



Figure S1: Distribution of predictions for $N = 100$ based on multiple subsamples of 20 diploid individuals from 1000 Genomes populations, expressed as a proportion of the correct value. We display the jackknife prediction, and upper and lower 95% bootstrap confidence intervals based on the Jackknife estimator and Linear Programming. Recently admixed populations (ASW,CLM,MXL,PUR), and populations with cryptic relatedness (ASW,CHS,MXL,LWK) show more variation across sub-samples, reflecting sample heterogeneity.