

Supplementary Figures

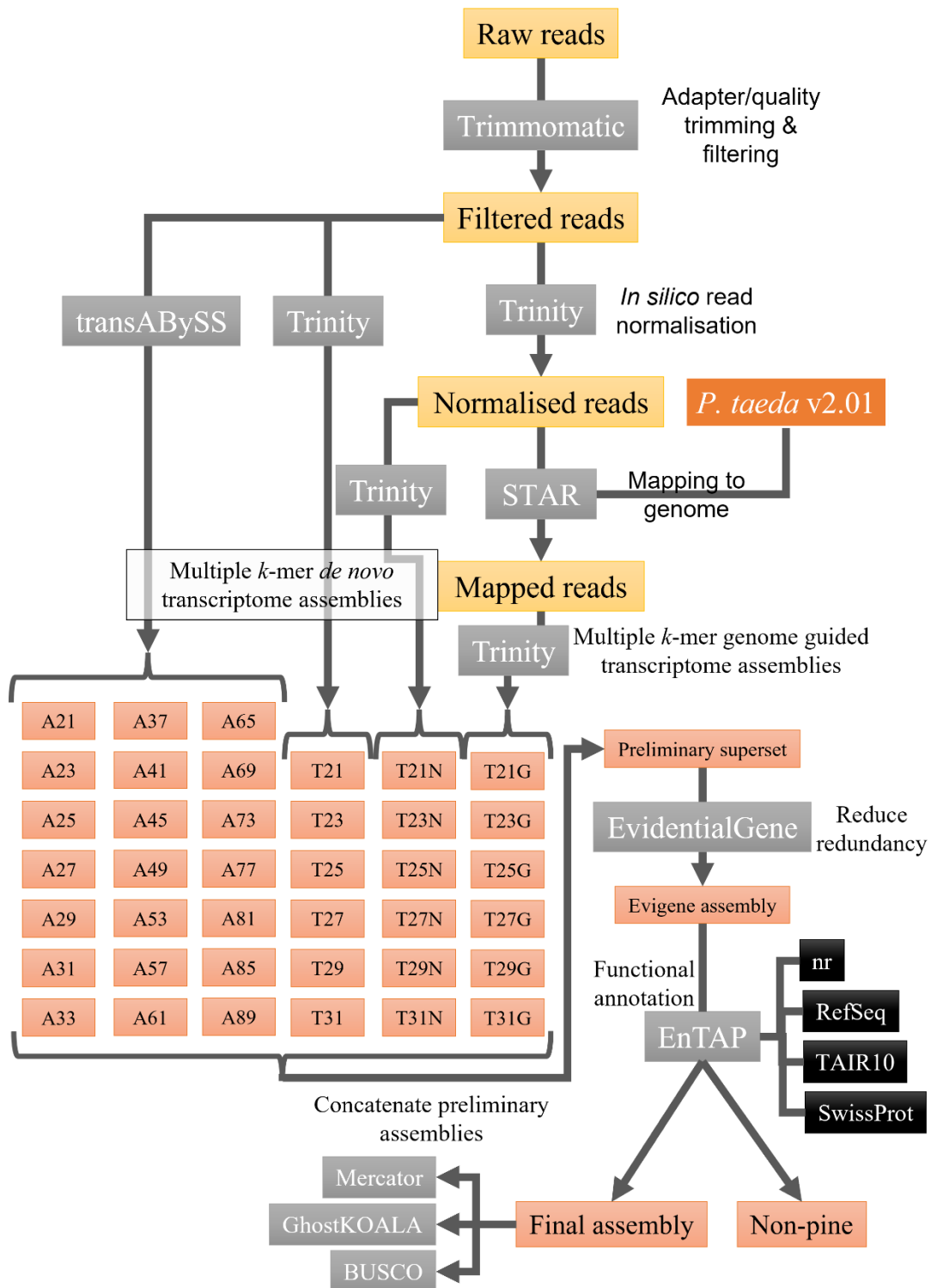


Figure S1: Transcriptome assembly pipeline. For the multi *k*-mer transcriptome assemblies, numbers represent the *k*-mer length, A identifies *de novo* transABySS assemblies, T identifies *de novo* Trinity assemblies using quality trimmed non-normalised data, N identifies *de novo* Trinity assemblies using normalised data, G identifies *P. taeda* v2.01 genome-guided Trinity assemblies. Yellow boxes represent RNAseq read data, grey boxes represent bioinformatic tools and pipelines, orange boxes represent genomes (white text) or transcriptomes (black text), black boxes represent protein databases.

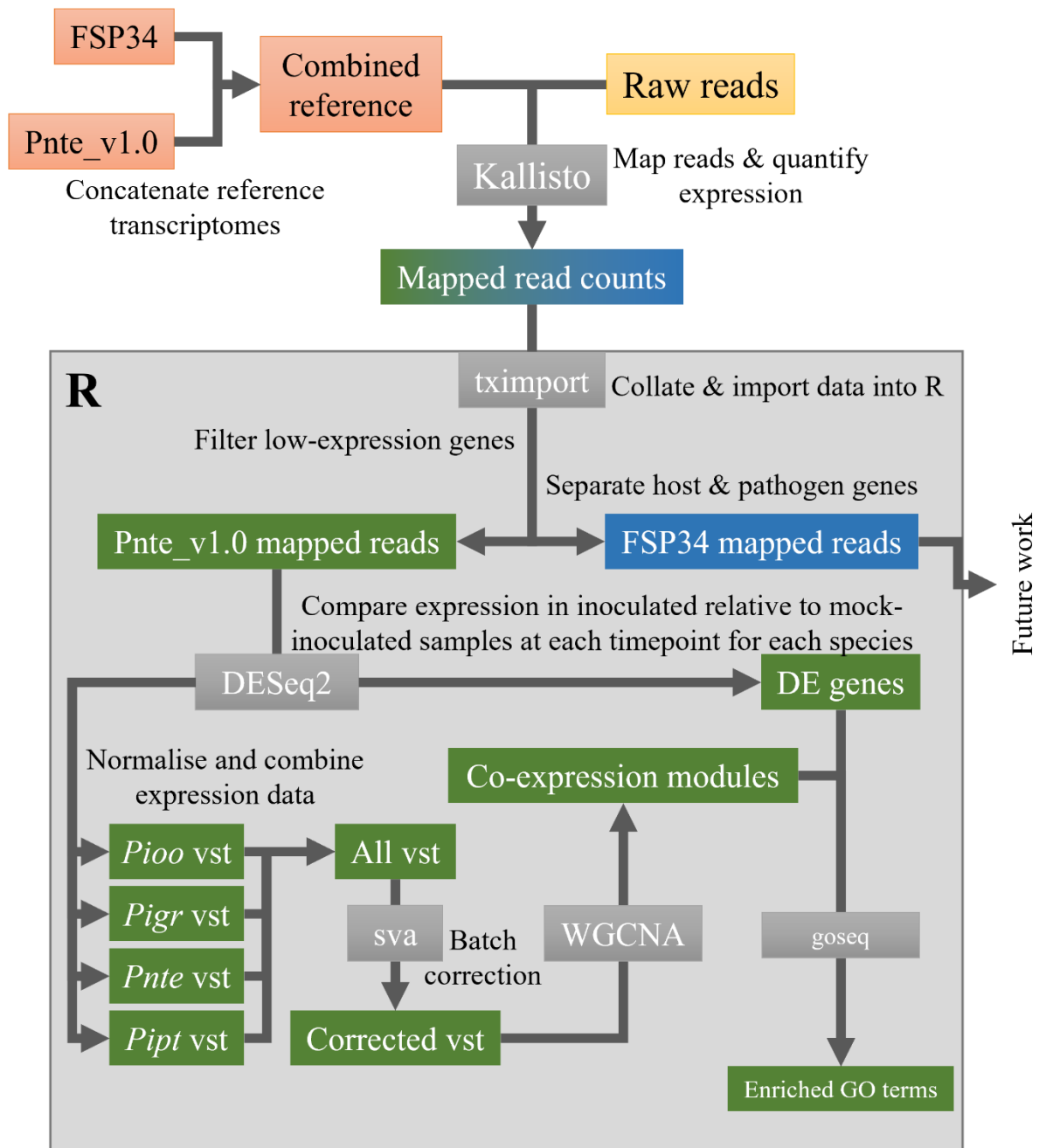


Figure S2: Expression analysis pipeline. Yellow boxes represent RNAseq read data, grey boxes represent bioinformatic tools and pipelines, orange boxes represent transcriptomes, green boxes represent pine expression data, blue boxes represent *F. circinatum* expression data. FSP34 – *F. circinatum* transcriptome (Wingfield *et al.* 2012), Pnte_v1.0 – *P. tecunumanii* transcriptome (Visser *et al.* 2018), Pioo – *P. oocarpa*, Pigr – *P. greggii*, Pnte – *P. tecunumanii*, Pipt – *P. patula*, vst – variance stabilising transformed data, DE – differentially expressed, GO – gene ontology.

