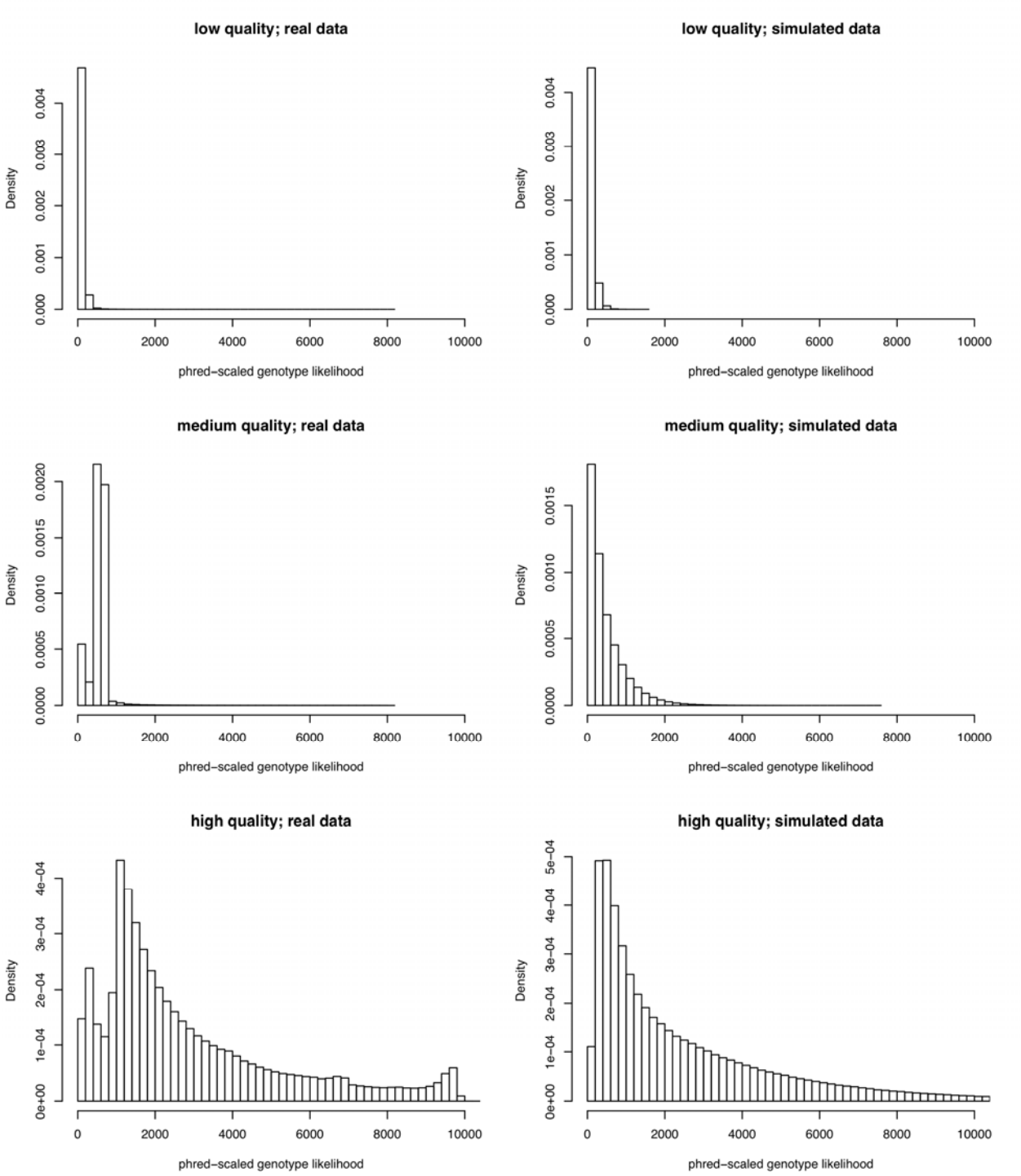

Figure S1 Distributions of phred-scaled genotype likelihoods of the third most likely genotype for low, medium, and high quality sites. Distributions for real GBS data are shown on the left, and distributions from simulated data are shown on the right. The most likely genotype was always assigned a Phred-scaled likelihood of 0, and distributions for the second most likely genotype are qualitatively similar to those for the third most likely genotype (except with lower means) and therefore are not shown. Note that the values shown are phred-scaled likelihoods for all possible genotypes given the called alleles (PL field of VCF files), not the overall genotype quality (GQ field of VCF files).

