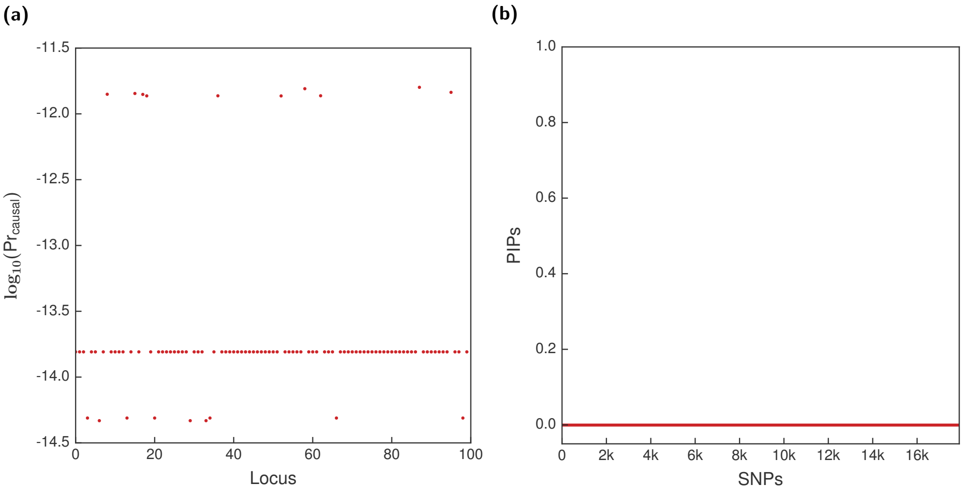

Figure S2. Performance of B-LORE on null data. We performed a simulation with randomly generated binary phenotype on 13082 samples across five populations, using 17218 SNPs distributed over 100 loci. We show (a) the log posterior probability of each locus being causal ($\log_{10}(\mathrm{Pr}_{\mathrm{causal}})$), and (b) the posterior inclusion probability (PIP) for each SNP.