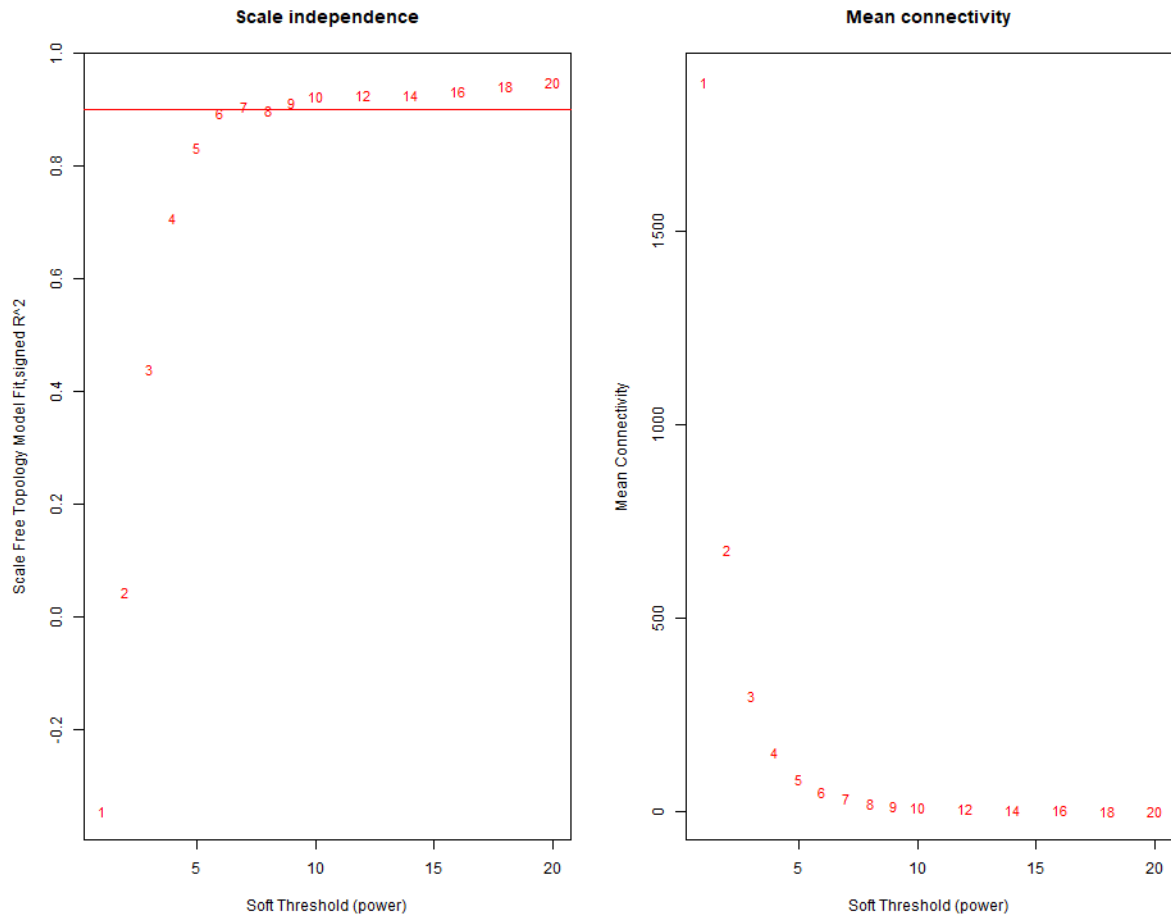


Figure S3: Network topology analysis across multiple soft-thresholding powers.

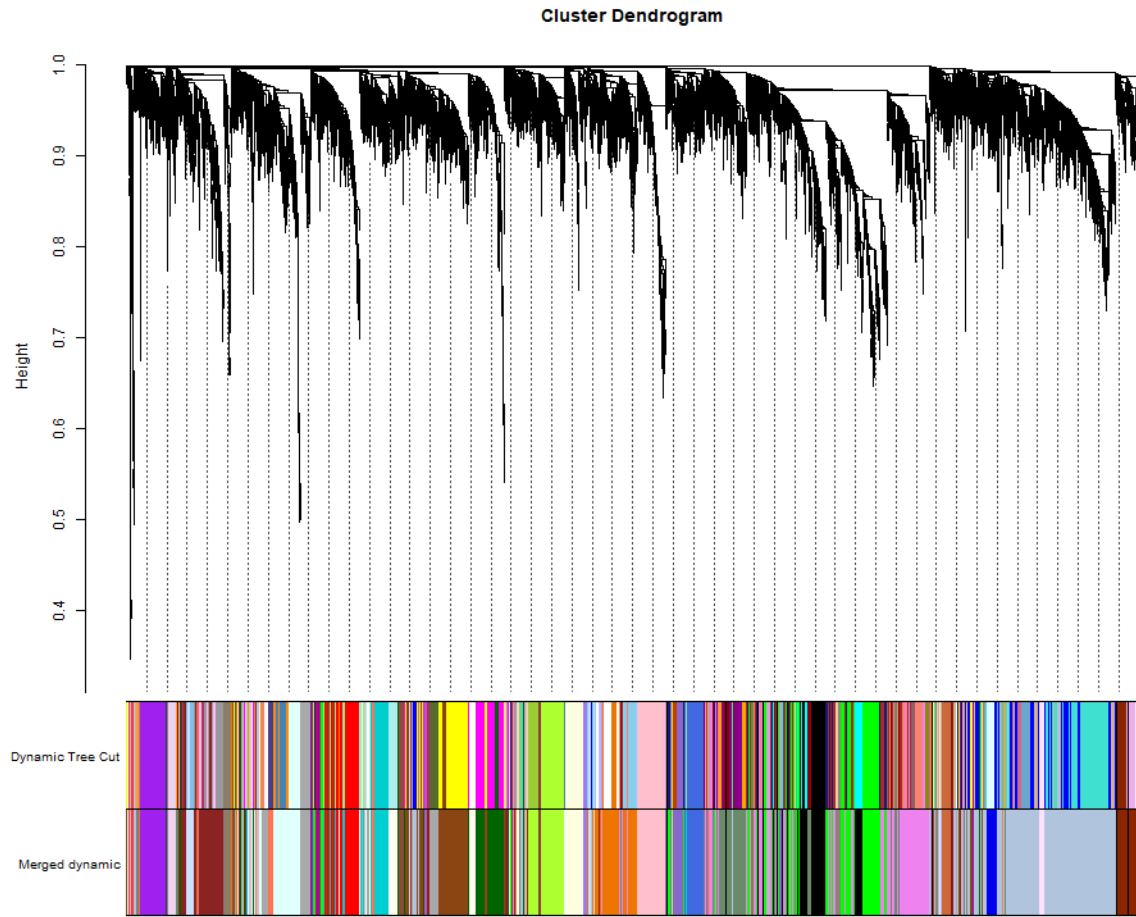


Figure S4: Topological overlap-based gene dissimilarity clustering dendrogram showing original and merged module colors.

