

1 **SUPPLEMENTARY MATERIALS FOR "WEIGHTED MULTIPLE TESTING**
 2 **PROCEDURES IN GENOME-WIDE ASSOCIATION STUDIES"**

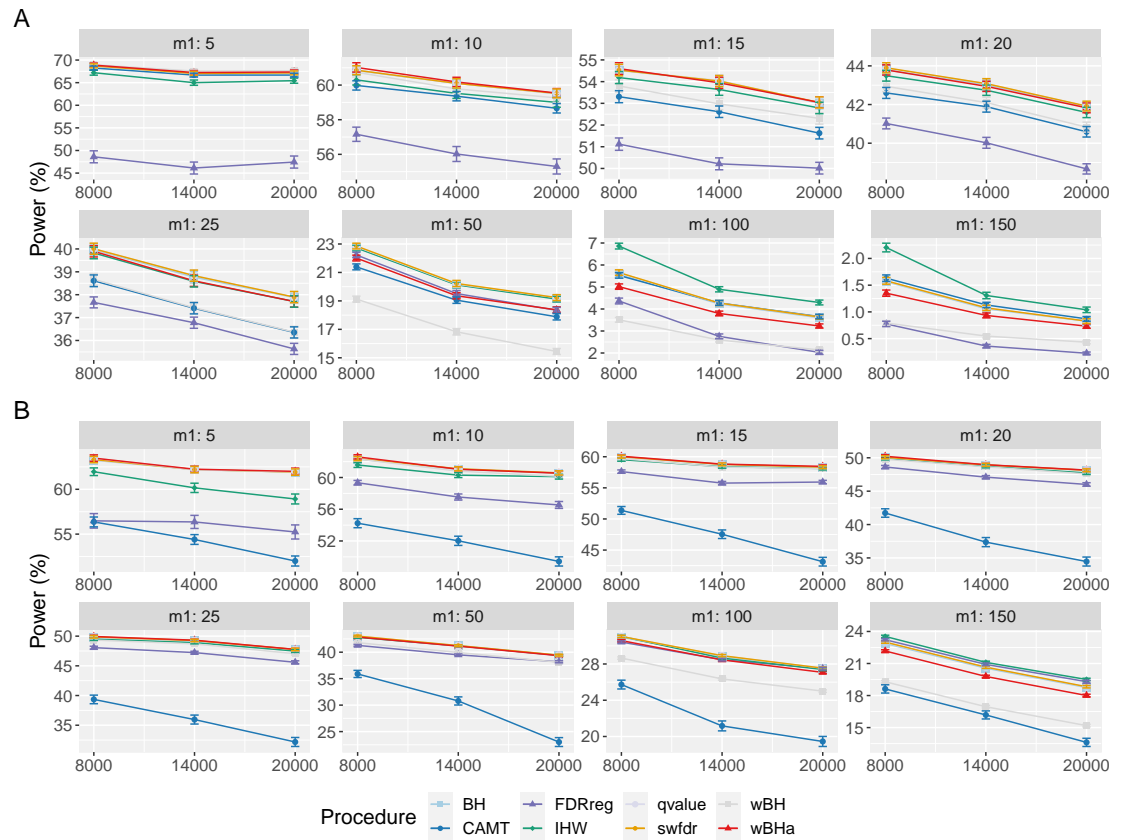


Figure S1. Overall power comparison in **scenario 2**, with **independent** markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

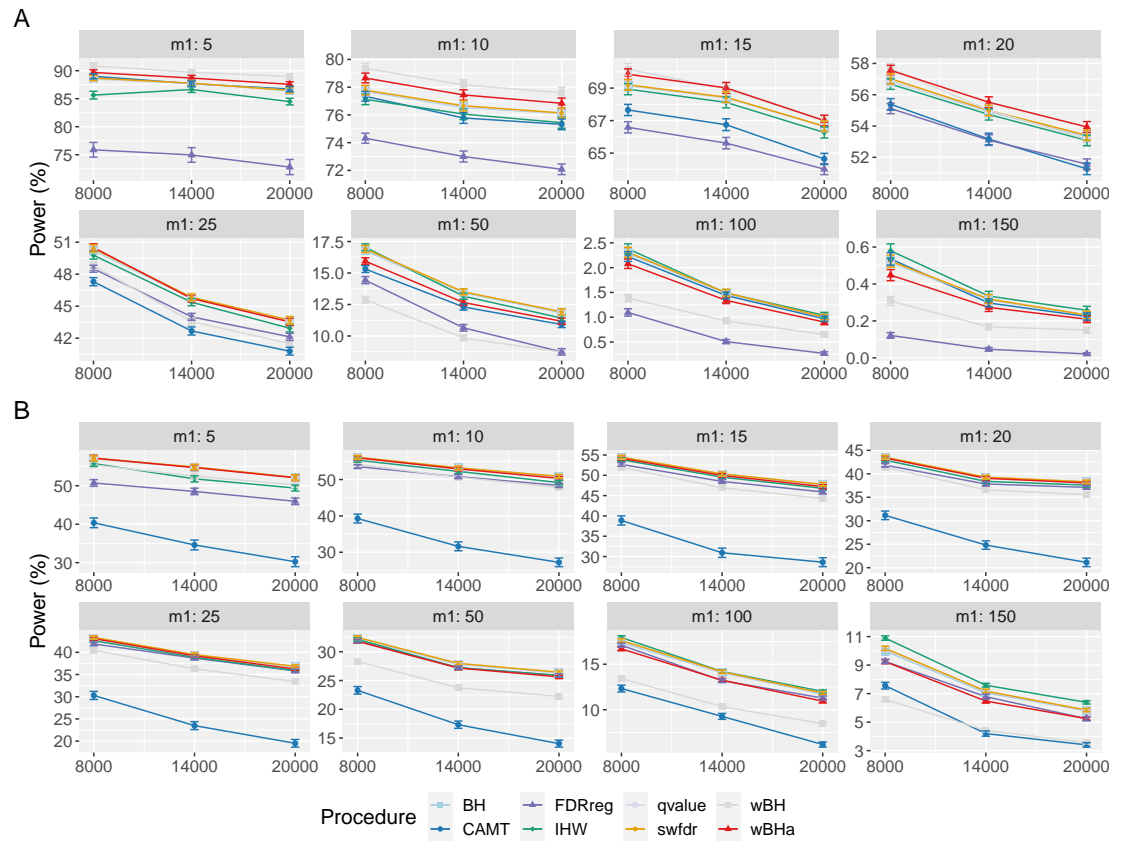


Figure S2. Overall power comparison in **scenario 3**, with **independent** markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

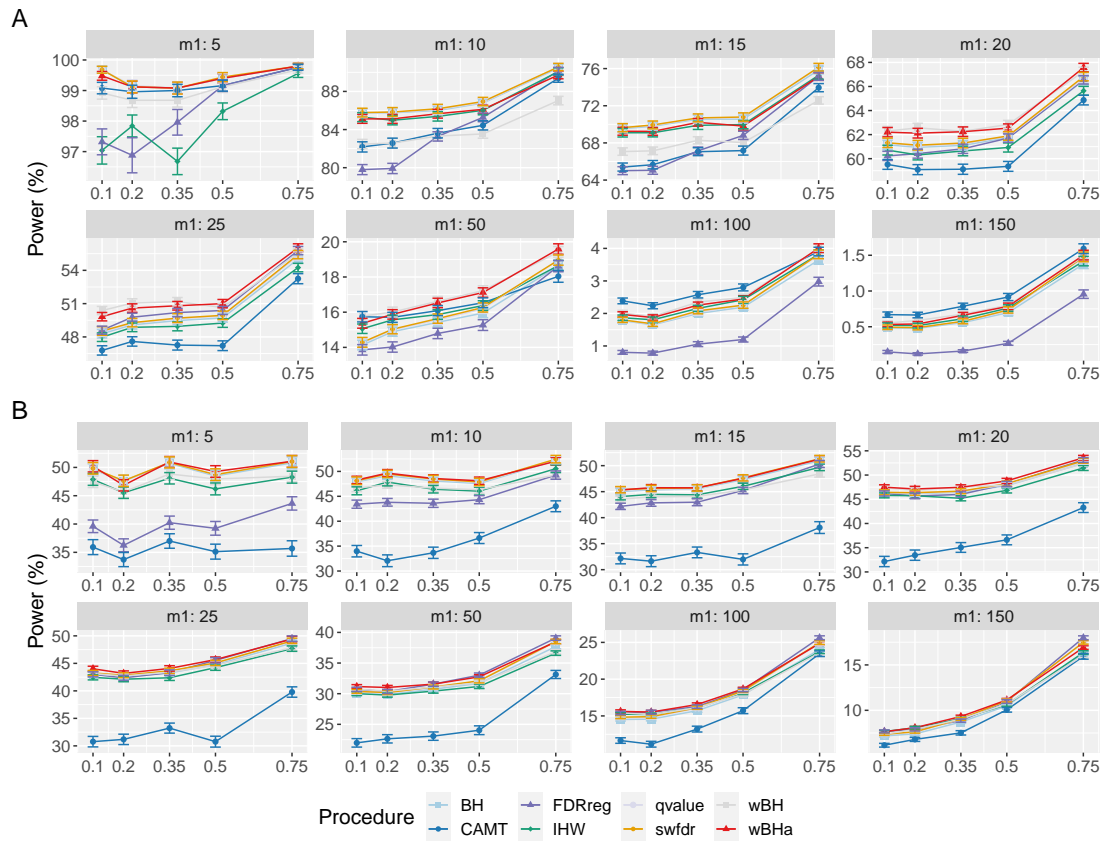


Figure S3. Overall power comparison in **scenario 1**, with **correlated** markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

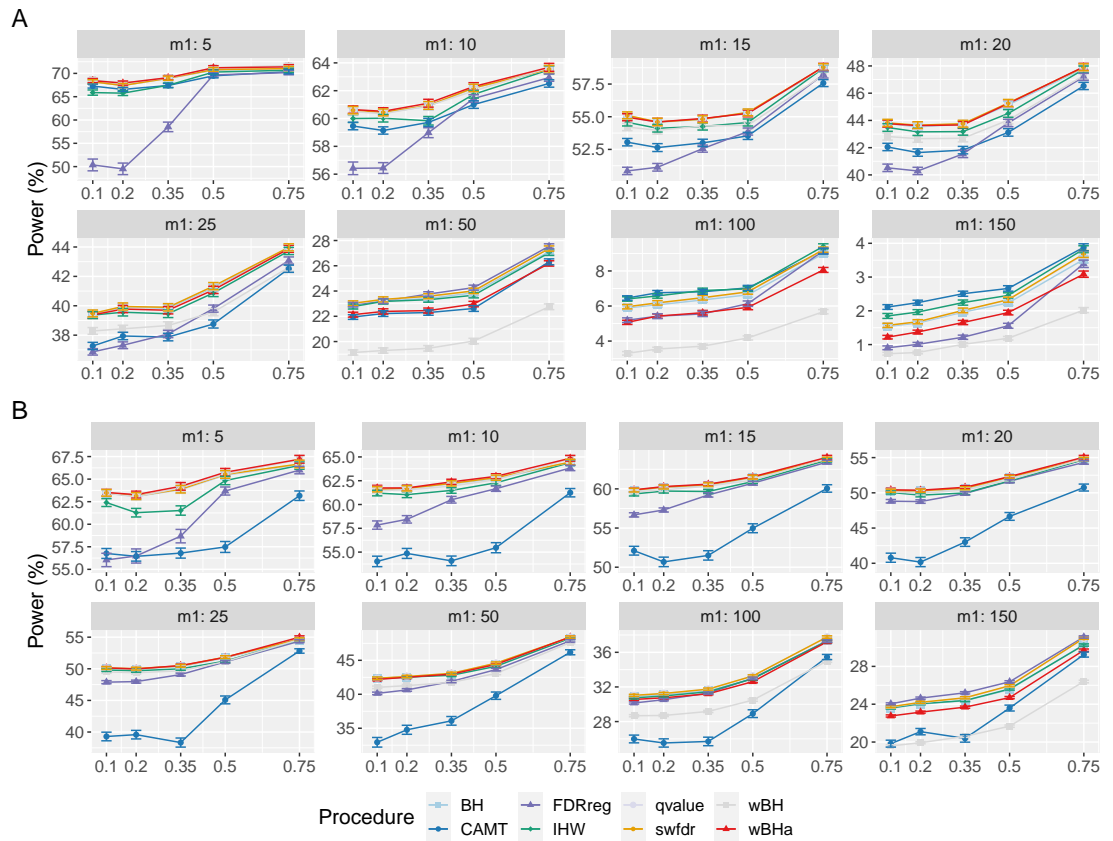


Figure S4. Overall power comparison in **scenario 2**, with **correlated** markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

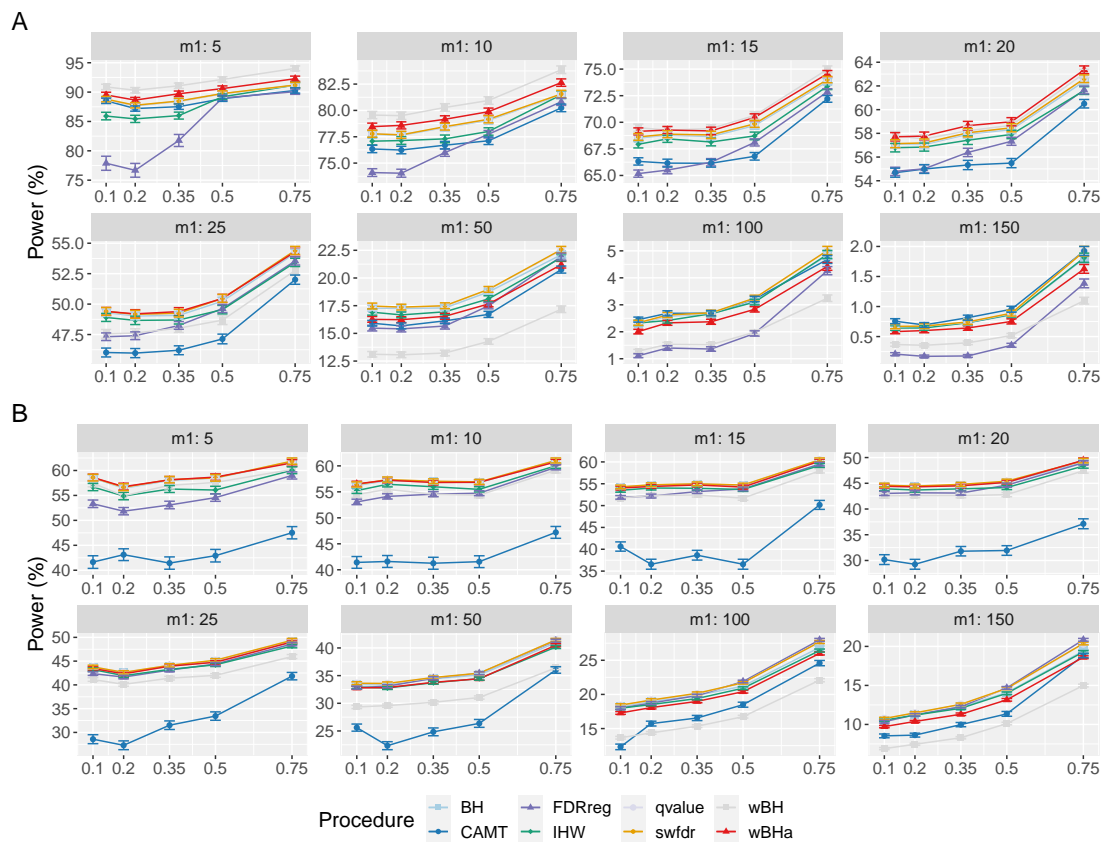


Figure S5. Overall power comparison in **scenario 3**, with **correlated** markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

