Haploview notes

<https://www.broadinstitute.org/haploview/>

Data: five formats, standard linkage format, completely or partially phased haplotypes, [HapMap Project](http://www.hapmap.org/" \t "_blank) data dumps, PHASE format, and PLINK outputs

Data: \*.ped

Locus: \*.map

Appears to take only binary phenotypes?

And need to check SNP formatting

Chr 2.2 BcT4\_6001

Haploview 4.2 File > open new data>

Linkage format >

Data file: C:\Users\nesoltis\Documents\Projects\BcSolGWAS\data\genome\chr2\_analysis\PLINK\myCHR2\_A.ped NULL PHENO

Locus file: C:\Users\nesoltis\Documents\Projects\BcSolGWAS\data\genome\chr2\_analysis\PLINK\myCHR2\_A.map

Exclude invididuals with >50% missing genotypes

Ignore pairwise comparisons of markers > 0 kb apart

Null pheno .ped:

Input file format error on line 1. “snp1” should be of type long. Info file must be of format: <markername> <markerposition>

Run as-is.