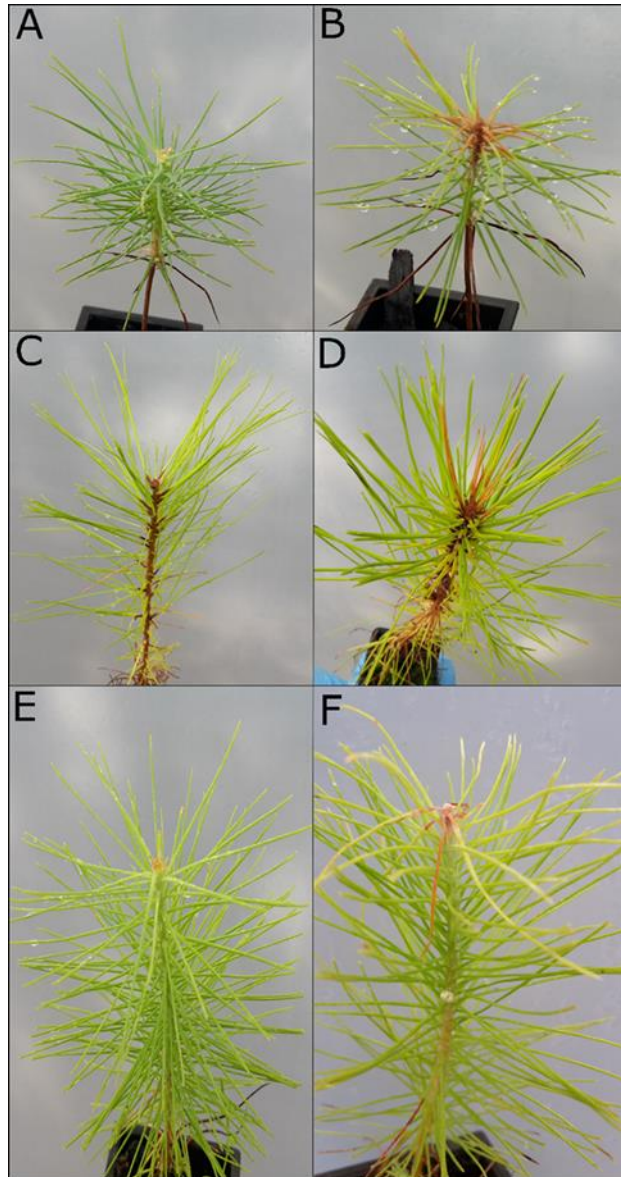


Figure S5: Visible symptoms of *F. circinatum* infection on inoculated relative to mock-inoculated seedlings at 21 days post inoculation. (A) Mock- and (B) inoculated *Pinus greggii* seedlings. (C) Mock- and (D) inoculated *Pinus maximinoi* cuttings. (E) Mock- and (F) inoculated *Pinus oocarpa* seedlings.

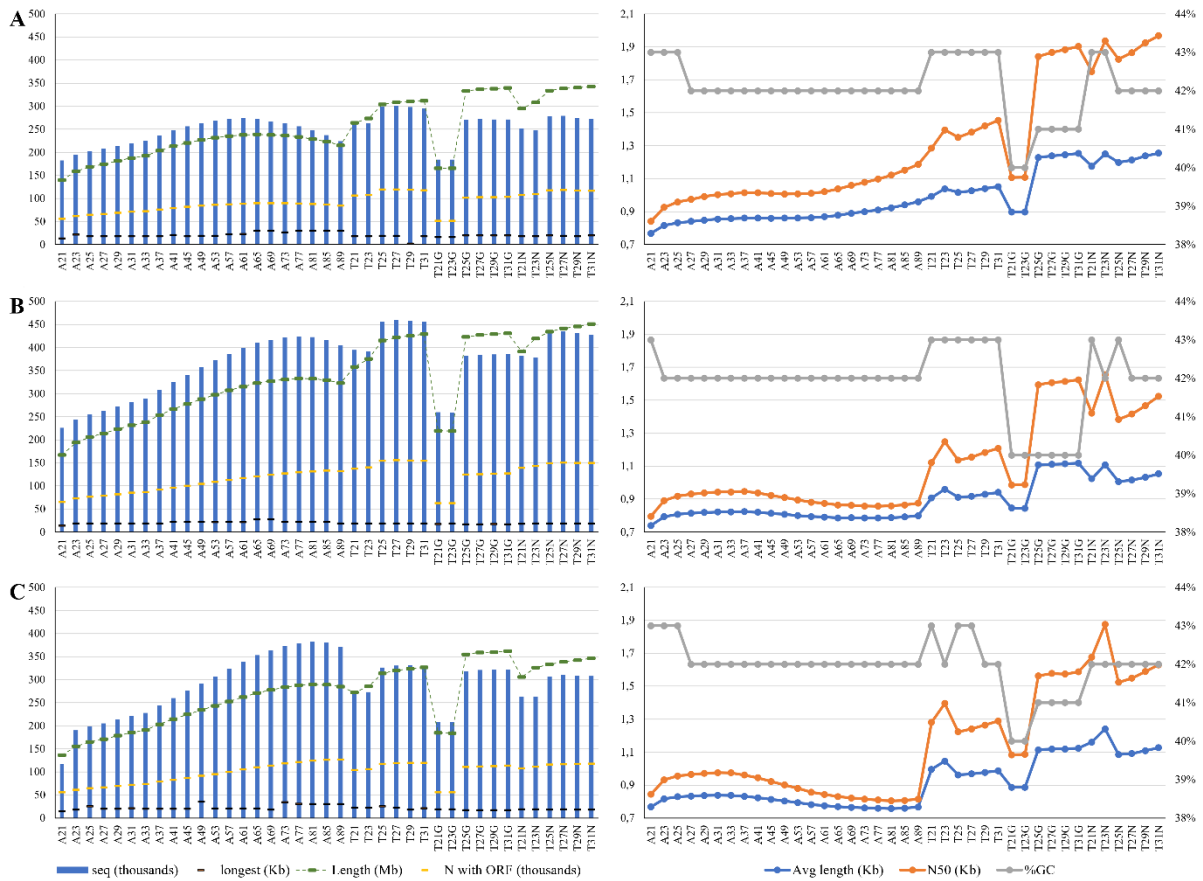


Figure S6: Summarised statistics for preliminary transcriptome assemblies. **A** – *P. greggii*, **B** – *P. maximinoi*, **C** – *P. oocarpa*. **Left** – Number of sequences per assembly, length of the longest transcript, overall assembly length and predicted number of open reading frames within each assembly. **Right** – Average sequence length, N50 and percentage GC for each assembly, the right hand axis only applies to %GC. The x-axis represents the respective assemblies for each species using, where numbers represent the *k*-mer value used for the assembly in ‘A’ trans-AbySS or ‘T’ trinity, using filtered RNA-seq data. For trinity assemblies ‘G’ represent genome guided assemblies and ‘N’ represents assemblies from *in silico* normalised read data.