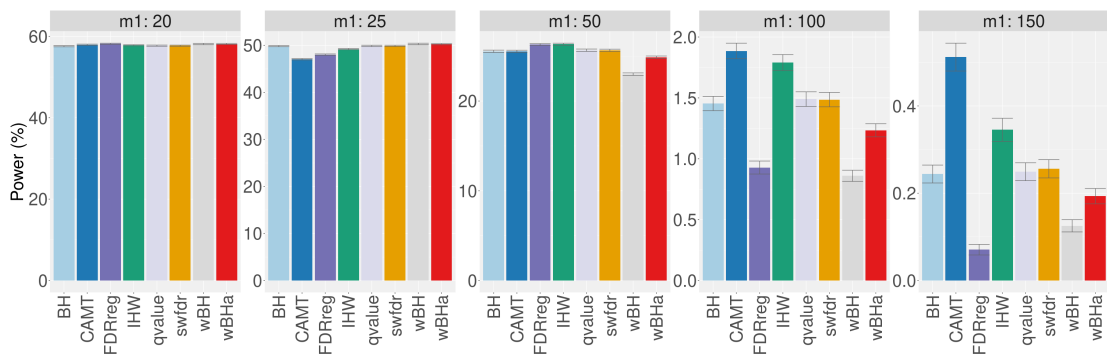


Figure S6. Overall power comparison in **scenario 2**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

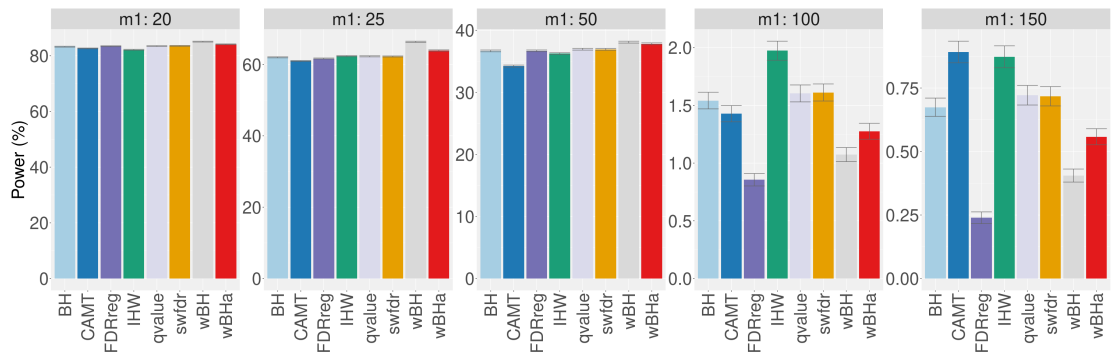


Figure S7. Overall power comparison in **scenario 3**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

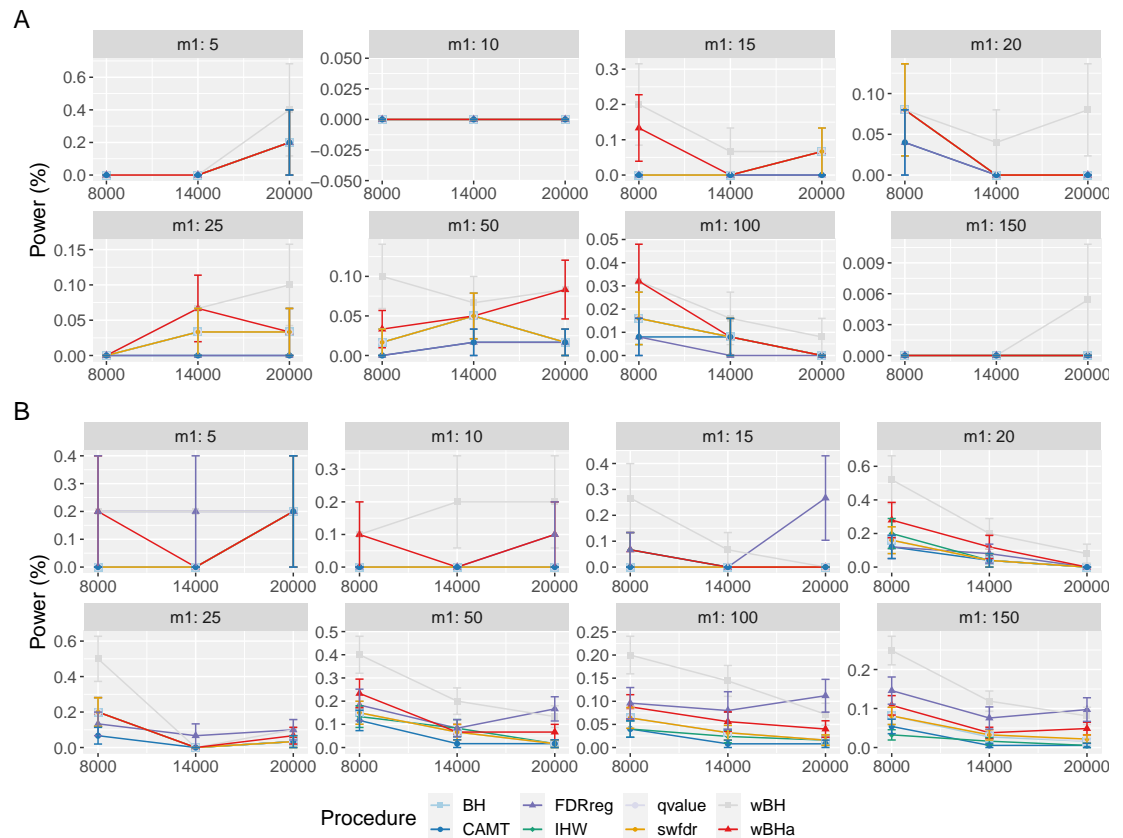


Figure S8. Power comparison in subgroup of **rare variants** in **scenario 2**, with **independent** markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

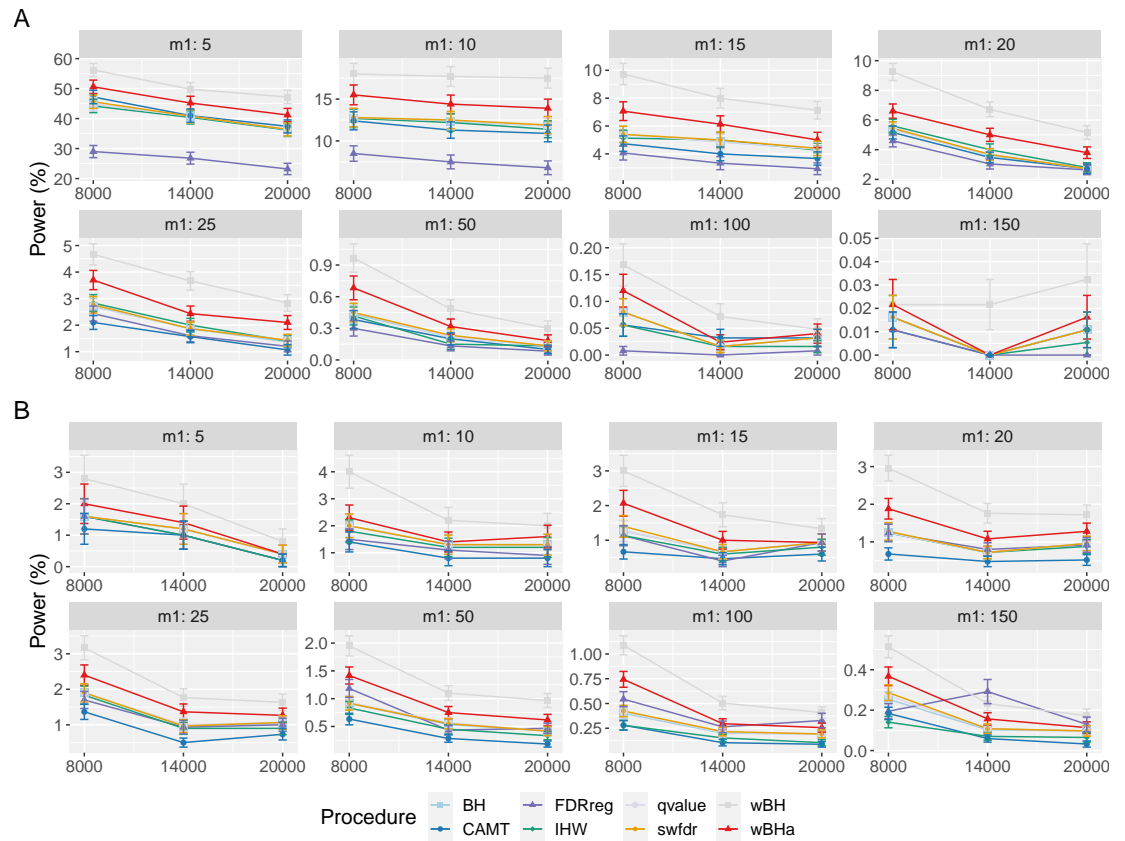


Figure S9. Power comparison in subgroup of **rare variants** in **scenario 3**, with **independent** markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

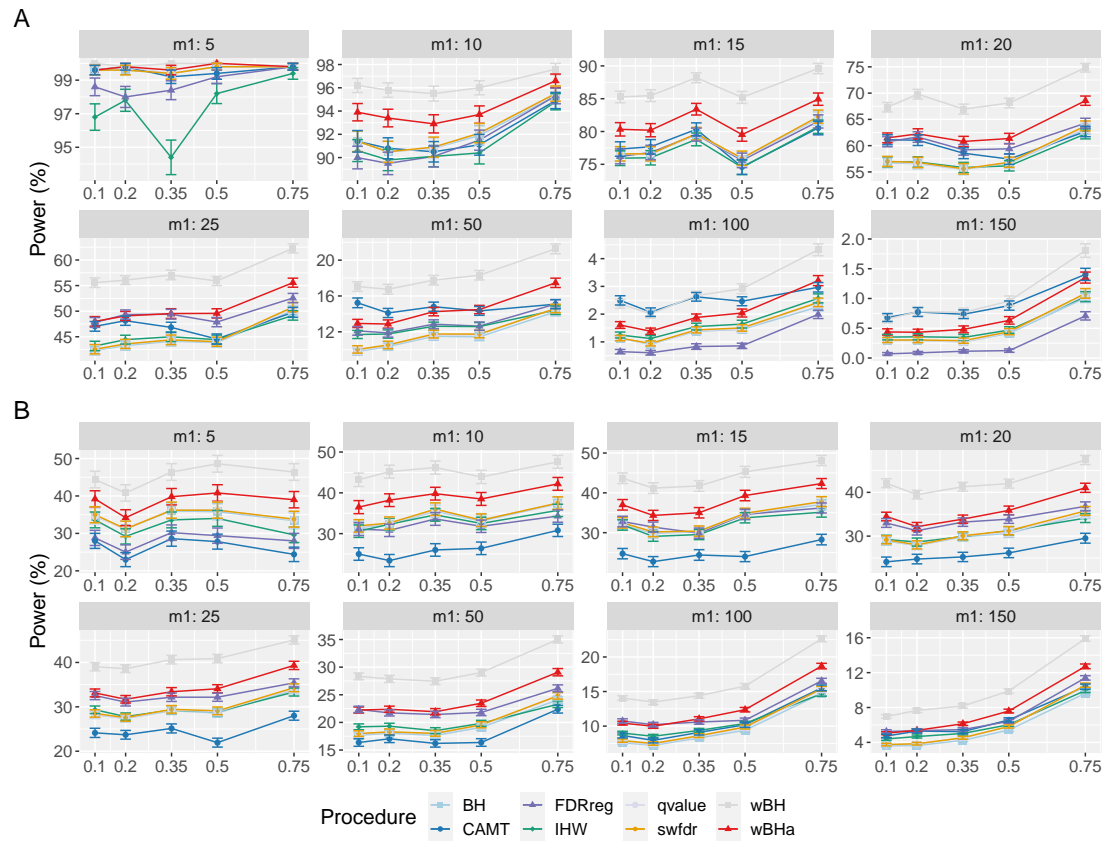


Figure S10. Power comparison in subgroup of rare variants in scenario 1, with correlated markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

