* Figure legend and results: Vertical stripes of SNPs are indicative of *trans*-eQTL hotspots; loci which modulate expression variation across many genes in the pathogen.
  + Could plot and describe the same thing in the host
* Additional analysis options
  + Polygenicity in B. cinerea eQTL for A. thaliana transcripts: are most genes only linked to one SNP/ locus? Or multiple?
  + Could also look at gene ontology (GO) and tissue/ ontogeny expression (Atlas) for A. thaliana genes linked to B. cinerea eQTL
    - Also, can do GO enrichment across full gene list or across individual clusters (if condensing eQTL and targets into interaction networks)
  + Could filter A. thaliana transcripts by high B. cinerea heritability prior to further analysis (optional filtering step)
    - Could do the same for B. cinerea genes with high B. cinerea heritability
  + Look at the total number of significant locus-transcript connections ~ eQTL “edges”
    - For A. thaliana
    - For B. cinerea
    - Have the option of clustering into linked networks based on these. Could look at network structure, gene ontology, look for overlap with Wei’s networks, etc.
  + Which chromosomes are the hotspots on?
    - Where on the chromosomes?
    - Any trend toward center/ teleomere?
    - Any physical linkage between hotspots?
  + Could add a map of workflow- see Wu 2015 Figure 1A for inspiration
  + In the future, could use Wu 2015 GPLS approach rather than coexpression network analysis- may have higher predictive power