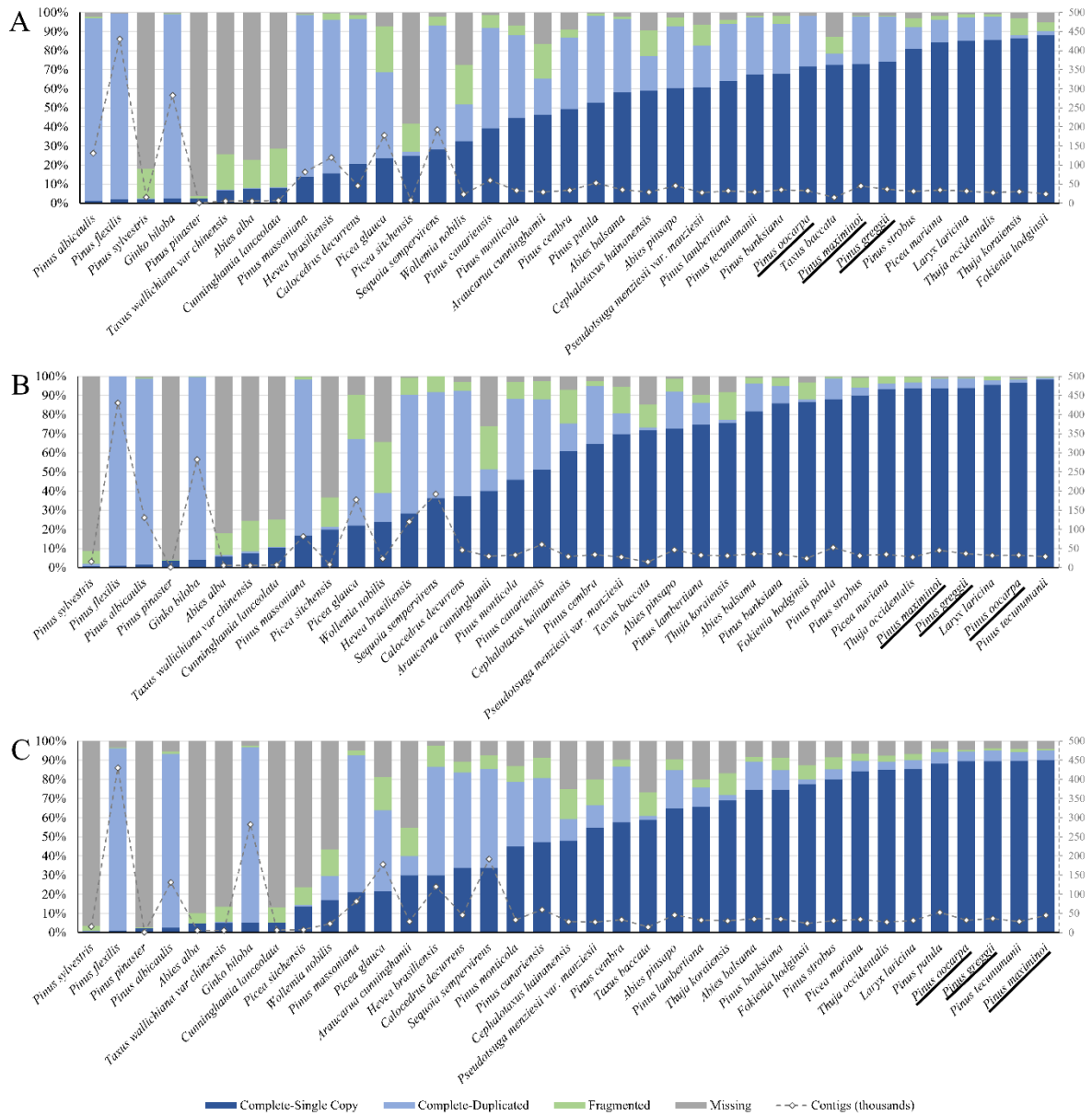


Figure S7: Assembly quality metrics compared to publicly available gymnosperm transcriptomes. BUSCOs were identified for the (A) eukaryotic (n = 255), (B) viridiplantae (n = 425), and (C) embryophyte (n = 1 614) lineages. Assembled transcriptomes for *P. oocarpa*, *P. maximinoi*, and *P. greggii* have been underlined. The left y-axis represents the percentage of BUSCOs in each category. The right y-axis represents the number of predicted proteins for each assembly.

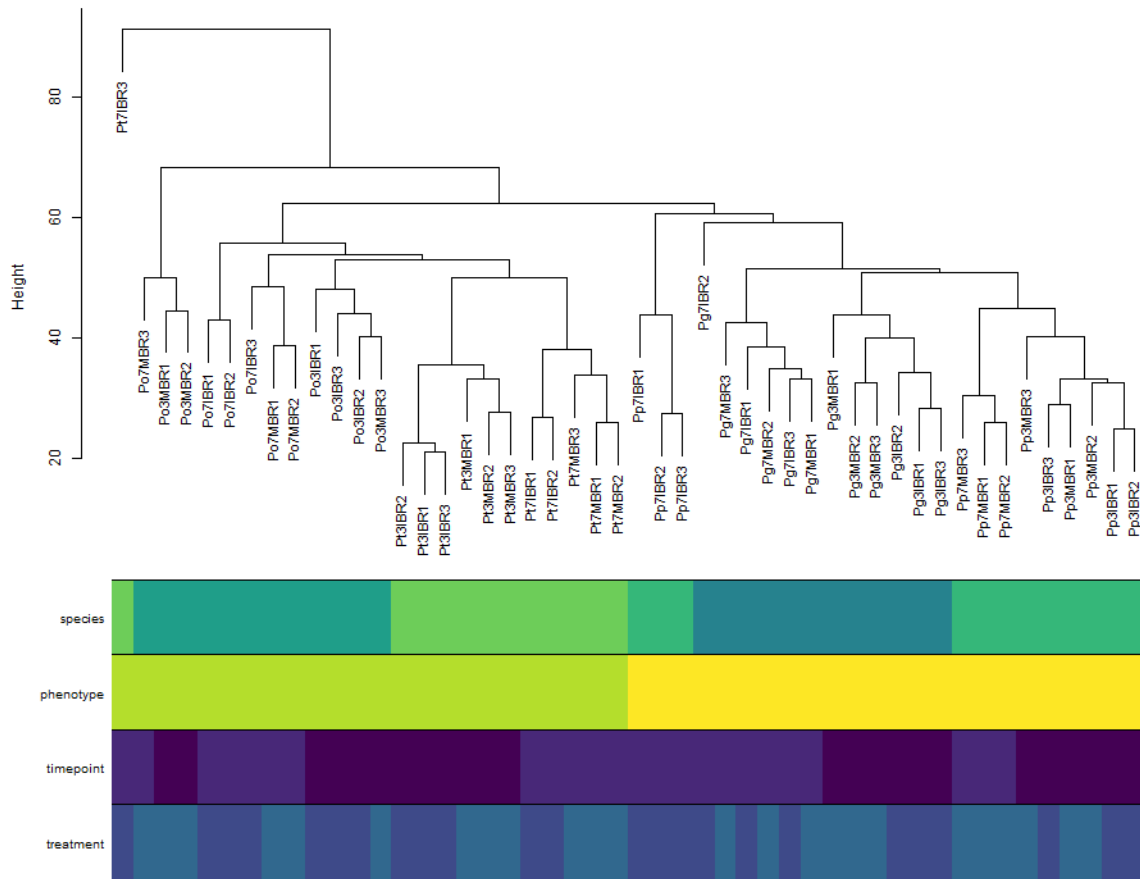
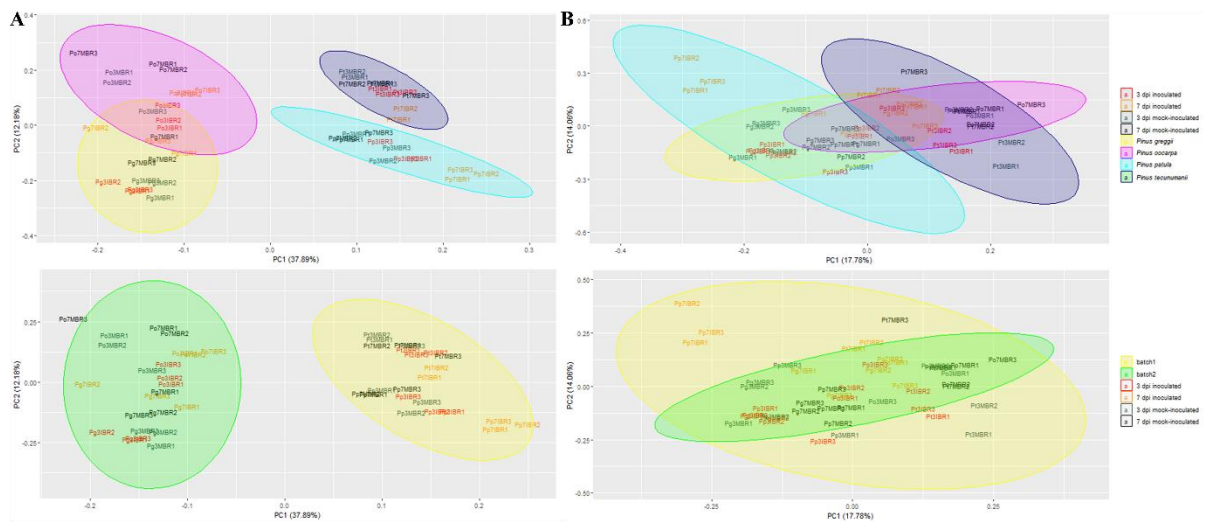


