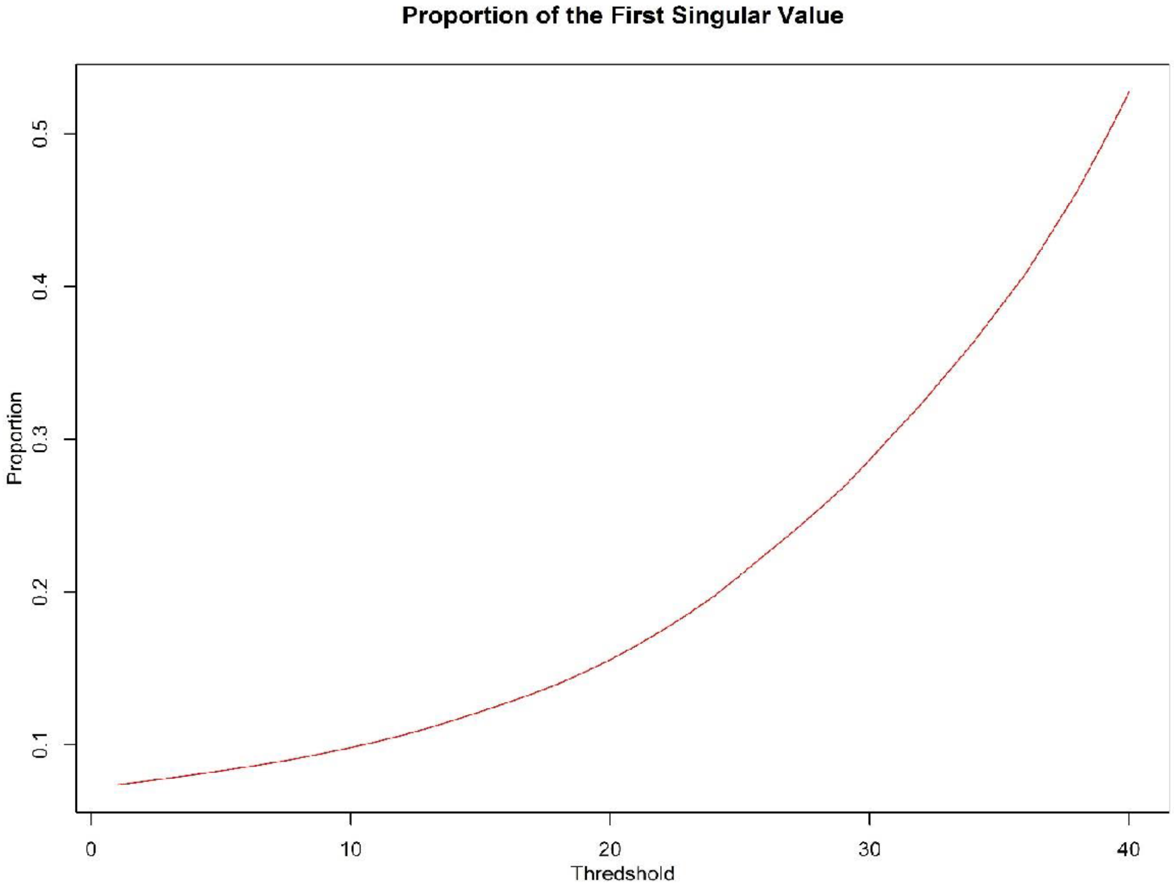


Fig S1. Proportion of the first singular value over the total singular values.

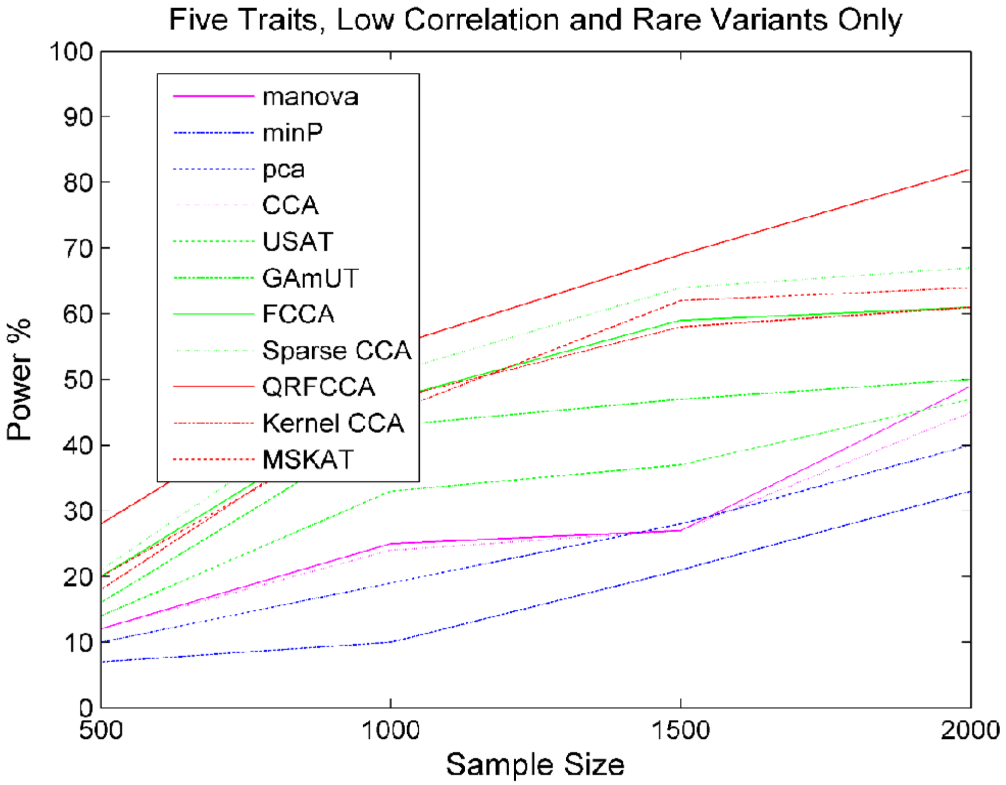


Fig S2. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 5 traits with low correlations for scenario 1 at the significance level $\alpha = 0.05$.

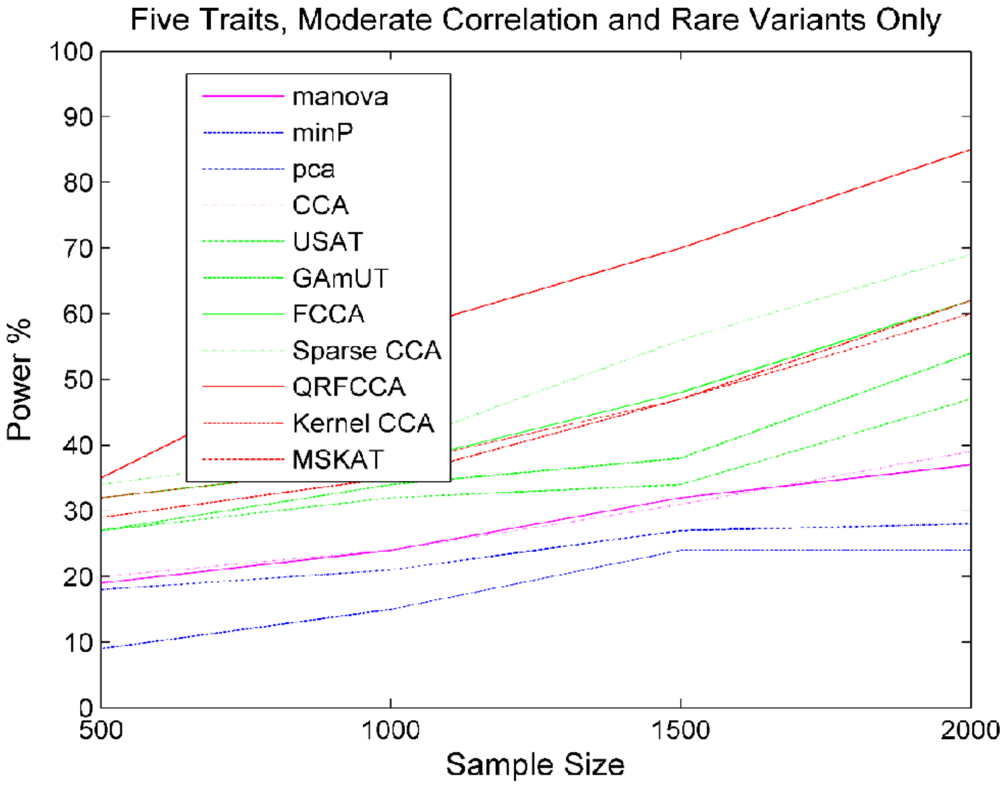


Fig S3. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 5 traits with moderate correlations for scenario 1at the significance level $\alpha = 0.05$.

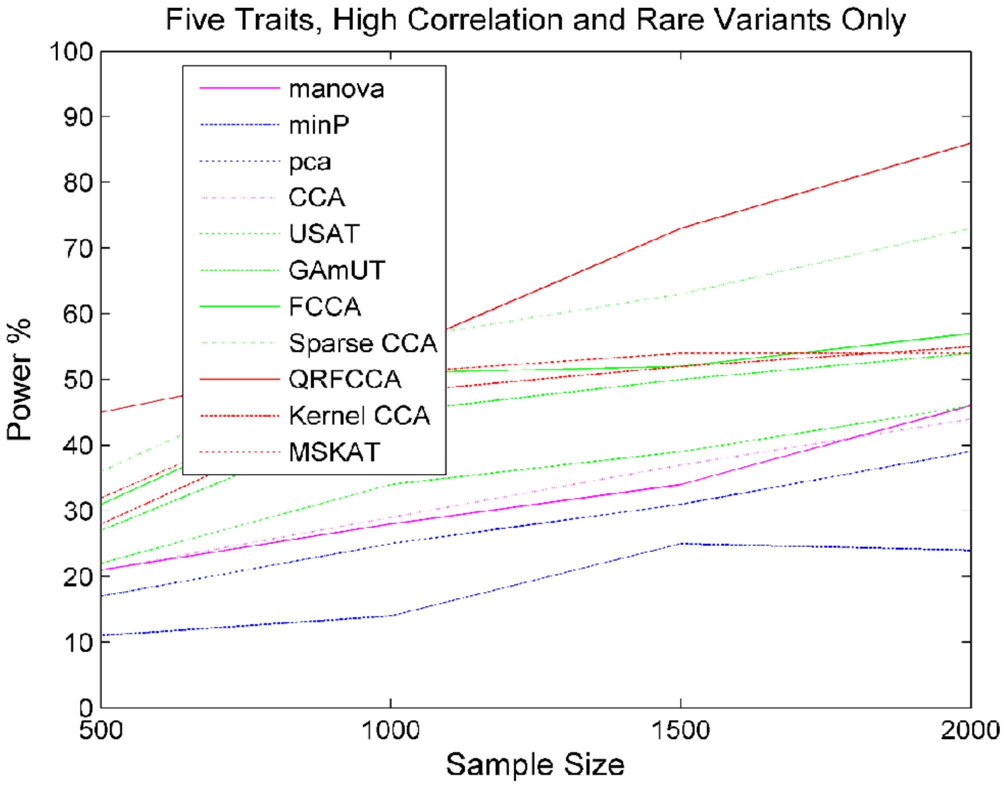


Fig S4. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 5 traits with high correlations for scenario 1 at the significance level $\alpha = 0.05$.

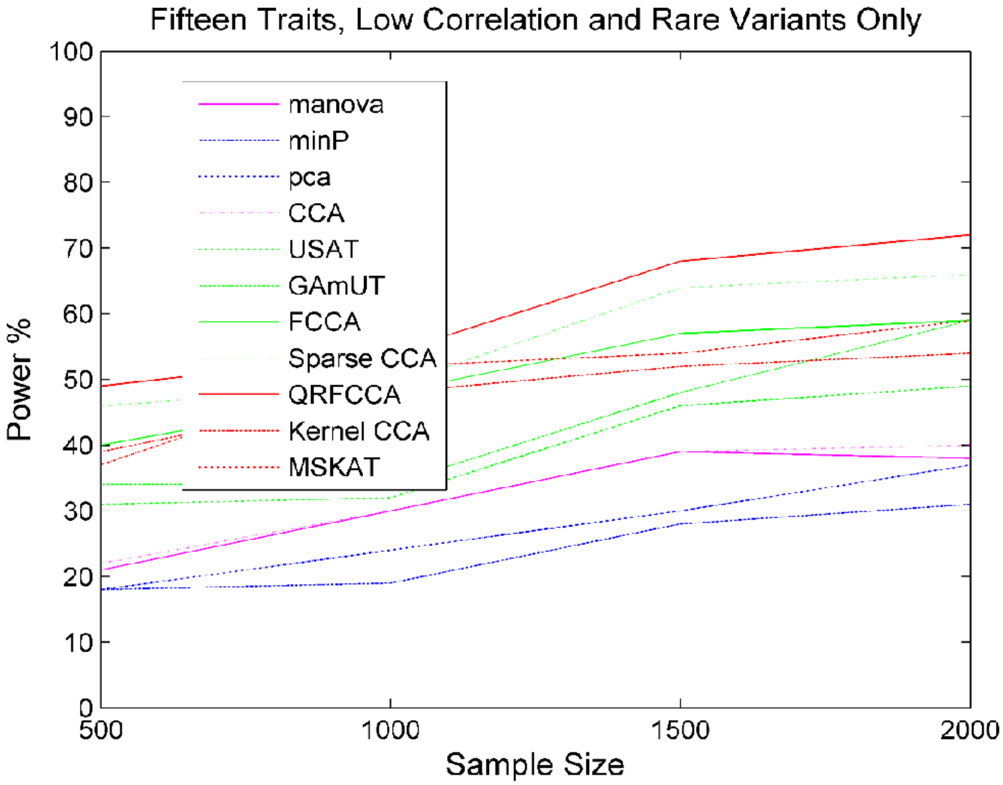


Fig S5. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 15 traits with low correlations for scenario 1 at the significance level $\alpha = 0.05$.