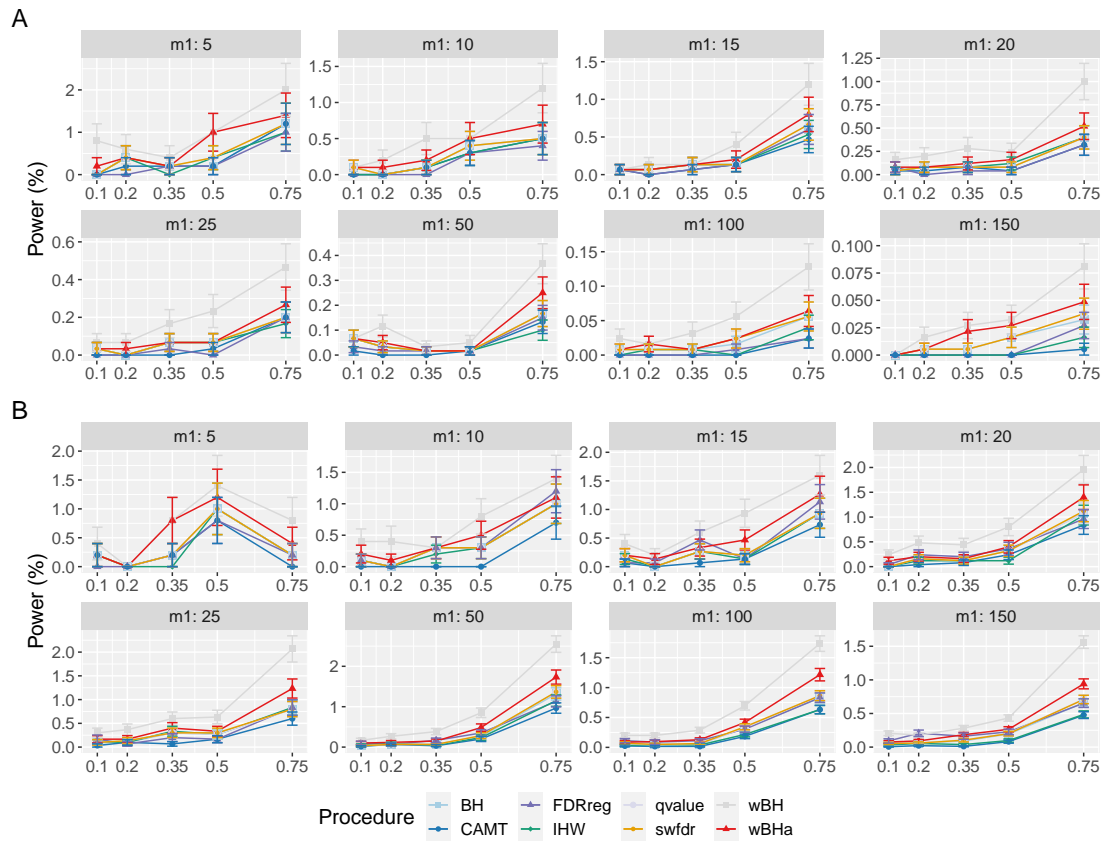


Figure S11. Power comparison in subgroup of **rare variants** in **scenario 2**, with **correlated** markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

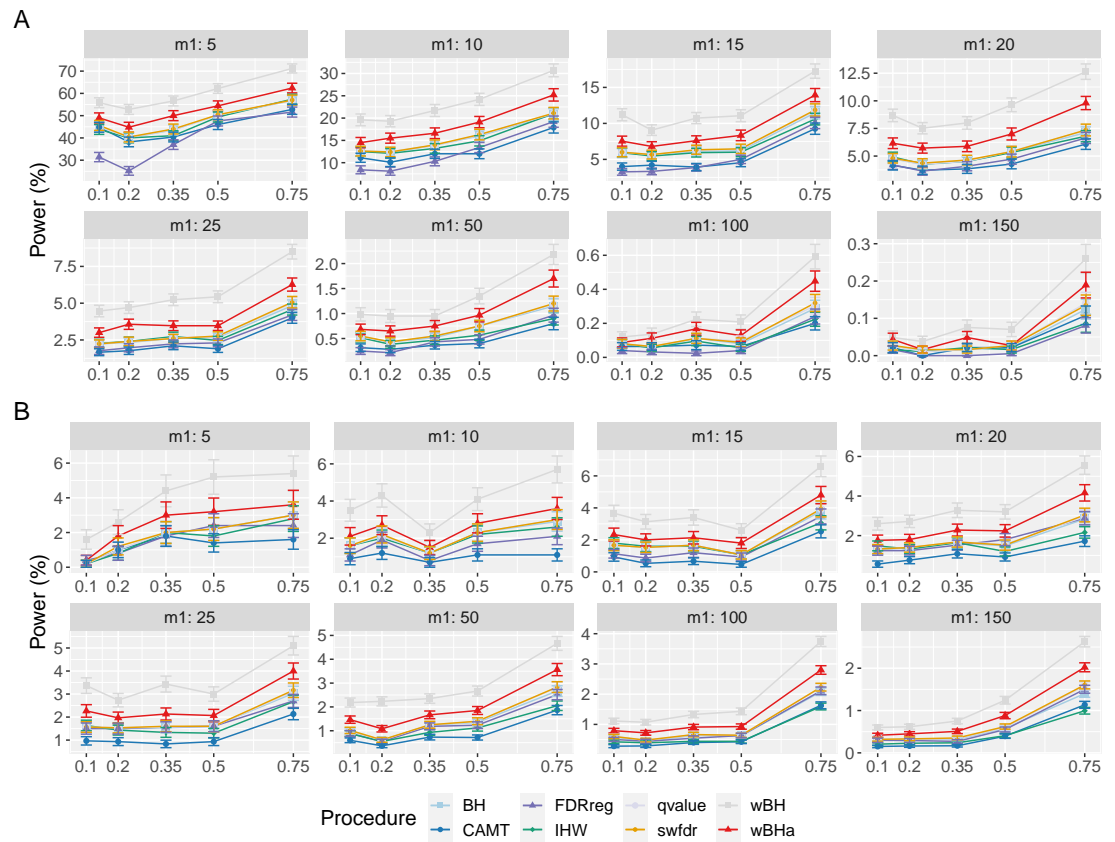


Figure S12. Power comparison in subgroup of **rare variants** in **scenario 3**, with **correlated** markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

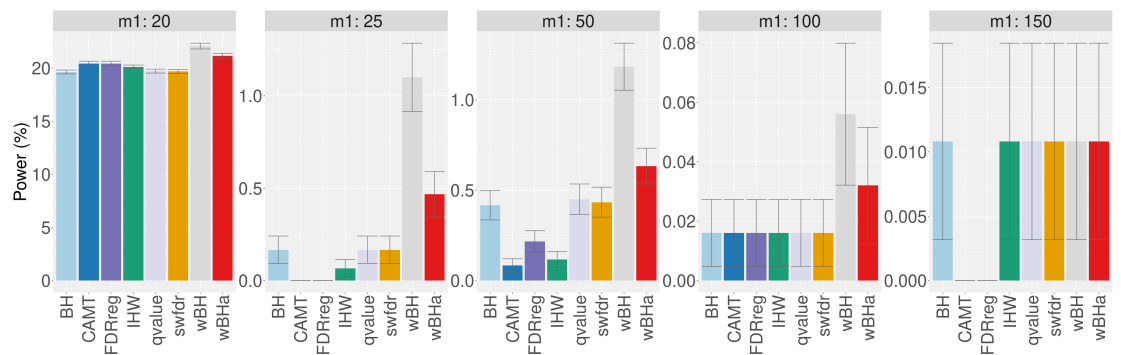


Figure S13. Power comparison in subgroup of **rare variants** in **scenario 2**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

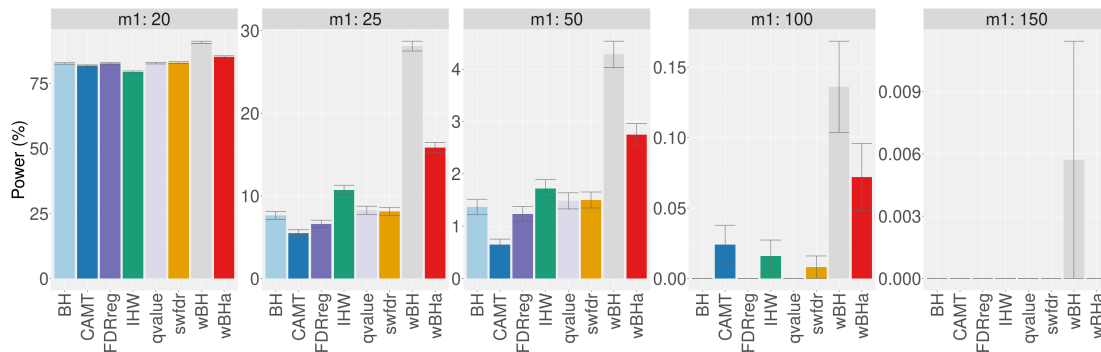


Figure S14. Power comparison in subgroup of **rare variants** in **scenario 3**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

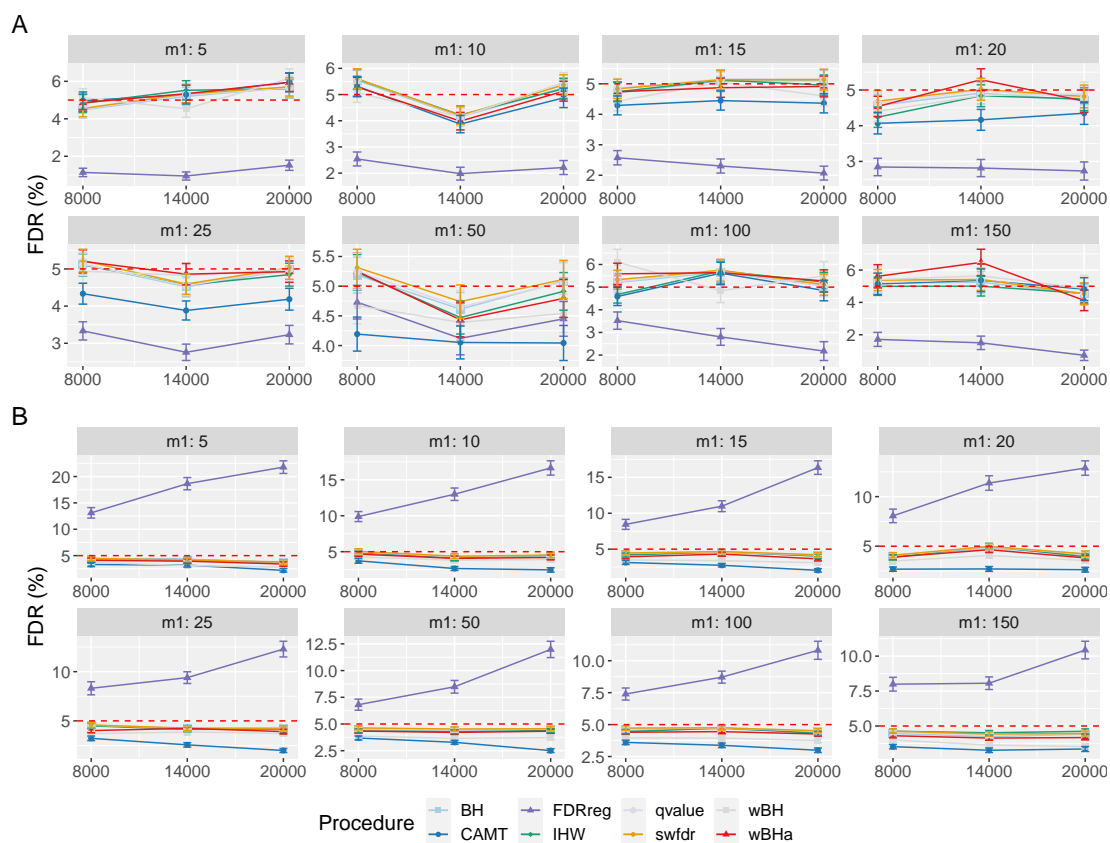


Figure S15. **FDR** comparison in **scenario 2**, with **independent** markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Red dashed line corresponds to target FDR level (5%). Vertical bars illustrate standard errors.

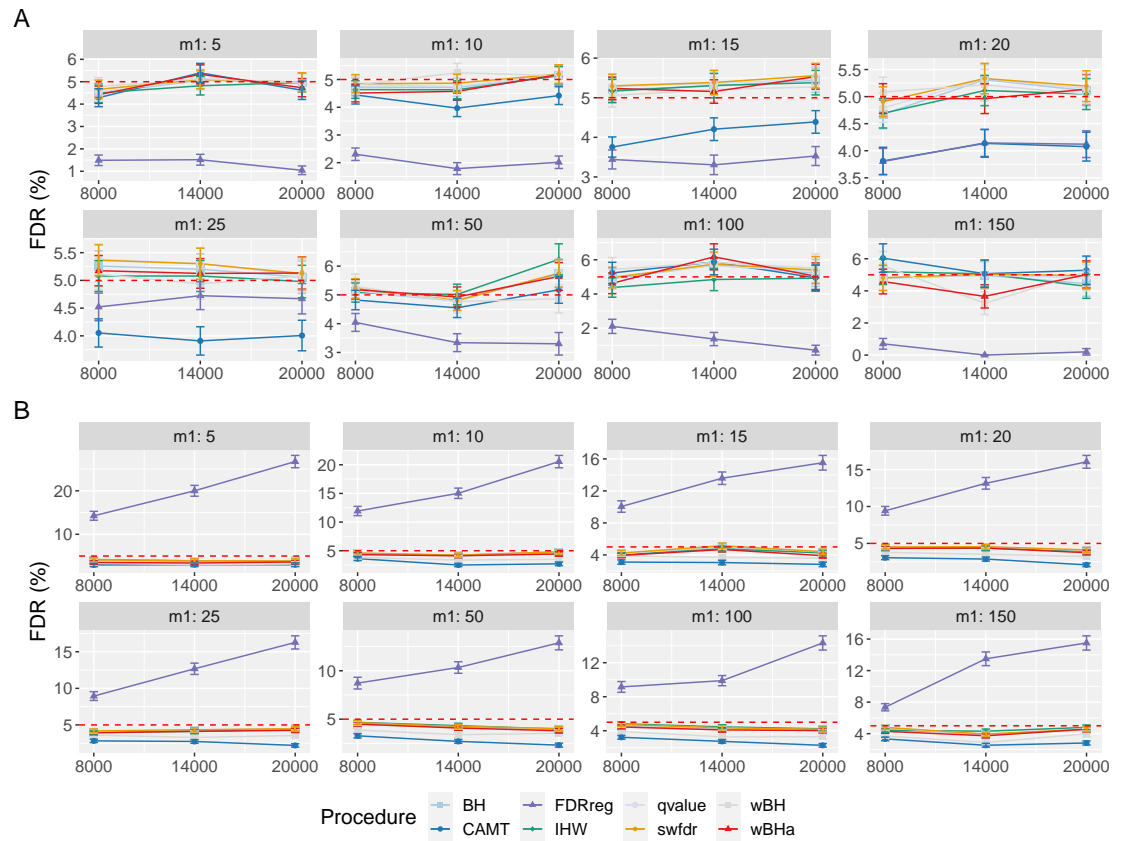


Figure S16. FDR comparison in scenario 3, with independent markers ($\rho = 0$), for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Red dashed line corresponds to target FDR level (5%). Vertical bars illustrate standard errors.