Figure S8: Cluster dendrogram of samples and corresponding traits. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.



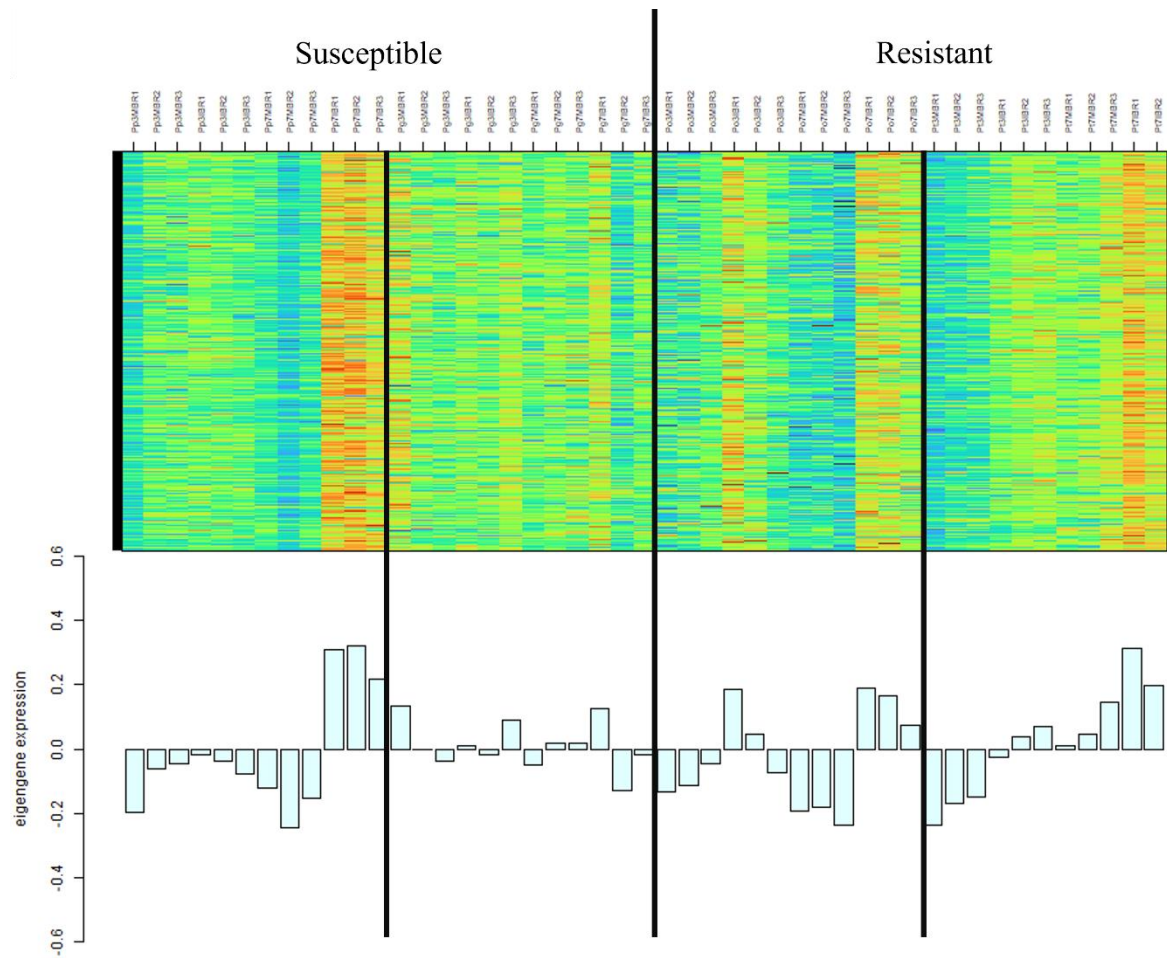


Figure S10: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M07 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

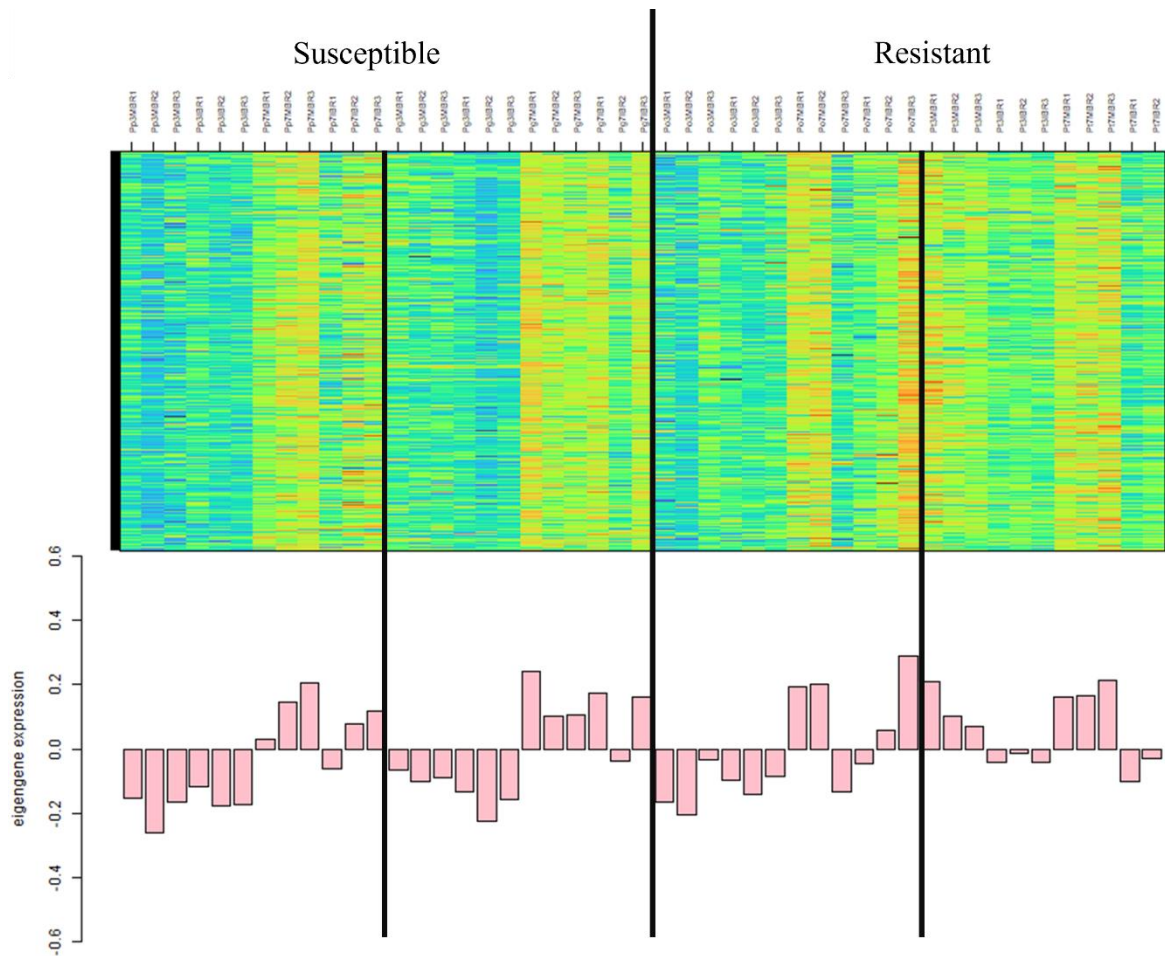


Figure S11: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M15 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