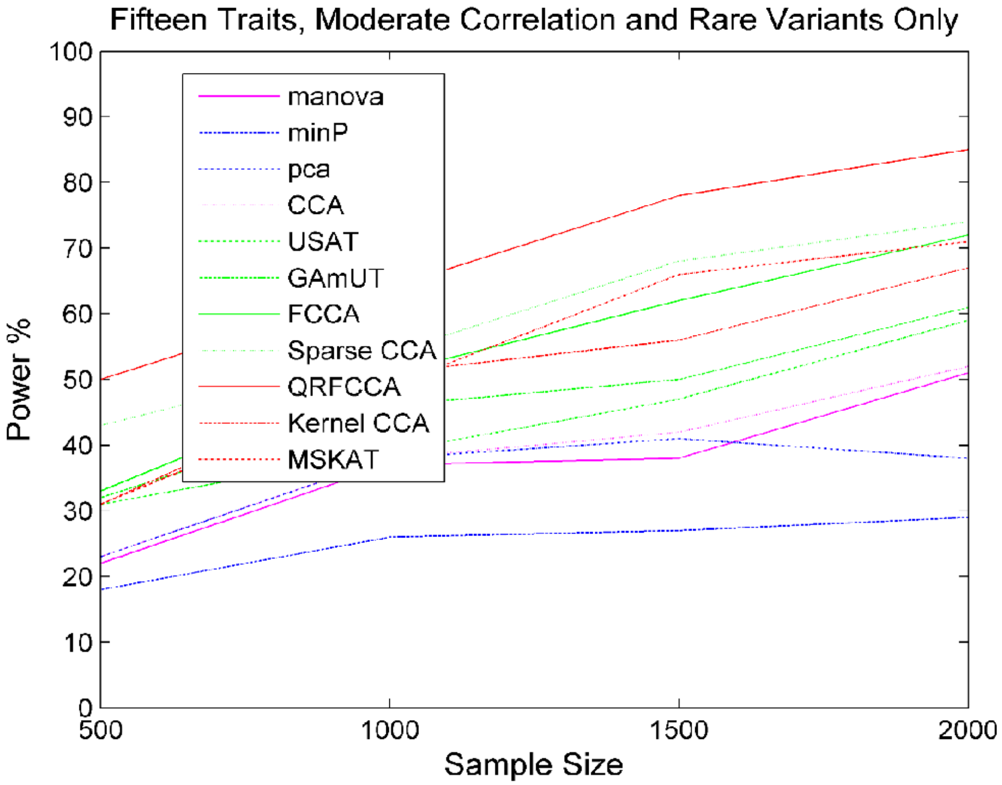


Fig S6. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 15 traits with moderate correlations for scenario 1 at the significance level $\alpha = 0.05$.

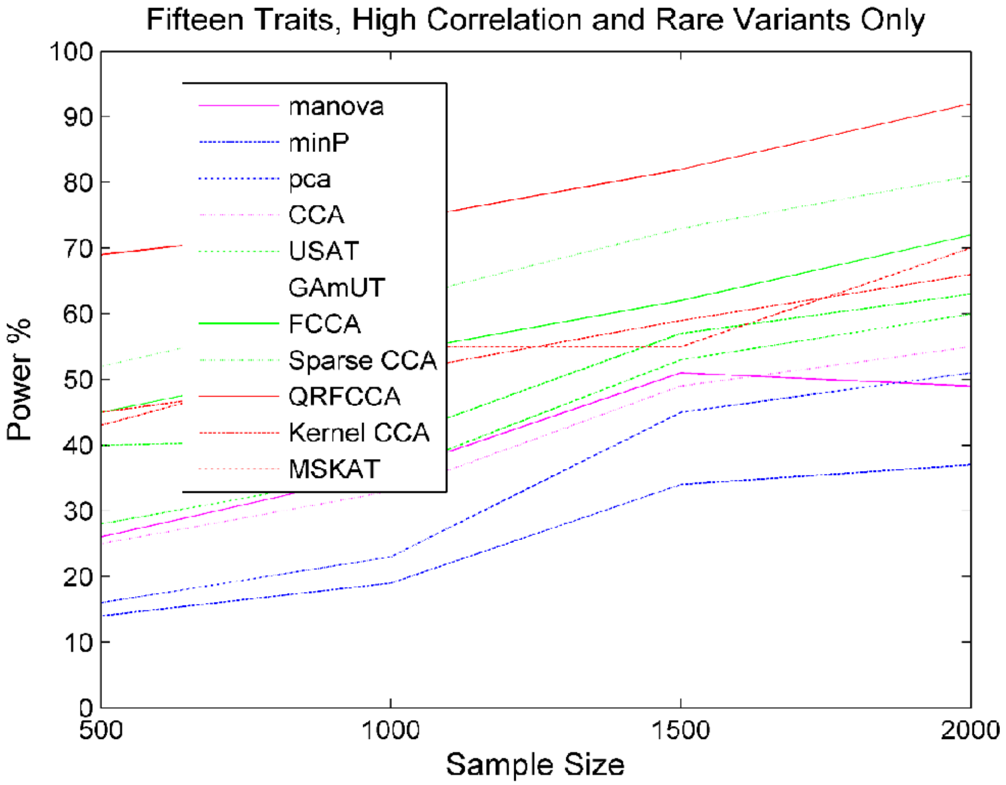


Fig S7. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 15 traits with high correlations for the scenario 1 at the significance level $\alpha = 0.05$.

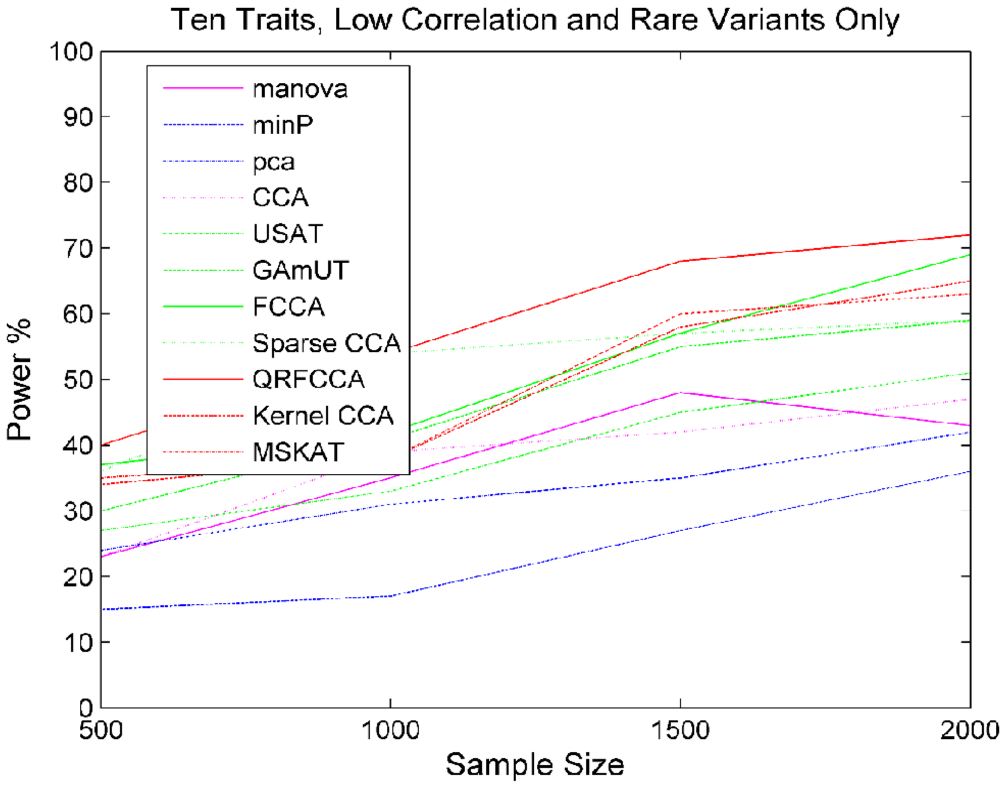


Fig S8. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 10 traits with low correlations for the scenario 2 at the significance level $\alpha = 0.05$.

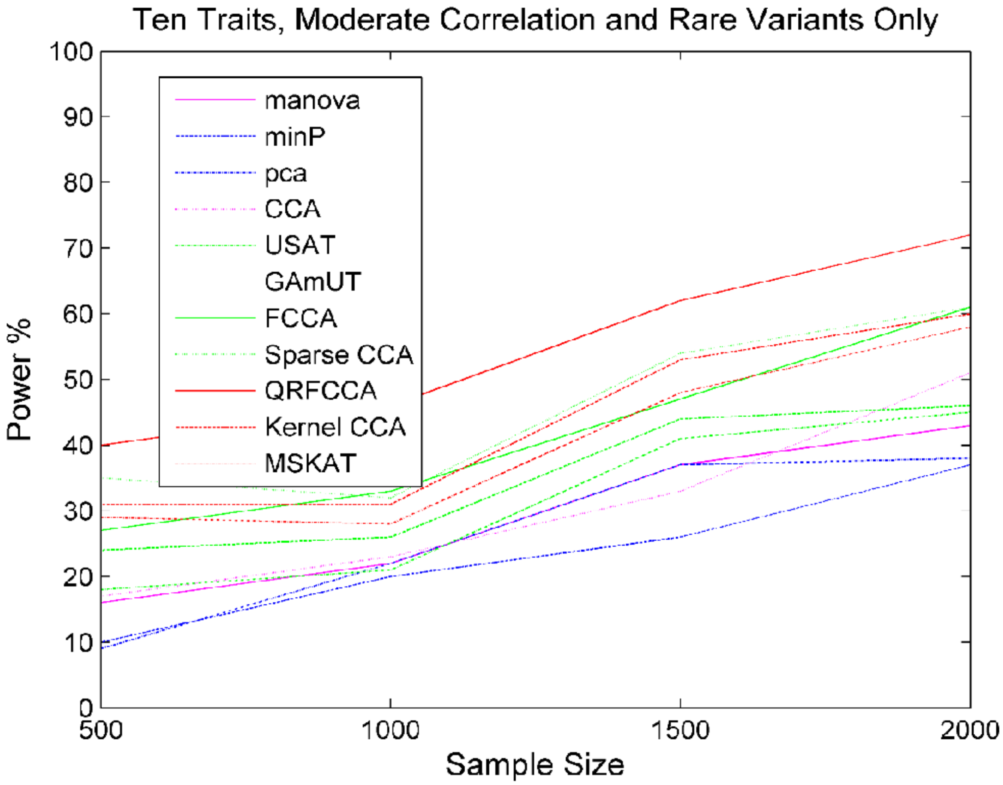


Fig S9. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 15 traits with moderate correlations for the scenario 2 at the significance level $\alpha = 0.05$.

