Figure S7: Scenario C simulations based on HapMap frequencies. We simulated 50 samples for 100,000 SNP sites. The sequencing depth is shown in the top plot. The true admixture proportions is shown in figure S3. The second panel shows the admixture proportions obtained from the simulated genotype likelihoods using NGSadmix. The remaining three panels shows the admixture proportions estimated from ML genotypes, HW genotypes and filtered genotypes.