

Figure 1: Power (top) and mean false positive rates (bottom) for a range of disease models. Each point on the x-axis corresponds to 50 datasets under each of the simulation parameters while keeping the rest at their default values.

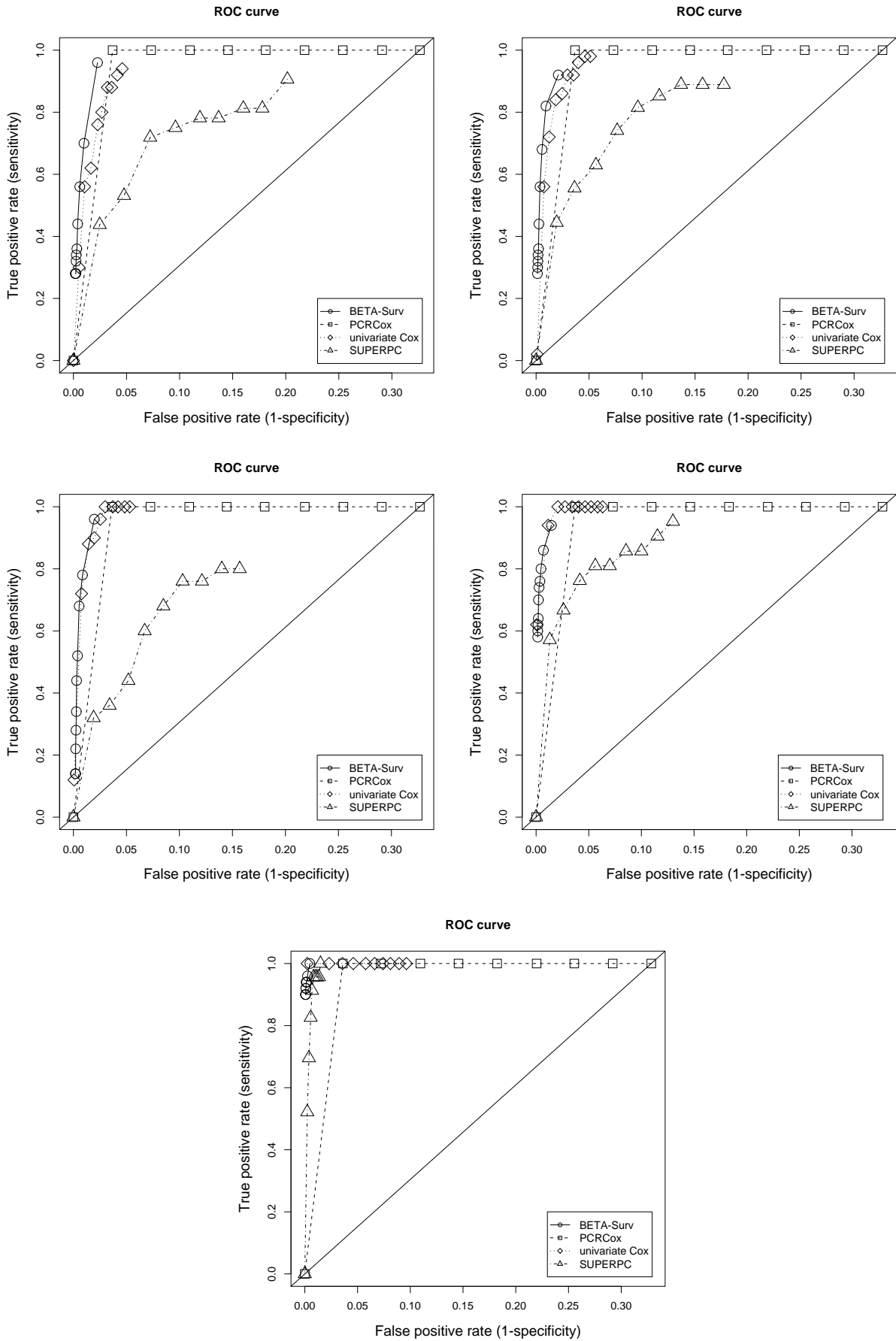


Figure 2: Heterozygote relative hazard 1.2 (top left), 1.6 (top right), 1.8 (middle left), 2.2 (middle right), 3 (bottom) while keeping the rest simulation parameters at their default values.