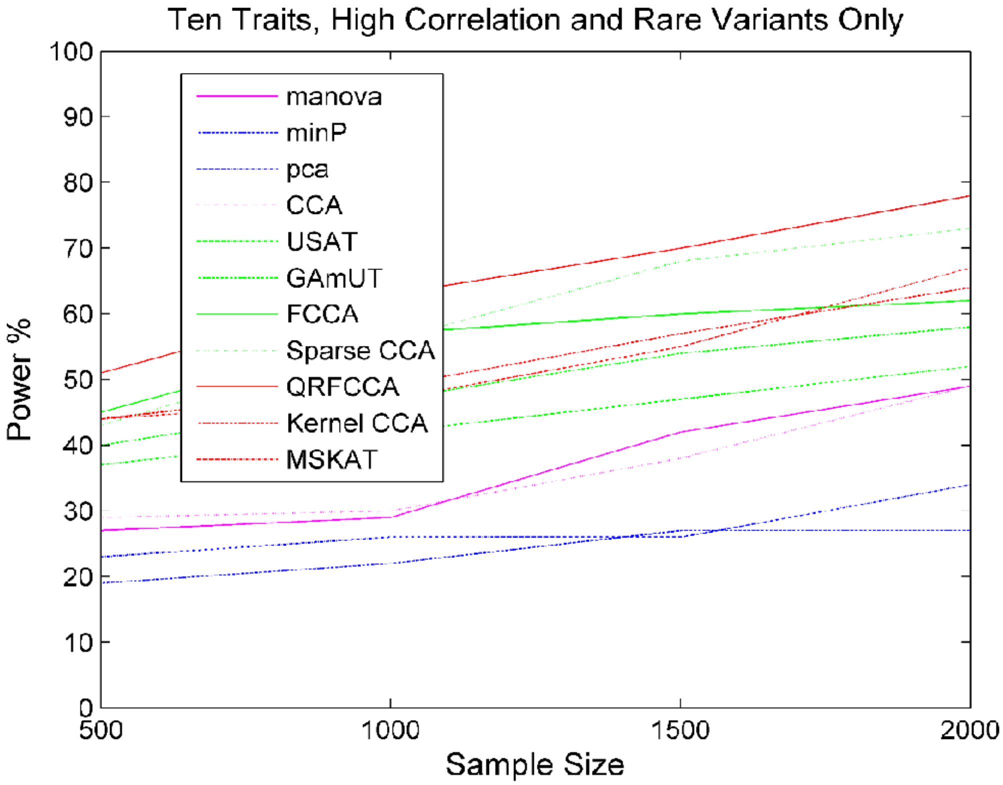


Fig S10. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 15 traits with high correlations for the scenario 2 at the significance level $\alpha = 0.05$.

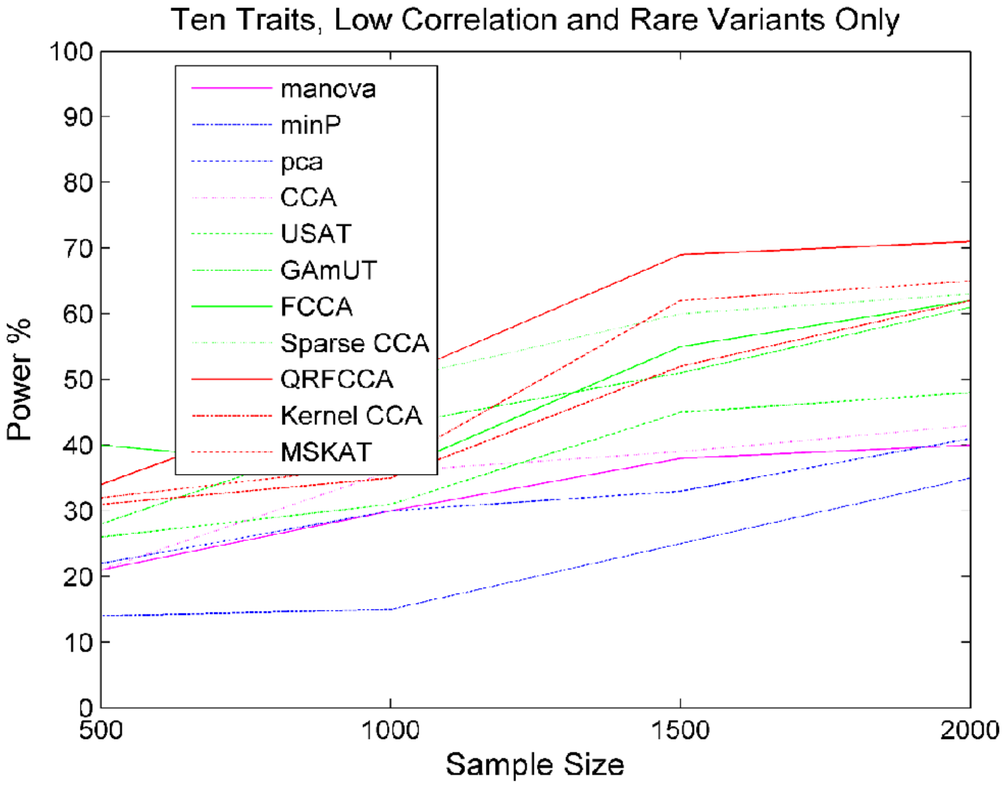


Fig S11. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 10 traits with low correlations for the scenario 3 at the significance level $\alpha = 0.05$.

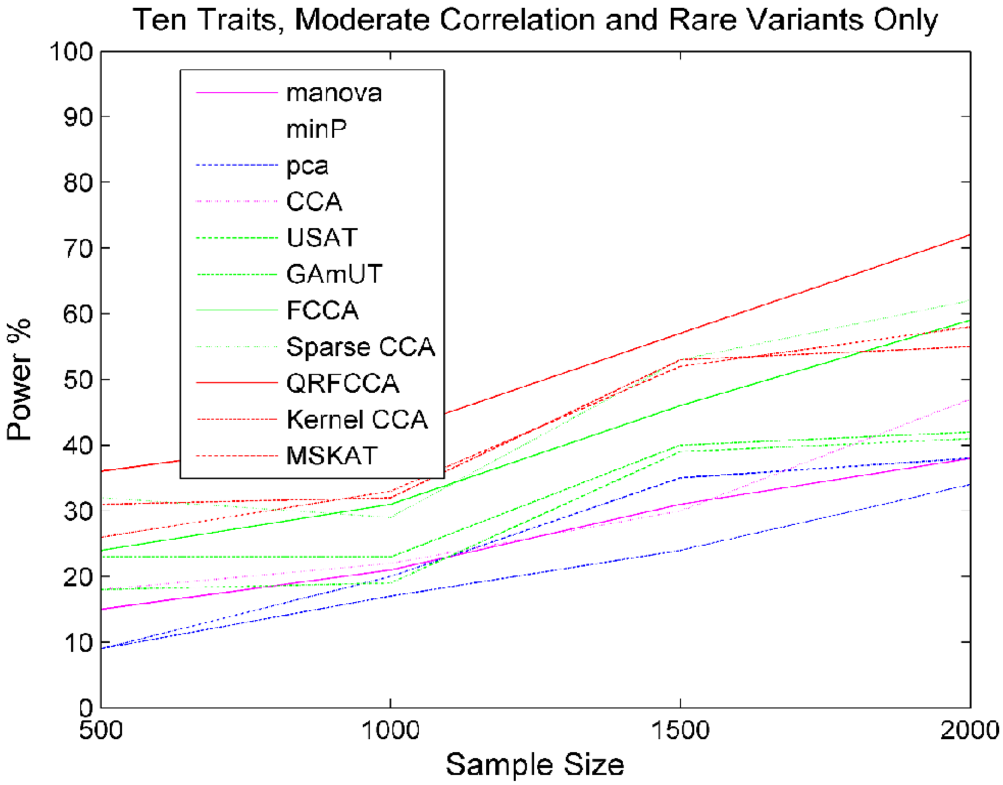


Fig S12. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 10 traits with moderate correlations for the scenario 3 at the significance level $\alpha = 0.05$.

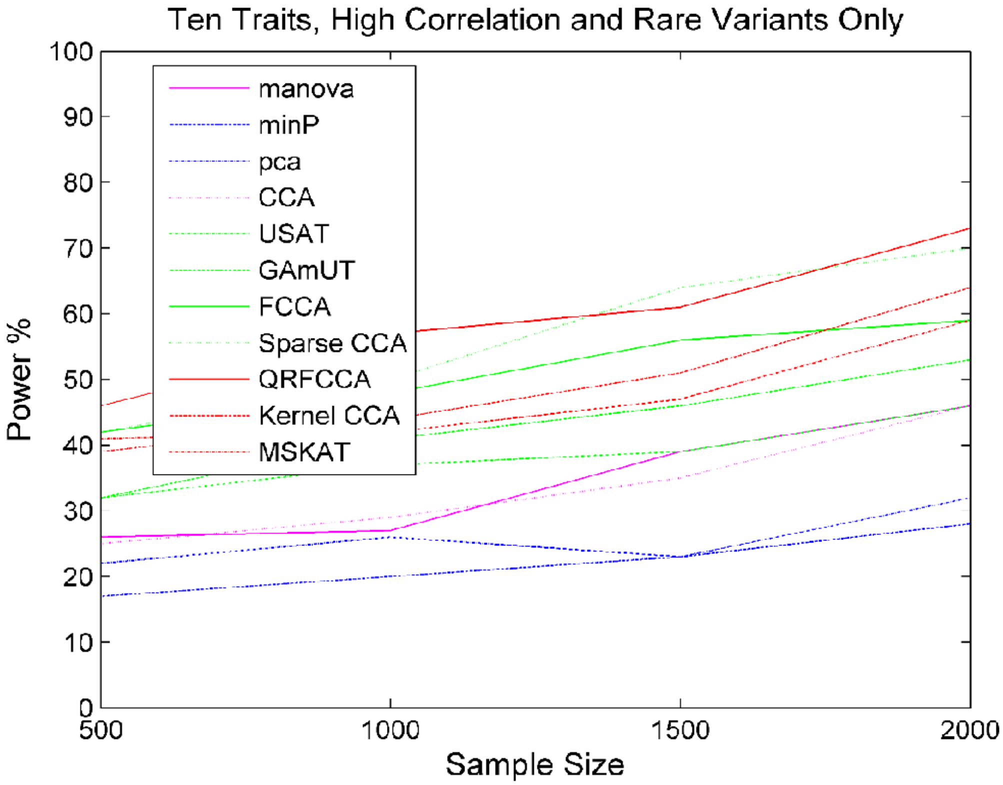


Fig S13. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of all rare variants in the gene with 10 traits with high correlations for the scenario 3 at the significance level $\alpha = 0.05$.

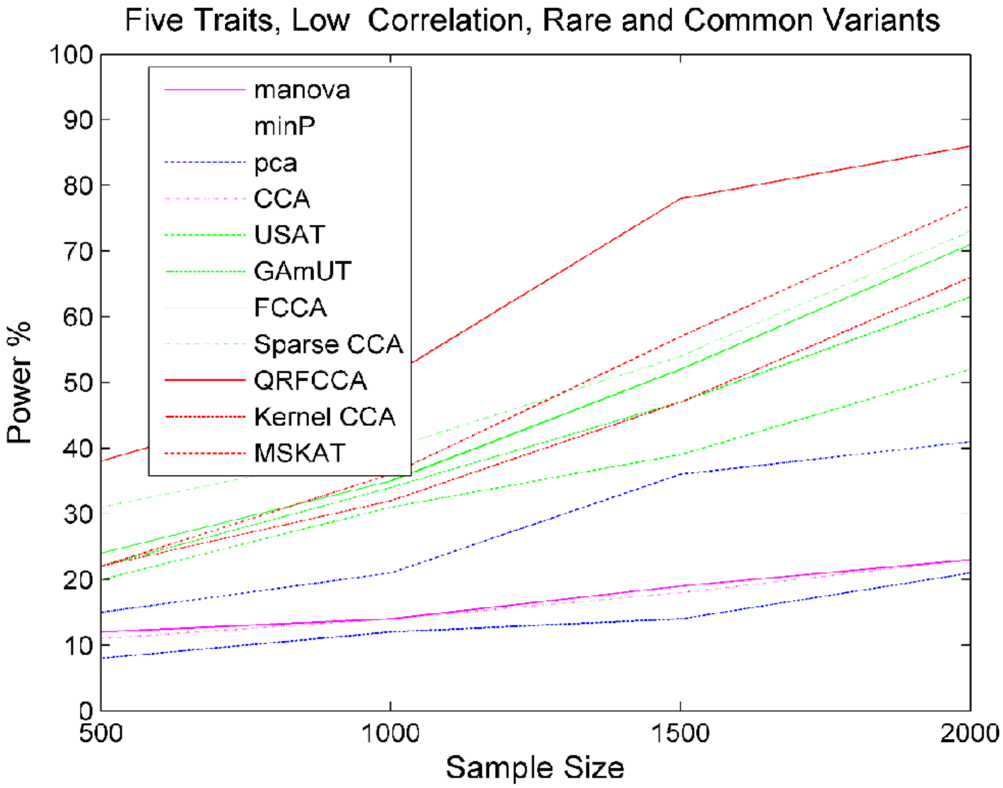


Fig S14. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 5 traits with low correlations for the scenario 1at the significance level $\alpha = 0.05$.

