**Figure S1**



LD statistics across distances.For each autosome, 1000 genotyped SNPs were sampled from the UK Biobank cohort used for analysis (N ~ 259,000). For each sampled SNP *j*, squared genotype correlations were computed between SNP *j* and SNP *j*+1, SNP *j* and SNP *j*+2…SNP *j* and SNP *j*+250.