Figure S12: Maximum deviance for 100 simulations of scenario D for each of the two sets of allele frequencies in the ancestral populations. The deviance is calculated as the maximum difference between the true and observed admixture proportion. “True genotypes” is for admixture proportions estimated from the true simulated genotypes. “NGSadmix” is based on admixture proportions estimated with NGSadmix from the simulated genotype likelihoods. “ML” is for admixture proportions estimated from ML genotypes and “HW” is the deviance for admixture proportions estimated from HW genotypes.