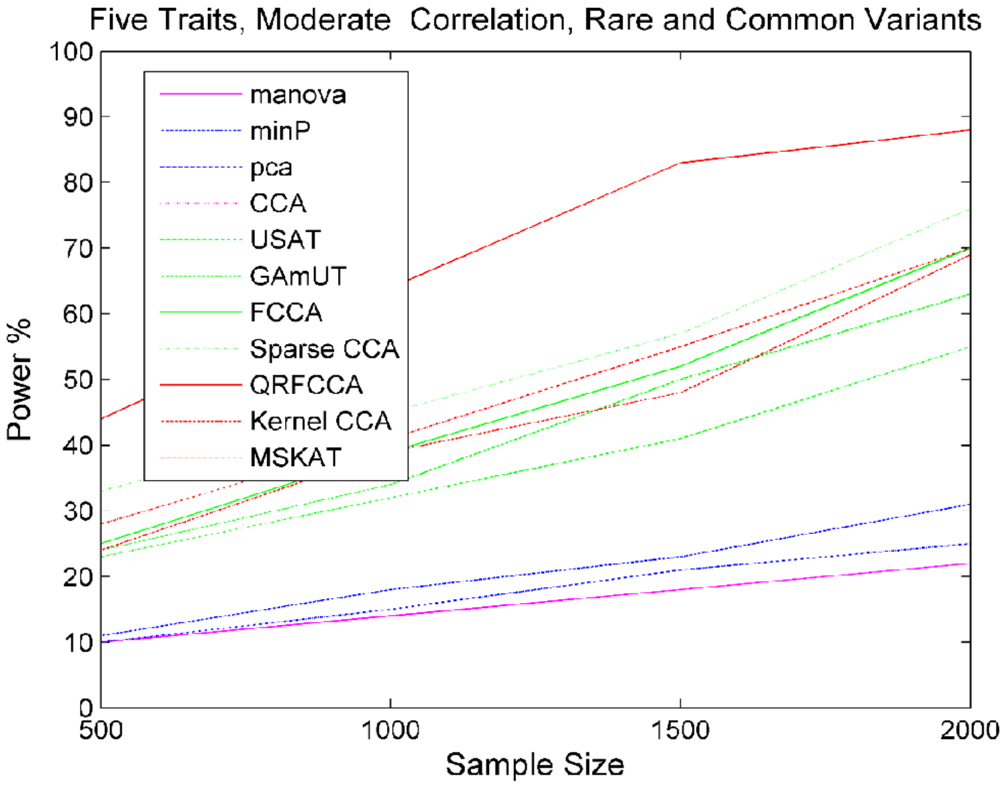


Fig S15. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 5 traits with moderate correlations for the scenario 1 at the significance level $\alpha = 0.05$.

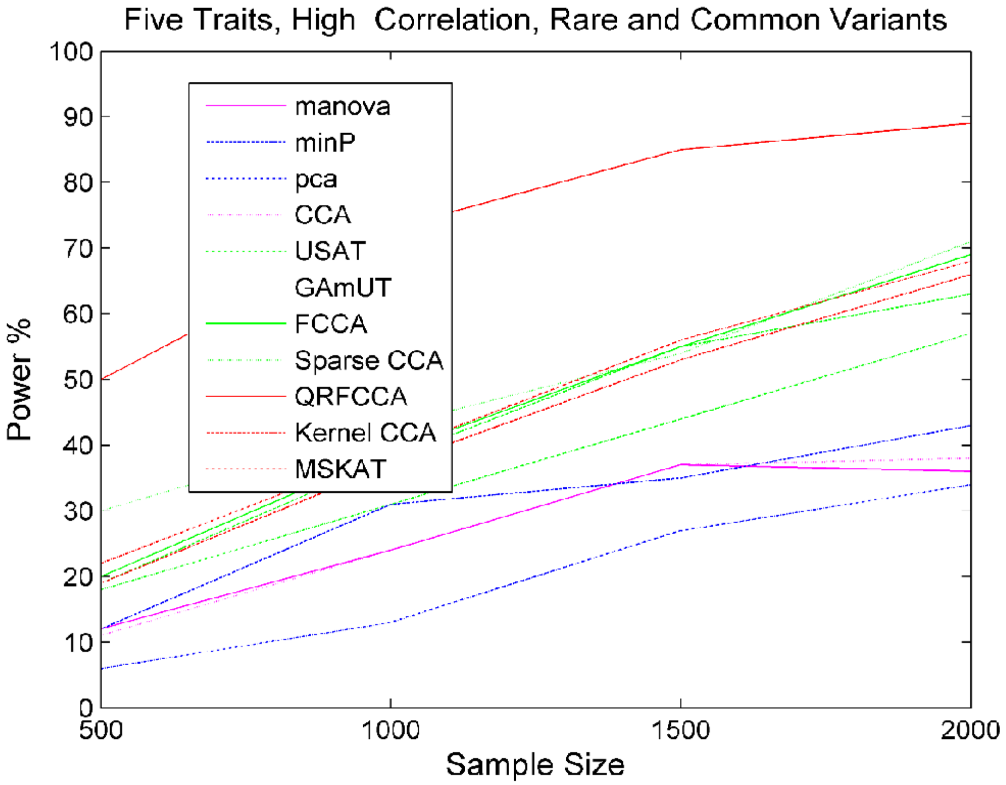


Fig S16. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 5 traits with high correlations for the scenario 1 at the significance level $\alpha = 0.05$.

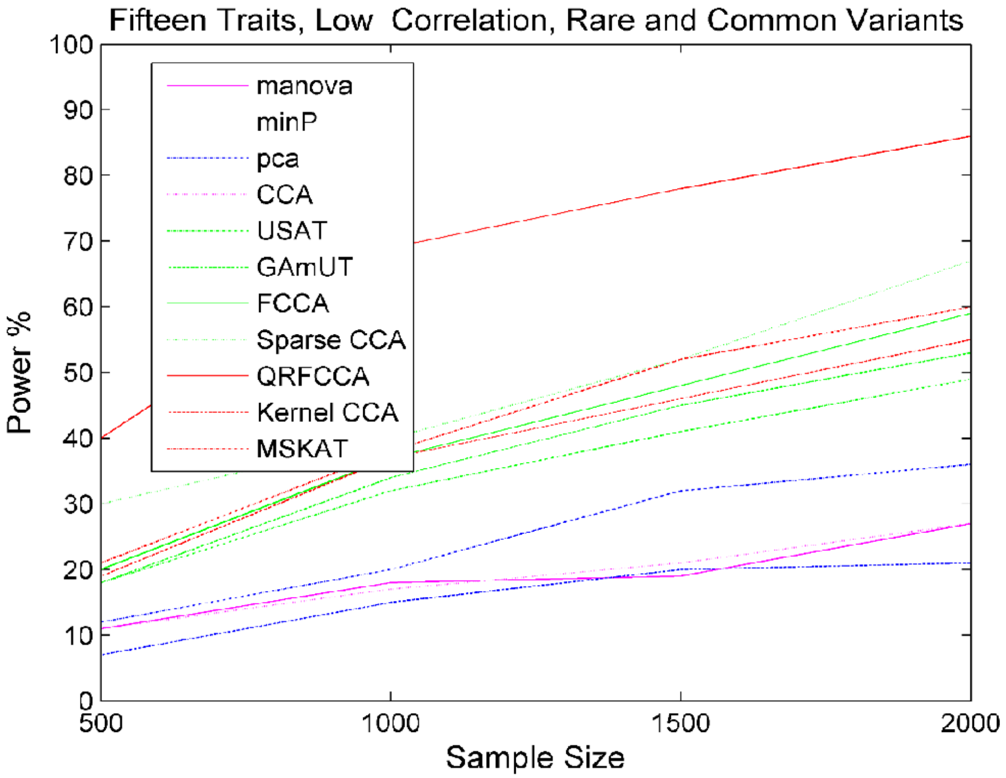


Fig S17. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 traits with low correlations for the scenario 1 at the significance level $\alpha = 0.05$.

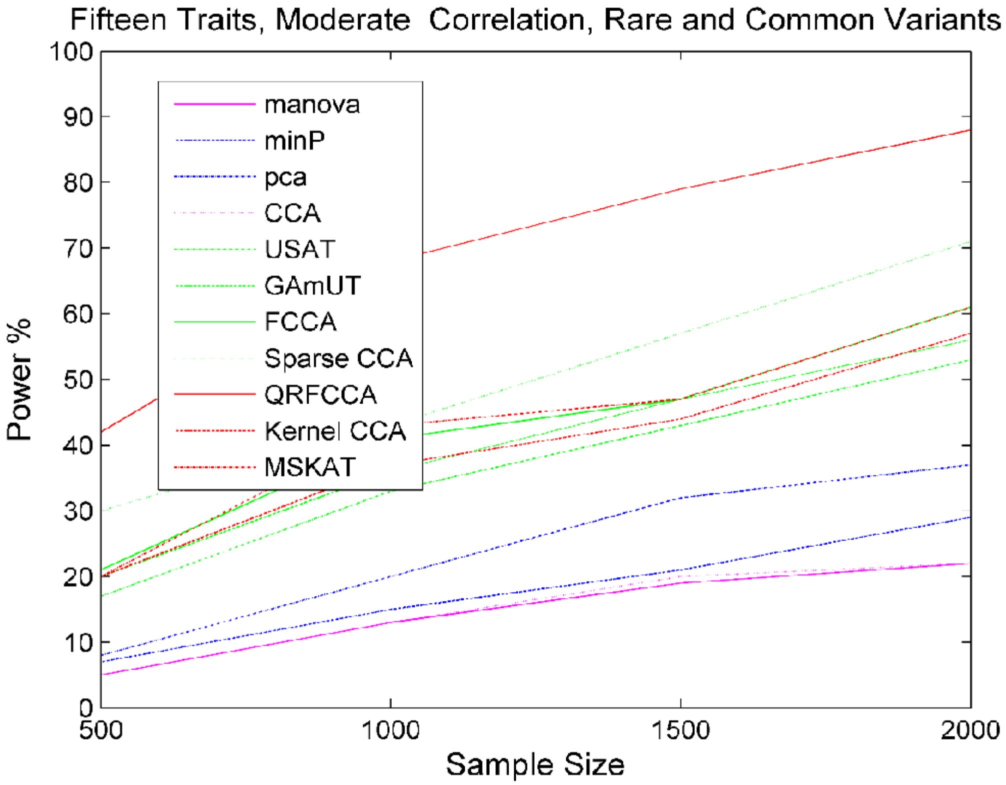


Fig S18. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 traits with moderate correlations for the scenario 1 at the significance level $\alpha = 0.05$.

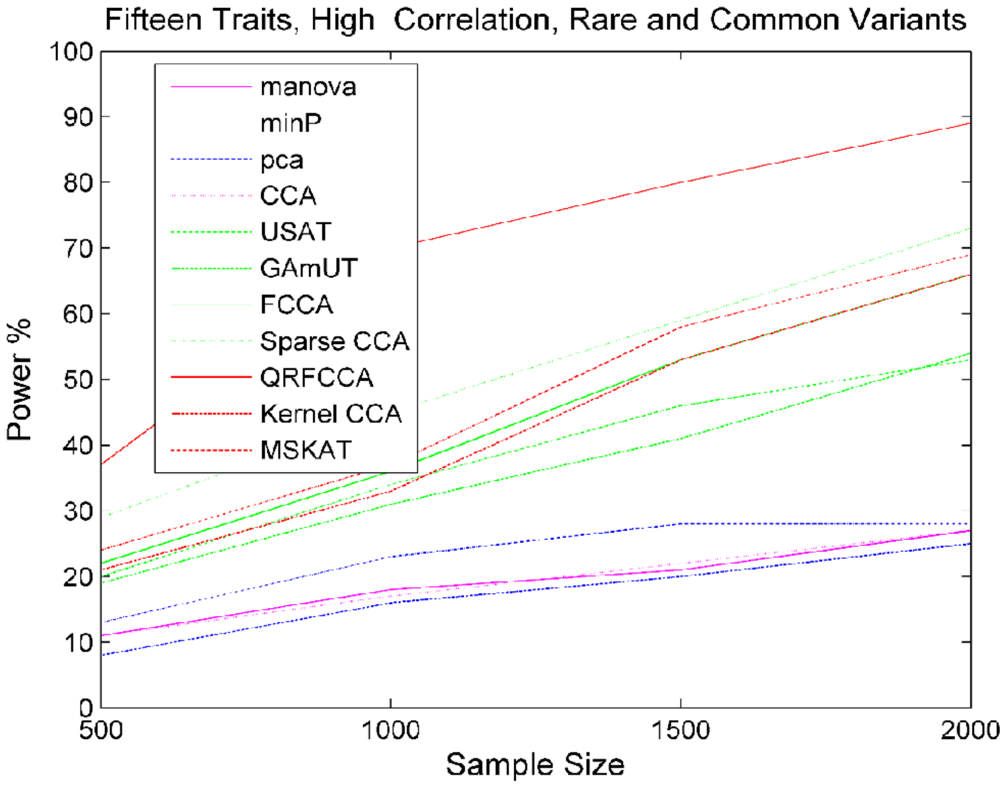


Fig S19. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 traits with high correlations for the scenario 1 at the significance level $\alpha = 0.05$.