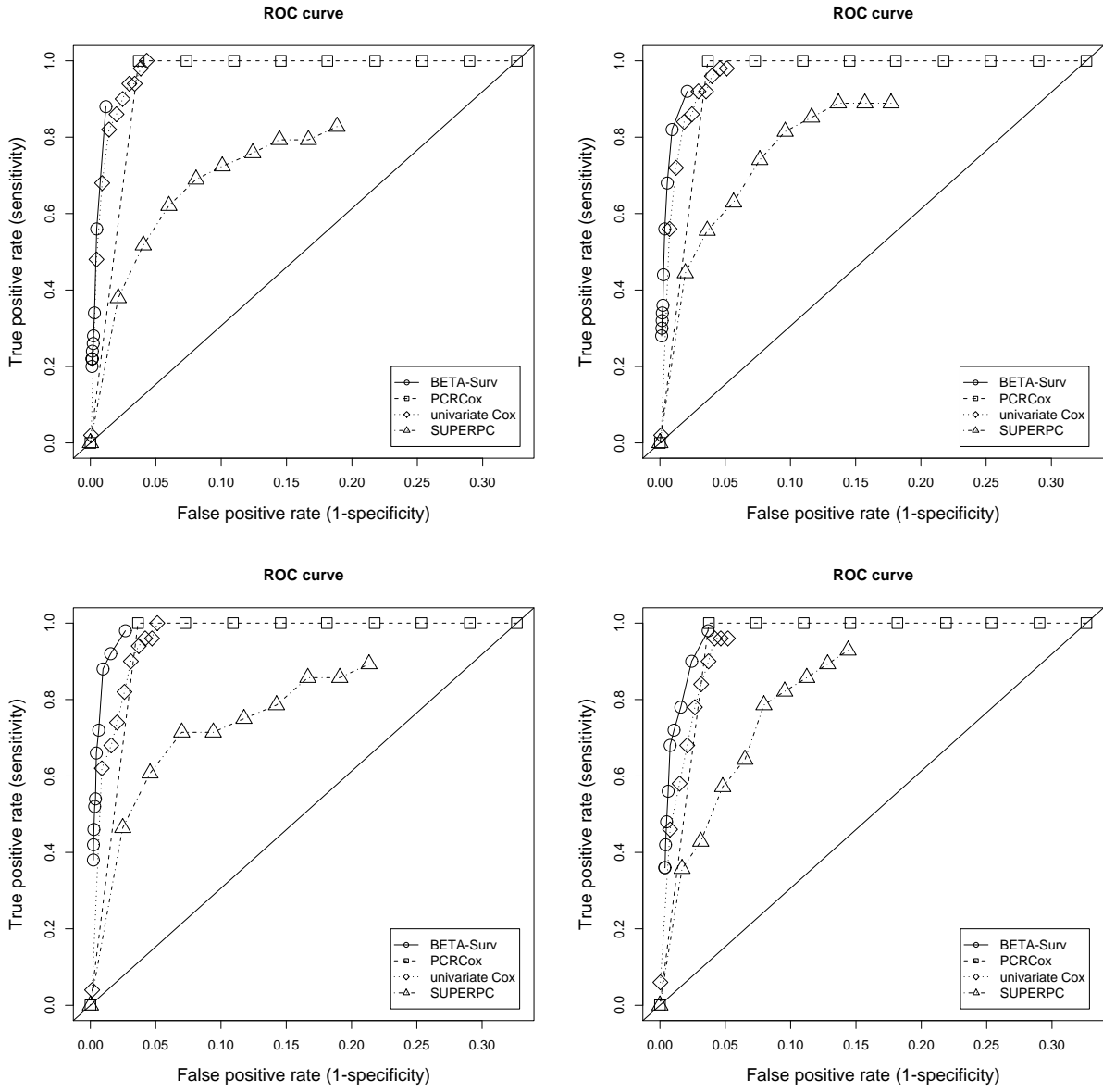


Figure 3: Censoring level 30% (top left), 50% (top right), 70% (bottom left), 90% (bottom right) while keeping the rest simulation parameters at their default values.

