

Supplementary Figures

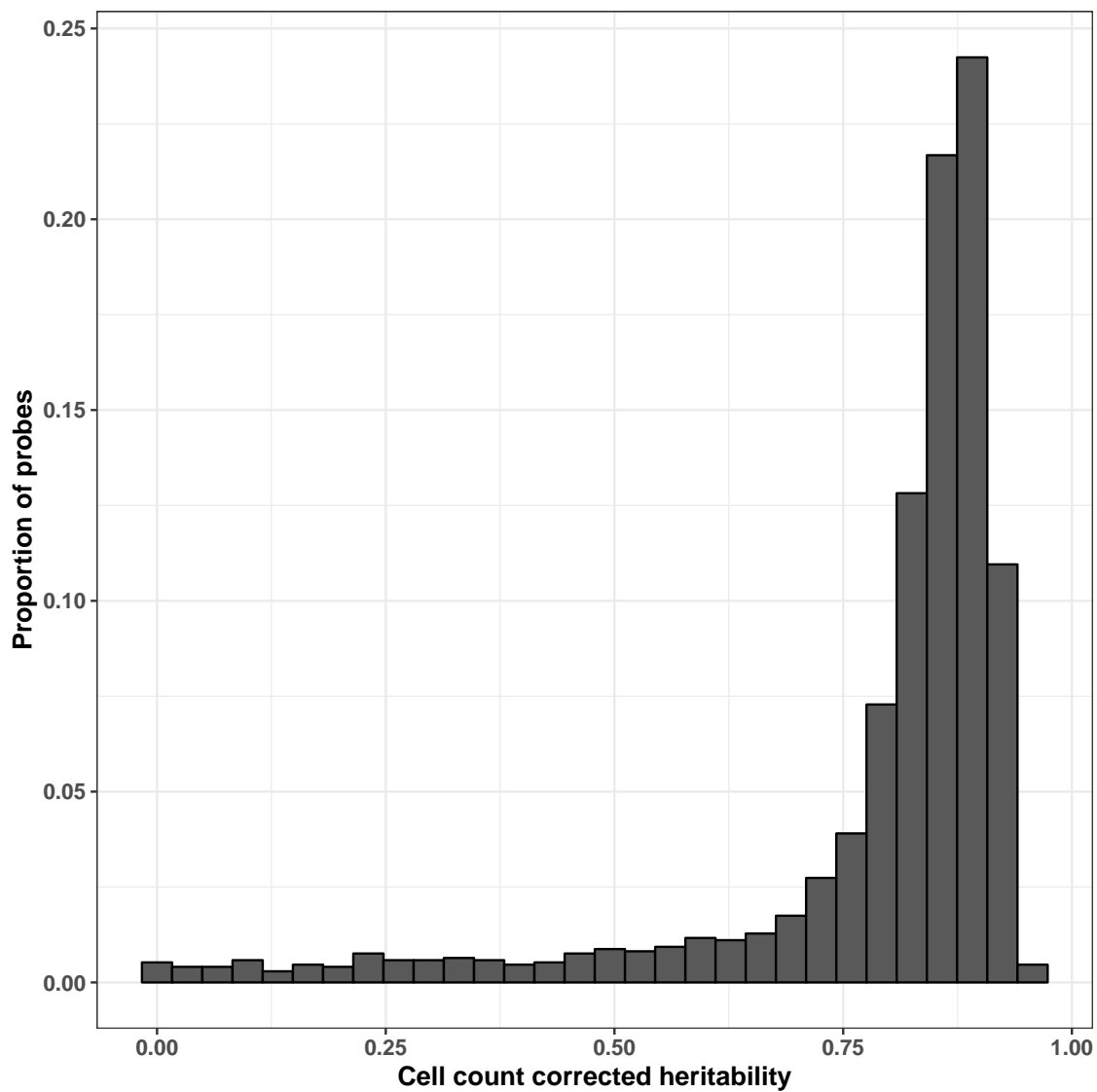


Figure S1: The distribution of heritabilities of the DNA methylation level at the CpG-SNP probes as calculated by (McRae et al., 2014) in a family based study design. The median $h^2 \sim 0.86$.