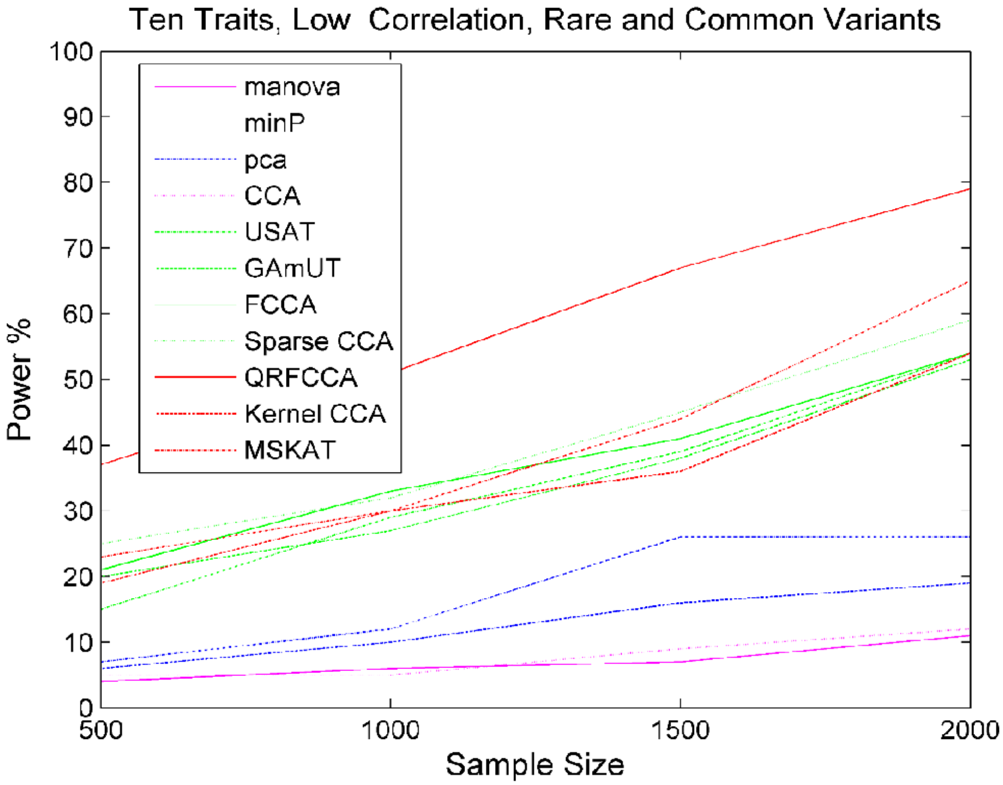


Fig S20. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with low correlations for the scenario 2 at the significance level $\alpha = 0.05$.

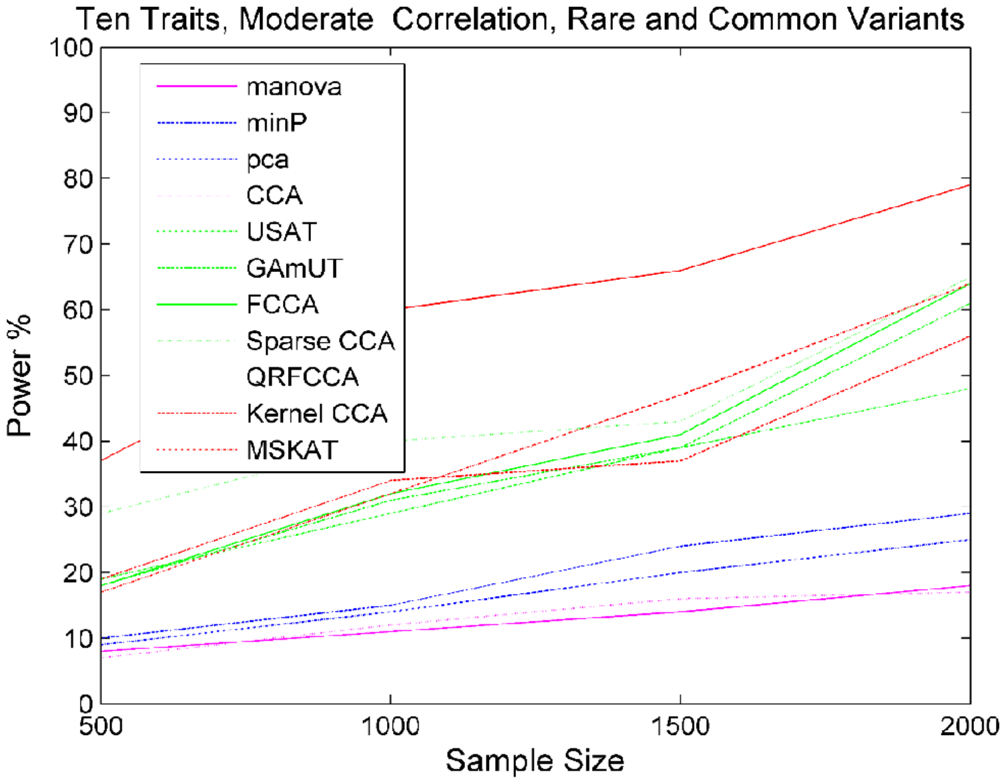


Fig S21. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with moderate correlations for the scenario 2 at the significance level $\alpha = 0.05$.

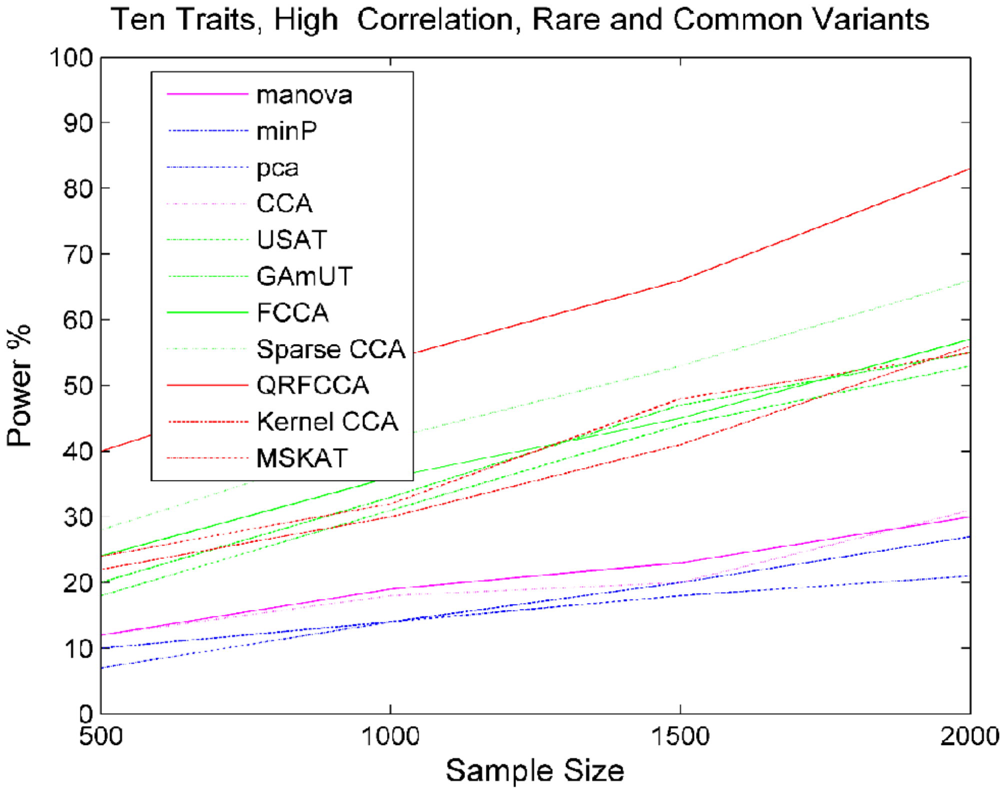


Fig S22. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with high correlations for the scenario 2 at the significance level $\alpha = 0.05$.

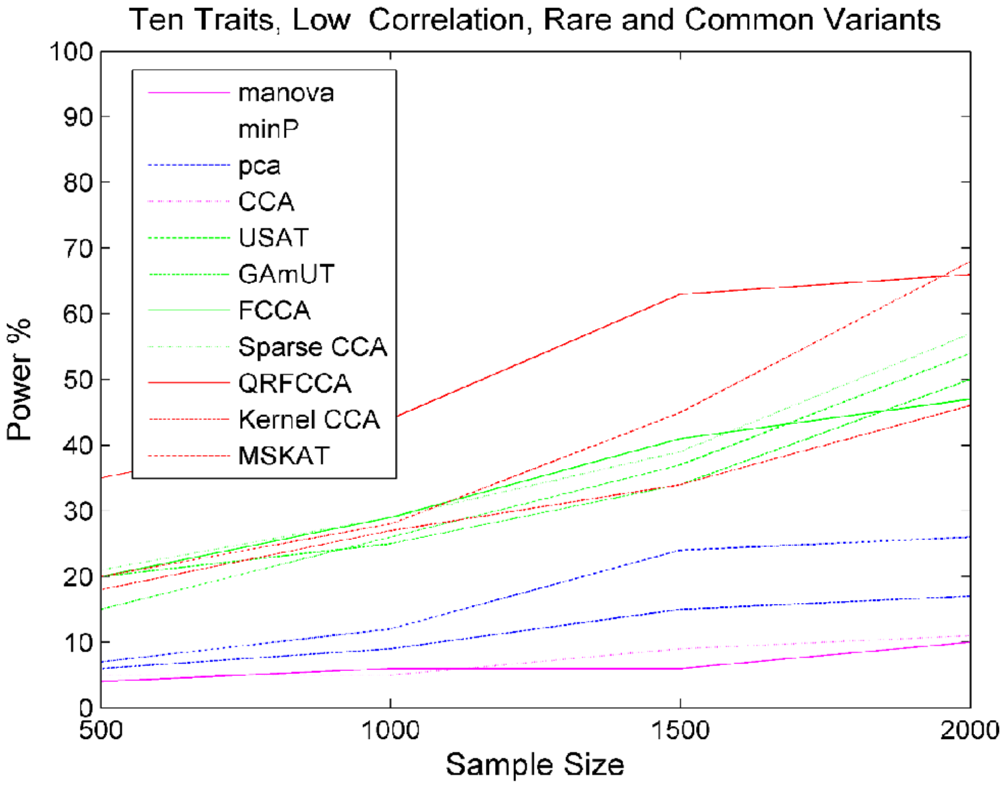


Fig S23. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with low correlations for the scenario 3 at the significance level $\alpha = 0.05$.

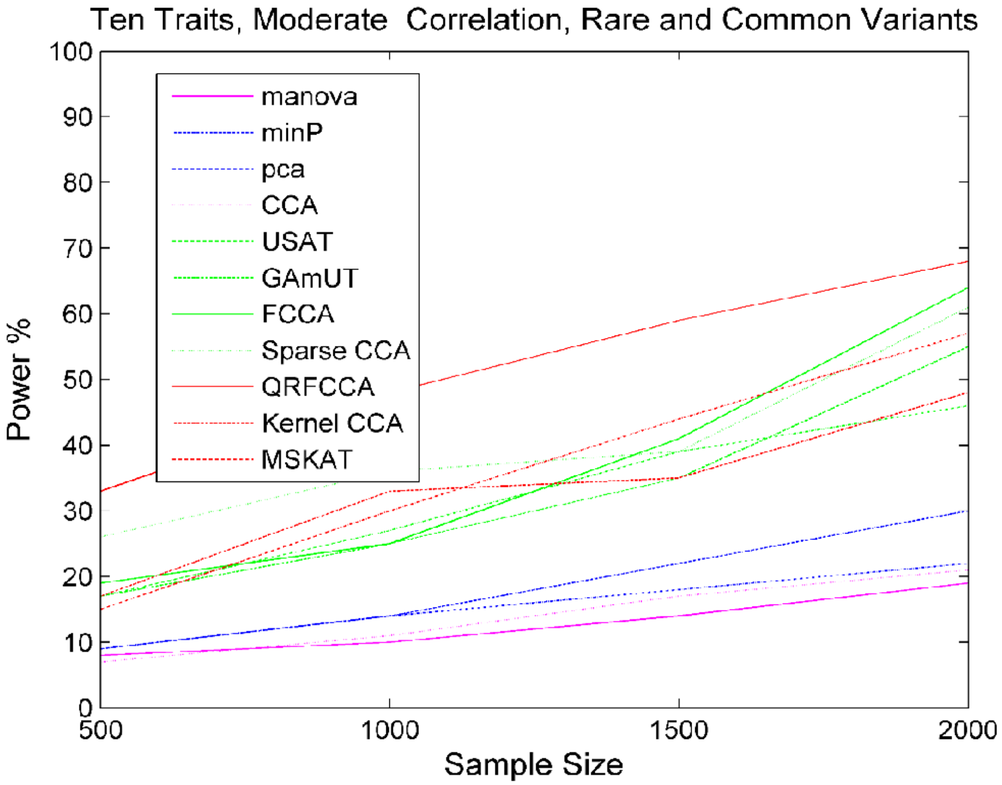


Fig S24. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with moderate correlations for the scenario 3 at the significance level $\alpha = 0.05$.

