

Figure S2. Comparison on datasets with 30% disease variants and MAF bounded at 0.05 on 4 disease models. x: significance. y: power for 4 models.

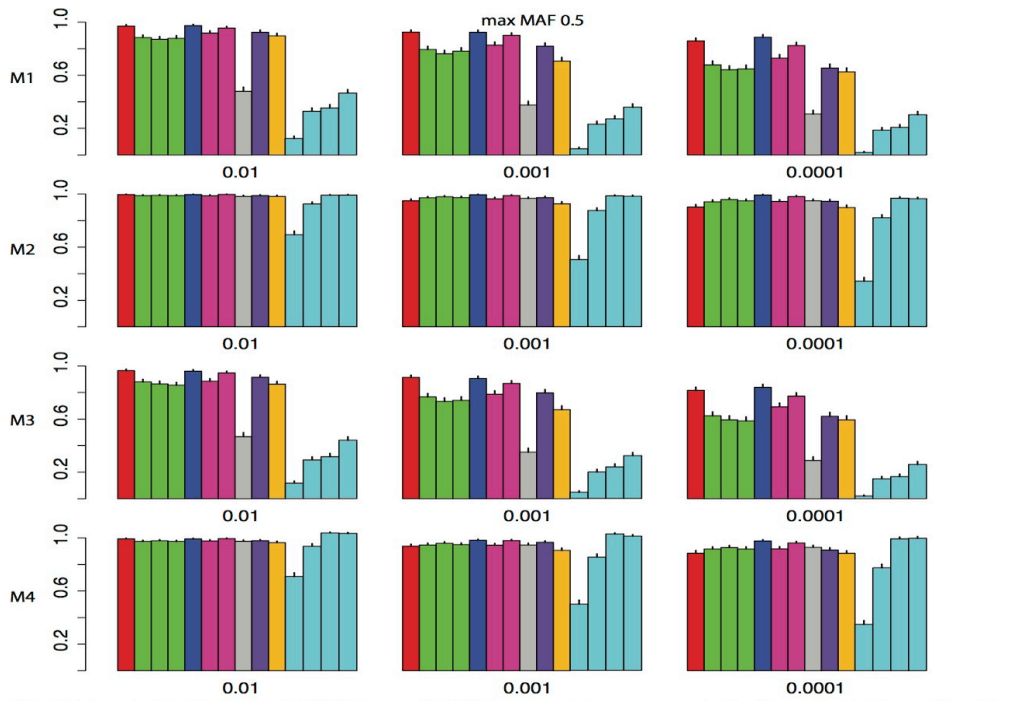


Figure S3. Comparison on datasets with 30% disease variants and MAF bounded at 0.5 on 4 disease models. x: significance. y: power for 4 models.

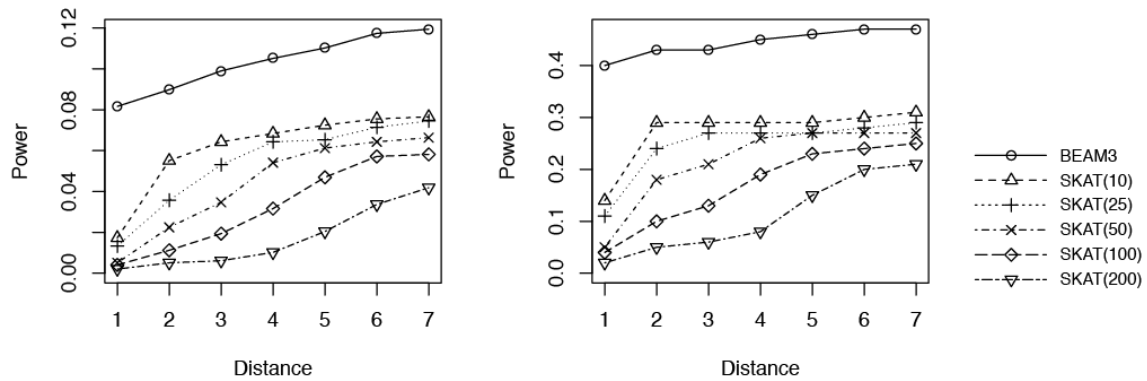


Figure S4. Power comparison between BEAM3 and SKAT on simulated datasets of 100,000 SNPs. “Distance”: maximum allowed # of SNPs between the center of a reported significant SNP set (data-wide p-value 0.01) and the nearest true disease variant, such that the true variant is counted towards power. SKAT: in the parenthesis shows the number of SNPs per set.