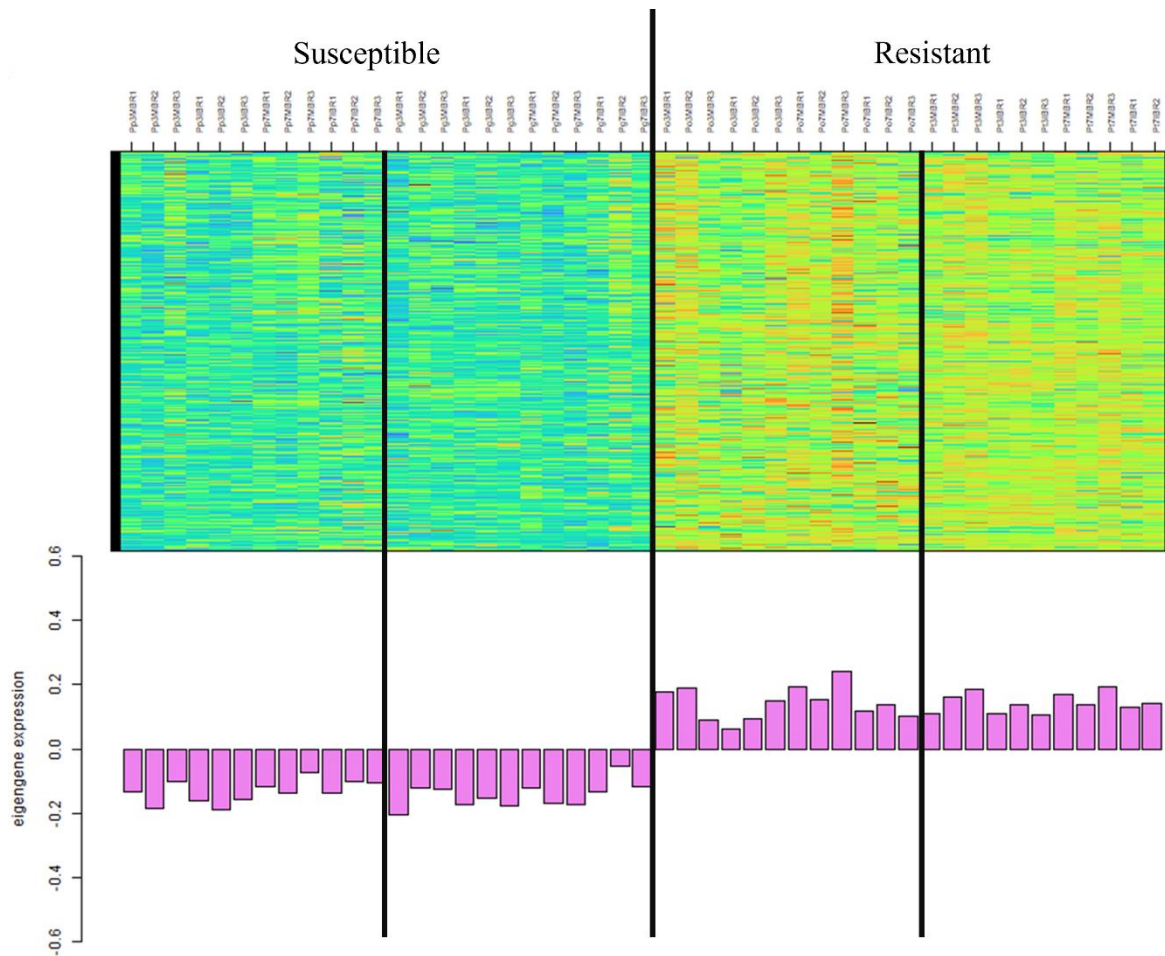


Figure S13: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M02 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

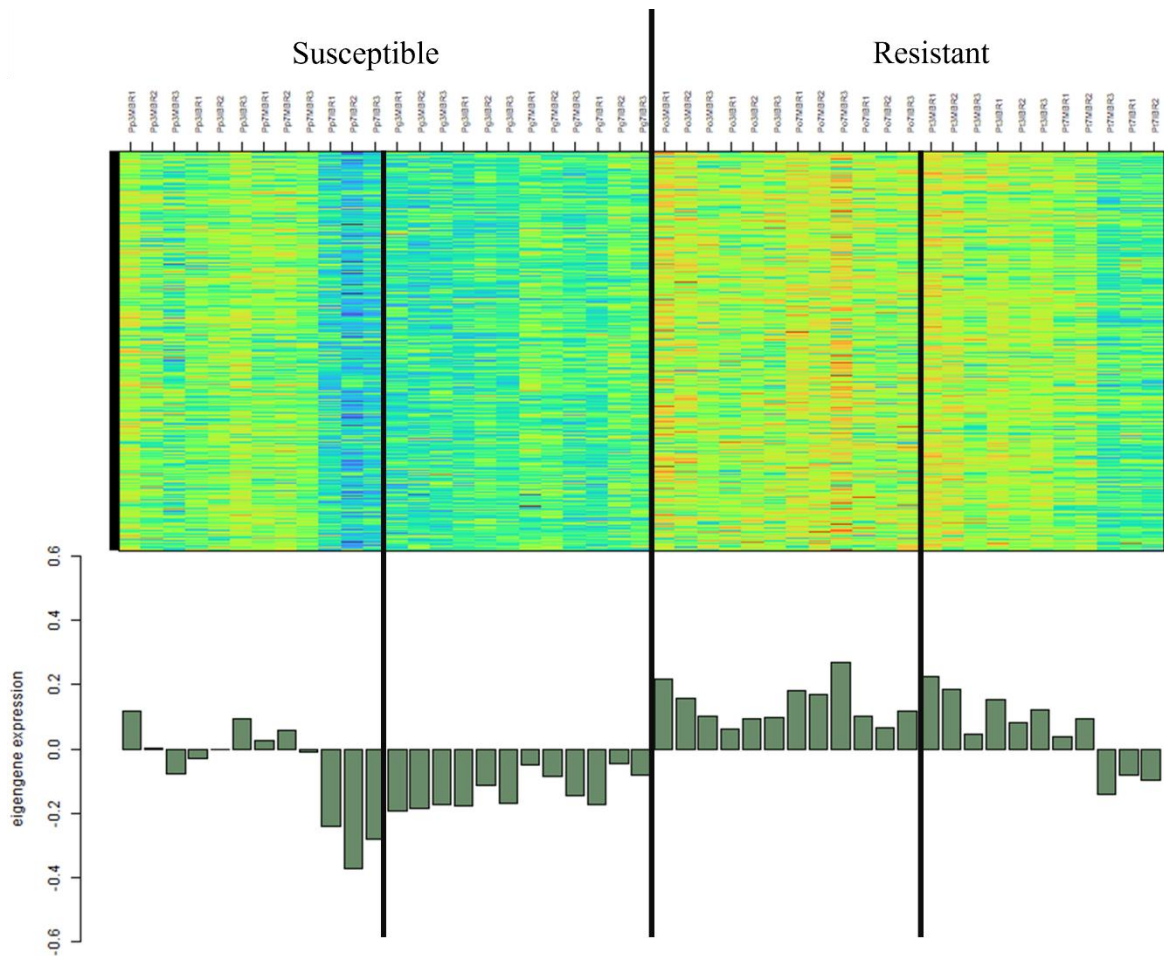


Figure S14: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M06 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