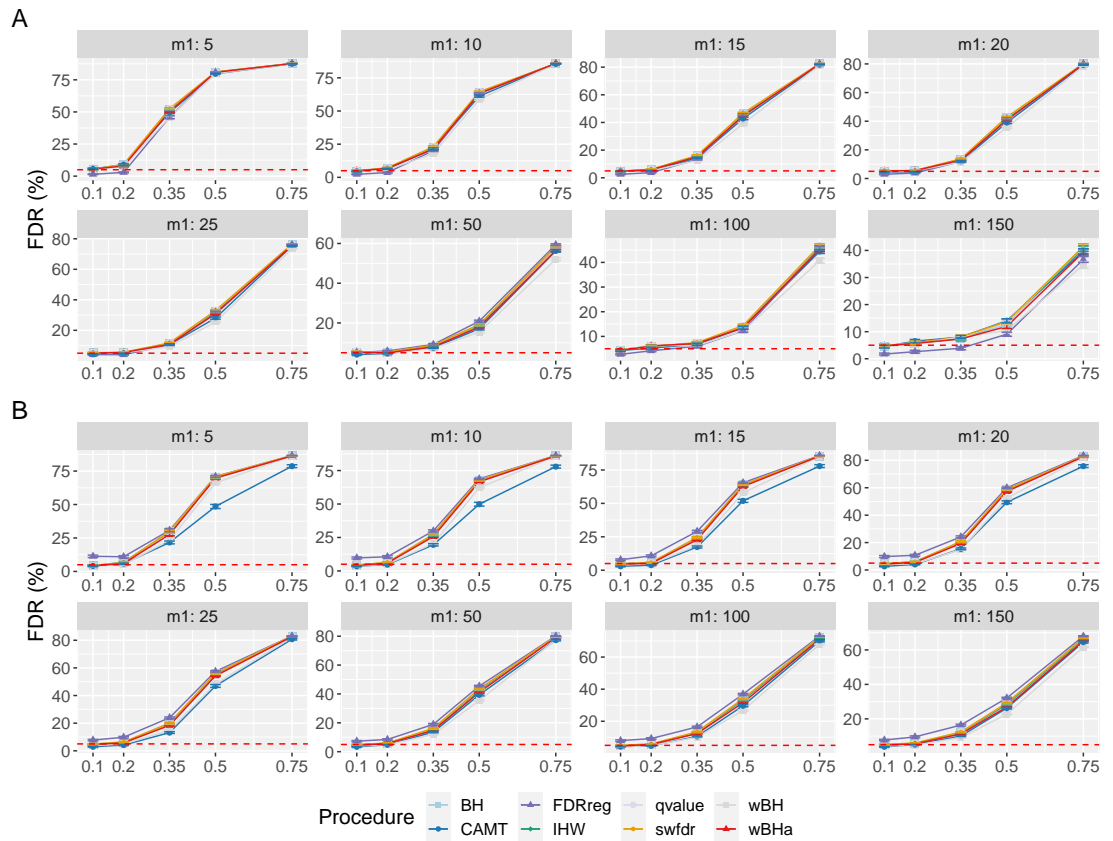


Figure S17. FDR comparison in scenario 2, with correlated markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Red dashed line corresponds to target FDR level (5%). Vertical bars illustrate standard errors.

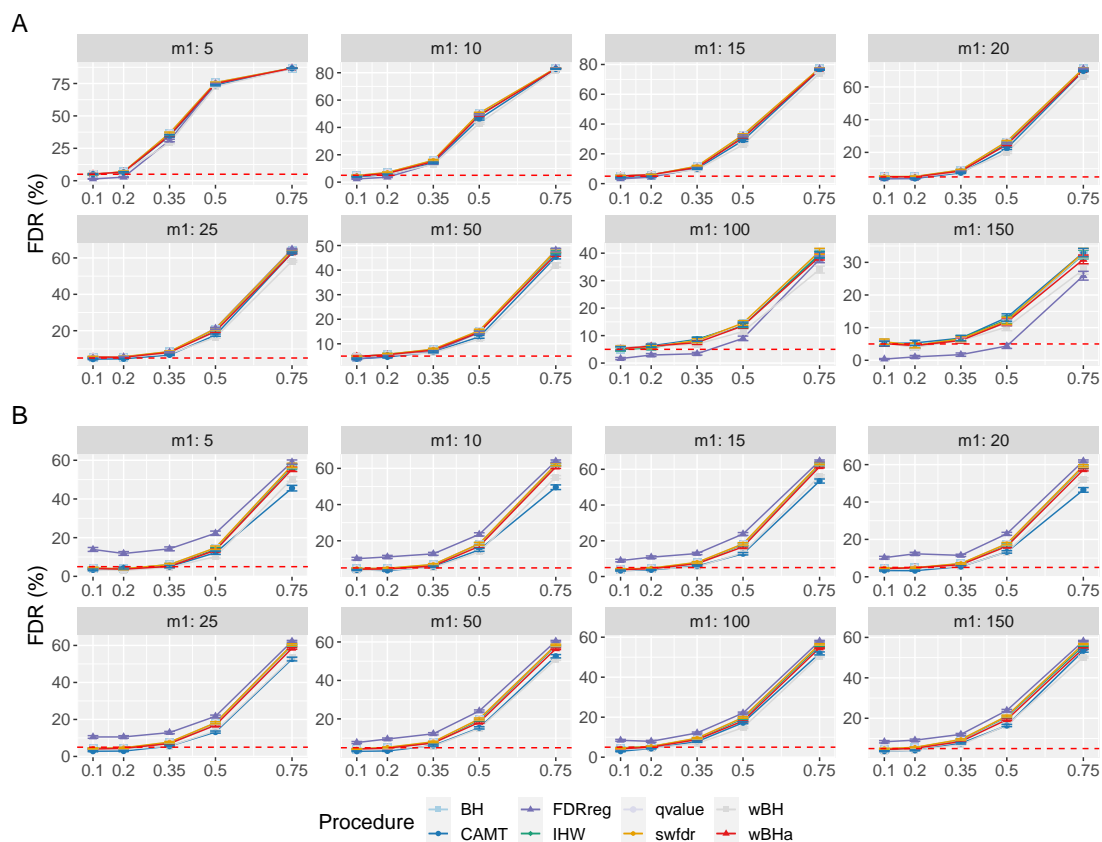


Figure S18. FDR comparison in scenario 3, with correlated markers, for different ρ and m_1 values with $m = 8000$. Panels A and B display results for quantitative and binary traits, respectively. Red dashed line corresponds to target FDR level (5%). Vertical bars illustrate standard errors.

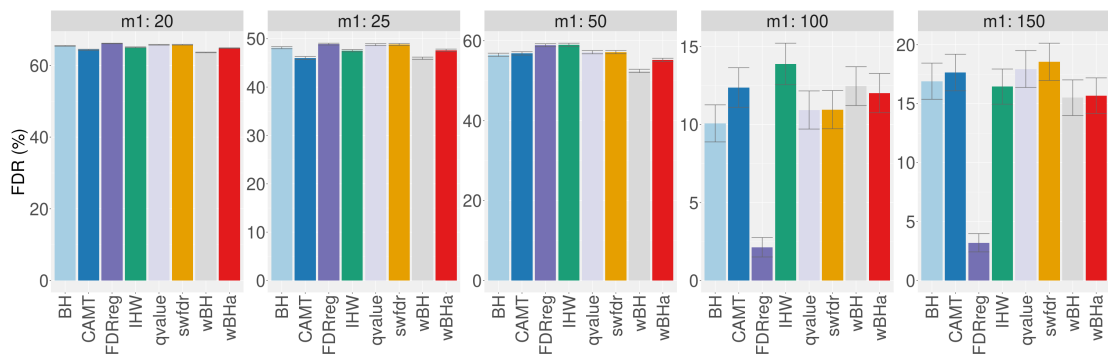


Figure S19. FDR comparison in scenario 1, with simulations based on real data, for different m_1 values. Vertical bars illustrate standard errors.

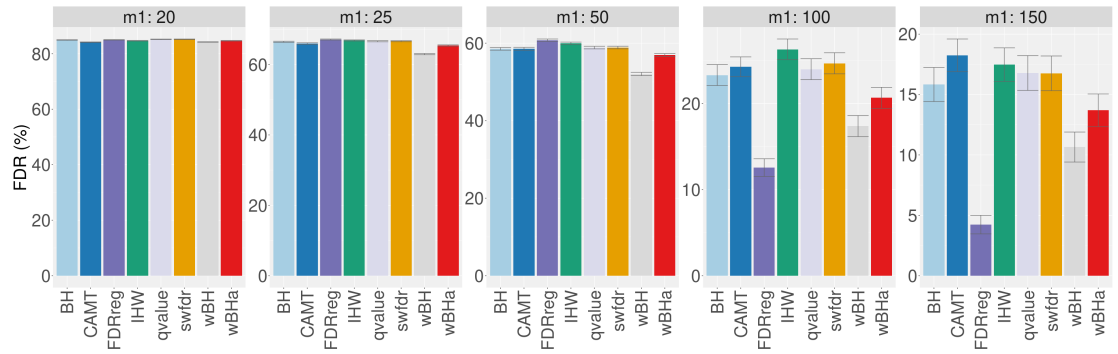


Figure S20. FDR comparison in **scenario 2**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

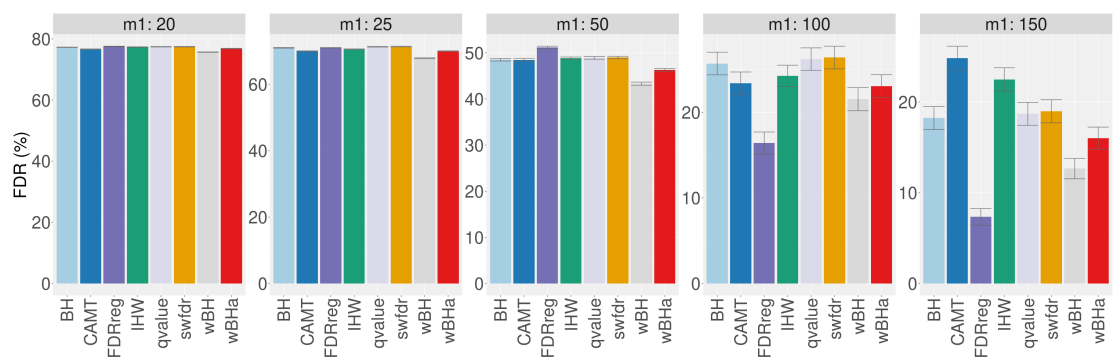


Figure S21. FDR comparison in **scenario 3**, with simulations based on **real data**, for different m_1 values. Vertical bars illustrate standard errors.

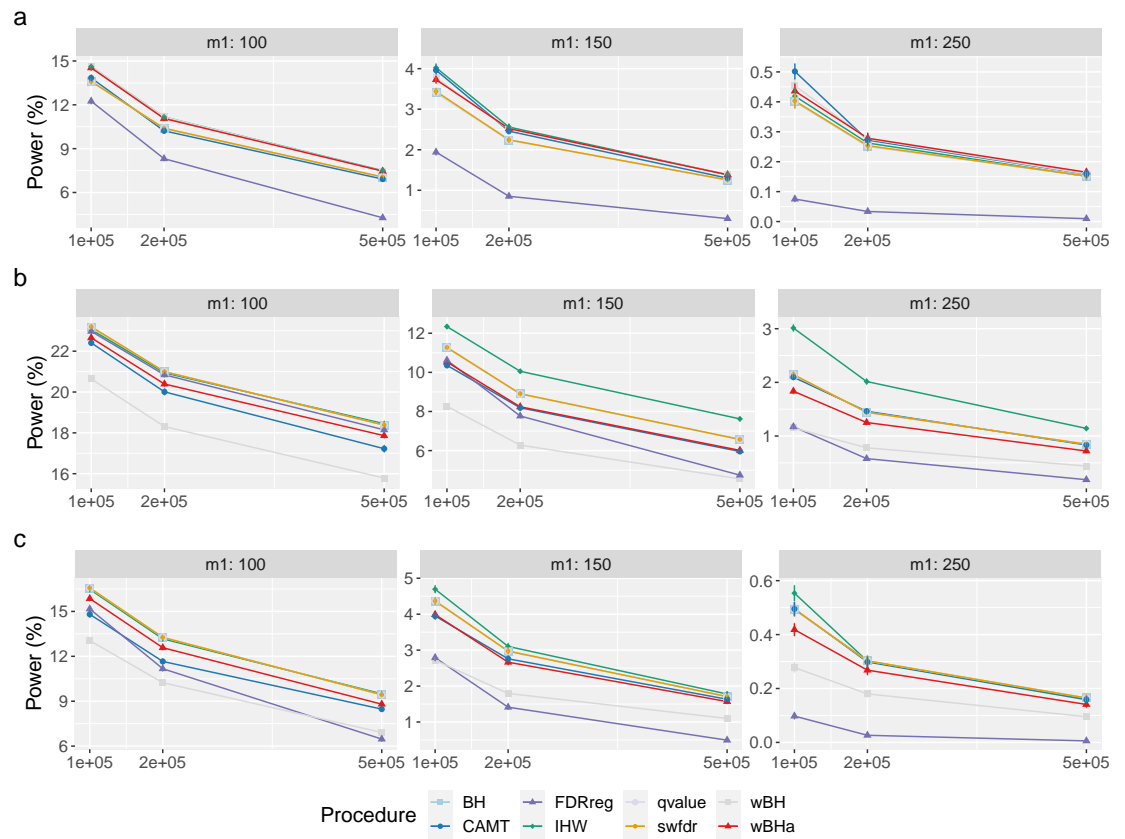


Figure S22. Overall power comparison with independent markers for **large m** values and m_1 values with quantitative phenotype. Panels a, b and c display results for scenario 1, scenario 2 and scenario 3, respectively. Vertical bars illustrate standard errors.

