Figure S3: Correcting the underestimation of observed heterozygosity for simulated data with genotyping errors other than allelic dropout. In each panel, a purple bar indicates the uncorrected observed heterozygosity averaged across all individuals in a simulated data set after applying allelic dropout; a green bar indicates the "true" observed heterozygosity averaged across all individuals in the same simulated data set before applying allelic dropout and before introducing genotyping errors; and a striped black bar indicates the corrected observed heterozygosity averaged across all individuals and across 100 imputed data sets. The x-axis indicates values of the inbreeding coefficient that were set for different simulations. Different panels correspond to different levels of simulated genotyping errors that come from sources other than allelic dropout. (A) $e = 0$; (B) $e = 0.02$; (C) $e = 0.04$; (D) $e = 0.06$; (E) $e = 0.08$; (F) $e = 0.10$.