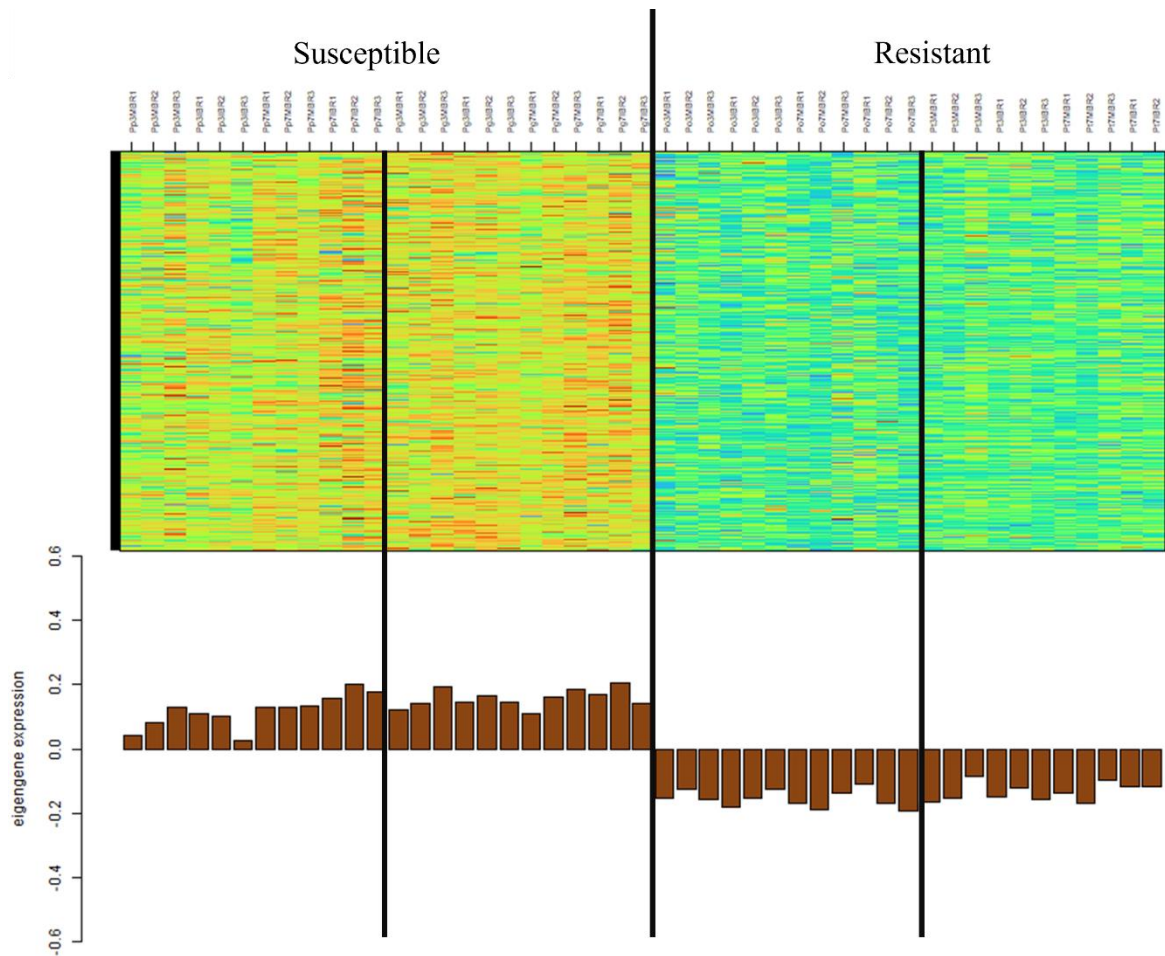


Figure S15: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M04 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

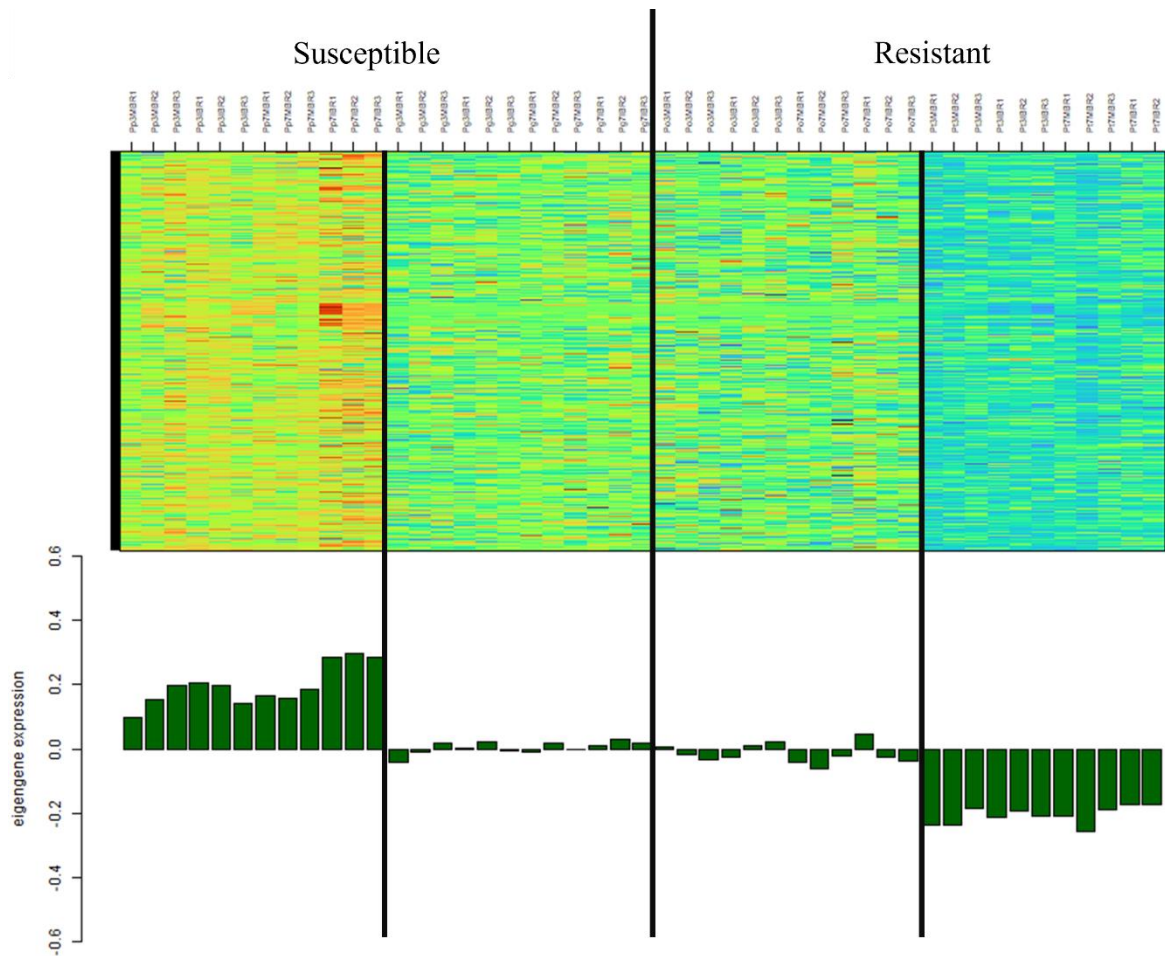


Figure S16: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M08 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