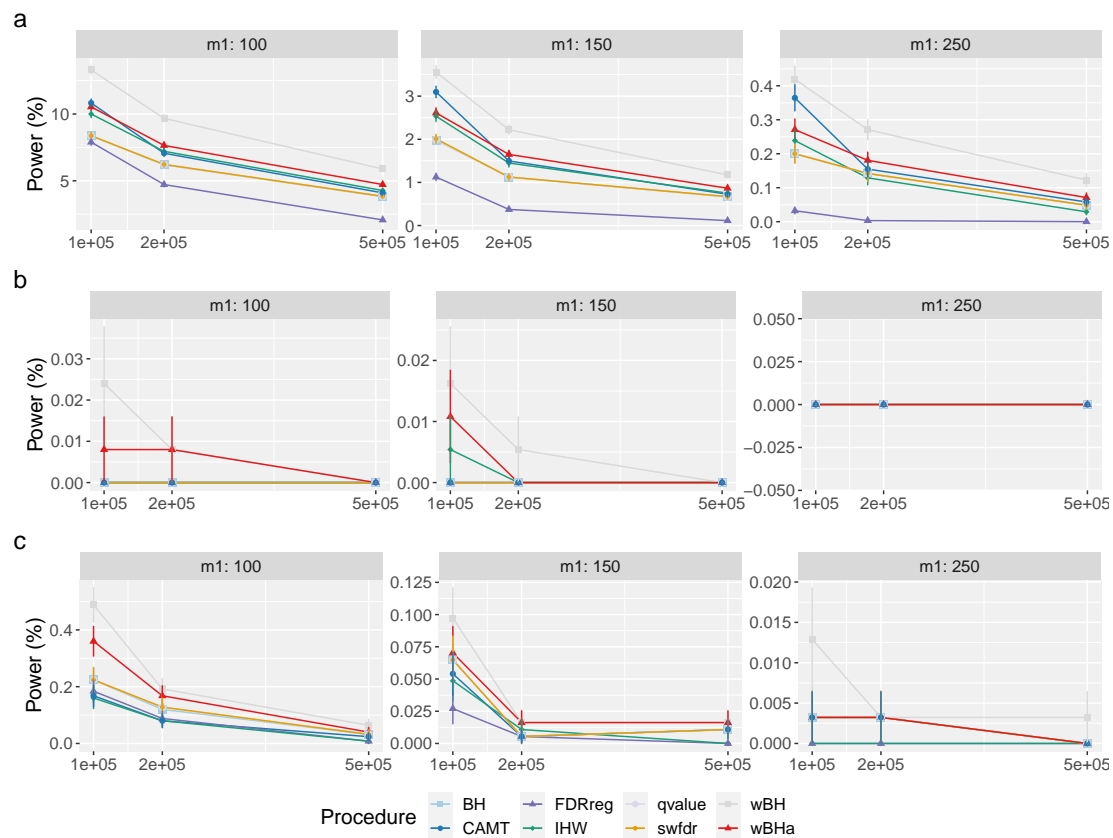


Figure S23. Power comparison in subgroup of **rare variants** with independent markers for **large m** values and m_1 values with quantitative phenotype. Panels a, b and c display results for scenario 1, scenario 2 and scenario 3, respectively. Vertical bars illustrate standard errors.

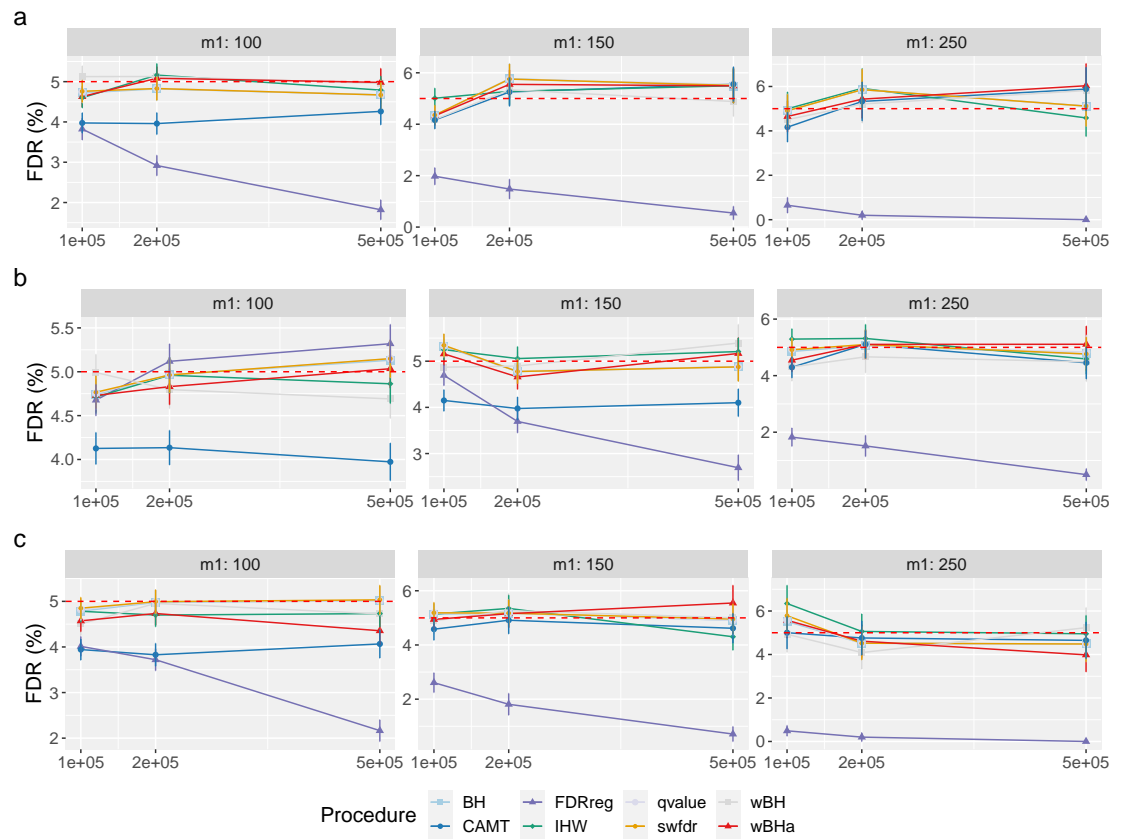


Figure S24. FDR comparison with independent markers for **large m** values and m_1 values with quantitative phenotype. Panels a, b and c display results for scenario 1, scenario 2 and scenario 3, respectively. Vertical bars illustrate standard errors.

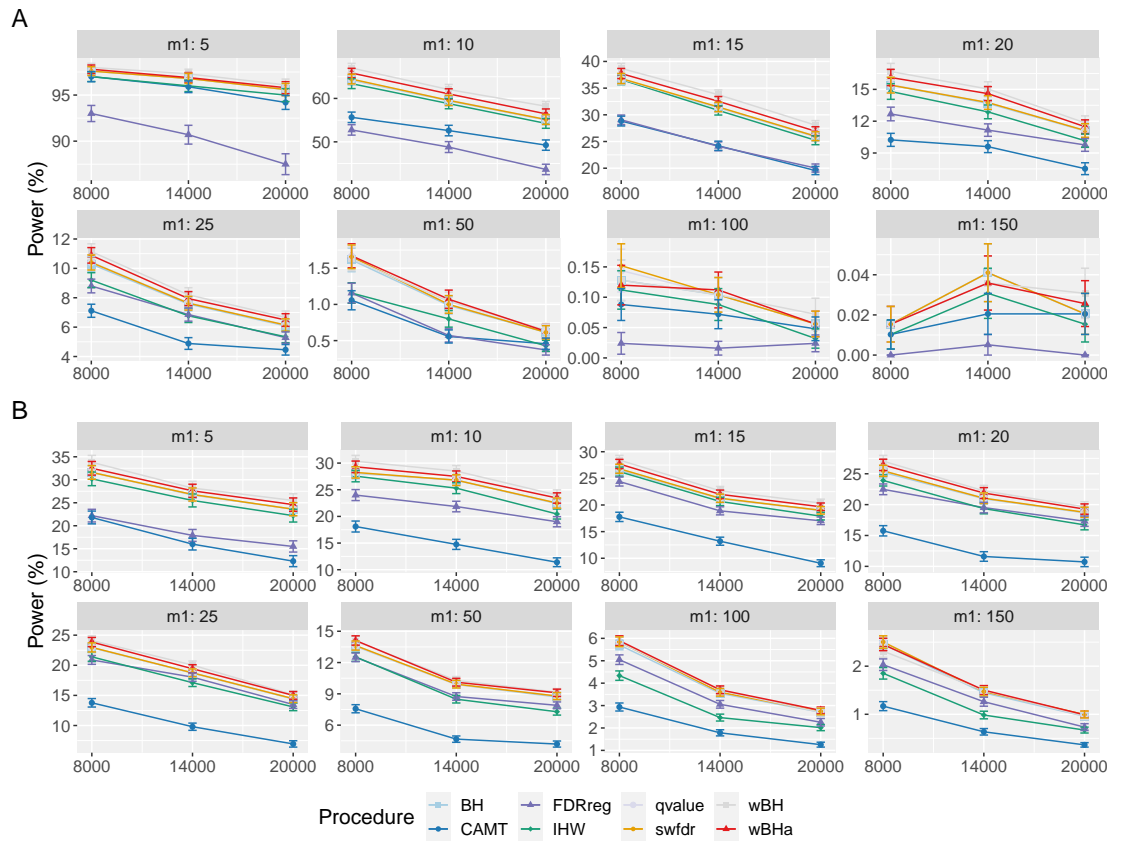


Figure S25. Power comparison in subgroup of **common variants** when using **1/MAF** as covariate in **scenario 1** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

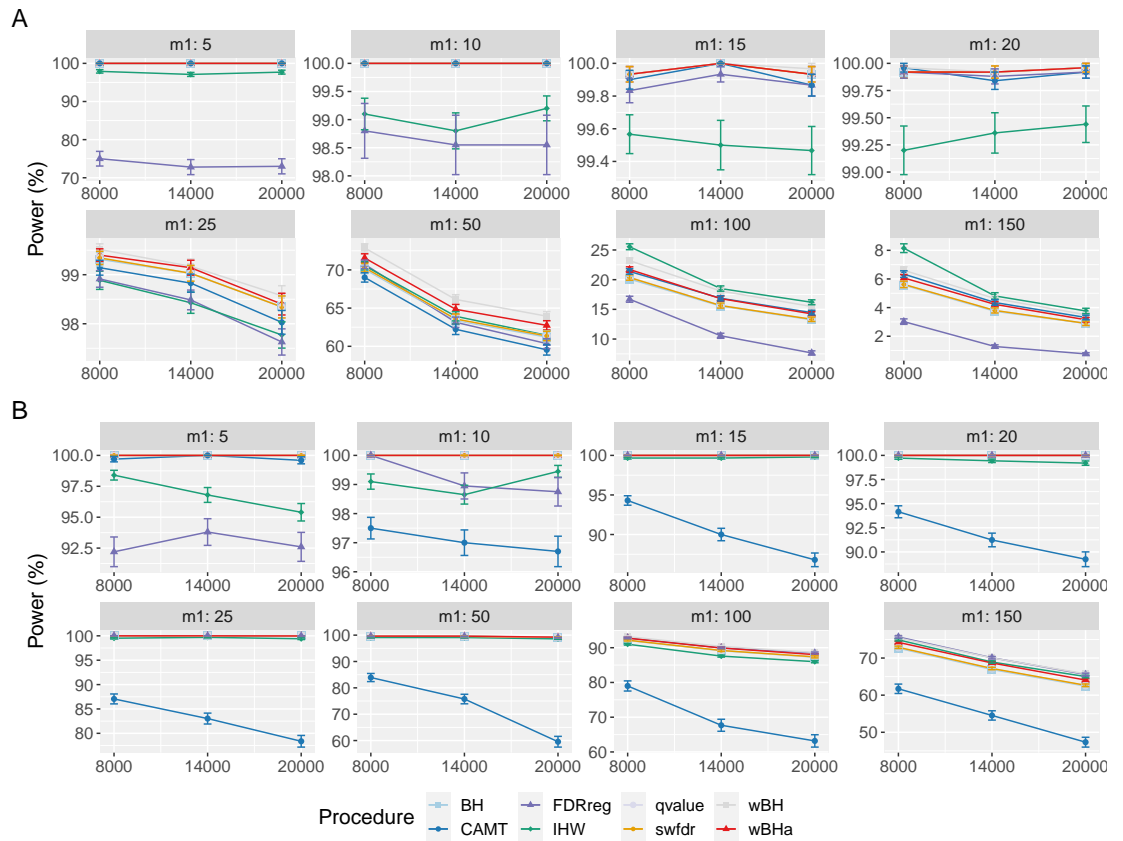


Figure S26. Power comparison in subgroup of **common variants** when using **1/MAF** as covariate in **scenario 2** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

