Genetics Research

Association analysis of rare and common variants with multiple traits based on variable reduction method

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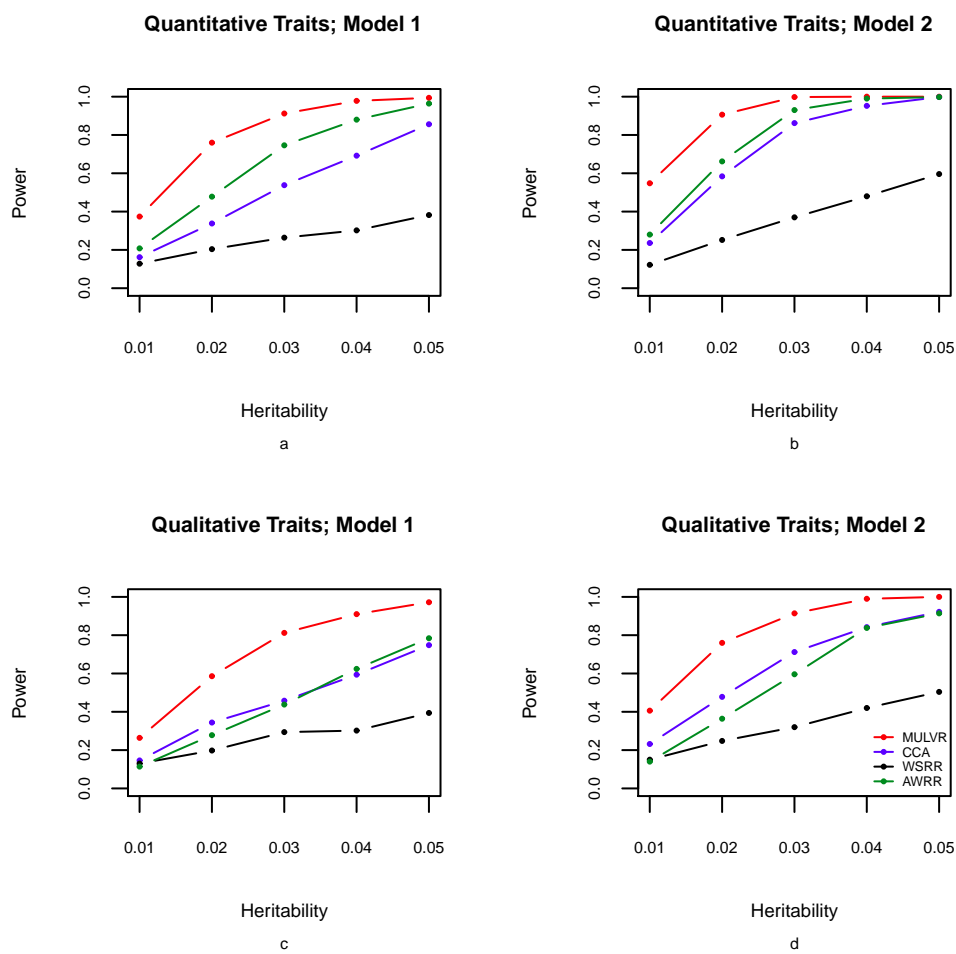## Supplementary Material

Power comparisons without noise traits

Figure S1: Power comparisons for different values of the total heritability in two models. Total number of traits is 4 and the four traits are associated with causal variants. One common variant and 10% of rare variants are causal, and 20% of rare causal variants are protective variants. The sample size is 1000, and $\rho = 0.5$.
