Supplementary Figures

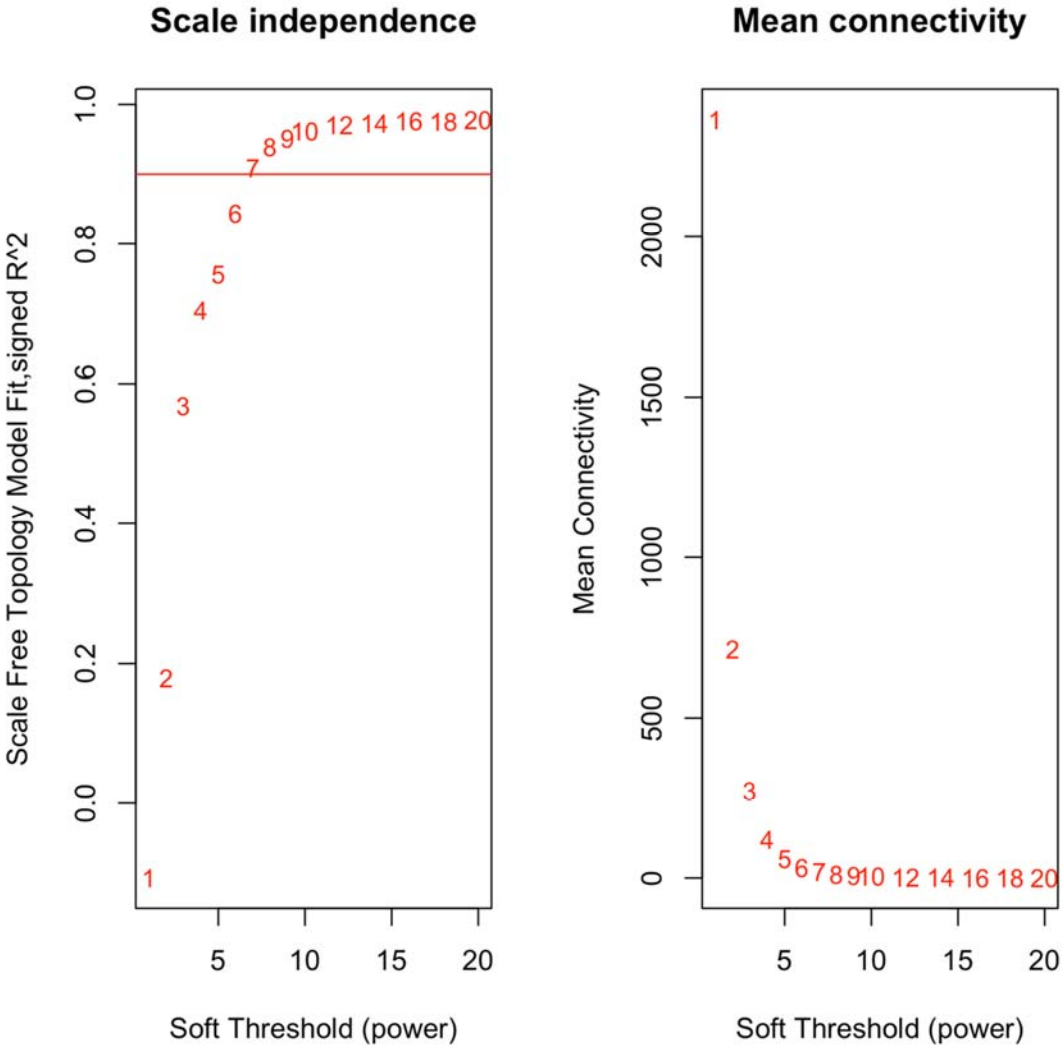

Fig. S1 Scale-free topology fit index as a function of the soft-thresholding power. A soft-thresholding power of seven was selected as it represented the lowest thresholding power for a scale-free topology of $R^2 = 0.9$