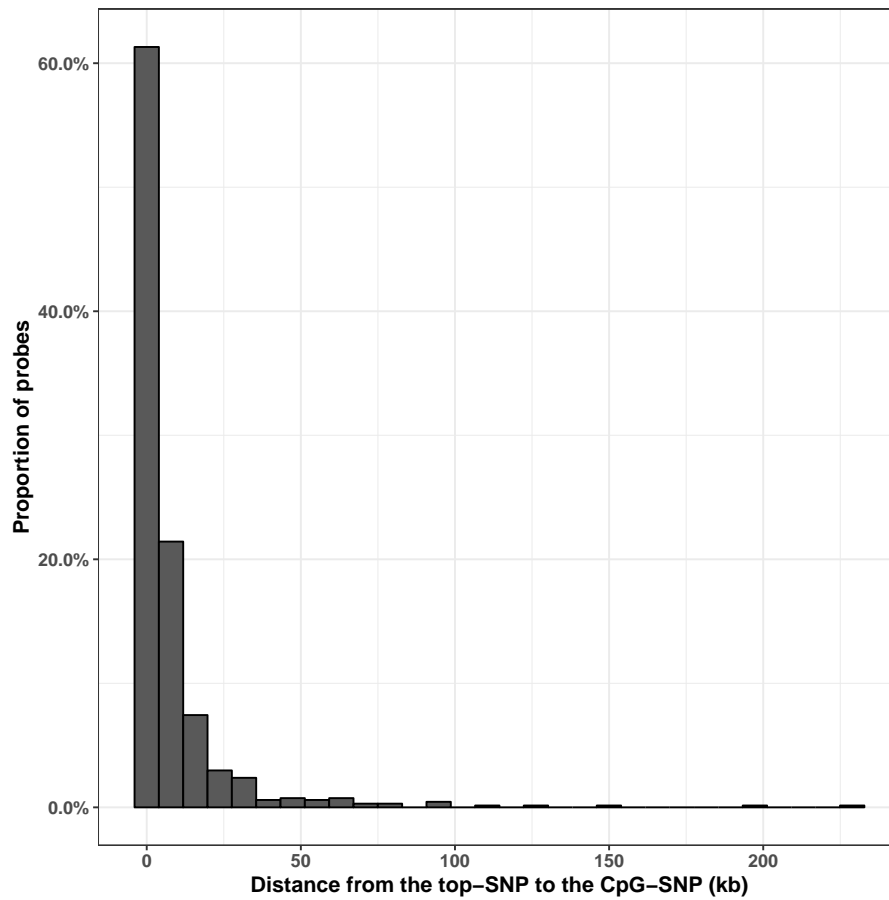


Figure S2: The distribution of distance between the CpG-SNP and the top-SNP in the GWAS using the WGS dataset, in the 672 cases where the CpG-SNP is not the top-SNP. The mean distance is 8kb, the median distance is 2kb, and the 95% quantile is 34kb.

