**Paper to do**

**BLAST search for names:**

Bcin01g10130

Bcin15g04110

**Check this estimate:**

Higher polymorphism rates are reported for the wheat stem rust pathogen *Puccinia graminis* f. sp. *tritici* (12.3 SNP/kb) (Upadhyaya, Garnica et al. 2014).

**pectinesterase gene (BcT4\_6001, Bcin14g00870)**

One block is associated with SNPs in the distal 3’UTR in SNPs 5-11 and the second block is SNPs that span the entirety of the gene in SNPs 13-26. Interestingly, there are only two SNPs in the open reading frame of the associated gene and this SNP is a silent site polymorphism (Figure 8). This suggests that the major variation surrounding this locus is controlling the regulatory motifs for this pectinesterase.

On figure:

32 SNPs for haplotype blocks

34 SNPs for effect estimates

DRAW LINES ACCORDINGLY:

R script: 14\_Fig8b\_LDplot.R

Select focal gene from

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 start\_codon 826343 826345 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 exon 826235 826345 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 CDS 826235 826345 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 exon 825306 826178 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 CDS 825309 826178 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Chromosome2.2 Botcin\_T4\_vankan\_IMPORTGTF\_3 stop\_codon 825306 825308 0 - 0 gene\_id "BcT4\_6001""; transcript\_id ""BcT4\_6001T1"";"

Lowest: 825306 (stop codon/ exon)

Highest: 8292710 (start codon)

Segments:

Stop 825306 825308

Exon1 825306 826178

CDS 825309 826178

Exon/ CDS 2 826235 826345

Start 826343 826345

For Fig 8a: range is 823323 to 828305

on linux:

bgzip Documents/GitRepos/BcSolGWAS/data/genome/big\_set\_v97iso\_SNPs\_filtered\_qual30\_dp6\_maf20\_recode.vcf

install vcftools

vcftools --gzvcf Documents/GitRepos/BcSolGWAS/data/genome/big\_set\_v97iso\_SNPs\_filtered\_qual30\_dp6\_maf20.recode.vcf.gz --chr Chromosome2 --recode --out Documents/GitRepos/BcSolGWAS/data/genome/chr2\_analysis/chr2\_analysis

this keeps only Chr2 sites

I’ll also make a shorter fragment with only 4kb around the gene of interest:

vcftools --gzvcf Documents/GitRepos/BcSolGWAS/data/genome/big\_set\_v97iso\_SNPs\_filtered\_qual30\_dp6\_maf20.recode.vcf.gz --chr Chromosome2 --from-bp 823323 --to-bp 828305 --recode --out Documents/GitRepos/BcSolGWAS/data/genome/chr2\_analysis/chr2\_analysis\_seg