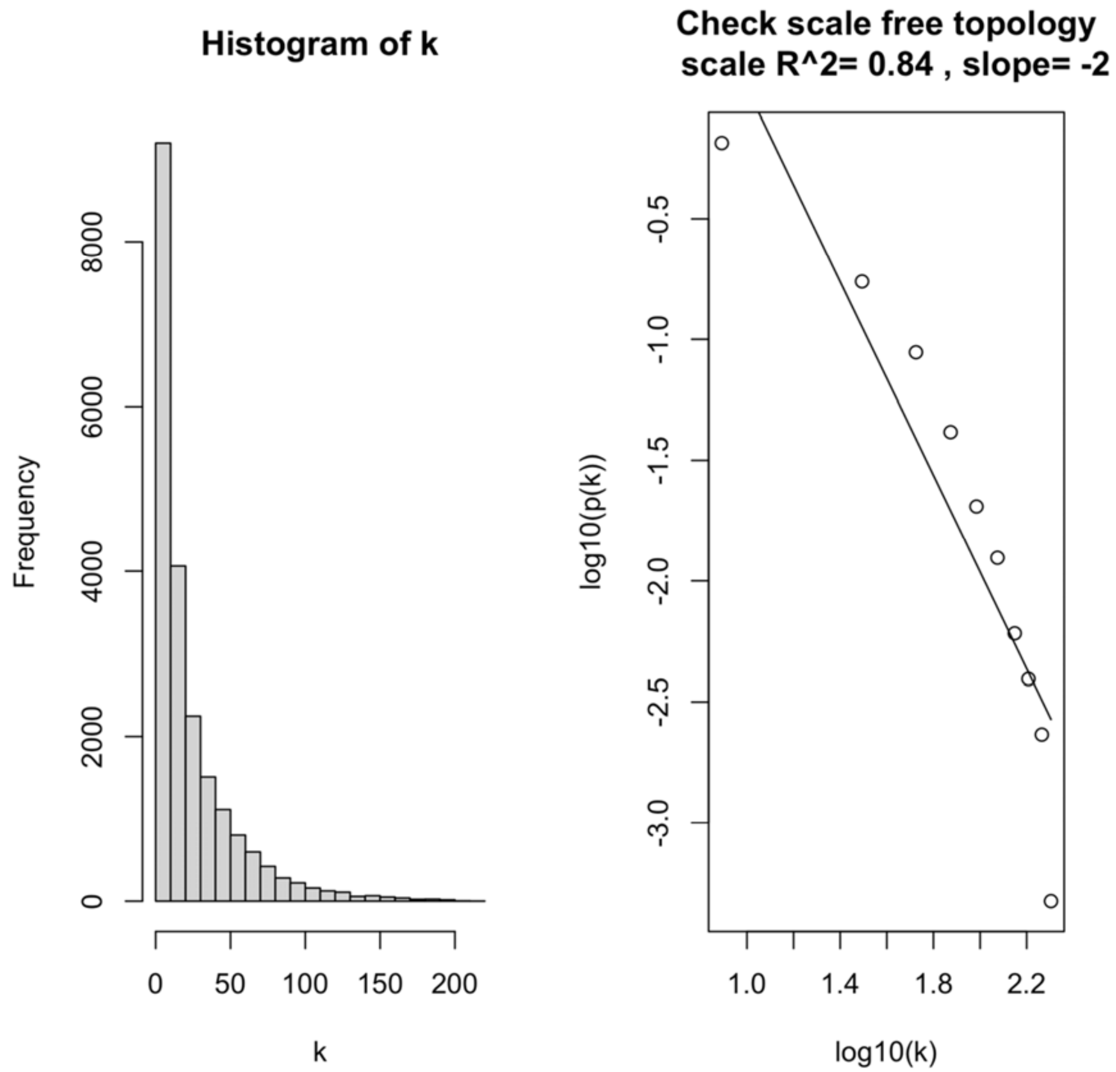

Fig. S2 Evaluation of scale free topology. The analysis shows approximate scale free topology based on the straight line relationship depicted in the log-log plot. The slight deviations can be attributed to the structure of the samples within the data (tissue and pathosystem differences) which still satisfies the assumptions of network construction (Horvath and Langfelder, 2008)