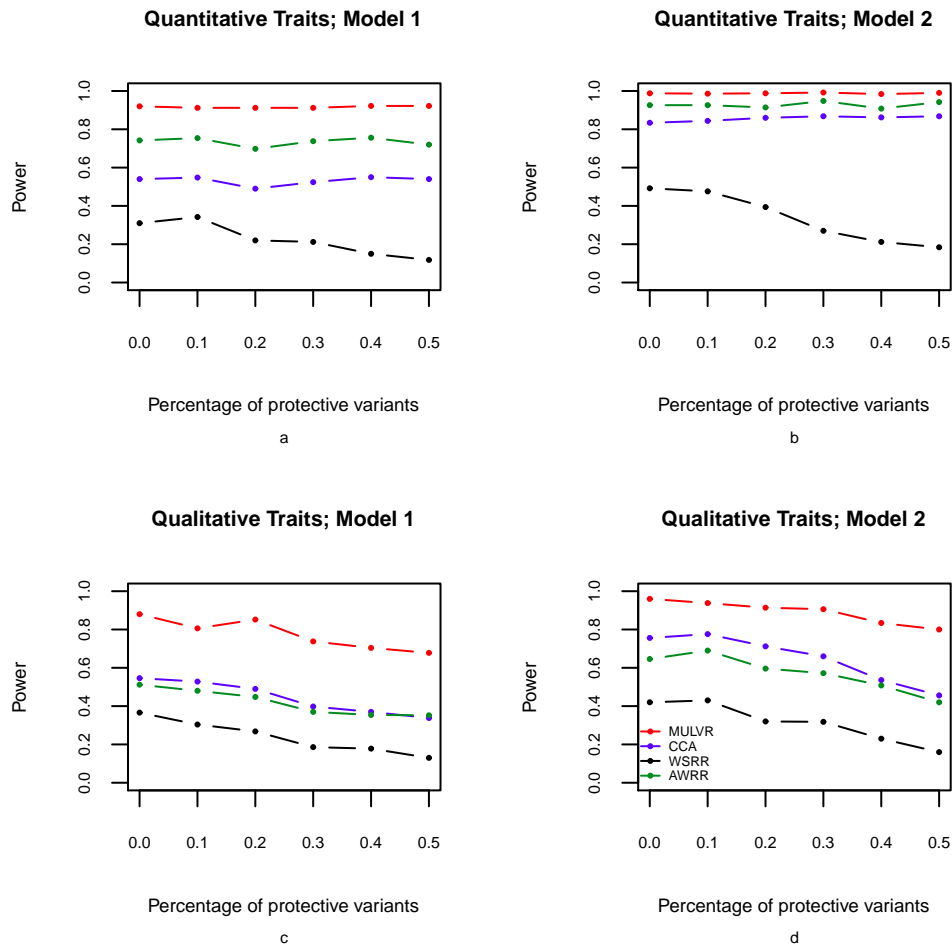
Figure S2: Power comparisons for different percentages of protective variants in two models. Total number of traits is 4 and the four traits are associated with causal variants. One common variant and 10% of rare variants are causal, and the total heritability of all causal variants is 0.03. The sample size is 1000, and $\rho = 0.5$.
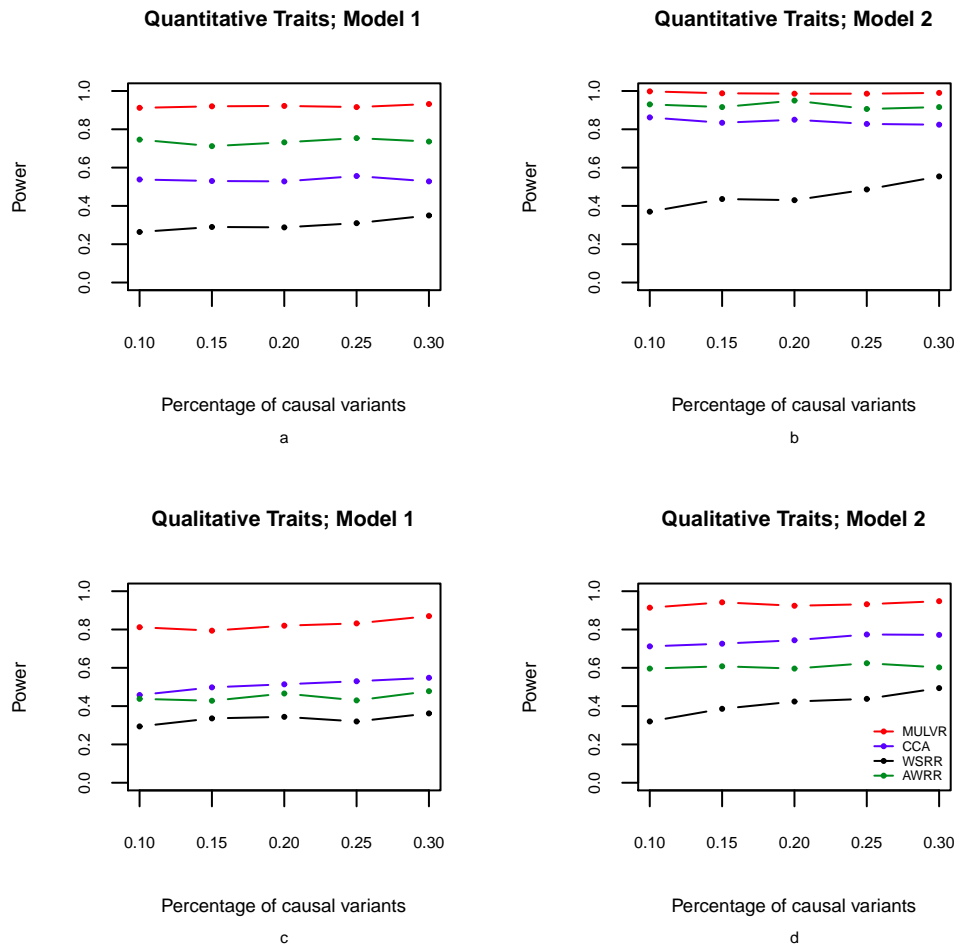
Figure S3: Power comparisons for different percentages of rare causal variants in two models. Total number of traits is 4 and the four traits are associated with