**Botrytis diversity**

We used a previously described collection of *B. cinerea* isolates that were isolated as single spores from natural infections of fruit and vegetable tissues collected in California and internationally {Atwell, 2015; Zhang, 2017; Zhang, 2018; Soltis, 2018}.

**Arabidopsis information**

We focused analysis on the *A. thaliana* accession Columbia-0 (Col-0), and all plants were grown as described in a previous study, with 6-fold replication of the full experimental design across two independent experiments {Zhang, 2017}.

**Expression analysis**

We used as input the model-adjusted means per transcript from previously published studies in the *A. thaliana* transcriptome and *B. cinerea* transcriptome {Zhang, 2017; Zhang, 2018}. We calculated linear models from the transcript data including the effects of isolate and host genotype. We extracted least-squares means (R emmeans package; {Lenth, 2018}) for each isolate across all plant genotypes. We z-scaled all transcript profiles prior to GWA.

**Genome data**

For GEMMA mapping, we used 95 isolates with a total of 237,878 SNPs against the *B. cinerea* B05.10 genome with MAF 0.20 or greater and less than 10% missing calls.

**GWAS**

We used haploid binary SNP calls with MAF > 0.20 and <20% missingness. We matched these phenotypes (9,267 B cinerea gene expression profiles) to the SNP data with custom R scripts, for a total of 95 isolates. We ran GEMMA once per phenotype, across 9,267 transcripts.

**Pathway focus**

We focused further cis-effects analysis on three networks which were highly conserved across *B. cinerea* isolates {Zhang 2018}. We clustered isolates by SNP data within focal networks. Hierarchical clustering was computed using the R package pvclust based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications {Suzuki 2015}. 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%.