Figure Legends

**Figure SR1. Distance between transcript center and top SNP location for all *B. cinerea* expression profiles on Col-0 *A. thaliana*.** Distances are in Mb, including only top SNPs on the same chromosome as the focal gene. Panel a data include the top 1 SNP identified by GEMMA association with each transcript expression profile (lowest p-value for association). Panel b describes the length of individual chromosomes. Panel c data include the shortest distance between transcript genomic location and top 1 SNP identified by GEMMA association with each transcript expression profile (lowest p-value for association) out of 5 permutations.

**Figure SR2. Manhattan-type plot of GEMMA results of transcriptome-wide *B. cinerea* expression phenotypes.** Each point represents a single transcript-SNP p-value of association. Panel a is a Manhattan-type plot of the top 1 SNP hit per *B. cinerea* transcript on Col-0 *A. thaliana*. Panel b is a Manhattan-type plot of the top 1 SNP hit per *A. thaliana* transcript when infected by *B. cinerea*.

**Figure SR3. *cis*-effect analysis of the botrydial biosynthetic gene network.** Panel a is hierarchical clustering of *B. cinerea* isolates from SNPs within the botrydial biosynthetic gene network. Clustering was based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications. AU p-values are reported in red, BP values in green. Edges with high AU values are considered strongly supported by the data, and clustering is drawn according to these edges with AU > 95%. Panel b is Violin plots of botrydial network-level expression within *B. cinerea* clusters. Isolates are clustered based membership in groups defined by hierarchical clustering of the SNPs within the botrydial biosynthesis network.

**Figure SR4. *cis*-effect analysis of the cyclic peptide biosynthetic gene network.** Panel a is hierarchical clustering of *B. cinerea* isolates from SNPs within the cyclic peptide biosynthetic gene network. Clustering was based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications. AU p-values are reported in red, BP values in green. Edges with high AU values are considered strongly supported by the data, and clustering is drawn according to these edges with AU > 95%. Panel b is Violin plots of cyclic peptide network-level expression within *B. cinerea* clusters. Isolates are clustered based membership in groups defined by hierarchical clustering of the SNPs within the botrydial biosynthesis network.

**Figure SR5. Interspecific hotspot comparison on the *B. cinerea* genome with the top 10 genes per SNP.** For each SNP that is a top hit for one or more transcripts, the number of associated transcripts is counted, across both the *B. cinerea* transcriptome and the *A. thaliana* transcriptome.

**Figure N4. *cis*-effect analysis of the botcinic acid biosynthetic gene network.** Panel a is hierarchical clustering of *B. cinerea* isolates from SNPs within the botcinic acid biosynthetic gene network. Clustering was based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications. AU p-values are reported in red, BP values in green. Edges with high AU values are considered strongly supported by the data, and clustering is drawn according to these edges with AU > 95%. Panel b is Violin plots of botcinic acid network-level expression within *B. cinerea* clusters. Isolates are clustered based membership in groups defined by hierarchical clustering of the SNPs within the botcinic acid biosynthesis network (Figure X5). Panel c is the gene models of the biosynthetic gene network, with the cluster 3 deletion indicated as a triangle.

Table N1. Hotspot eQTL in B. cinerea and A. thaliana

Table SN2. a. All target genes of B. cinerea hotspots

b. Functional summary of target genes

Table SN3. A. All target genes of A. thaliana hotspots

b. Significant GO hits by hotspot SNP