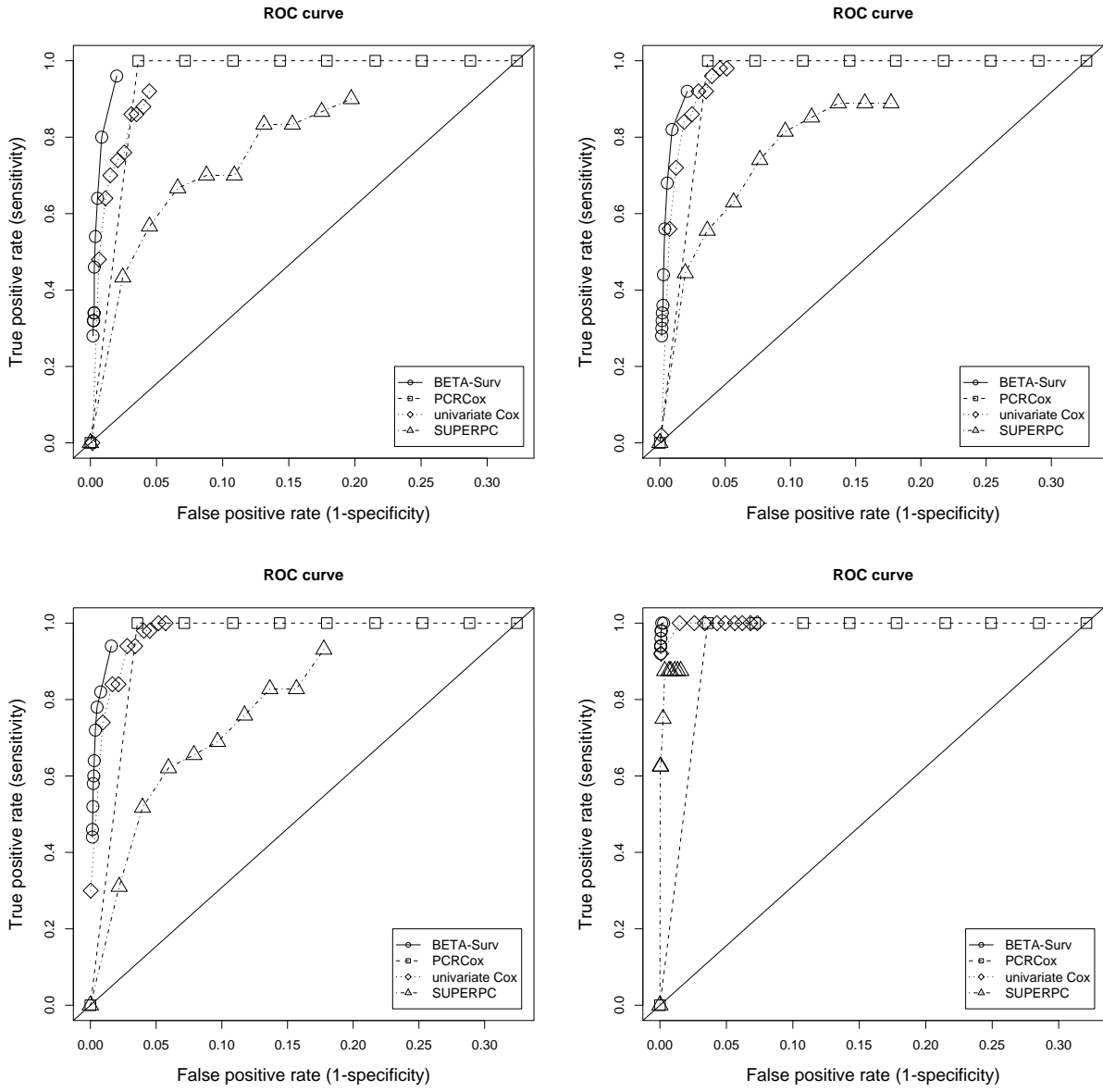


Figure 4: MAF of causal allele 0.02 (top left), 0.05 (top right), 0.1 (bottom left), 0.3 (bottom right) while keeping the rest simulation parameters at their default values.

