



Figure S1: Genetically indistinguishable SNPs in real datasets. This figure is identical to Fig. 4D-F in the main text but also includes results calculated from human data. (A-C) Statistics calculated from datasets downsampled randomly to match a sample size of 100 chromosomes and 100,000 SNPs. (A) Fraction of SNPs with at least one giSNP as a function of MAF. (B) Median number of giSNPs as a function of MAF. Small black notches indicate bootstrap 95% confidence intervals on the median. The median number of giSNPs for all MAFs > 0.08 is negligible in all datasets. (C) Maximum number of giSNPs across all allelic configurations, as a function of MAF. Dots indicate the number of giSNPs for the “worst” allelic configuration at each specific MAF. Solid lines provide a local smoothing via the loess method.