causal variants. One common variant is causal, 20% of rare causal variants are protective variants, and the total heritability of all causal variants is 0.03. The sample size is 1000, and $\rho = 0.5$.
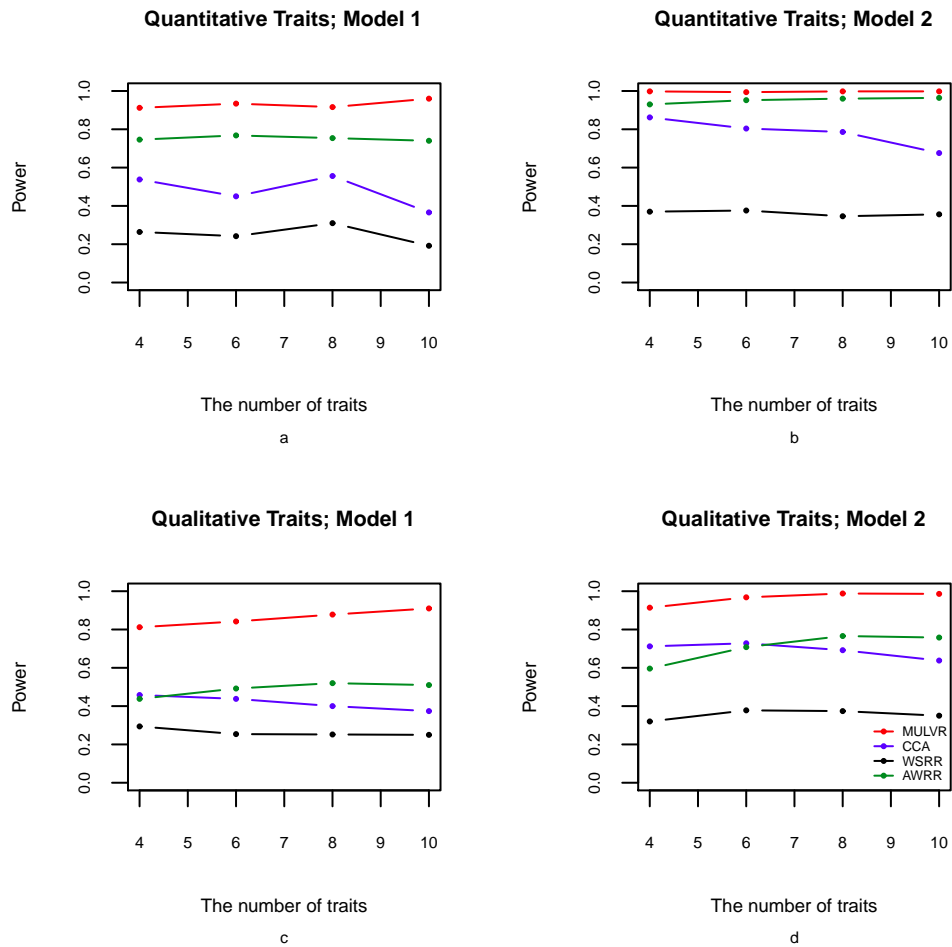
Figure S4: Power comparisons for different numbers of traits in two models. All traits are associated with causal variants. One common variant and 10% of rare variants are causal, 20% of rare causal variants are protective variants, and the total heritability of all causal variants is 0.03. The sample size is 1000, and $\rho = 0.5$.