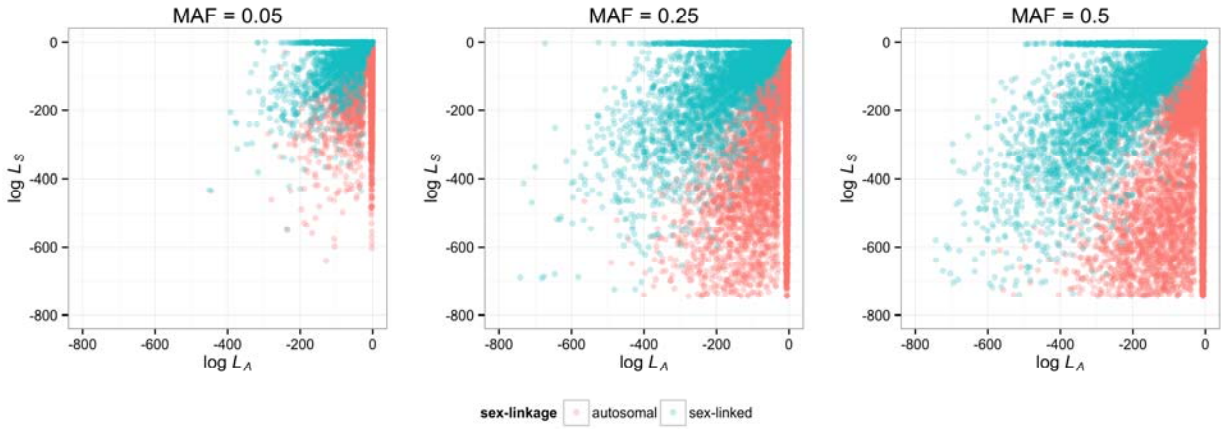

Figure S2 Pedigree likelihoods can be used to identify sex-linked sites. We simulated autosomal (pink) and sex-linked (blue) SNPs with medium to high quality genotypes and 0-20% missing data in 10 trios. For each SNP, we plot the likelihood of the pedigree under an autosomal model of inheritance (L_A) and the likelihood of the pedigree under a sex-linked model of inheritance (L_S). Plots are shown for SNPs with a MAF of 0.05, 0.25, and 0.5. Autosomal SNPs and sex-linked SNPs have different pedigree likelihoods. Therefore we can classify SNPs as autosomal or sex-linked based on L_A and L_S.