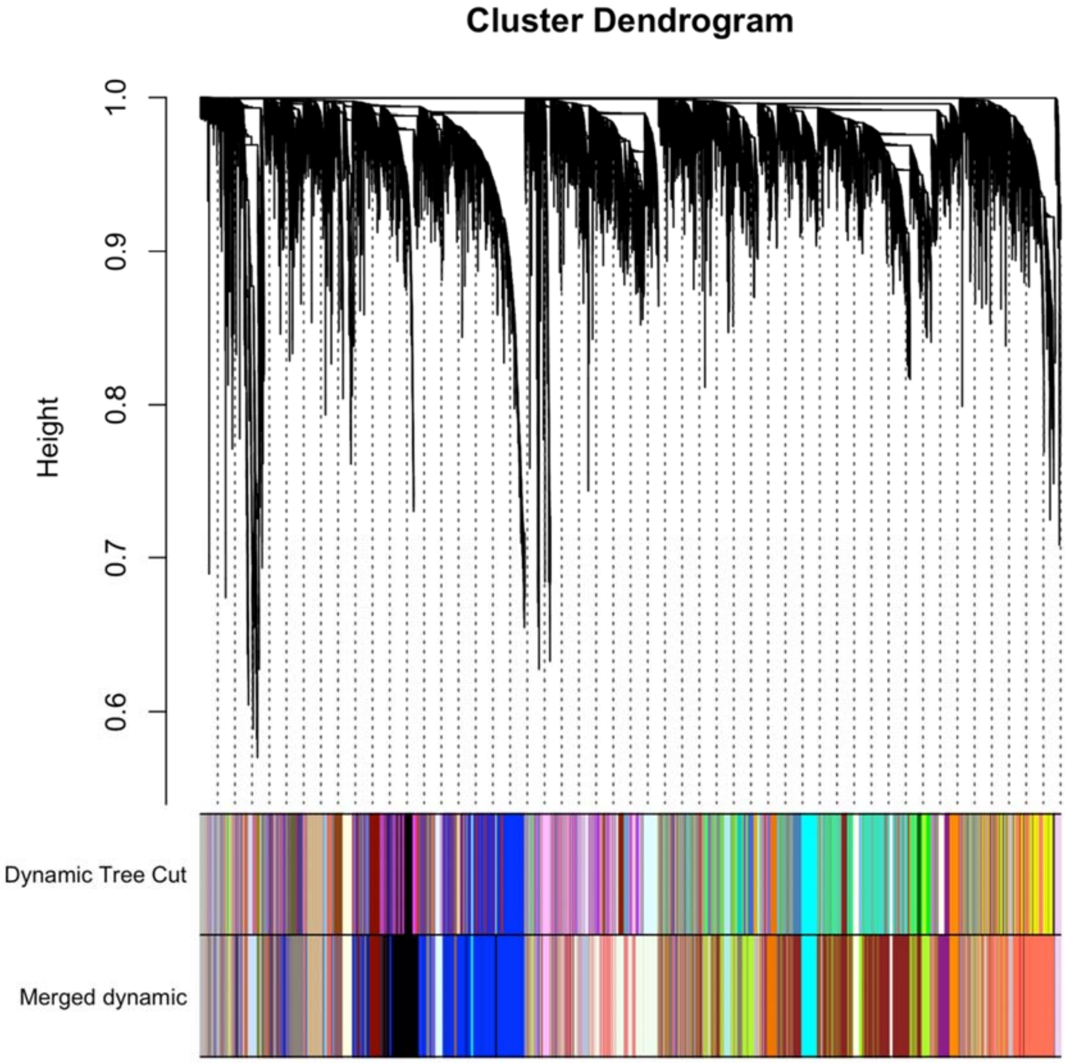

Fig. S3 Cluster dendrogram showing the topological overlap matrix based on co-expression dissimilarity representing dynamic and merged dynamic module colours. A minimum module size of 40 was selected and modules with similar dissimilarity were merged with a cut-off of 0.25

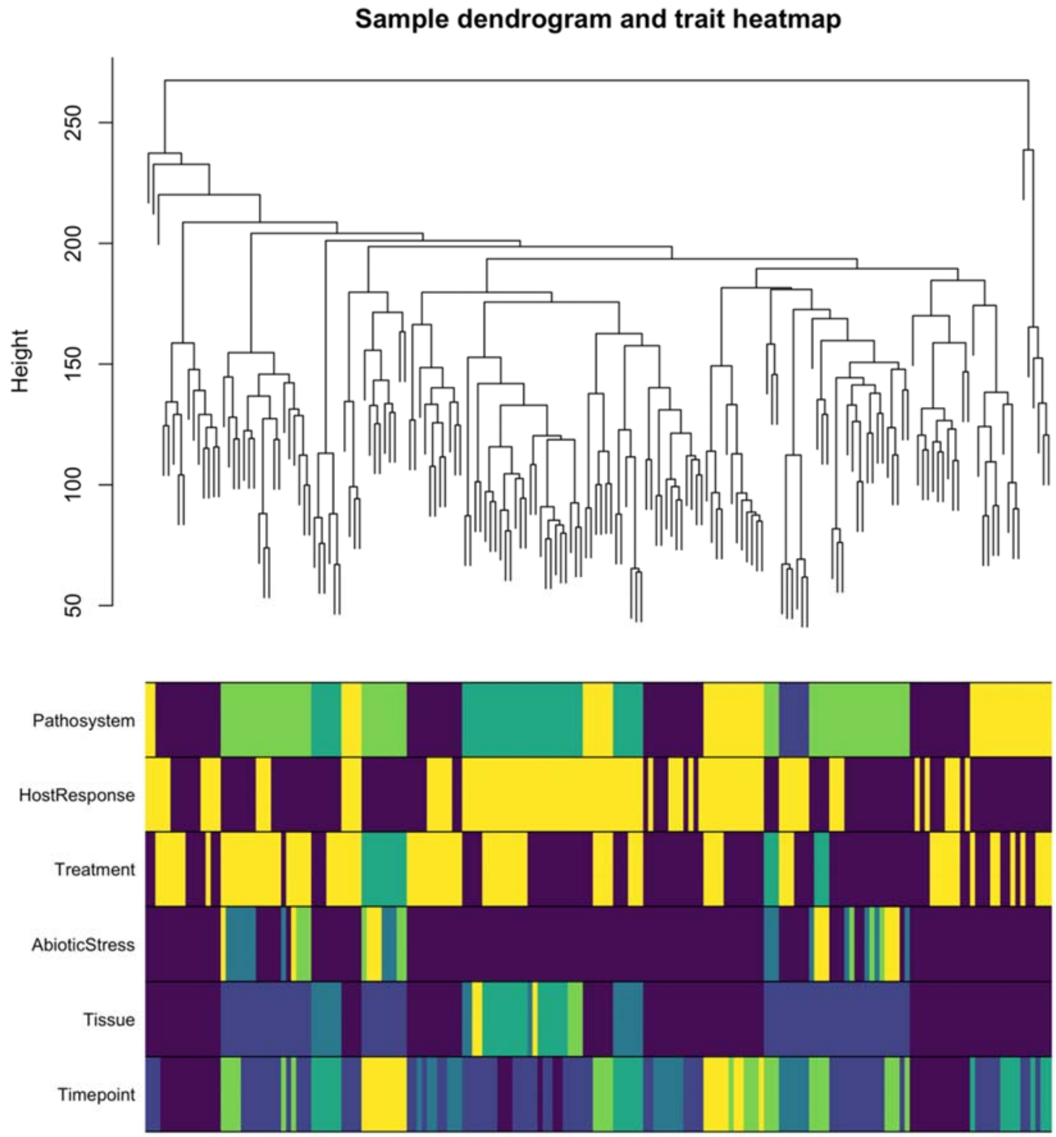

Fig. S4 Cluster dendrogram of samples and traits to determine sample outliers. Sample IDs have been omitted for clarity. Pathosystems included *A. psidii, C. austroafricana, P. cinnamomi,* and *T. destructans*. Host responses included resistant and susceptible hosts. Treatment included mock-inoculated, uninoculated and inoculated treatments

