#### LEGENDS FOR ADDITIONAL FILES

Additional Figure 1

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Additional Figure 1: Bar graph of total number of differentially expressed transcripts between inoculated and control treatments of Fish Creek (blue) and 94006 (orange) at 1-day intervals for 5 days. Dotted lines represent approximated trends of expression over duration of experiment.

Additional Figure 2

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Additional Figure 2: Module eigengene correlations with time point as calculated in WGCNA. Time point was coded as 0, 2, 3. The modules from the resistant network are on the left while the susceptible network modules are on the right. Significance was determined at the 0.05 value. Positive correlations become deeper red while negative correlations become blue.

Additional Figure 3

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Additional Figure S3: Schematic of greenhouse experiment. Each leaf was paintbrush inoculated with 1mg uredospores and image of heavily infected leaf was taken 12dpi after completion of the experiment. Imaged in bottom is Patrick McMullen.

Additional Table 1

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Gene ontology results for each group of differentially expressed genes defined though the contrast of susceptible and resistant genotypes.

Additional Table 2

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Gene ontology results for each group of differentially expressed genes defined though the contrast of inoculated and the uninoculated control treatments.

Additional Table 3

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Gene ontology results for each module from the network analysis of resistant genotypes.

Additional Table 4

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Gene ontology results for each module from the network analysis of susceptible genotypes.

Additional Table 5

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Gene ontology results for each eQTL hotspot.

Additional Table 6

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List of candidate genes identified through differential expression, network analysis, and eQTL mapping.

Additional Table 7

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Differentially expression and effector prediction results of *M. americana* transcripts.

Additional Table 8

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Analysis of the *in-silico* proteome of the *M. americana* reference genome using SignalPv5.0 with default settings to generate an *in silico* secretome.

Additional Table 9

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Analysis of the *M. americana* secretome for effector prediction using EffectorPv2.0 using the default settings.