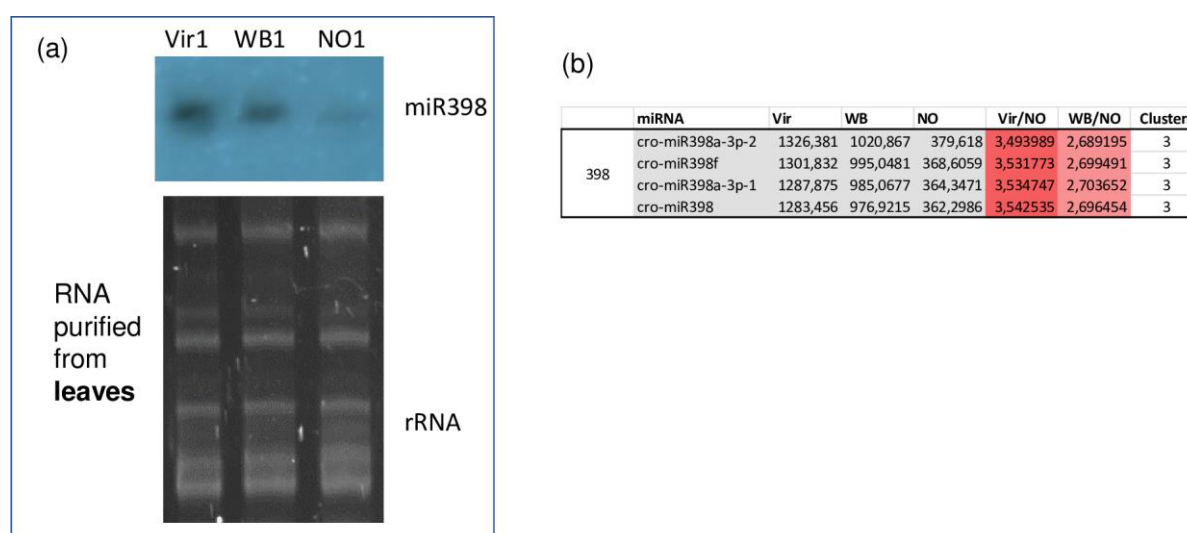


Figure S12. Northern-blot-based validation (a) of the expression changes (b) in miR398. (a) Northern blot hybridization using radioactively labelled LNA probe detecting the indicated miRNA in the extract of one of the Vir, WB and NO plants. EtBr-stained gel serves as a loading control. (b) RPM of miRNA sequenced in the different libraries (indicated as the average of results in three libraries) and relative expression (RMP in the Vir or WB libraries compared to the RPM of the same miRNA in NO libraries) green indicates, the most abundant form of the miRNA family. MiRNA forms indicated with grey have identical sequences. Down-regulation in the symptomatic plants is indicated with blue, while up-regulation is indicated with red colour.