Botrytis diversity and genotyping

Arabidopsis diversity

RNAseq

Transcripts were summarized as X for each gene per isolate:plant genotype interaction.

**GWA preparation**

We calculated linear models from the transcript data including the effects of isolate and host genotype. We extracted least-squares means (R {emmeans} package) for each isolate across all plant genotypes.

We z-scaled all least-squares means outputs prior to GWA. We used haploid binary SNP calls with MAF > 0.20 and <20% missingness. We matched these phenotypes (9267 B cinerea gene expression profiles) to the SNP data with custom R scripts, for a total of 95 isolates.

**BigRR**

We ran bigRR on GPU once per phenotype, imputing missing data as needed. We assumed a poisson distribution (RNAseq phenotype data). We calculated effect estimates for each SNP.

**GEMMA**

We ran GEMMA once per phenotype.