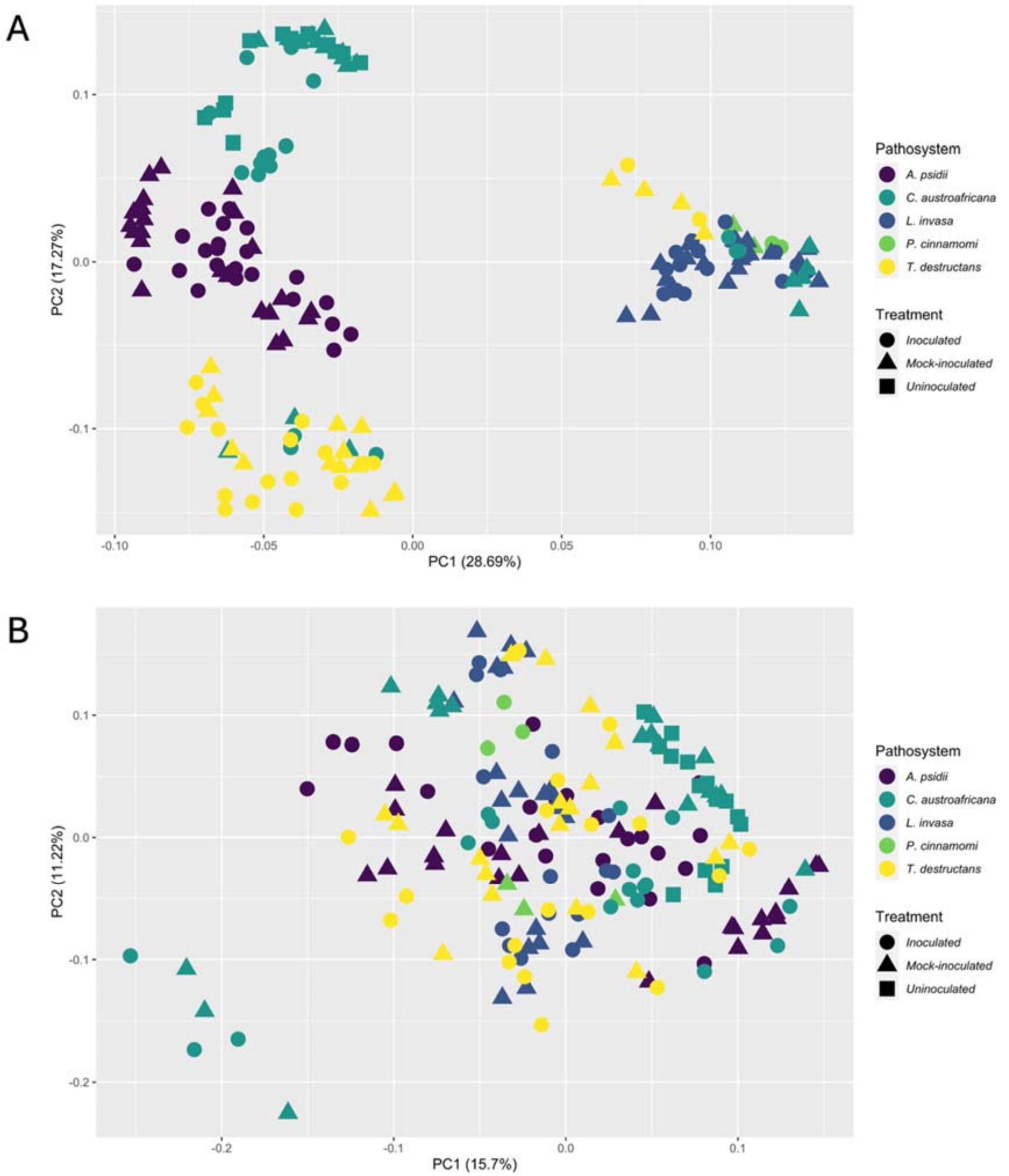

Fig. S5 Principal component analysis of log transformed expression data. (A) before batch correction, and (B) after batch correction. The PCA shows that batch correction removed clusters within datasets so data was no longer clustered by pathosystem. Outliers were identified as abiotic stressed samples and thus not removed

