**Supplemental Tables**

**Table S1:** Estimated Broad-sense heritability (H2) of each transcript in Botrytis and Arabidopsis. Heritability refers to the fraction of total variance that is ascribed to the particular term.

**Table S2.** List of GEMMA expression hotspots for Botrytis transcripts with the detailed annotation of the gene underlying the SNP and the number of transcripts in Botrytis regulated by the SNP.

**Table S3.** List of GEMMA expression hotspots for Arabidopsis transcripts with the detailed annotation of the gene underlying the SNP and the number of transcripts in Arabidopsis regulated by the SNP.

**Table S4:** Model estimated p-values and permutation derived alpha-error estimates from network ANOVAs.

**Table S5**: Annotation of genes underlying hotspots for both Botrytis transcripts and Arabidopsis transcripts.

**Table S6:** Summary of genes potentially under epistasis in Botrytis. True p-values and empirical estimates from network ANOVAs, estimated using single host epistasis model and multiple host epistasis model.

**Table S7.** Summary of enrichment analysis of genes underlying hotspots for Botrytis and Arabidopsis transcripts.