Figure S11: RMSD for 100 simulations of scenario D for each of the two sets of allele frequencies in the ancestral populations. The RMSD is calculated with respect to the true admixture proportions. “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 RMSD for admixture proportions estimated from HW genotypes.