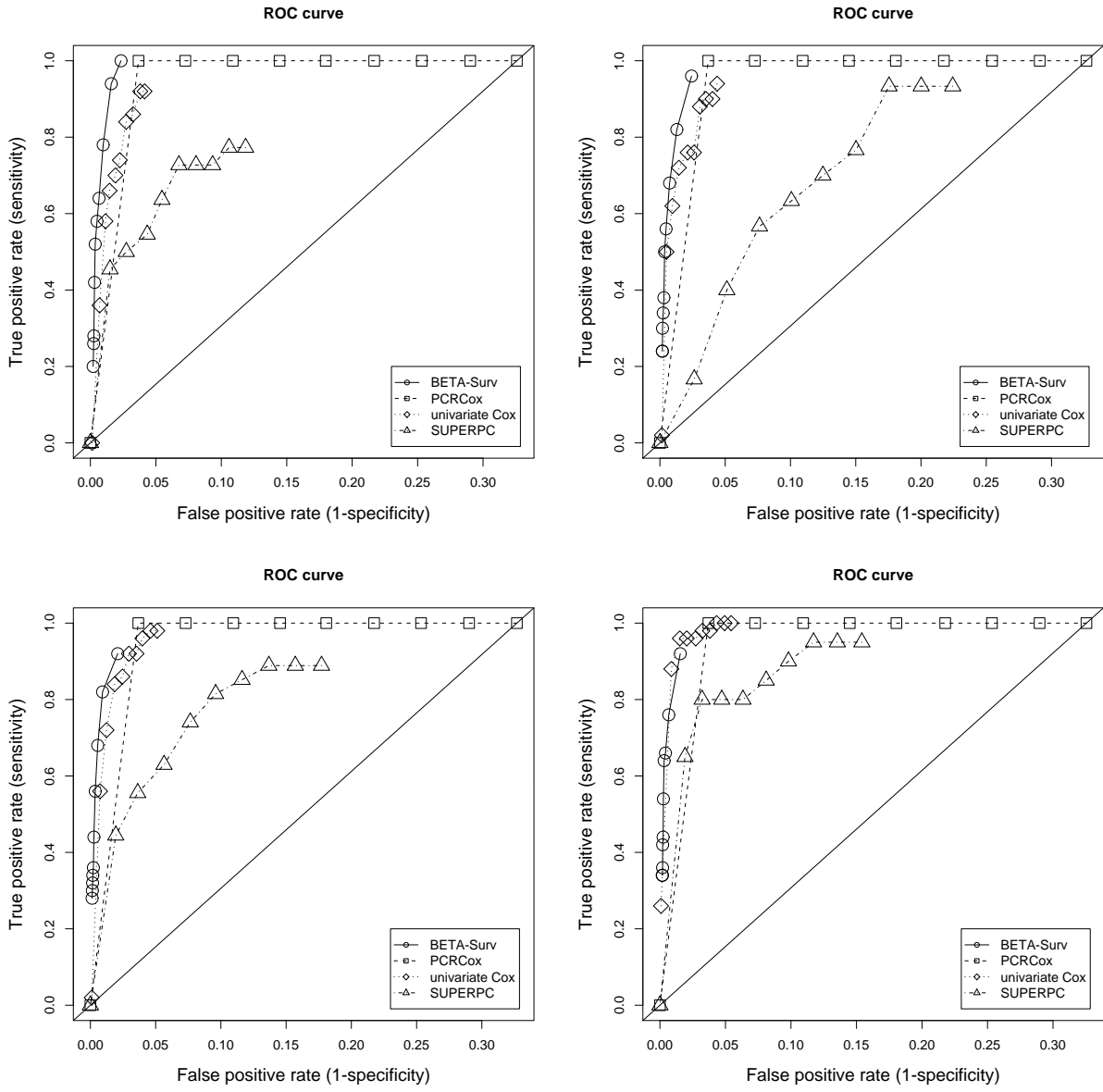


Figure 5: Sample size 400 (top left), 1000 (top right), 2000 (bottom left), 4000 (bottom right) while keeping the rest simulation parameters at their default values.