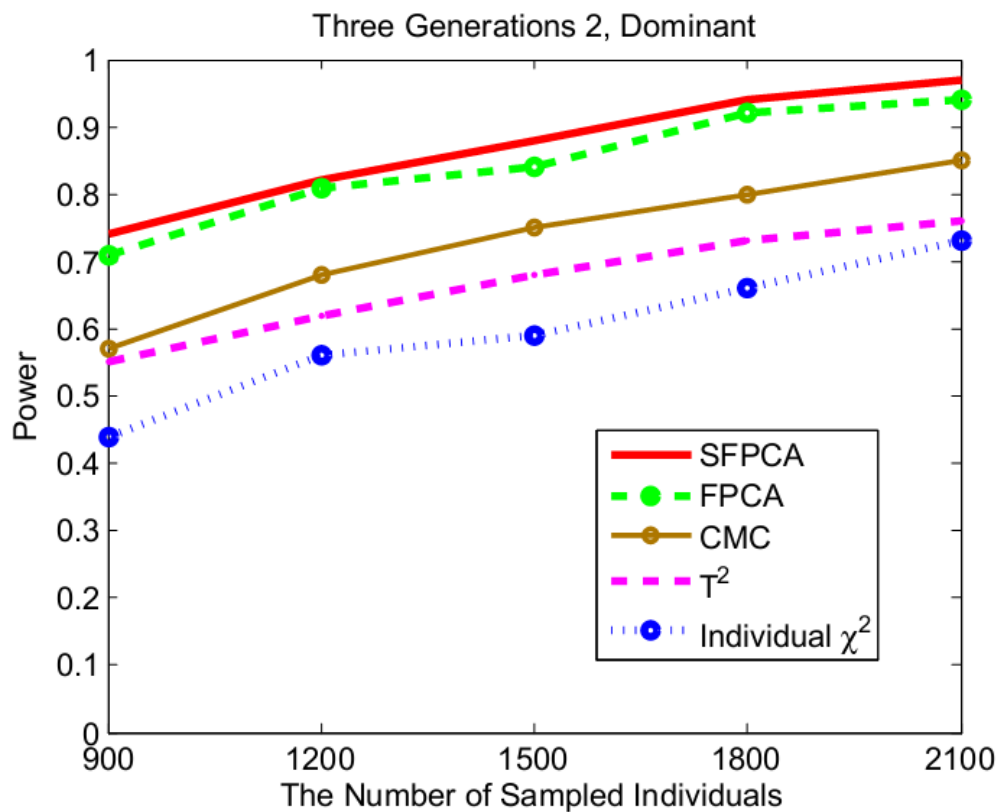# Supplemental Data

Family-Based Association Studies

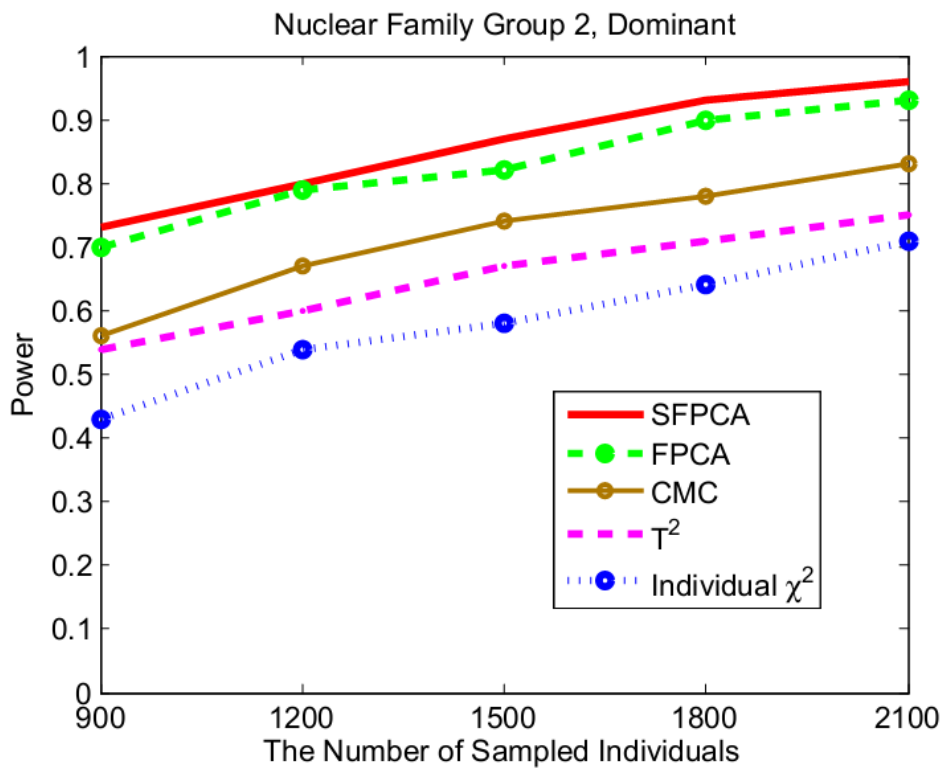# for Next-Generation Sequencing

Yun Zhu and Momiao Xiong

Figure S1. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for