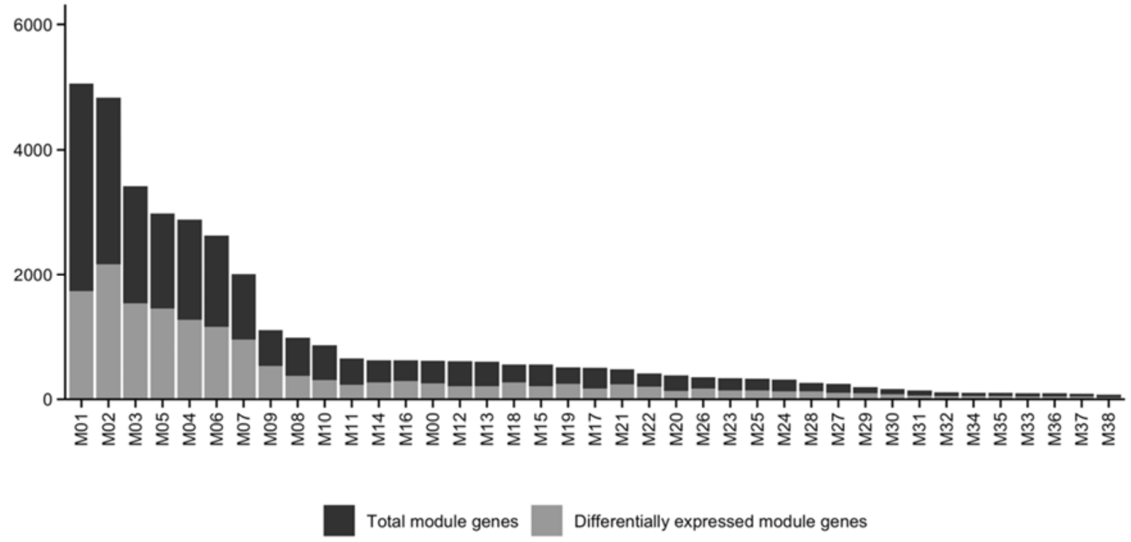

Fig. S6 The total number of genes and differentially expressed genes per module identified through a weighted gene co-expression network analysis

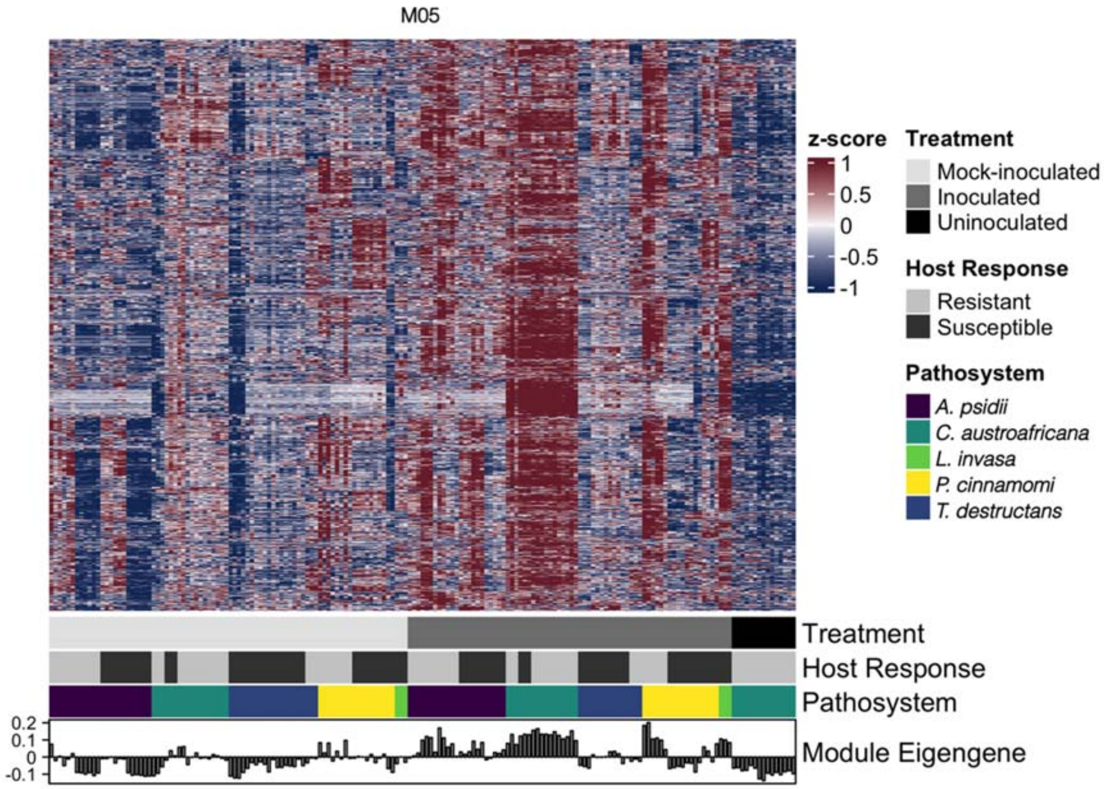

Fig. S7 Module heatmap and module eigengene expression plots for M05. In the heatmap, rows represent the 1,530 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by treatment and further annotated with host response and pathosystem

