



**S8 Fig. Distributions of likelihood ratio statistic calculated from GBS read data at known polymorphic restriction sites.** The test statistic was calculated as described in S1 Appendix for 333,058 autosomal SNPs in the HapMap GBS data set that had < 25% missing data. Each plot represents a group of SNPs that were sequenced to a different mean coverage, and within each group the test statistic is plotted versus the number of non-cut restriction site alleles present at the SNP. The blue lines represent the  $p = 0.05$  critical value from the theoretical null distribution, the one-half chi-squared distribution with one degree of freedom. The red lines represent the empirical  $p = 0.05$  critical value.