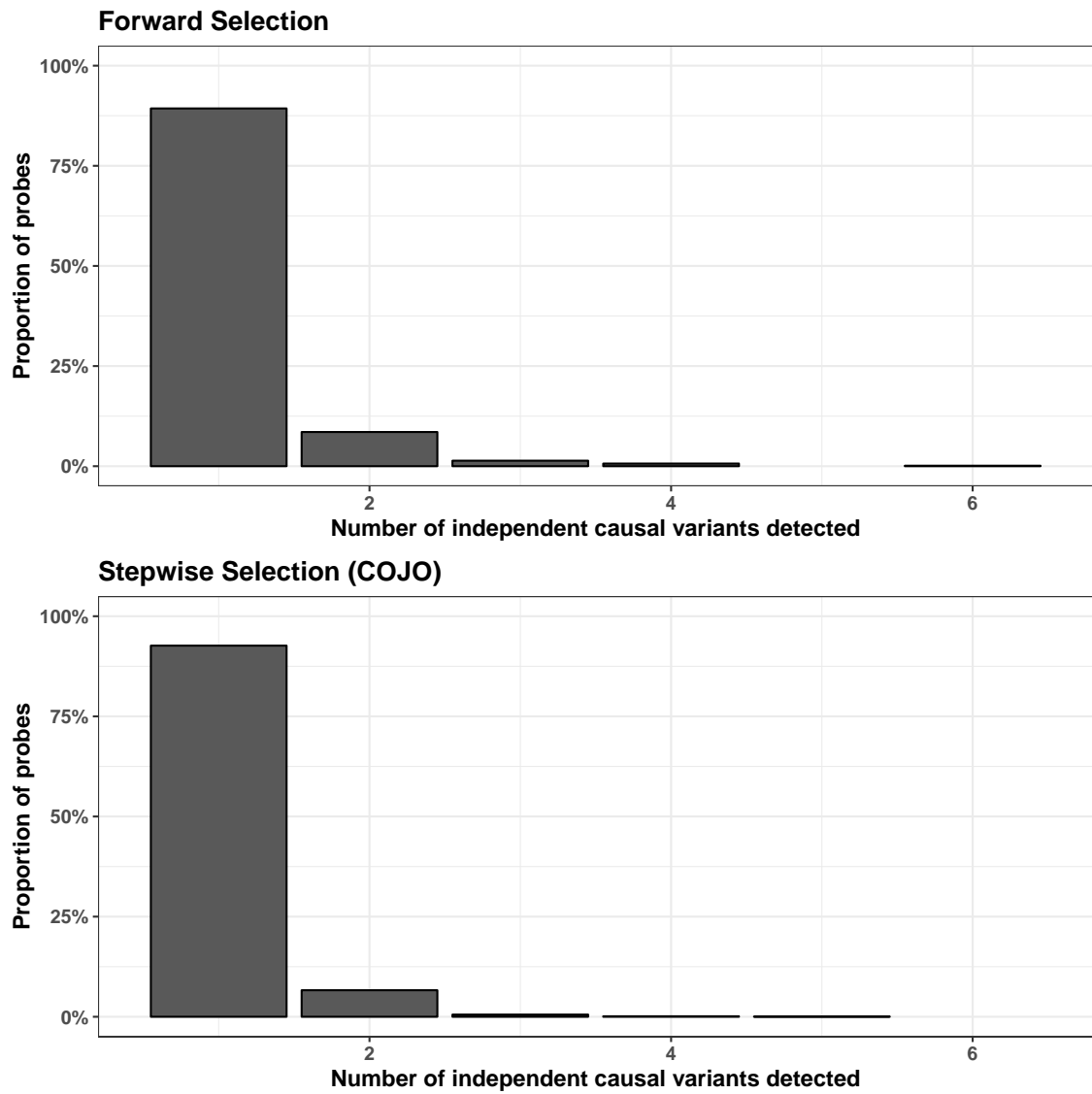


Figure S3: The estimated number of causal variants at each CpG-site using a forward selection method, and a stepwise selection using the Conditional and Joint model (CoJo) (Yang et al., 2012). Multiple signals were detected in 11% of the mQTL from at least one of methods.