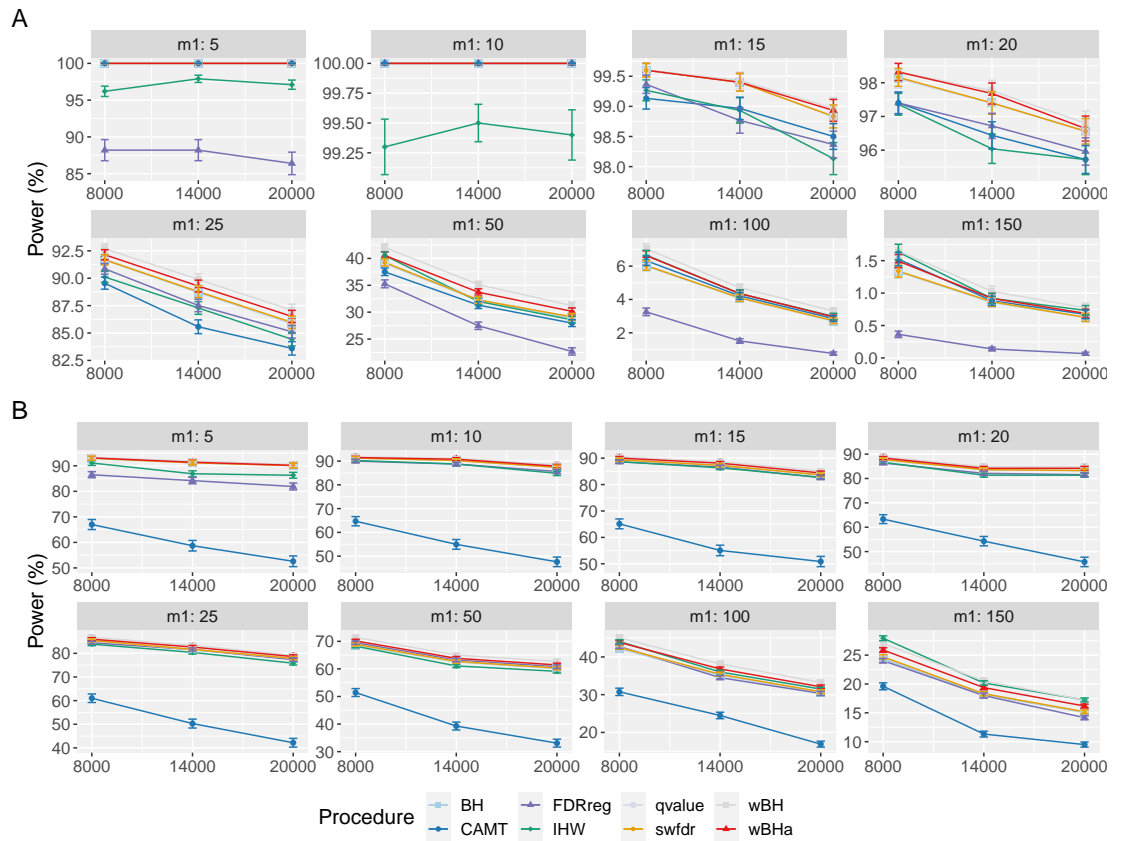


Figure S27. Power comparison in subgroup of **common variants** when using **1/MAF** as covariate in **scenario 3** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

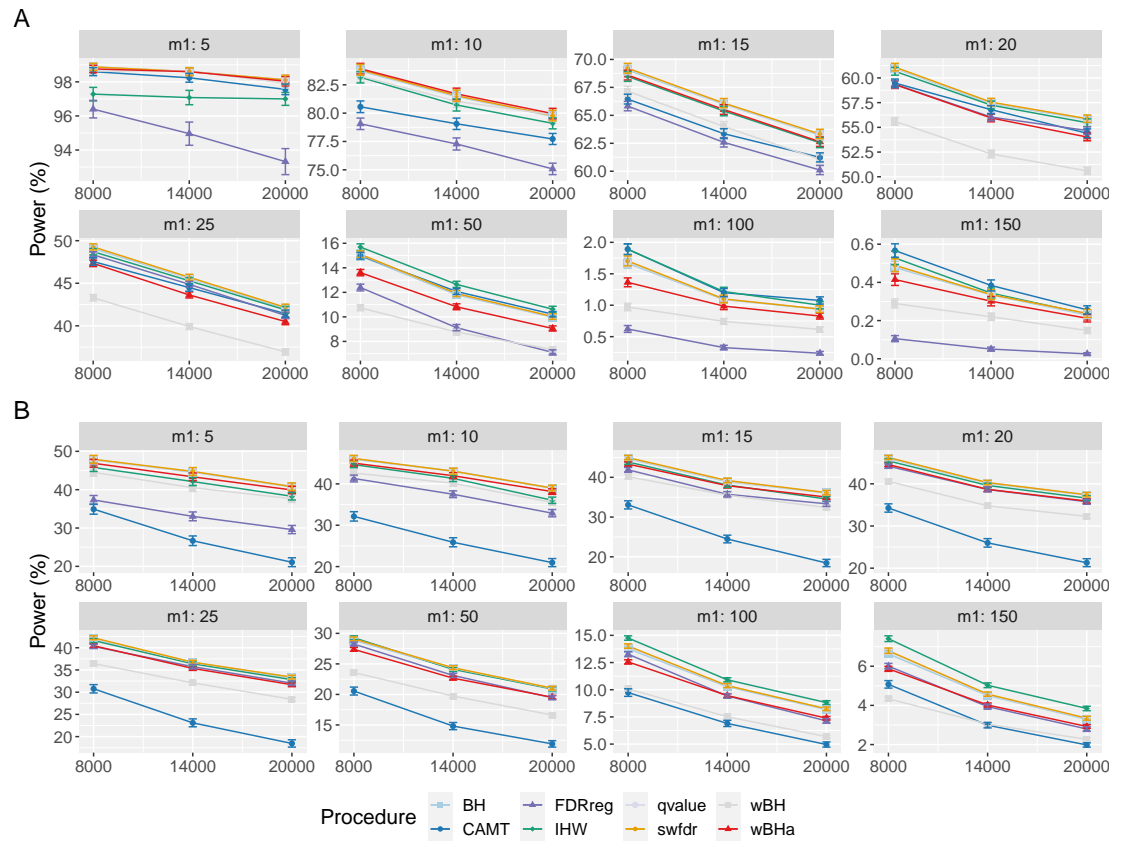


Figure S28. Overall power comparison when using $1/MAF$ as covariate in **scenario 1** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

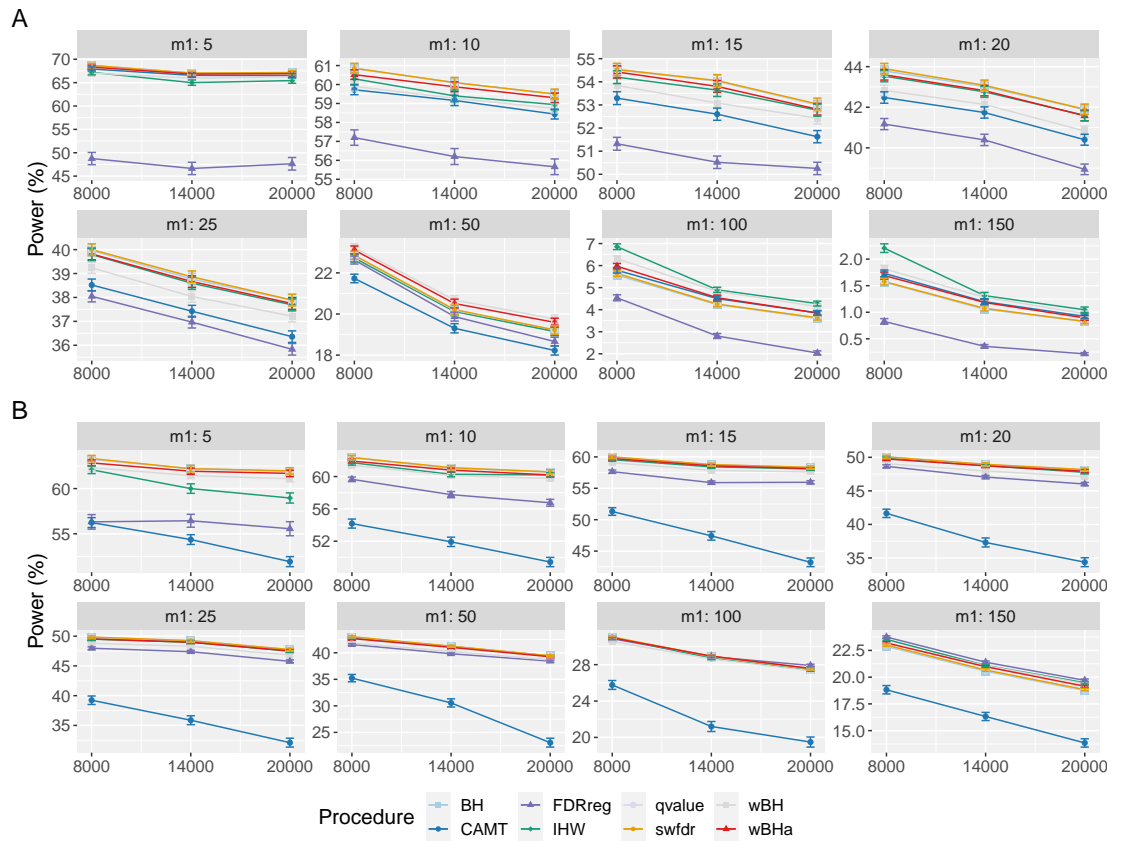


Figure S29. Overall power comparison when using $1/MAF$ as covariate in **scenario 2** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

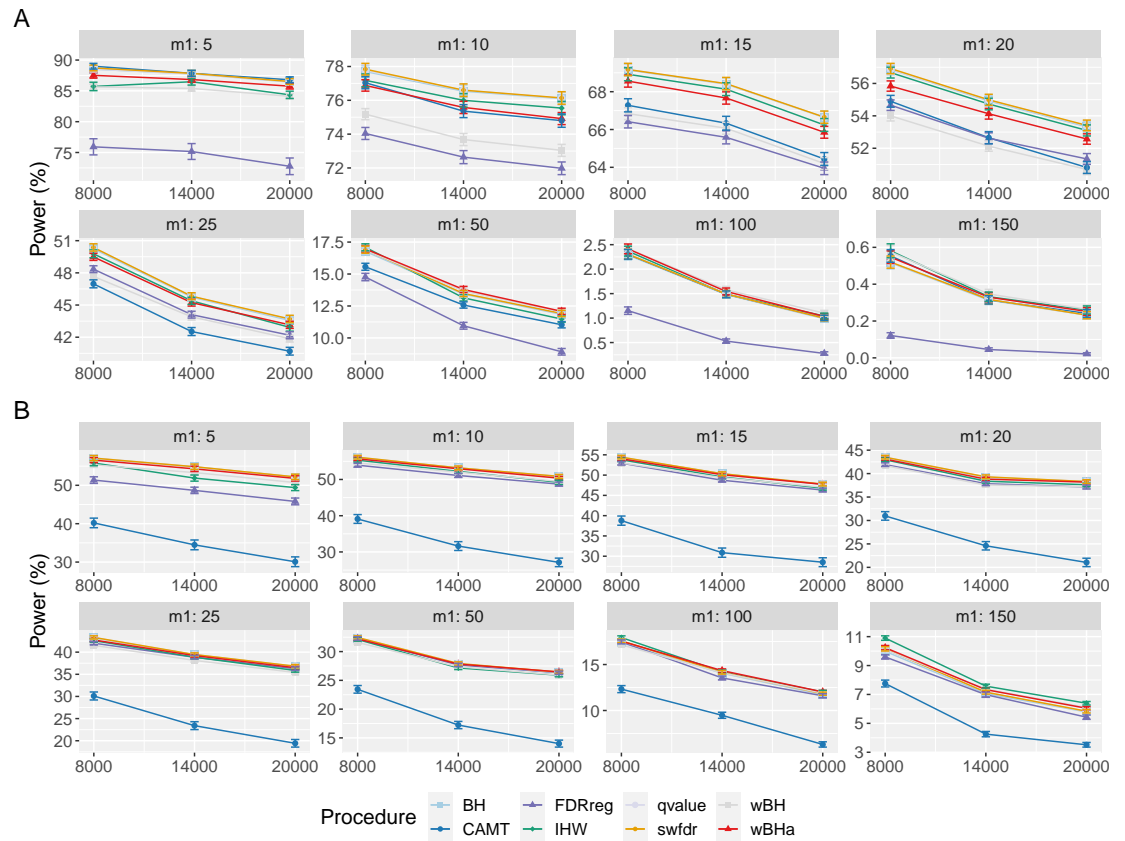


Figure S30. Overall power comparison when using $1/MAF$ as covariate in **scenario 3** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

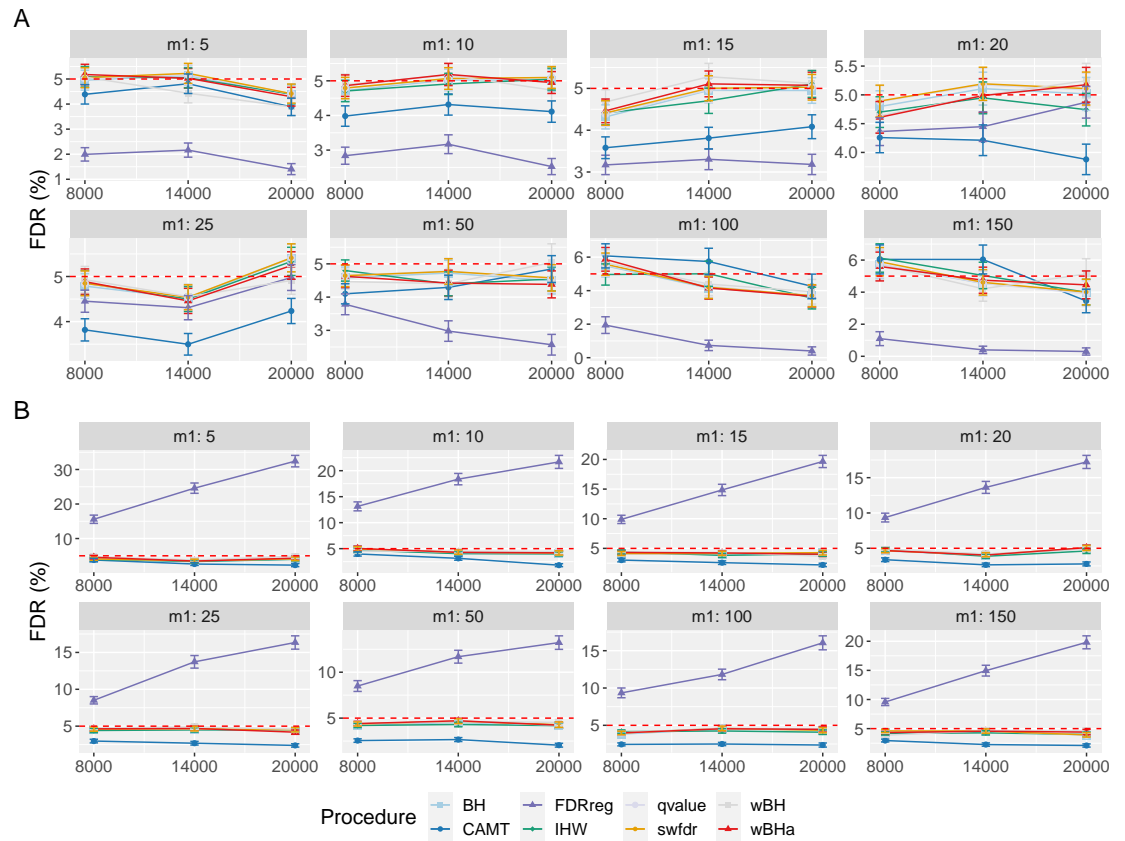


Figure S31. FDR comparison when using $1/MAF$ as covariate in scenario 1 with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

