



**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.