



Figure S9: Theoretical difference in mean squared error between the unbiased estimator \hat{H}_{red} (left), \tilde{H} (center), or \tilde{H}_{BLUE} (right) and the biased estimator \hat{H}_{full} calculated at each of 50 SNP simulated loci ($0.0198 \leq H \leq 0.5$) for samples of 60 diploid individuals containing some inbred relative pairs. Each sampled individual was related to exactly one other, and samples contained 10 pairs of inbred full-siblings ($\Phi = 3/8$), 10 pairs of outbred full-siblings ($\Phi = 1/4$), and 10 outbred avuncular pairs ($\Phi = 1/8$). Dotted lines in each plot correspond to a difference in MSE of zero with \hat{H}_{full} . See Supplementary Data for the true expected heterozygosity values incorporated into analytical calculations (SNP loci are labeled as SNP01-SNP50).