



Figure S3. Elevation in H12 values in Zambian and Raleigh data with less stringent filters. H12 values measured in windows of 801 SNPs down sampled to 401 SNPs in Zambian data (A) windows of 401 SNP in Raleigh data (B) along the four autosomal arms were elevated as compared to expectations under any neutral demographic model tested. In this data set, we did not mask inversions, IBD tracts, or admixture tracts. Instead, we excluded individuals with > 20% of the autosomal arms sharing IBD tracts of 0.5 similarity or greater with any other another individual in the sample. H12 values were measured in sample sizes of 145 and in genomic regions with $\rho \geq 0.5$ cM/Mb. H12 values were measured in neutral demographic simulations of 145 individuals generated with $\rho = 0.5$ cM/Mb. Plotted are the result of approximately 1.5×10^5 simulations under each neutral demographic model, representing 10 times the number of analysis windows in the data.