S1 Fig. **Sample disease prevalences of cohorts simulated according to logistic and liability threshold models.** Each sample comprises 100,000 individuals with randomly sampled genotypes, and case/control status was assigned according to either a logistic or liability threshold model with a desired prevalence of 0.01. The resulting fraction of individuals assigned to cases by each model is plotted. Colors indicate a fixed odds ratio assigned to 10 SNPs, with each value simulated over 10 trials.