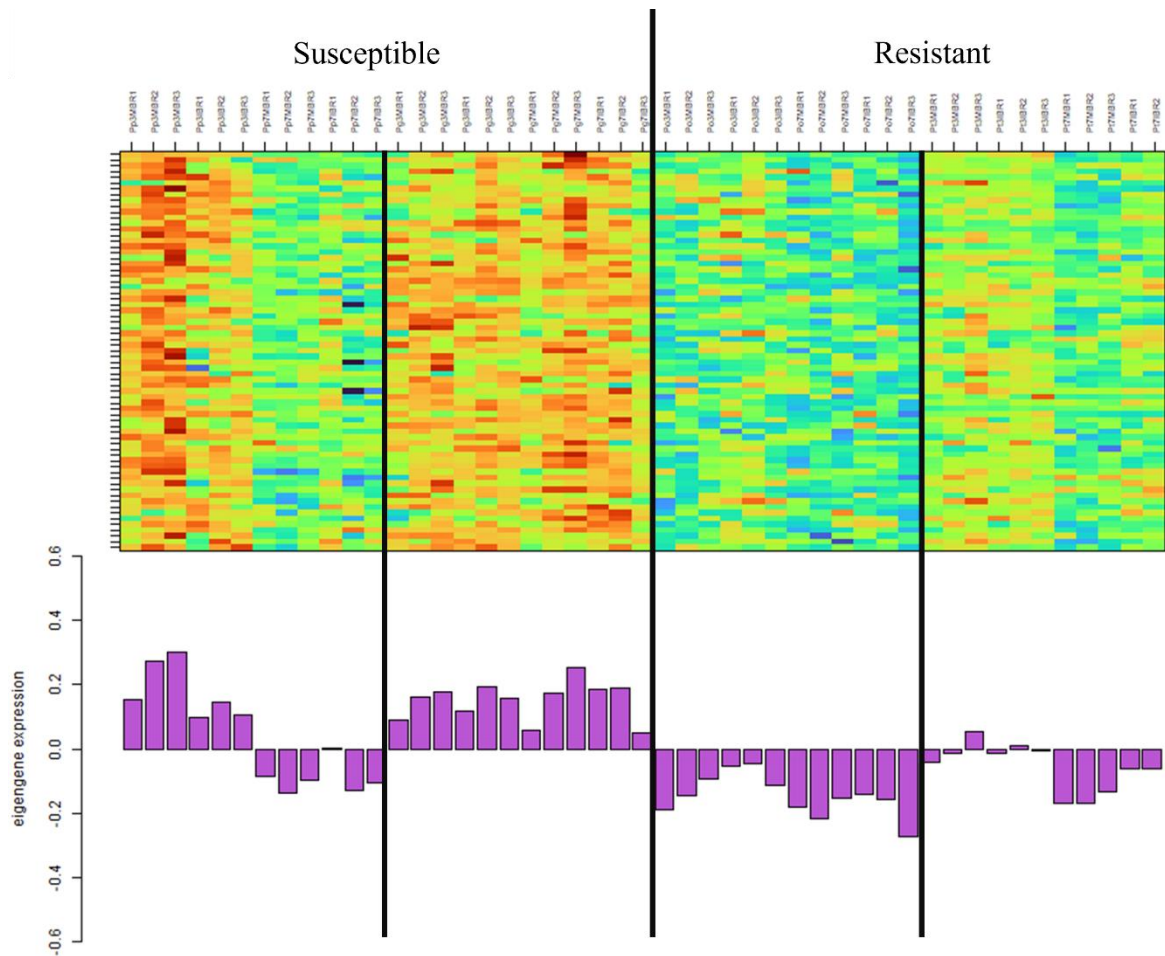


Figure S17: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M33 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.

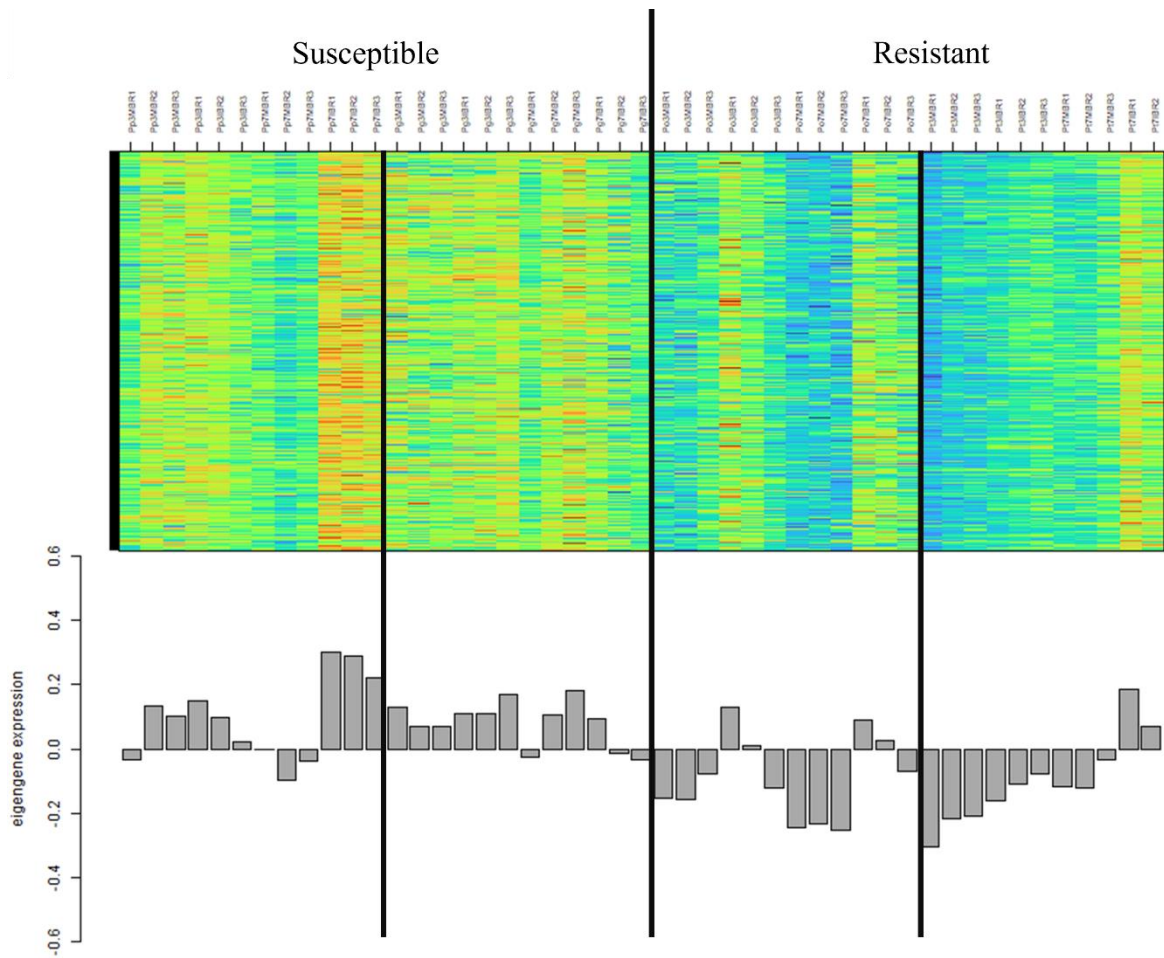


Figure S18: Module heatmap (top) and module eigengene (ME) expression (bottom) for the M11 module. For the heatmap, rows represent genes and columns represent samples, yellow to red corresponds to over-expression relative to the sample mean and light to dark blue corresponds to under-expression. The ME expression values correspond to the heatmap samples and can be considered a representative expression profile of genes in the module. Sample IDs encode the species of origin; **Pg** – *Pinus greggii*, **Pp** – *Pinus patula*, **Po** – *Pinus oocarpa*, **Pt** – *Pinus tecunumanii* – the harvesting timepoint; **3-** and **7-**days post inoculation – the treatment; inoculated (**I**) and mock-inoculated (**M**) – as well as the biological replicate (**BR**) count.