Figure S5: Power comparisons for different sample sizes in two models. Total number of traits is 4 and the four traits are associated with causal variants. One common variant and 10% of rare variants are causal, 20% of rare causal variants are protective variants, and the total heritability of all causal variants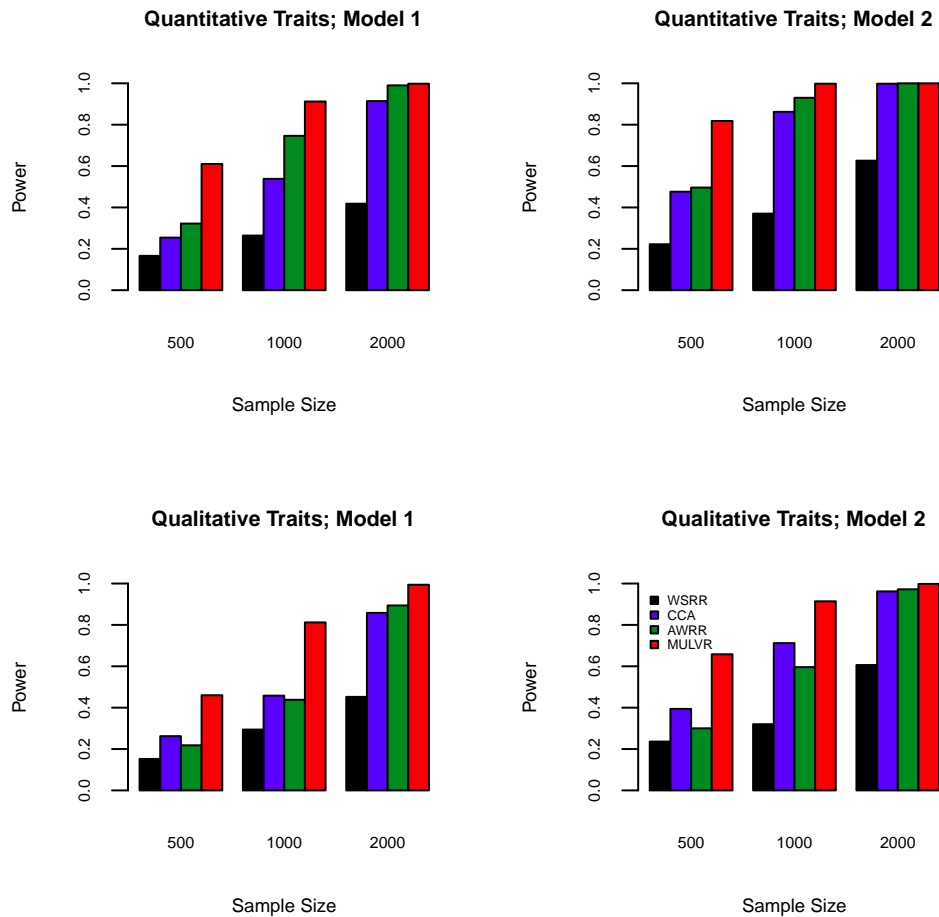 is 0.03. The sample size is 1000, and $\rho = 0.5$.