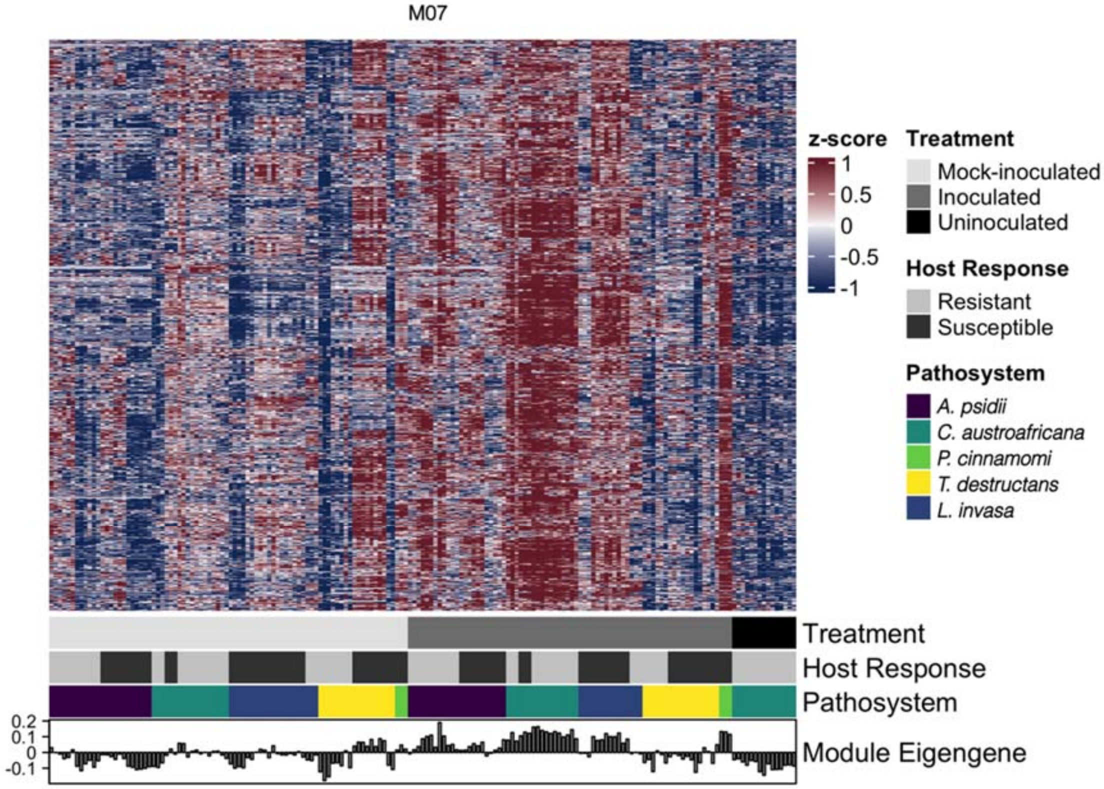

Fig. S8 Module heatmap and module eigengene expression plots for M07. In the heatmap, rows represent the 1,052 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by treatment and further annotated with host response and pathosystem

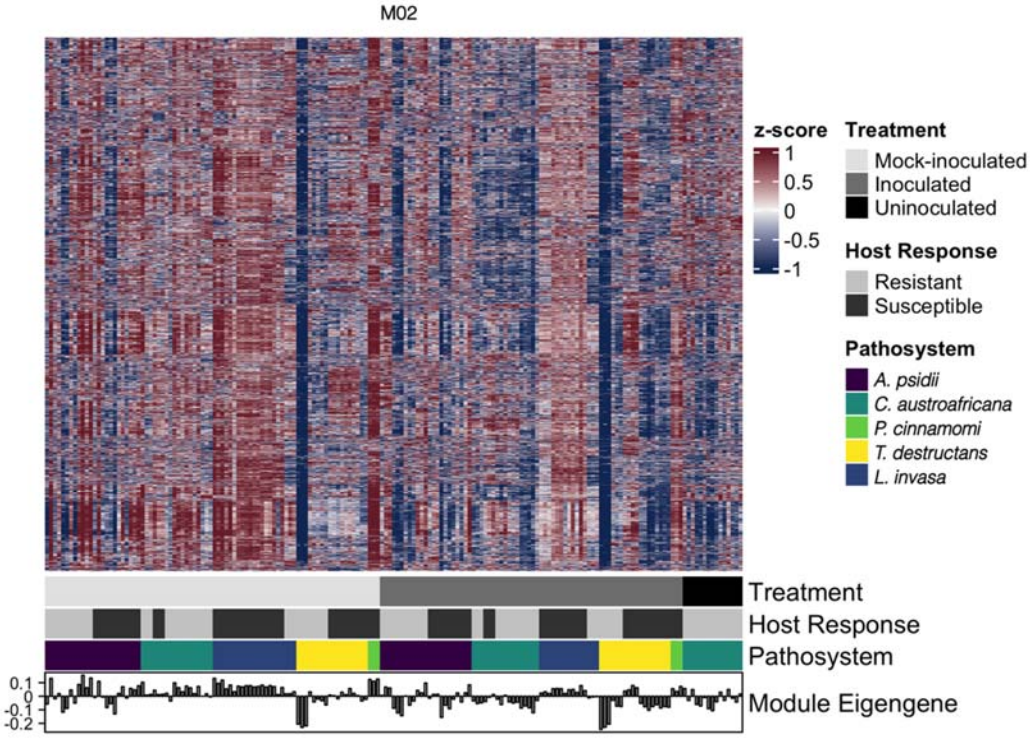

Fig. S9 Module heatmap and module eigengene expression plots for M02. In the heatmap, rows represent the 2,660 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by treatment and further annotated with host response and pathosystem