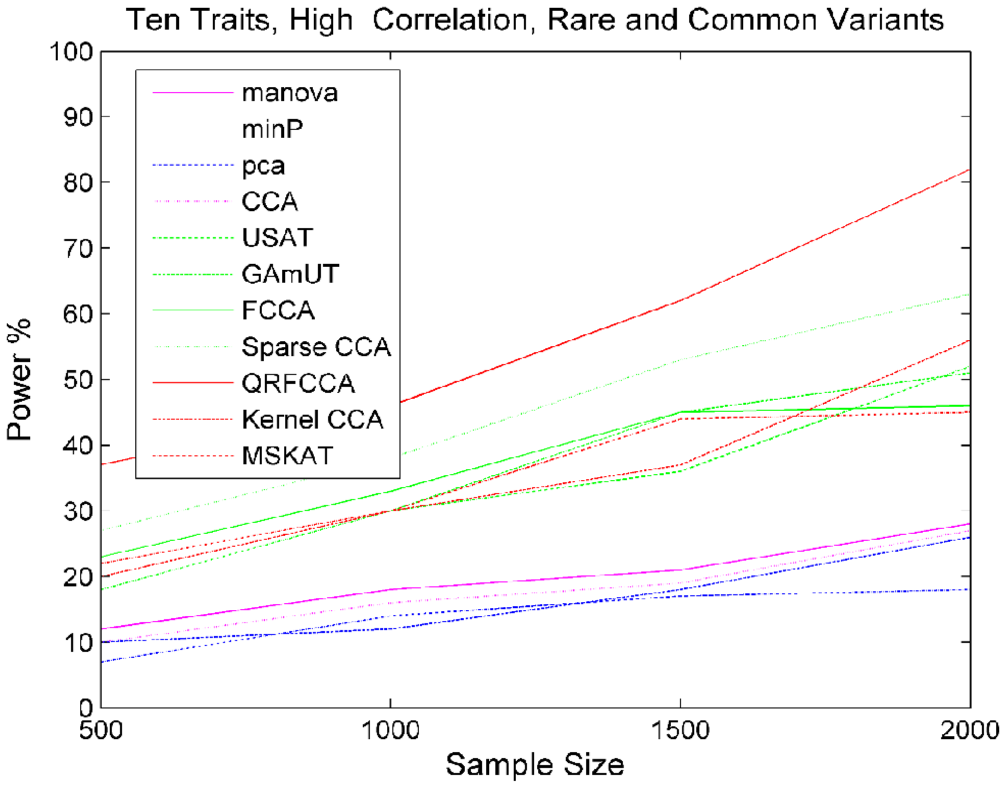


Fig S25. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 10 traits with high correlations for the scenario 3 at the significance level $\alpha = 0.05$.

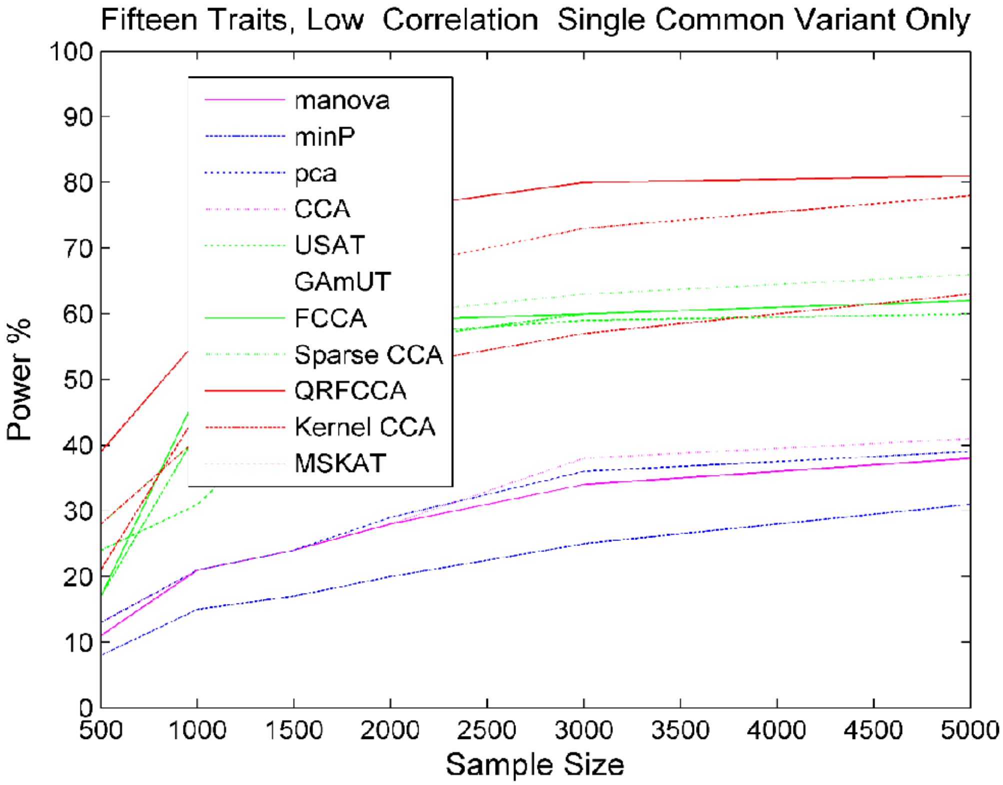


Fig S26. The power of curves as a function of sample sizes of 11 statistics for testing the power of a single common variant with 15 low correlated traits at the significance level $\alpha = 0.05$.

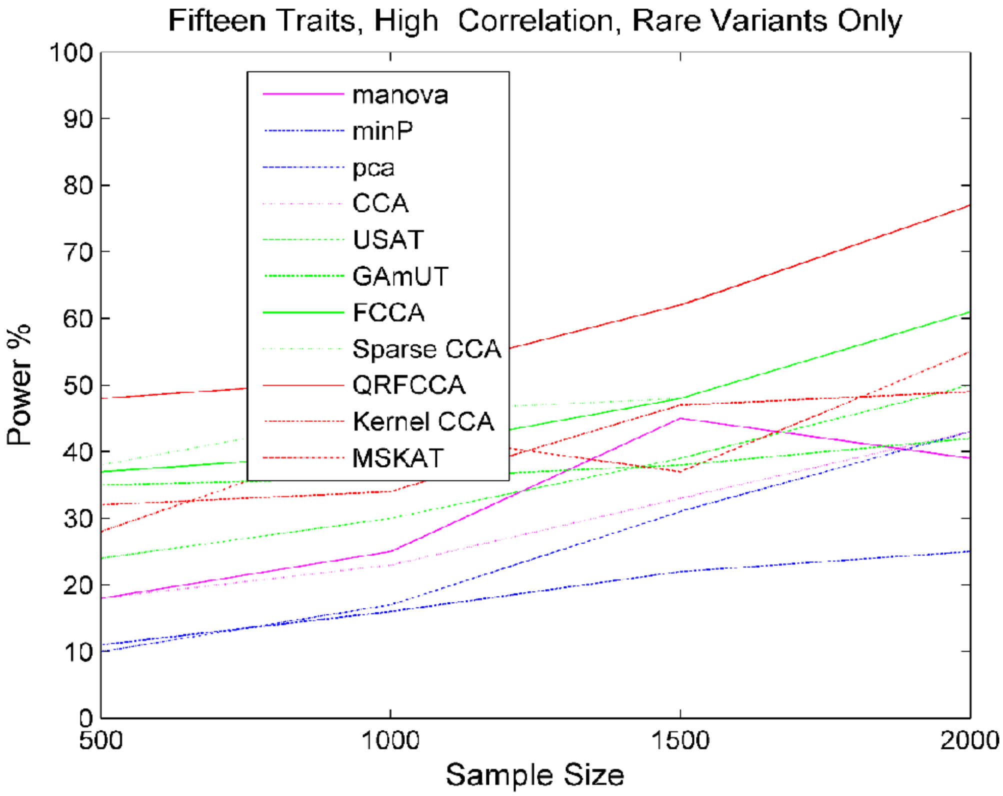


Fig S27. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including rare variants only with 15 highly correlated traits in scenario 1 at the significance level $\alpha = 0.00001$.

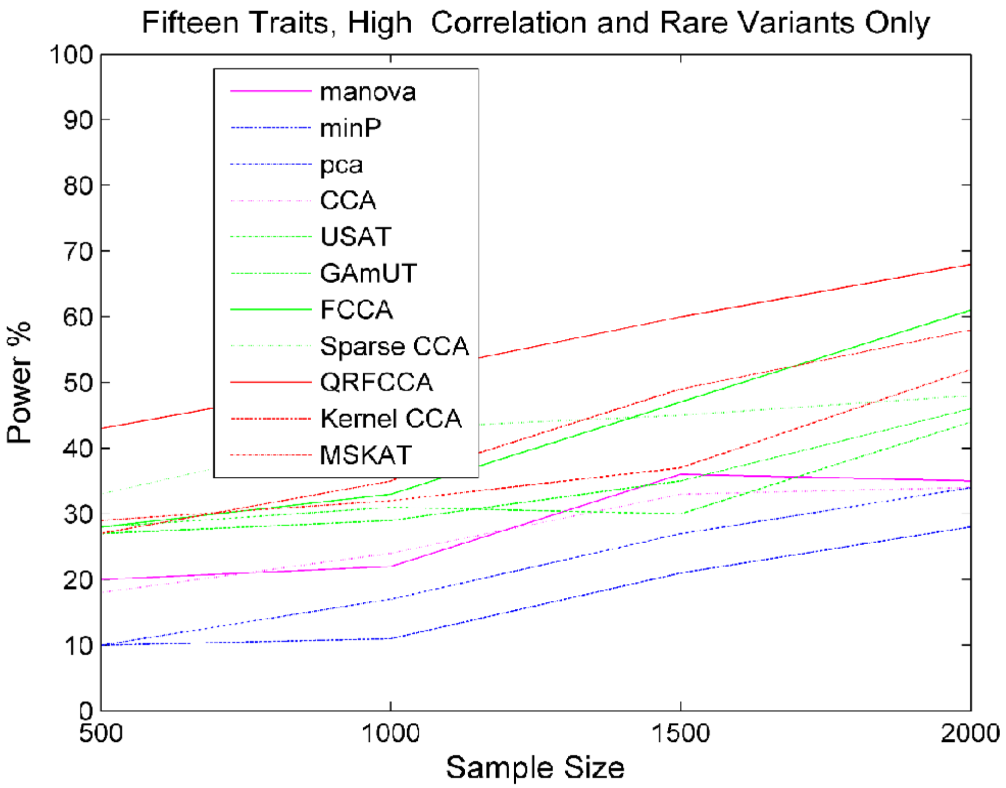


Fig S28. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including rare variants only with 15 highly correlated traits in scenario 2 at the significance level $\alpha = 0.00001$.

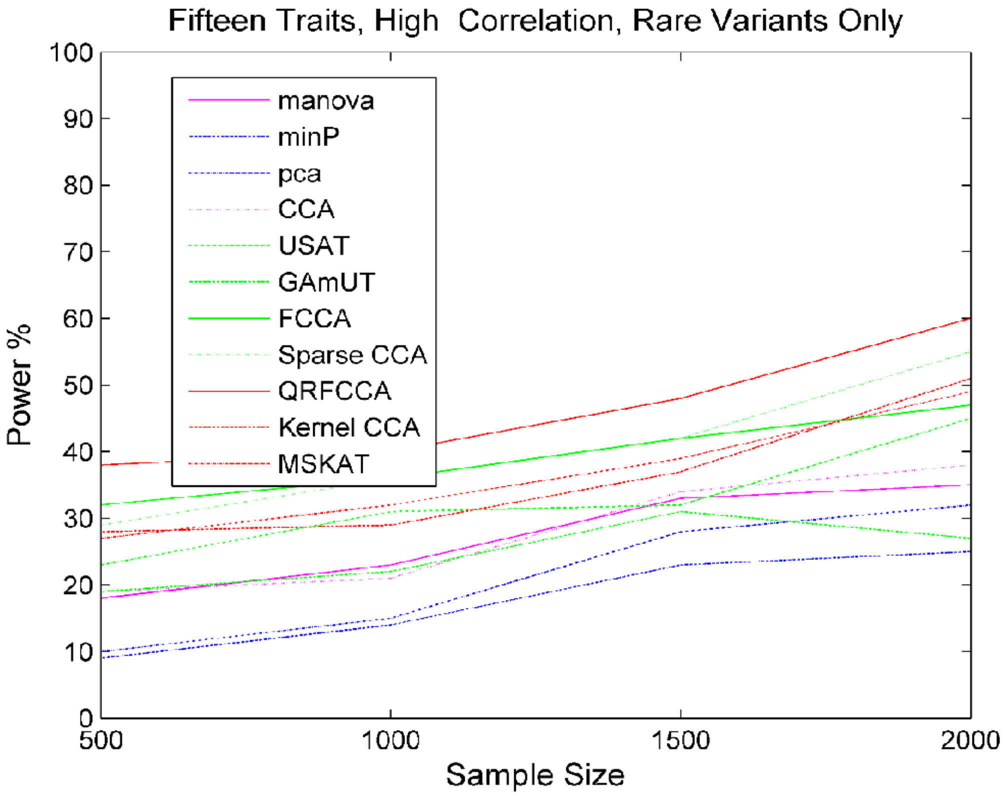


Fig S29. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including rare variants only with 15 highly correlated traits in scenario 3 at the significance level $\alpha = 0.00001$.