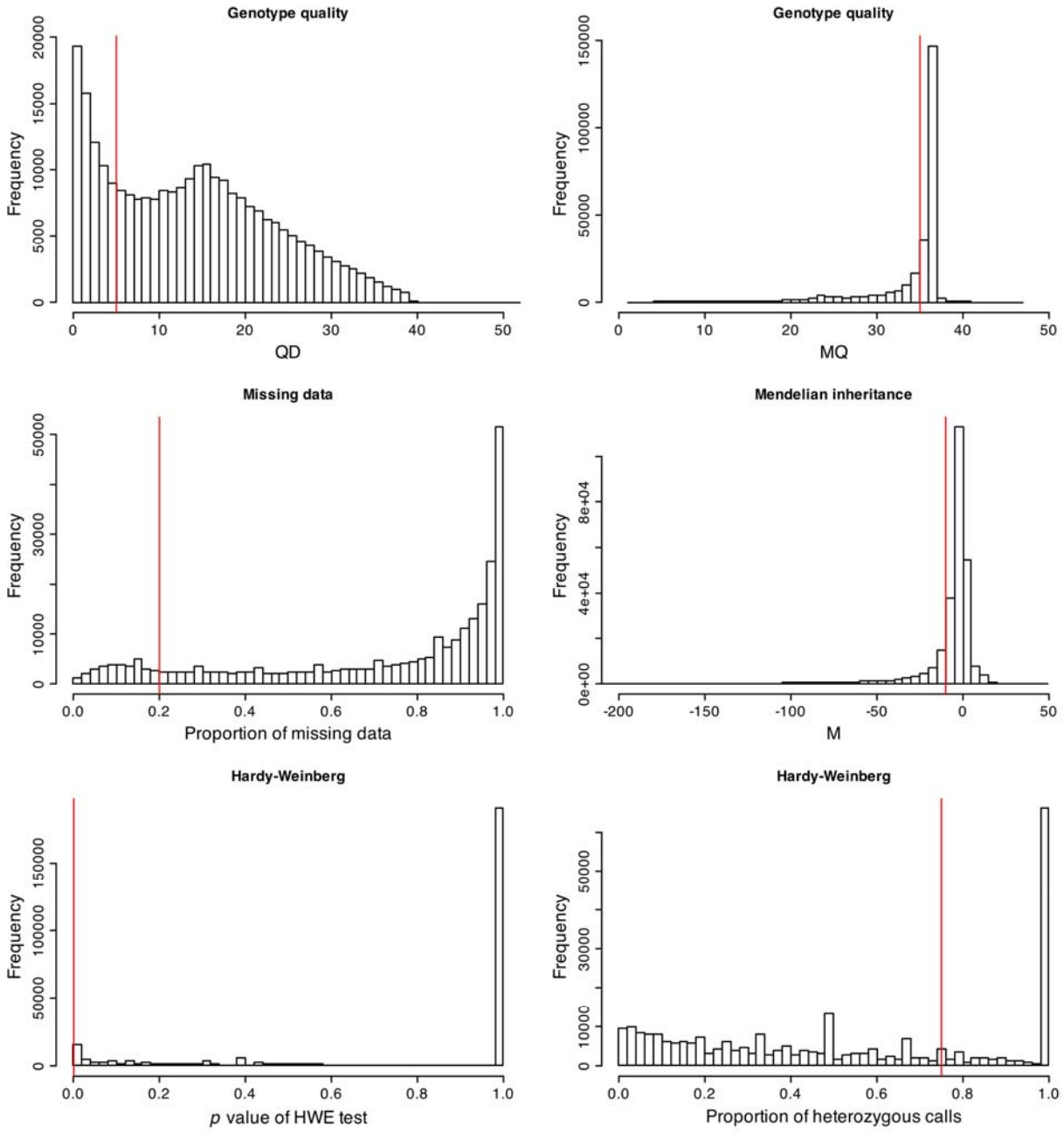

Figure S3 Distributions of various quality metrics (genotype quality, missing data, Mendelian inheritance, and Hardy-Weinberg) for unfiltered SNPs discovered using GBS in Florida Scrub-Jays. Thresholds for each metric are shown in red. We filtered out sites with QD<5, MQ<35, >20% missing data, *M*<-10, HWE *p*<0.001, and >75% heterozygous calls.

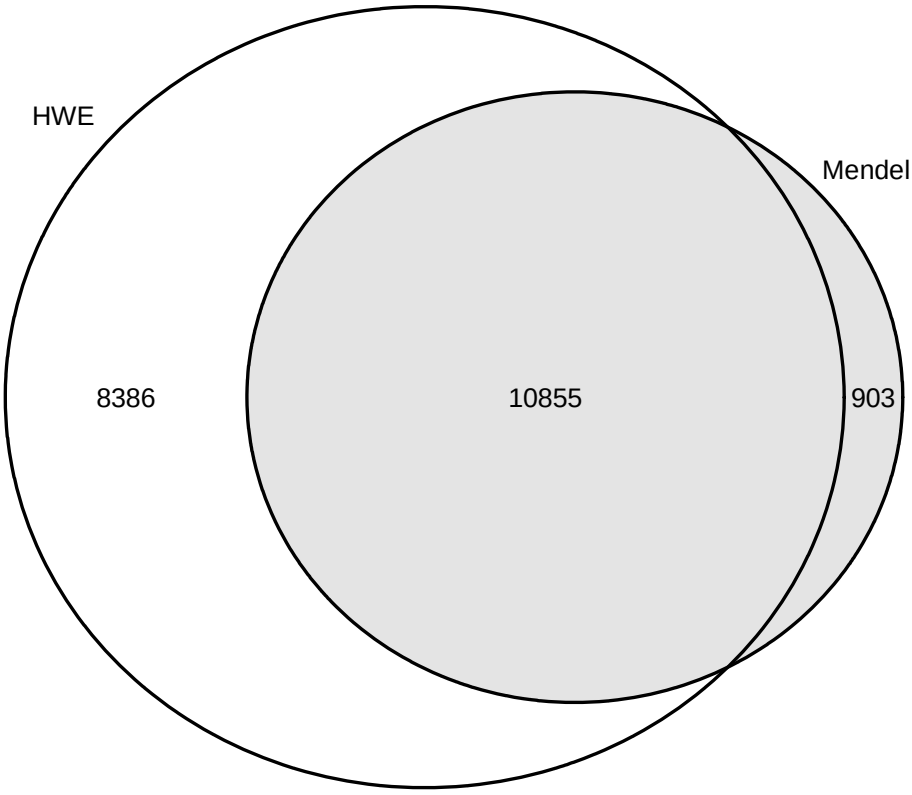

Figure S4 Number of high-quality SNPs from the real data that pass a Hardy-Weinberg test or the Mendelian inheritance filter. SNPs have already been filtered for quality and proportion of missing data. The Mendelian inheritance filter is more rigorous: 44% of the SNPs that pass the HWE test fail MendelChecker but only 8% of the SNPs that pass MendelChecker fail HWE.

File S1

GBSscripts.zip

File S1 is available for download as a zip archive at

http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.169052/-/DC1