



Figure S5: (Left) Predicted and observed discovery rates as a function of sample composition when the sample has both European and West African ancestry, based on a simulated evolutionary model from (TENNESSEN *et al.* 2012, GRAVEL *et al.* 2011). LP and jackknife predictions for discovery rates were generated using a sample of 100 European and 100 African haplotypes, for varying proportions of European and West African ancestries. These were compared to simulated values according to the model. (Right) Predictions based on 100 haplotypes drawn from 1000 Genomes YRI and CEU samples, as a function of sample composition.