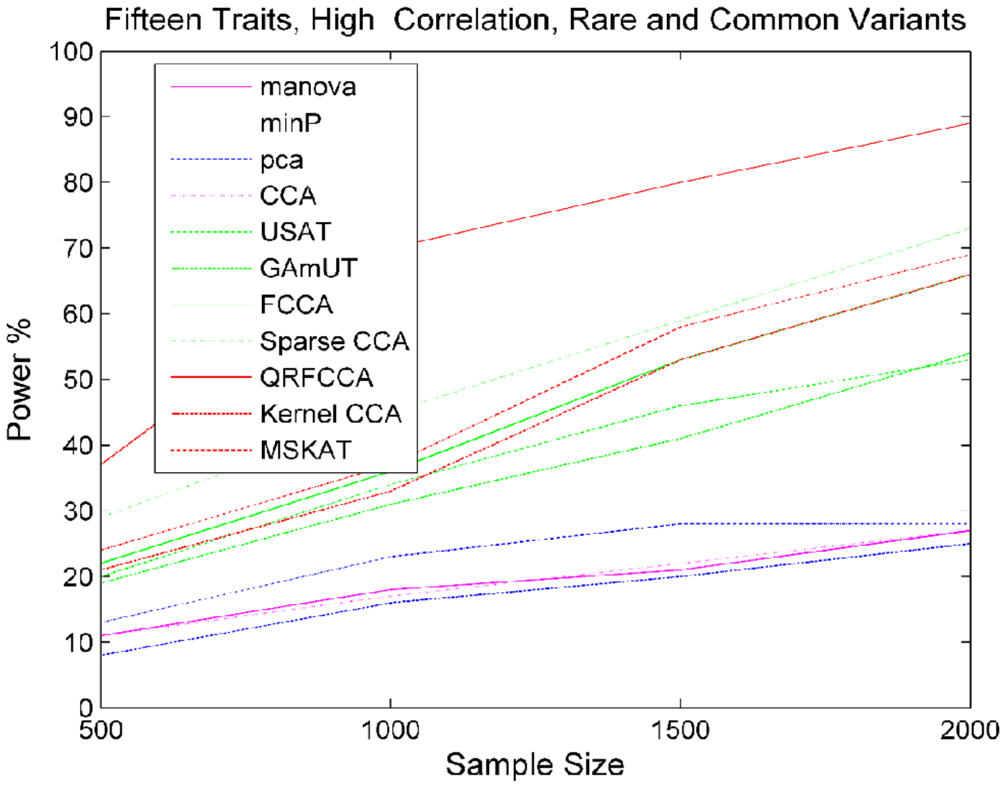


Fig S30. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 highly correlated traits in scenario 1 at the significance level $\alpha = 0.00001$.

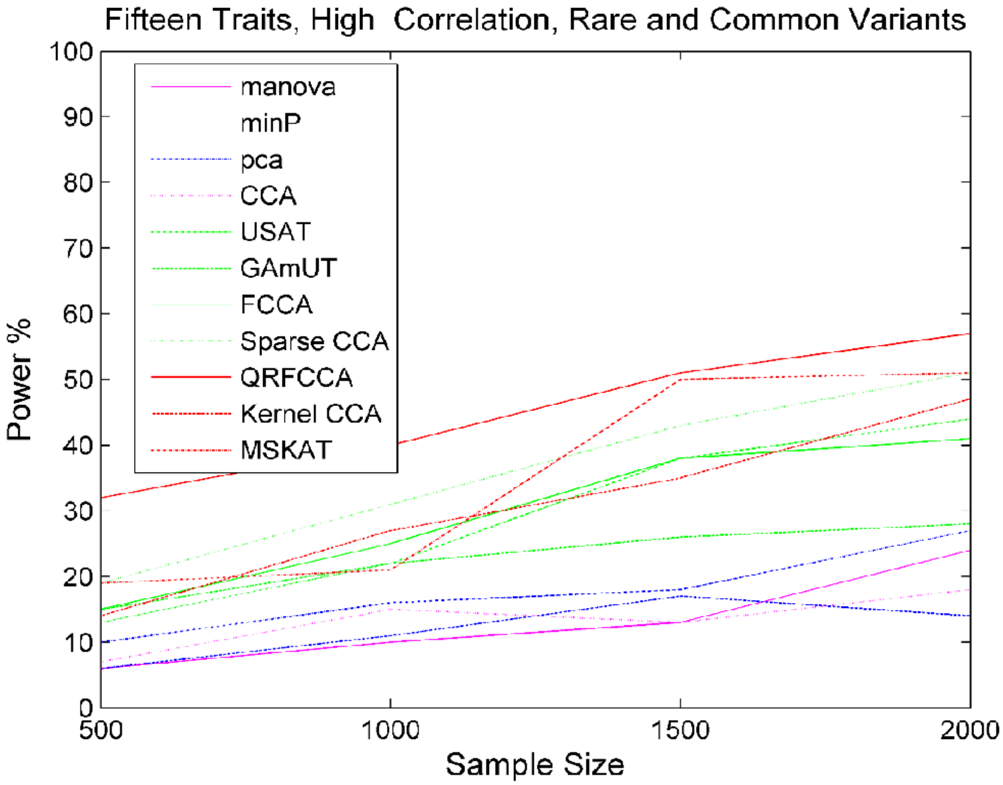


Fig S31. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 highly correlated traits in scenario 2 at the significance level $\alpha = 0.00001$.

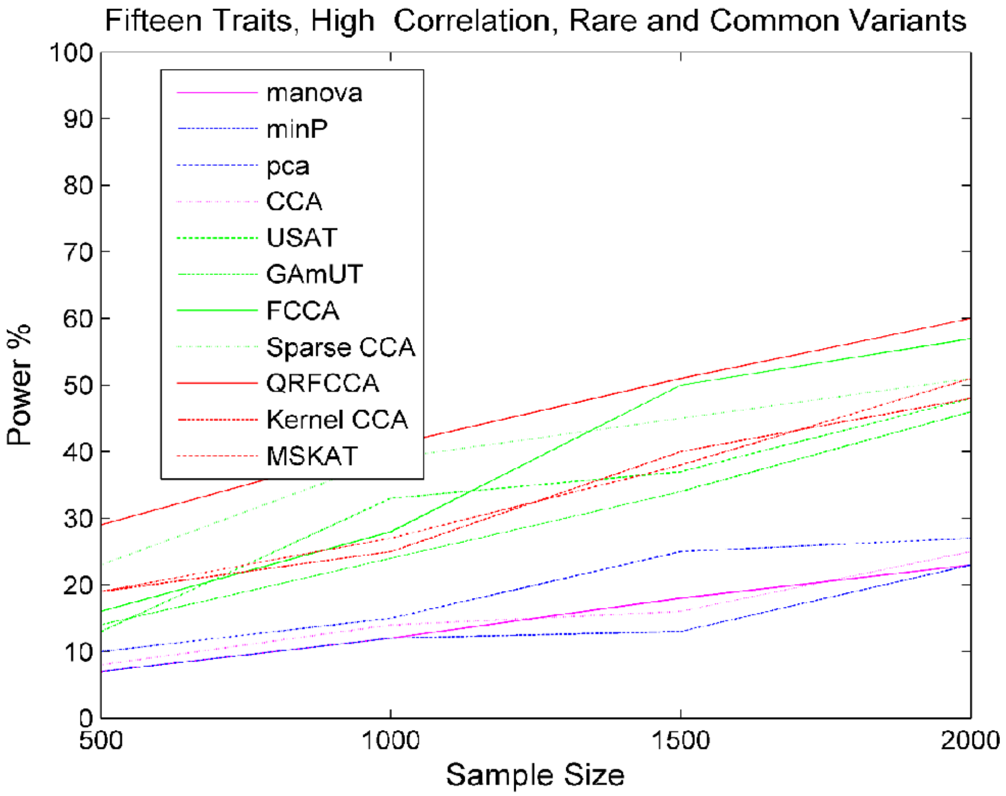


Fig S32. The power of curves as a function of sample sizes of 11 statistics for collectively testing the association of the gene including both rare and common variants with 15 highly correlated traits in scenario 3 at the significance level $\alpha = 0.00001$.

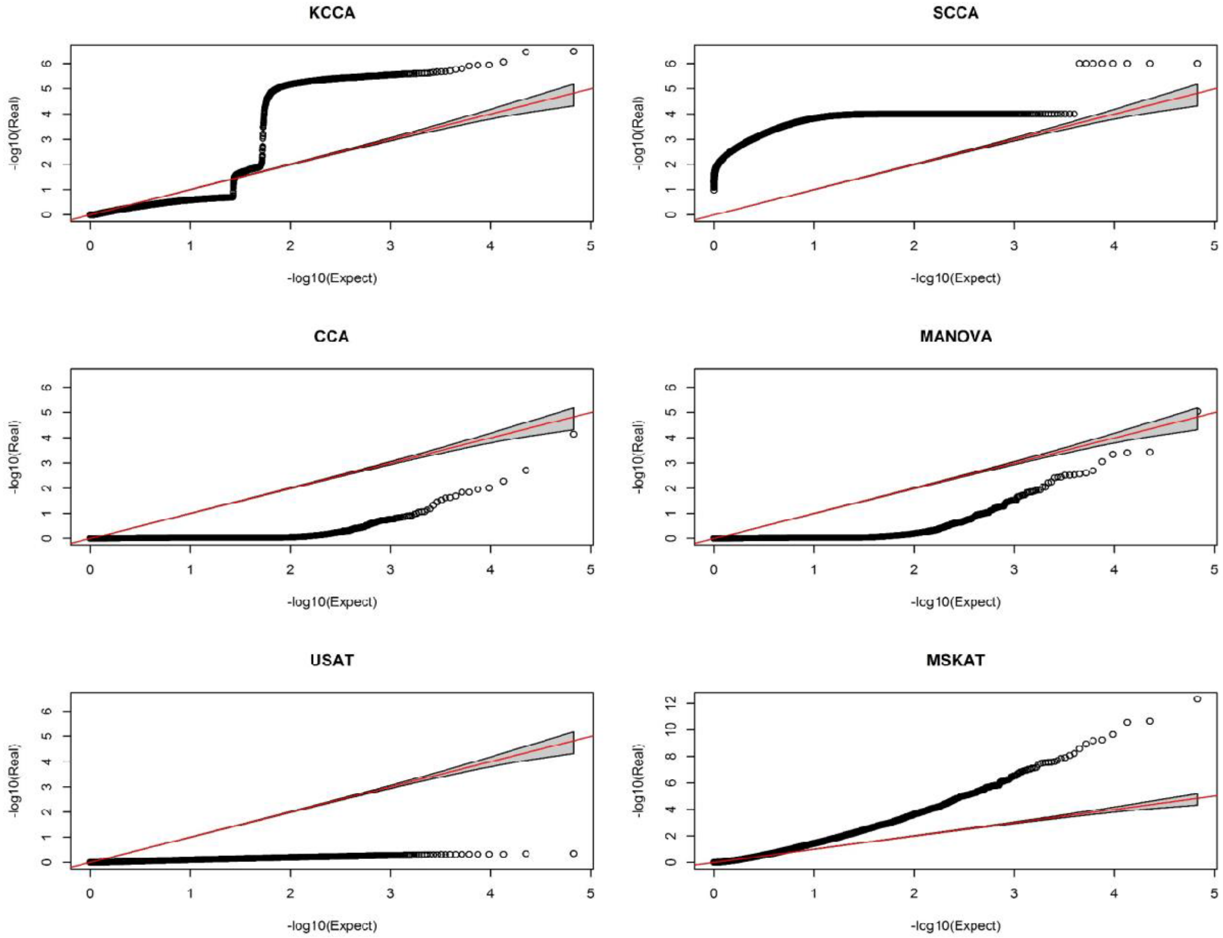


Fig S33. QQ plot of MSKAT, KCCA, CCA, USAT, SCCA, and MANOVA with 95% confidence interval for rare variants. The negative logarithm of the observed (y axis) and the expected (x axis) P value is plotted for each gene (dot), and the red line indicates the null hypothesis of no true association.

