S4 Fig. Effect of restriction site polymorphisms on genotyping accuracy and site frequency spectrum estimation in simulated GBS data. A. Double-digest GBS genotype data ($5 \times 10^5$ SNPs) were simulated for 100 diploid individuals under a neutral coalescent model with population mutation rates between $1 \times 10^{-3}$ and $2 \times 10^{-2}$, and the genotype error rates plotted vs scaled mutation rate after removing sites with > 10% missing genotypes. The error rates after removing sites with a GBStools likelihood ratio > 2.71 are also shown for the same data with 40X mean coverage. B. Site frequency spectrum for restriction site polymorphisms for data simulated under a population mutation rate of $1 \times 10^{-3}$. Samples that carried two non-cut restriction site alleles were considered missing. C. The number of SNP genotyping errors is shown for each frequency class in B. D. The non-normalized SNP site frequency spectra for the same data as in A, represented as a subsample of size 50. E. The normalized site frequency spectra corresponding to those shown in D.