To Do BcAtGWAS\_RNAseq

* Col-0 bigRR
  + First run of bigRR
  + Troubleshooting done: need to rerun 500 phenos at a time
  + rerun: only saved bigRR outputs from about 500 / 9k phenos
  + Run through z-scaling of effect estimates R script: 05\_zscale…R
* Lsmeans bigRR
  + Model: transcript ~ plant (fixed) + isolate
  + Wait for linux run to finish (ongoing 01/23 12pm)
    - Started 01/22 ~3pm
    - Failed 01/24 ~12pm with only ~900 phenotypes done.
  + Linux run on 500 phenos at once: done, took 16 hours (output b.csv)
  + Wait for linux batched run (500 phenos at once) to finish (started 01/25, 12pm)
    - Error: appending outputs to create huge files. Restarting 01/29.
    - Trying with writing out 1 csv per phenotype – faster?
      * And garbage collection gc()
  + Waiting for edited batched run (500 phenos at once, individual output files) to finish (started 01/29, 1pm)
    - One pheno failed, restarted 01/30/18 1pm
    - One more pheno failed, stopped 01/30/18 7pm
    - Paused 01/31 11am to run testMethods
  + Check lsmeans values: any large negative outliers?
    - Approach: save minimum lsmeans value per read, plot histogram of all mins
      * Mins as low as -30
    - Do same for max
      * Highs up to 12
    - Email Dan result
      * Comparing in testMethods:
        + Use default low minimums
        + OR set all mins <-5 to equal -5
        + OR use z-scaled lsmeans as phenotypes
  + Run through z-scaling of effect estimates R script: 05\_zscale…R
    - Extract gene position information for each phenotype
      * BcinXgX <- Chr.g.position
  + How many SNPs associate with each phenotype?
    - Summary data: for each read, number of snps over: z-scaled 3, 4, 5, 6… etc.
      * Summary plots of this
        + Scatter plot: x = genome location, y = # SNPs > z thr, z = z thr color
        + Histograms: frequency of SNP counts over each z thr
        + X = z threshold, y = number of transcripts with any SNP > thr? Or y = distribution of effect sizes of top SNPs (as violin)?

Ask Dan what he meant for this plot

* + Where are the SNPs associated with phenotype?
    - Phenotype-blind SNP locations
      * Keep only the SNP of largest effect for each phenotype
      * Lump all of these SNPs together, with their effect size info
      * Scatterplot this: x = SNP position on genome, y = effect size estimate
        + To get really crazy, could color points (z) by chromosome of origin for the read that gave us this SNP, and add color bars on x axis to denote chromosomes
    - SNP locations with transcript location
      * X = rank order of all transcript (phenotypes), y = rank order of TOP SNP (abs val z)
      * Expect tracts of synteny for cis effects
  + Annotate SNPs? Maybe someday, but only after filtering
  + All analysis so far is on T4 SNPs, and Wei mapped transcripts to T4 genome
    - Add bigRR to B05.10?
    - email Wei whether reads are aligned to B05.10 or T4
    - ask Wei for T4 to B05.10 positional index file – convert SNP locations?
* BcBOT bigRR
  + Quality check work so far
  + Annotate outputs
  + Evaluate cis/trans loci
* Network bigRR
  + GWAS on the Botrydial network and the Arabidopsis genes that show co-expression with these transcripts
    - For At genes correlated with any Botrydial transcript – expression variation across 96 Bc isolates
      * Including only At genes with >=2 associations with the Botrydial genes?
    - For At genes correlated with only the expressed Botrydial transcripts (removed transcripts with 0 expression in XX isolates)
      * Email Wei for transcript removal details
    - Option 1: Can bigRR run each gene in these networks individually, then batch analyze downstream
    - Option 2: can bigRR run z-scaled average of all genes in a network??
  + GWAS on network z-scores of the top Bc networks on col-0 background
    - Wait for Wei to send z-scaled network variation
* General analysis
  + Test of z scaling
    - z-scale effect sizes from BcSlGWAS : see file scripts/testMethods
    - plot z-scaled vs. original fx
    - find where threshold lands on z scale
  + Data management for large files (many SNPs x many phenotypes)
    - Slow to read in/ write out: batch process split files?
    - Slow to repeat calculations across all phenotypes
  + Give GEMMA another shot
    - Step one: assess progress so far and skim through old code
    - Test on BOT reads first
  + Check in with Celine about EMMAX
* Writing
  + Write methods so far
    - Modify methods description from Vivian’s paper
    - Update my analysis methods
    - Start bibliography
  + Start introduction
    - Background reading
    - Annotated bibliography / early citations
  + Start results
    - Thought map of figures and analyses that I want to include
    - Save outputs in a .ppt as I go
    - Start writing up results text
* Reading
  + PNAS Hevia 2015: Circadian clock Botrytis. In my lit folder