



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).