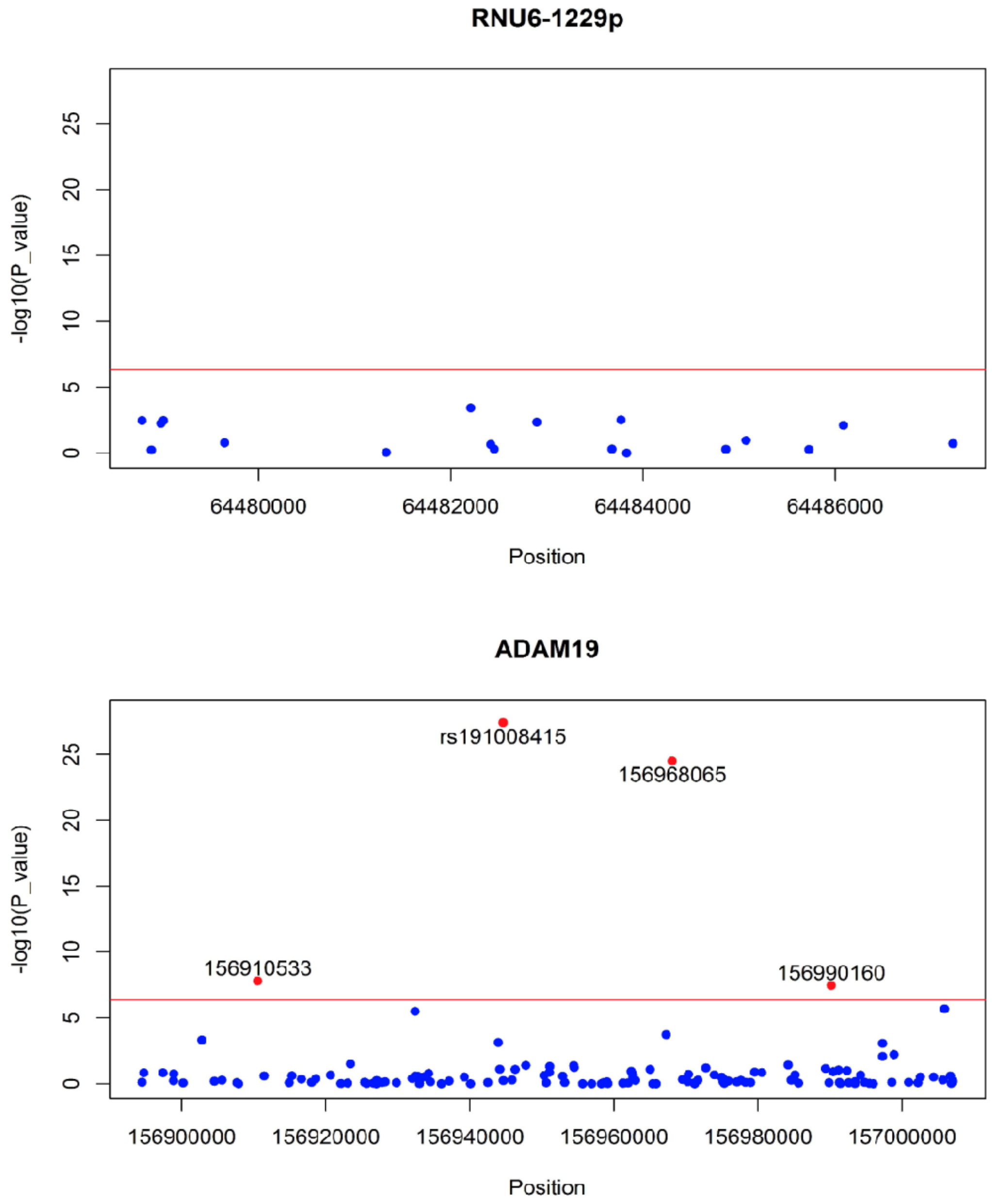


Fig S34. Association signals of SNPs within genes *RNU6-1229P* and *ADAM19*. In the top plot, we showed the P-valuesof the SNPs within *RNU6-1229P* associated with 46 traits. In the bottom plot, we showed the P-valuesof the SNPs within *ADAM19* associated with 46 traits where the numbers next to the red points were the RS number or genomic position of the SNPs.

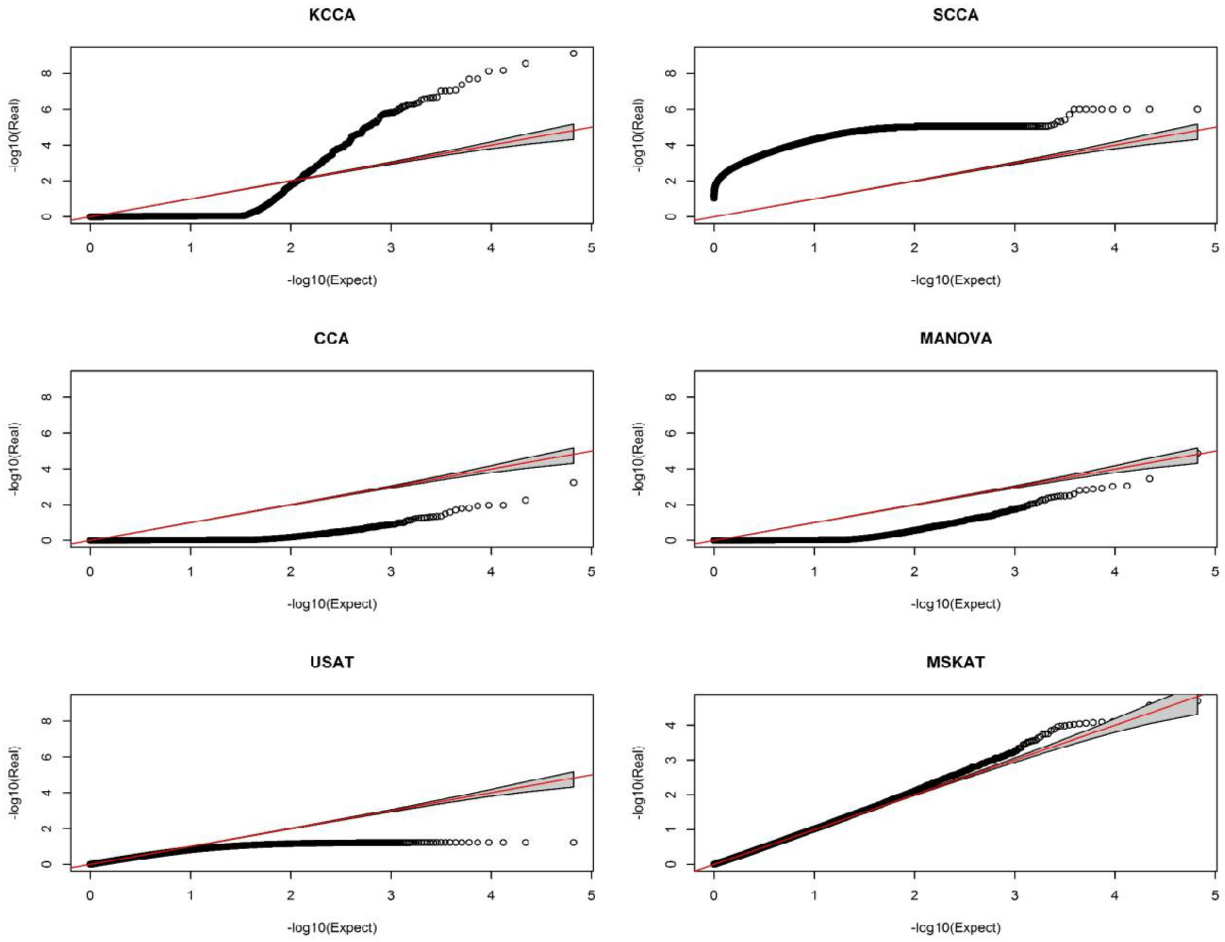
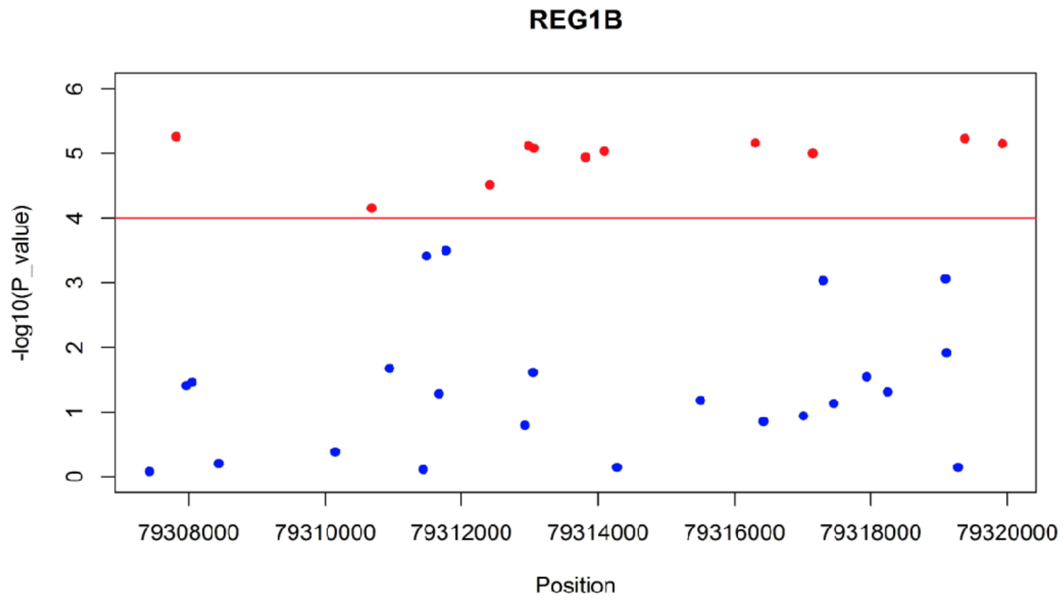


Fig S35. QQ plot of KCCA, CCA, USAT, SCCA, and MANOVA with 95% confidence interval for common variants. The negative logarithm of the observed (y axis) and the expected (x axis) P value is plotted for each gene (dot), and the red line indicates the null hypothesis of no true association.



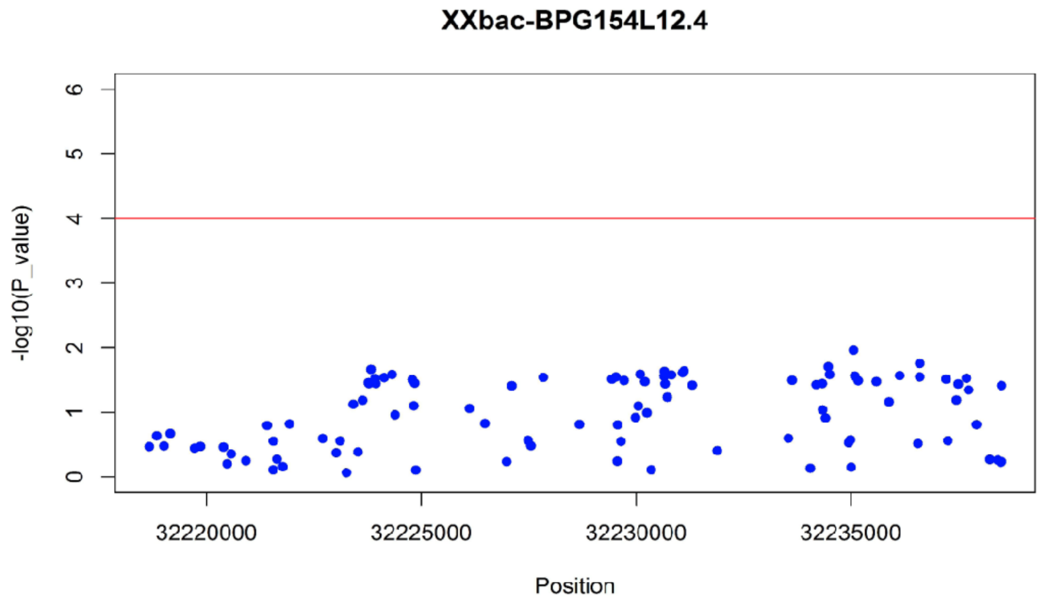


Fig S36. Association signals of SNPs within genes *REG1B* and *XXbac-BPG154L12.4*. In the top plot, we showed the P-values of the SNPs within *REG1B* associated with the 46 traits. In the bottom plot, we showed the P-values of the SNPs within *XXbac-BPG154L12.4* associated with the 46 traits where the numbers next to the red points were the RS number or genomic position of the SNPs.