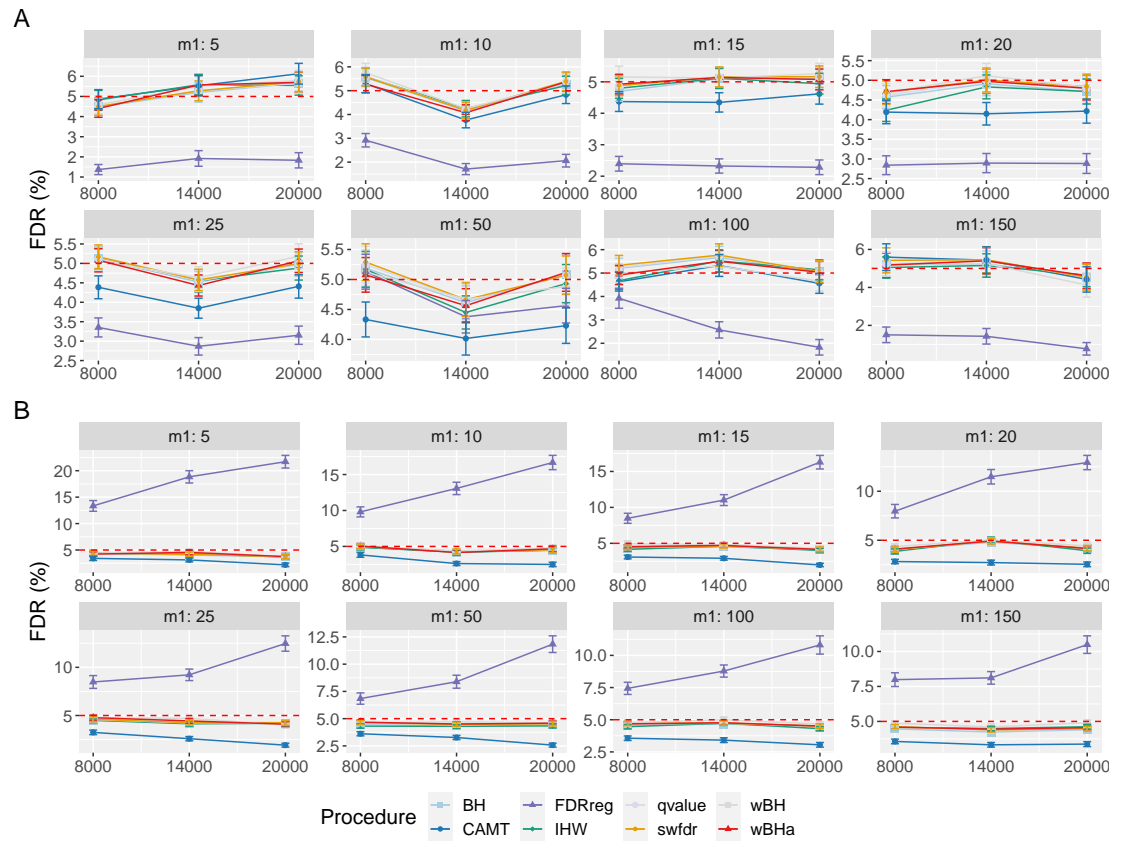


Figure S32. FDR comparison when using **1/MAF** as covariate in **scenario 2** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

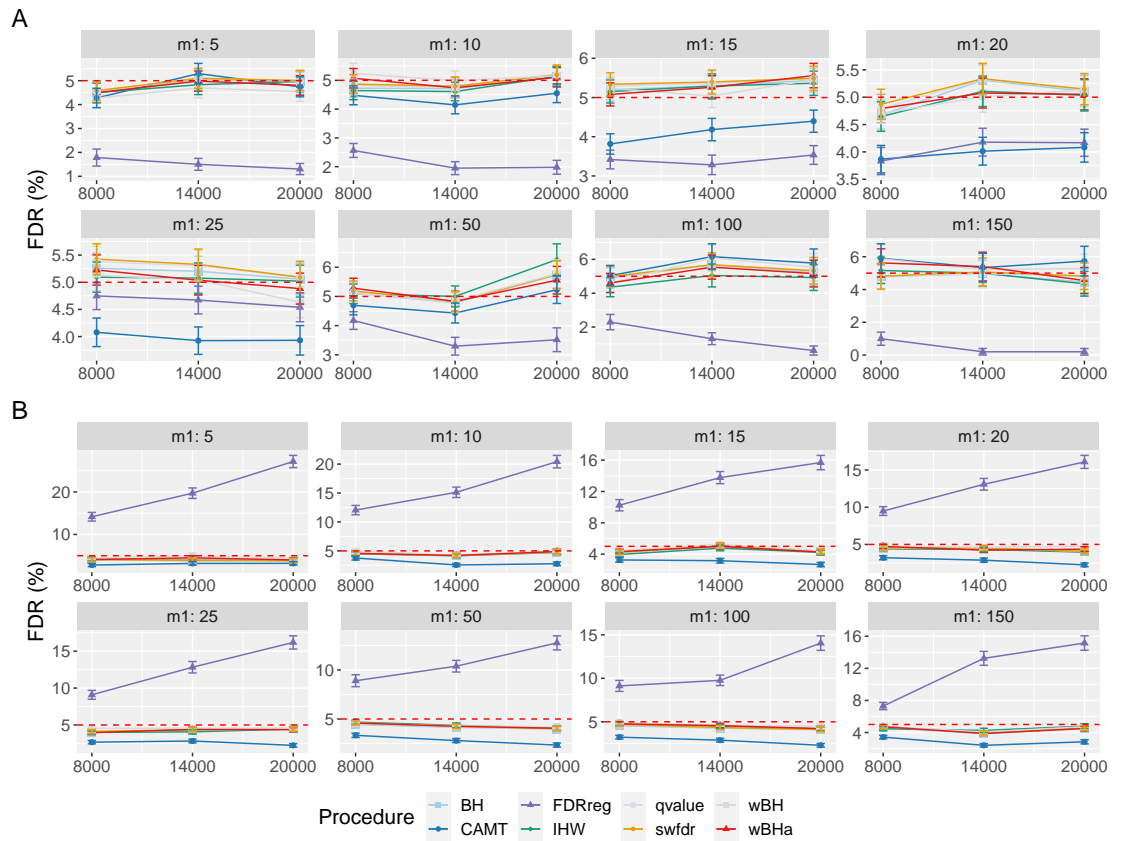


Figure S33. FDR comparison when using $1/MAF$ as covariate in **scenario 3** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

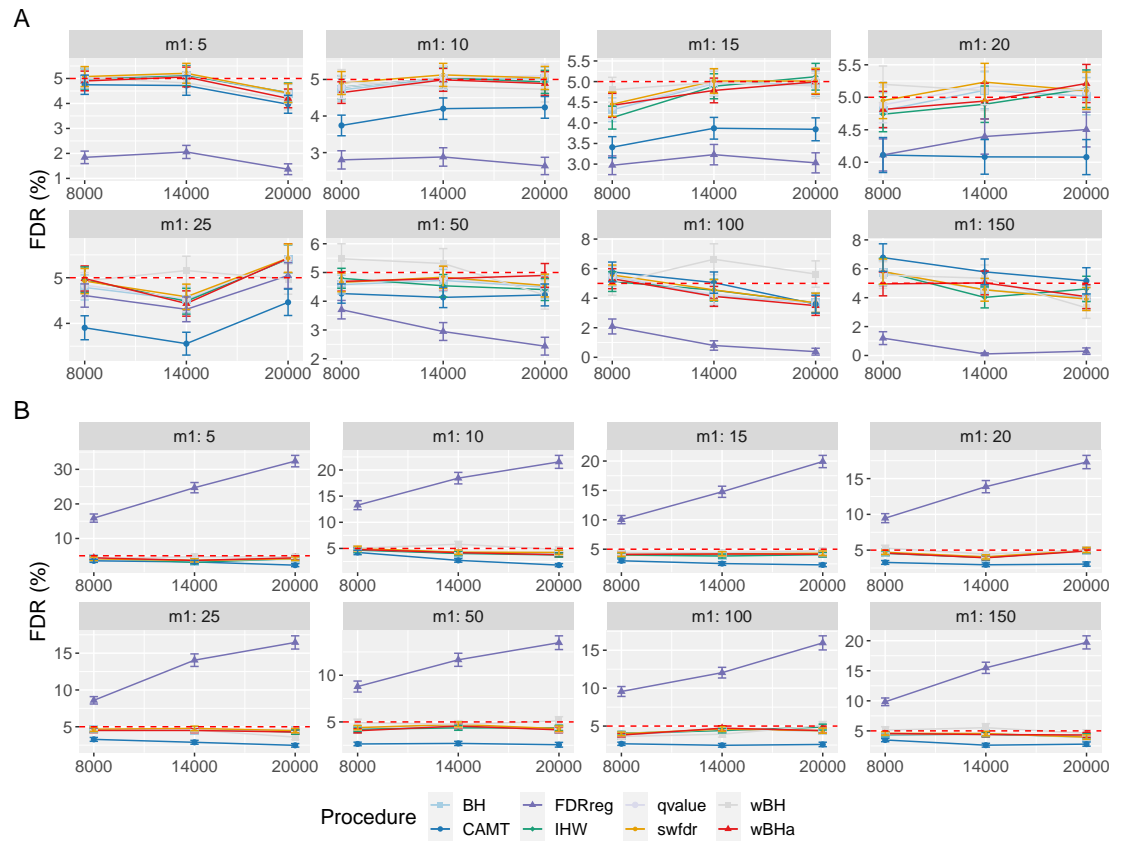


Figure S34. FDR comparison when using **uninformative** covariates in **scenario 1** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

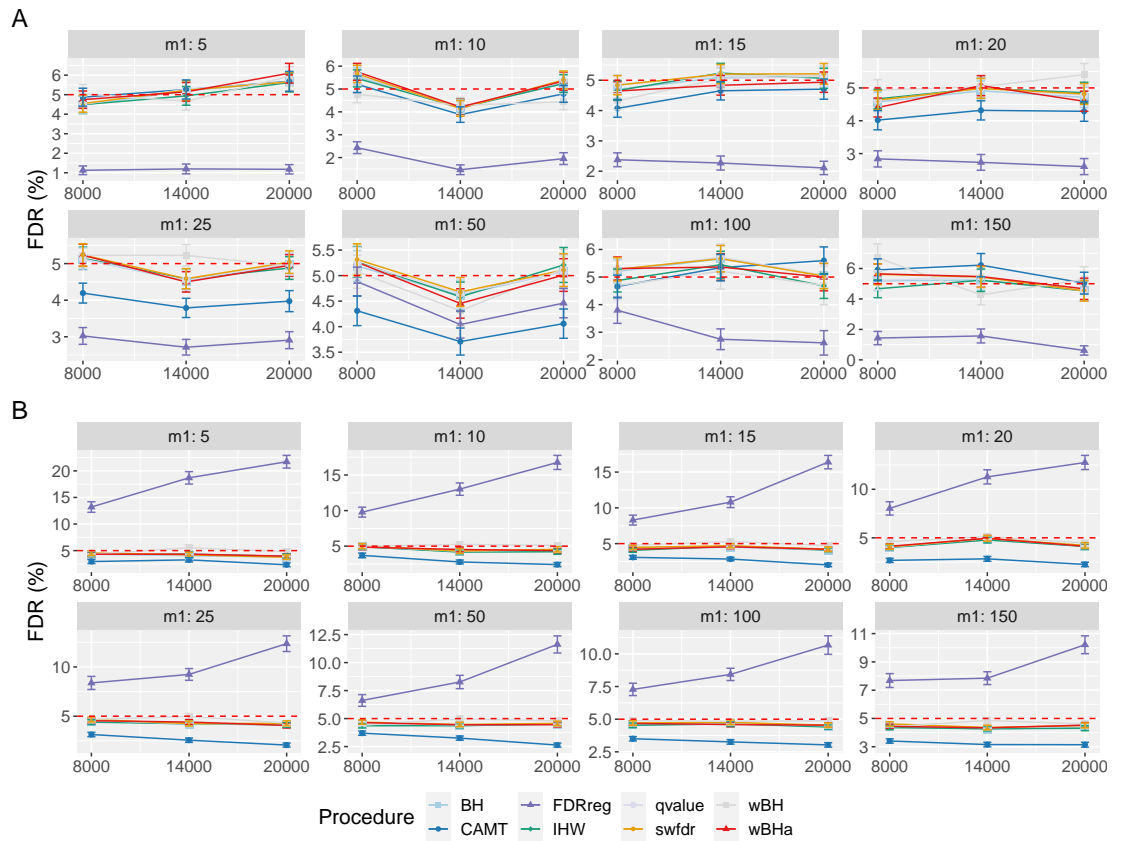


Figure S35. FDR comparison when using **uninformative** covariates in **scenario 2** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

