Figure S19: Admixture using two different genotype likelihood estimators. Estimated admixture proportions from both SNP chip (top) and low depth sequencing data from the 1000 genomes. Results are based on 20 individuals from each of the five populations: African Americans (ASW), European (CEU), Han Chinese (CHB), Mexicans (MXL) and Yoruban (YRI), assuming three ancestral populations. Only sites overlapping the two data sets were used. The first plot is the admixture proportions estimated from SNP chip data. The two last plots shown are based on NGSadmix using GATK genotype likelihoods and SAMtools modified MAQ model for genotype likelihoods. The sites included in the analysis are inferred from the sequencing data from 50 random 10Mb regions.