Figure S3: Scenario B (low depth 2X) with 50 samples for 100,000 SNP sites simulated from HapMap frequencies. The first panel shows the true admixture proportions, the second shows the result of NGSadmix on the simulated genotype likelihoods and the last three panels show the estimated admixture proportions from called genotypes (ML, HW and filtered genotypes as described in the Materials and Methods section).