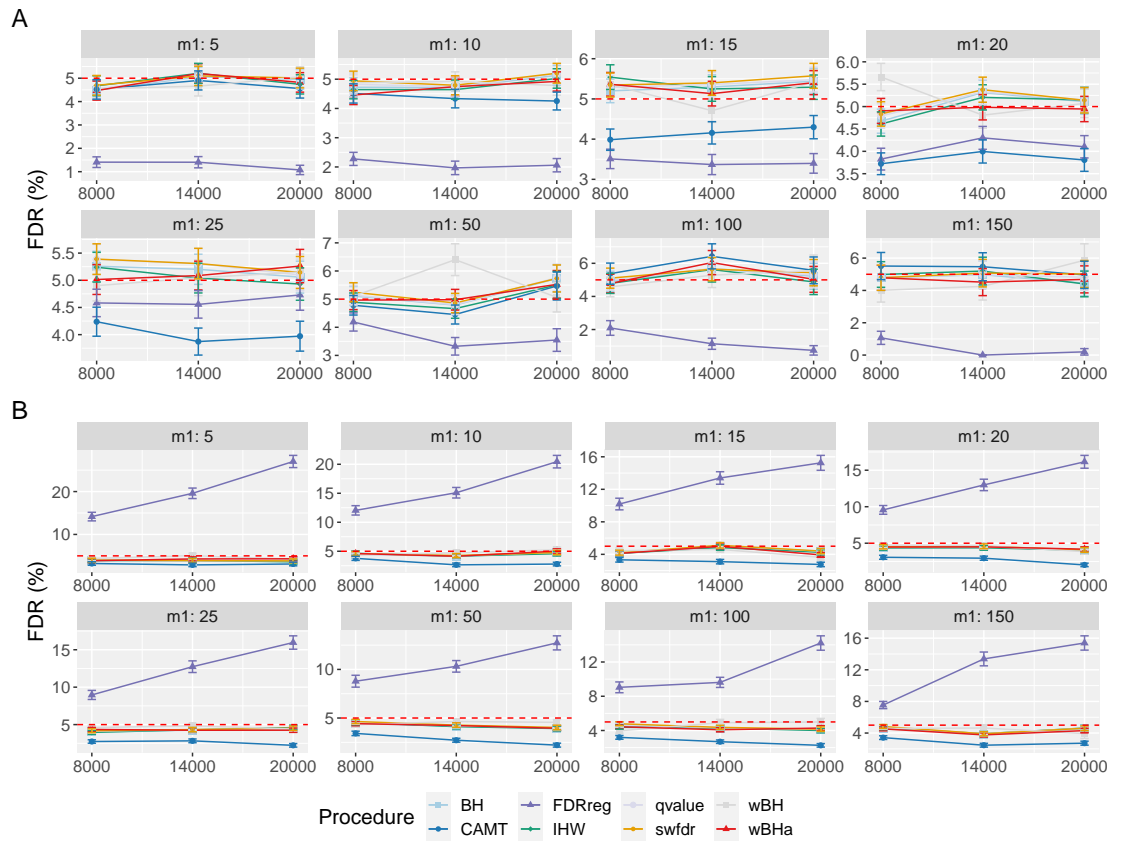


Figure S36. FDR comparison when using **uninformative** covariates in **scenario 3** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively. Vertical bars illustrate standard errors.

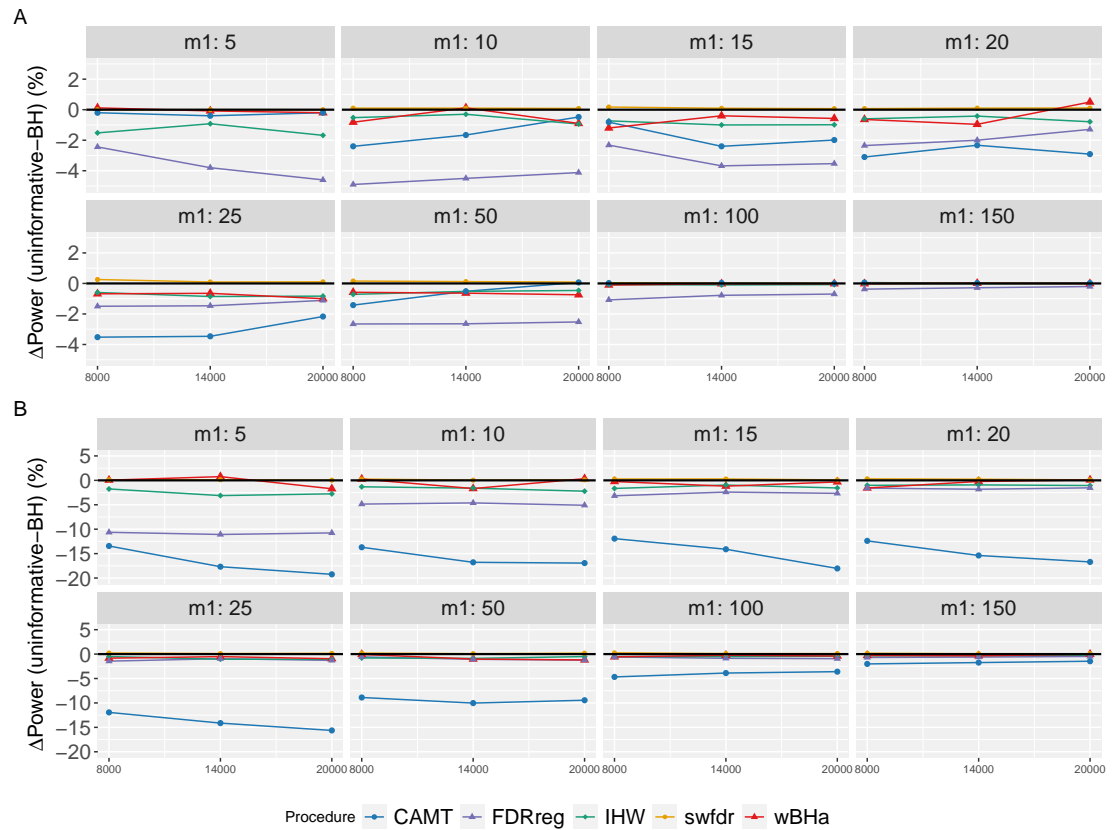


Figure S37. Overall power difference between uninformative covariates and BH procedure in **scenario 1** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively.

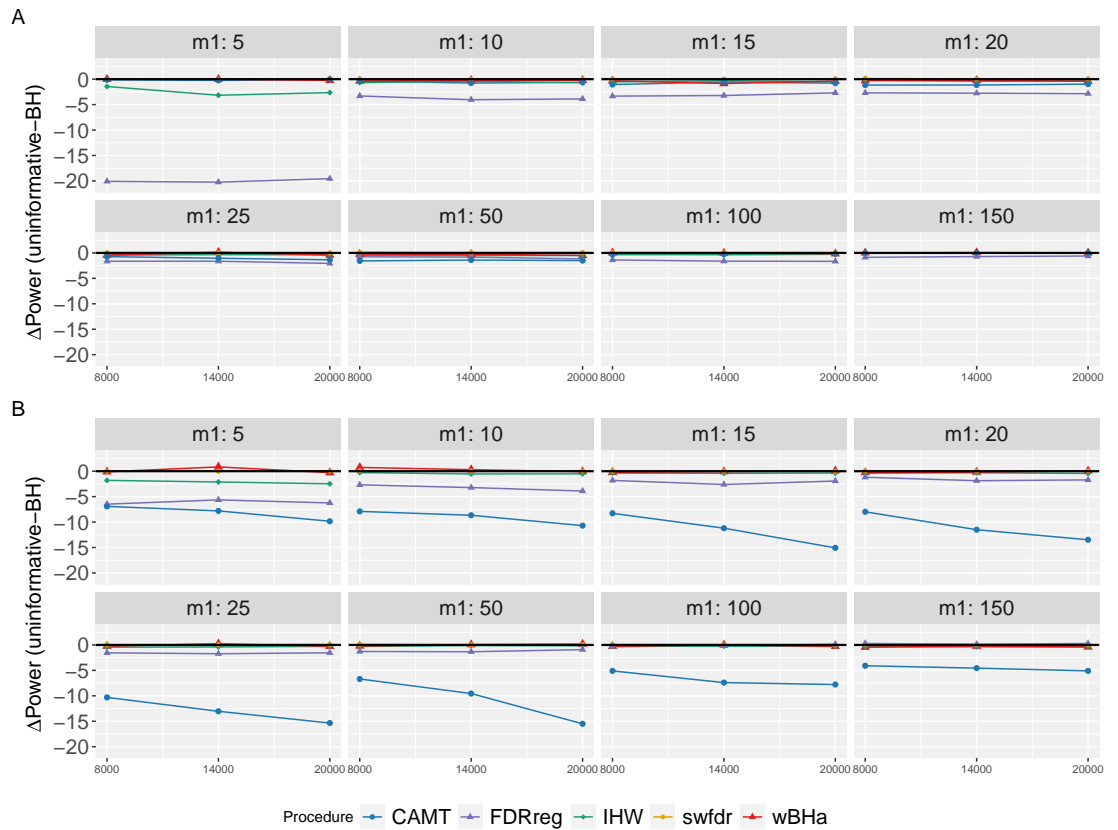


Figure S38. Overall power difference between uninformative covariates and BH procedure in **scenario 2** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively.

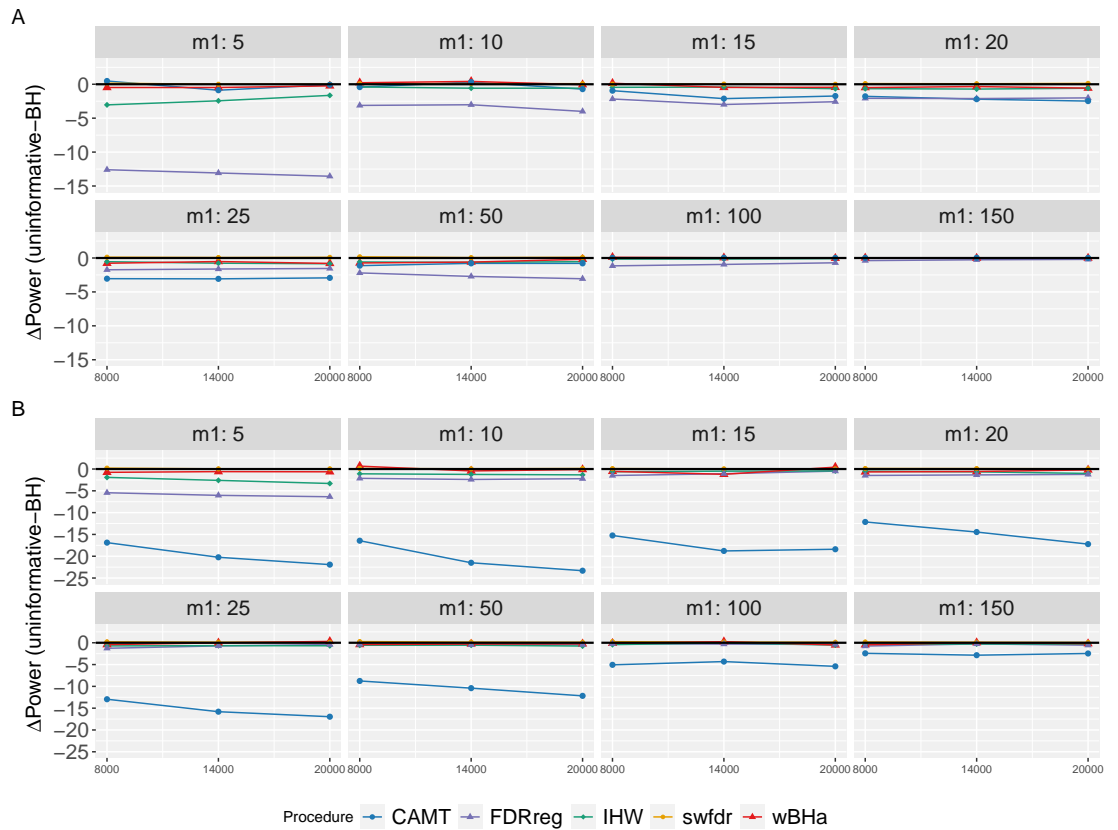


Figure S39. Overall power difference between uninformative covariates and BH procedure in **scenario 3** with independent markers for different m and m_1 values. Panels A and B display results for quantitative and binary traits, respectively.

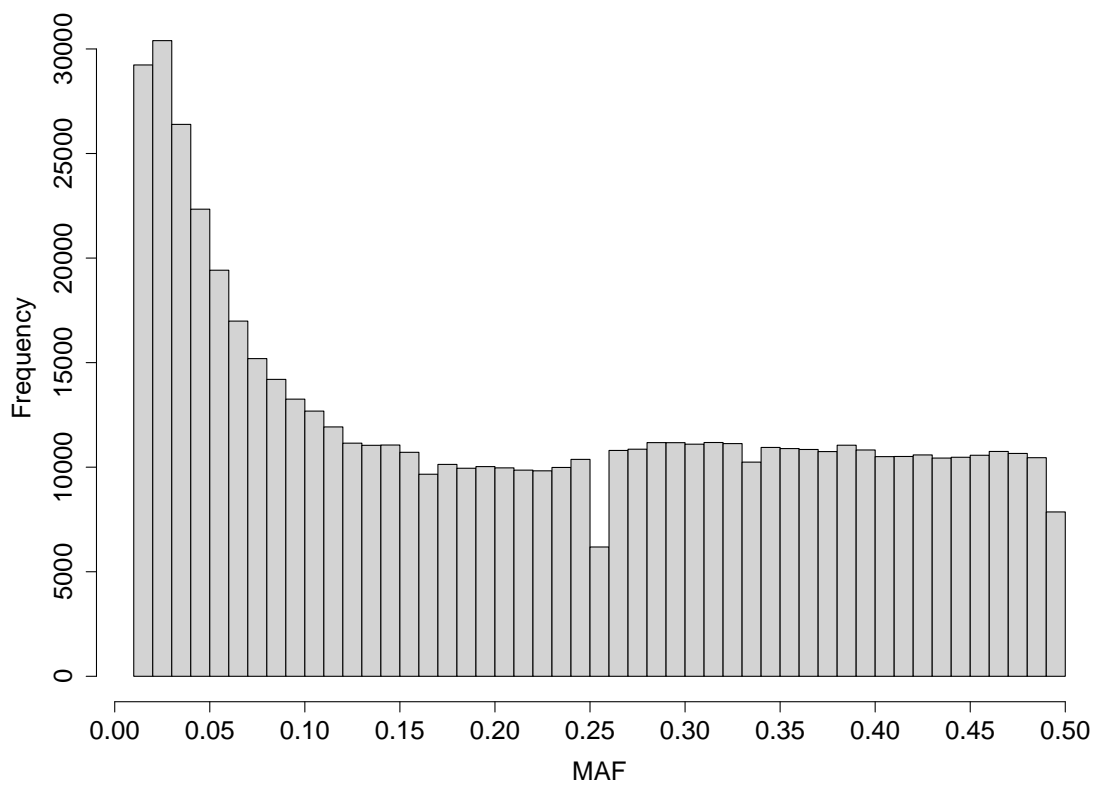


Figure S40. MAF distribution of all SNPs for the Crohn's disease dataset.