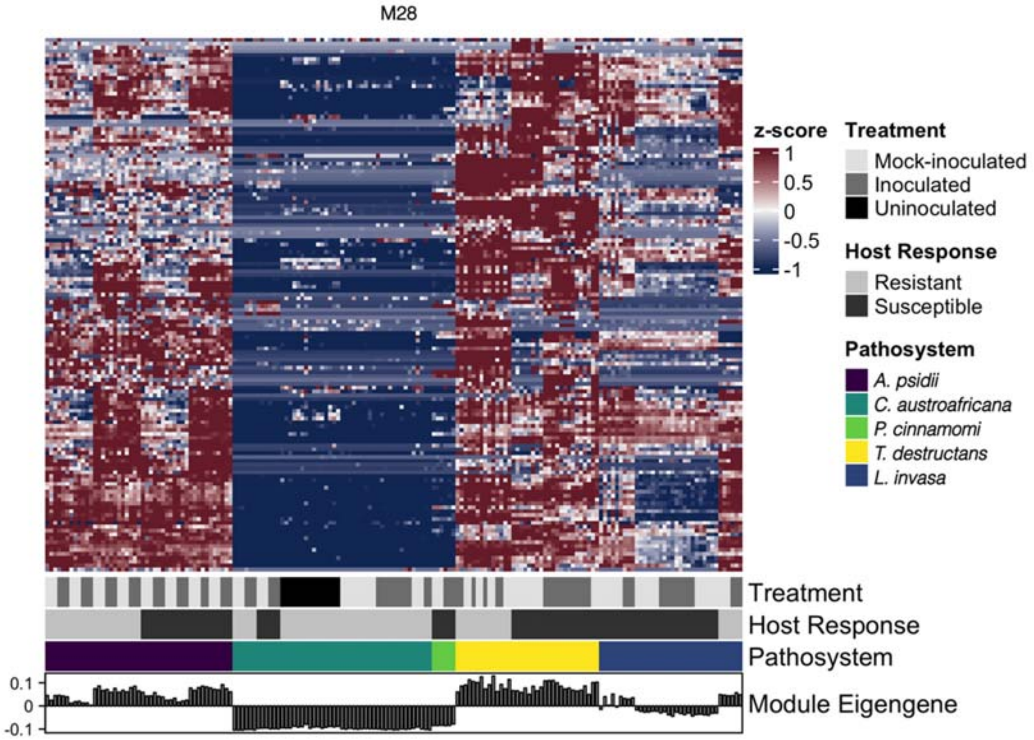

Fig. S10 Module heatmap and module eigengene expression plots for M28. In the heatmap, rows represent the 138 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by pathosystem and further annotated with host response and treatment

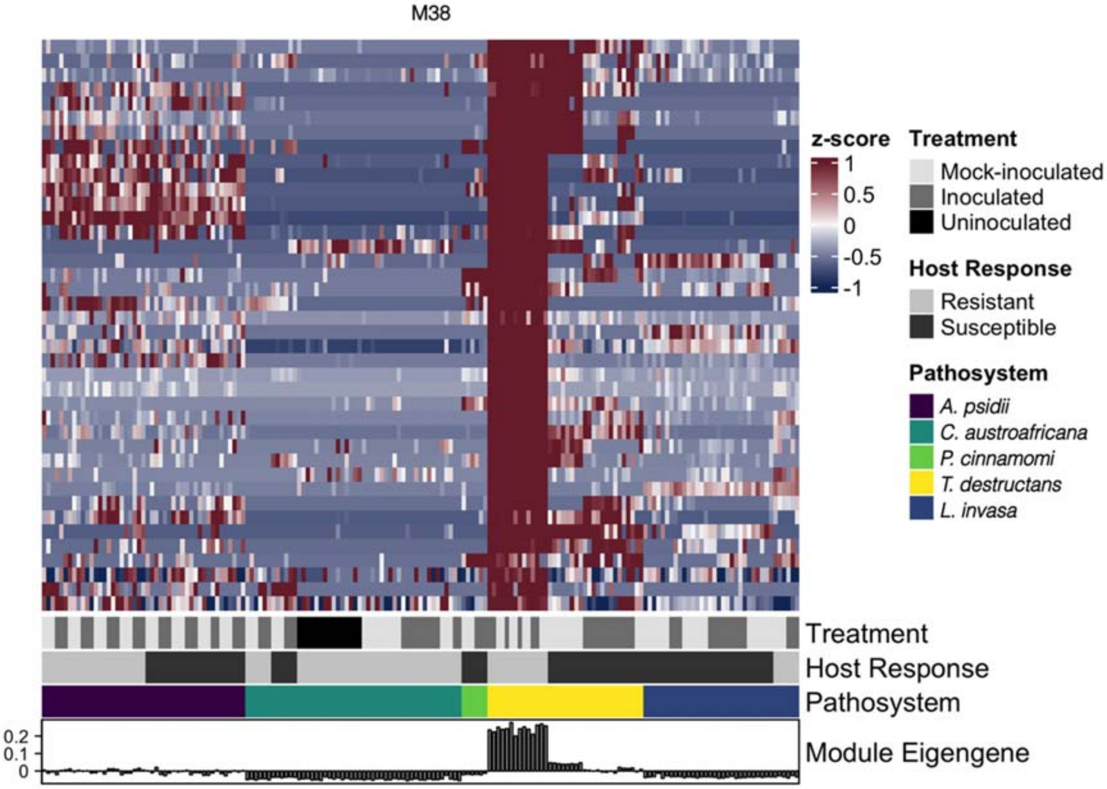

Fig. S11 Module heatmap and module eigengene expression plots for M38. In the heatmap, rows represent the 40 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by pathosystem and further annotated with host response and treatment

