Commands run:

```
gunzip BYxRM_segs_saccer3.bam.simplified.vcf

plink --pca --allow-extra-chr --mind --vcf BYxRM_segs_saccer3.bam.simplified.vcf

./PCAplot.py plink.eigenvec
open PCAplot.png

./allelefreq.py BYxRM_segs_saccer3.bam.simplified.vcf
open allelefreqPlot.png

./parsePhenotype.py BYxRM_PhenoData.txt > parsed_PhenoData.txt

plink --vcf BYxRM_segs_saccer3.bam.simplified.vcf --assoc --mind --allow-no-sex --pheno
parsed_PhenoData.txt --allow-extra-chr --all-pheno

./manhattanplot.py plink.P*.qassoc
```