Concerns to address:

We do not see evidence for specialization of these 5 tomato-collected isolates on the selected tomato varieties. BUT other isolates in our collection could also have a history of growing on tomato. And these isolates may be specialized to a different tomato variety.

Our methods did not find evidence of the expected pathogenicity loci for Botrytis contributing to the variation in virulence on tomato. BUT

* Do we have sufficient genetic variation at those pathogenicity loci to test this?
  + How many SNPs within those genes in our collection?
  + MAF > 20 at those genes? How many SNPs?
* If we DO have significant genetic variation, all we know is…
  + Genetic variation at these loci is not the major contributor to Botrytis virulence *on tomato.*

With T4 genome… Can look into haplotype diversity at the significant loci. Expectation is we have >2 alleles contributing to Botrytis response to tomato domestication. If 2 alleles at causal loci, would see a clear Domesticated effect OPPOSITE Wild effect at candidate SNPs.

Can I say quantitatively that the genetic basis of Botrytis virulence is \*as quantitative (many loci of small effect)\* as Arabidopsis?