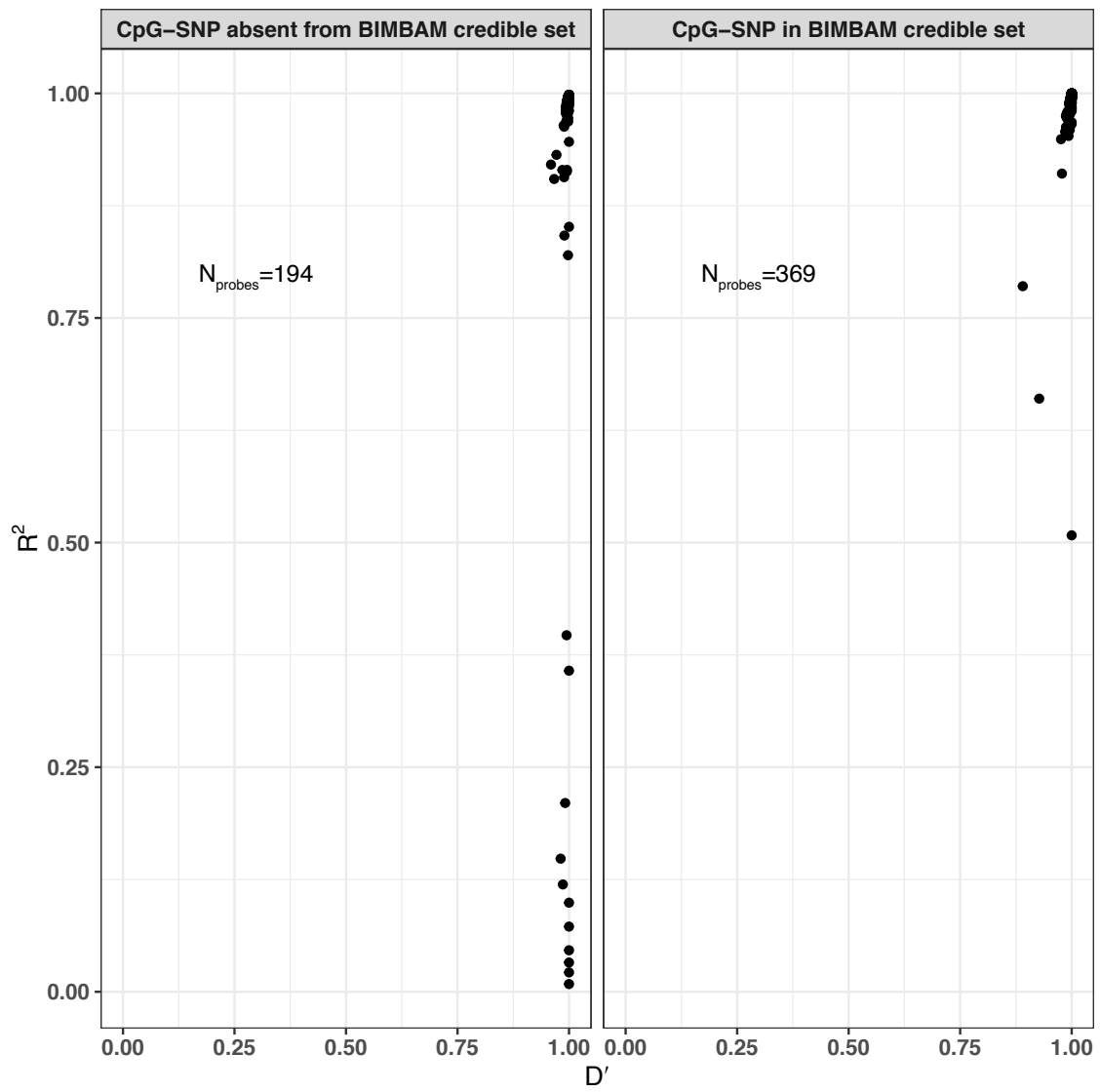


Figure S4: The LD D' vs LD R^2 of the top-SNP vs the CpG-SNP for the probes with a single independent signal in the conditional analyses, and a top-SNP different to the CpG-SNP.

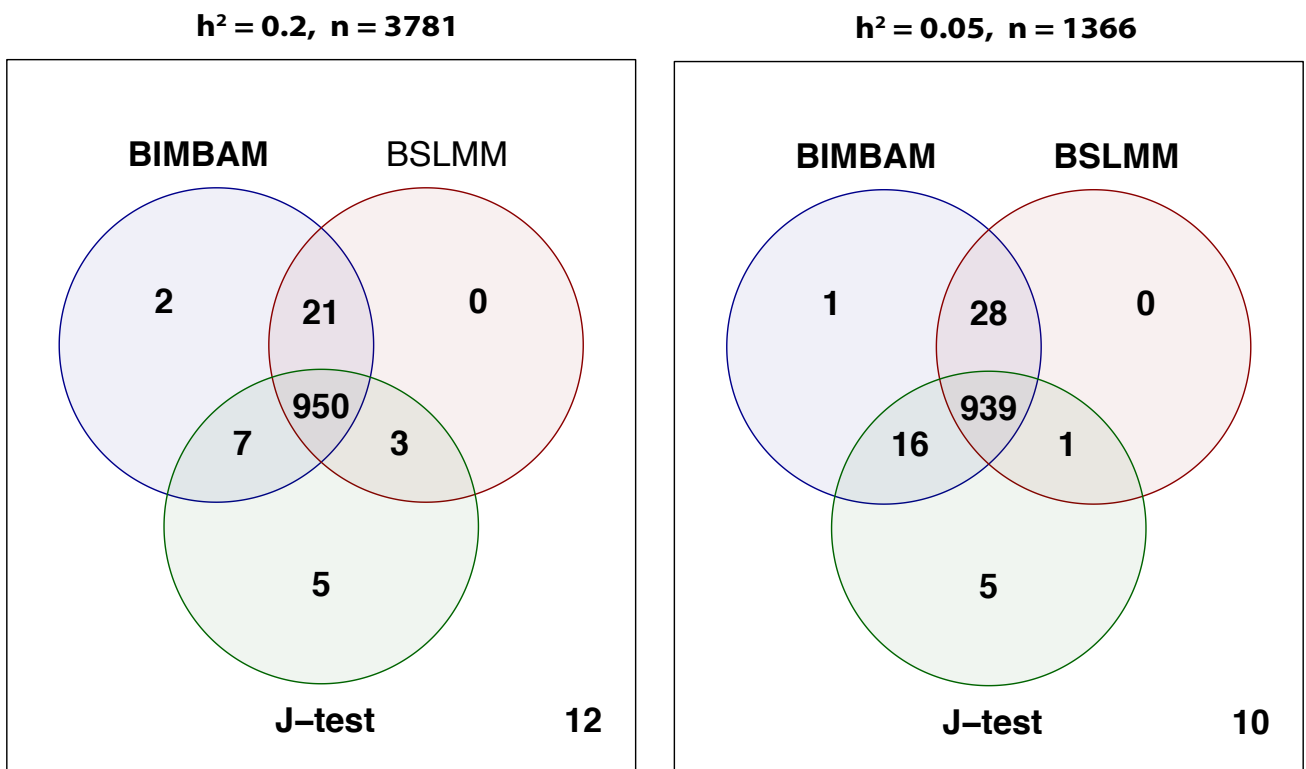


Figure S5: The overlap in the simulated causal variants included in the 95% credible sets from each method, in two of the simulation scenarios. Here we show the results from the simulation with highest effect size ($h^2 = 0.2$) and largest sample size ($n=3781$), and results from the simulation with the lowest effect size ($h^2 = 0.05$) and smallest sample size ($n=1366$)