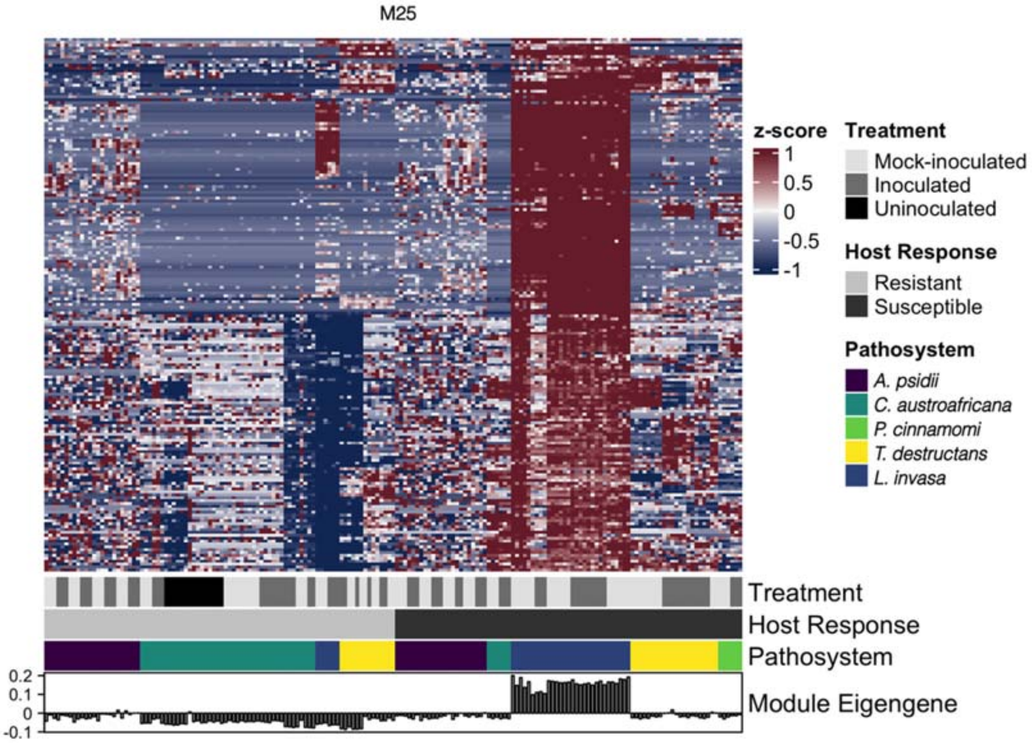

Fig. S12 Module heatmap and module eigengene expression plots for M25. In the heatmap, rows represent the 185 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by pathosystem and further annotated with host response and treatment

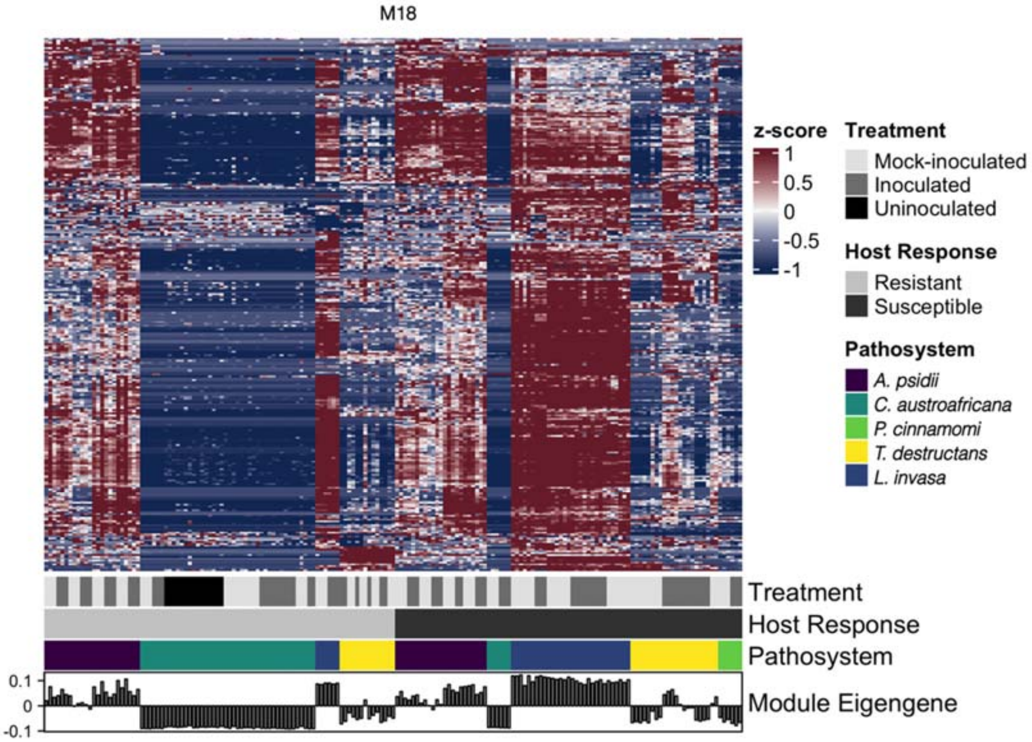

Fig. S13 Module heatmap and module eigengene expression plots for M18. In the heatmap, rows represent the 286 genes and columns represent samples. Red to blue represents the z-score normalisation of gene expression within the module. Module eigengene expression values are separated by pathosystem and further annotated with host response and treatment