Supplementary Figures

Supplementary Figure 1. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of proportion of risk increasing variants for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, with the disease under the additive disease model, assuming baseline penetrance of 0.01 and 2,000 cases and 2,000 controls.

Supplementary Figure 2. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of proportion of risk increasing variants for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, with the disease under the dominant disease model, assuming baseline penetrance of 0.01 and 2,000 cases and 2,000 controls.

Supplementary Figure 3. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of proportion of risk increasing variants for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, with the disease under the multiplicative disease model, assuming baseline penetrance of 0.01 and 2,000 cases and 2,000 controls.

Supplementary Figure 4. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of proportion of risk increasing variants for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, with the disease under the recessive disease model, assuming baseline penetrance of 0.01 and 3,000 cases and 3,000 controls.

Supplementary Figure 5. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of sample sizes for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, half of which were risk increasing variants, with the disease under the additive disease model, assuming baseline penetrance of 0.01.

Supplementary Figure 6. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of sample sizes for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, half of which were risk increasing variants, with the disease under the dominant disease model, assuming baseline penetrance of 0.01.

Supplementary Figure 7. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of sample sizes for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, half of which were risk increasing variants, with the disease under the multiplicative disease model, assuming baseline penetrance of 0.01.

Supplementary Figure 8. Power of nine statistics: FPCA (discretization approach) –based statistics, FPCA (Fourier expansion approach) –based statistic, multivariate PC-based statistic, WSS, VT, collapsing method, generalized T^2 statistic, single marker χ^2 test and CMC method (the variants with frequencies $\leq$ 0.005 were collapsed) as a function of sample sizes for testing association of 80 rare variants, the MAF of which ranges from 0.0003 to 0.036, 70% of which were risk increasing variants, with the disease under the recessive disease model, assuming baseline penetrance of 0.01.