three generation family group 2 as a function of the total number of individuals at the significance level $\alpha = 0.05$ under the dominant model, assuming 20% of risk variants and a baseline penetrance of 0.01.
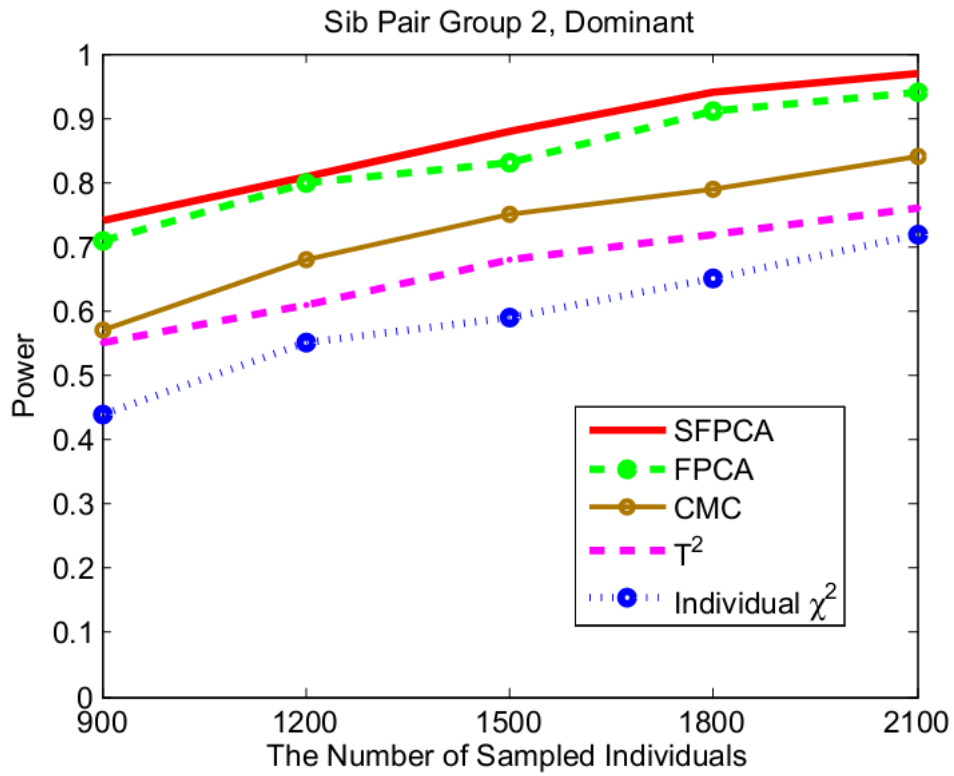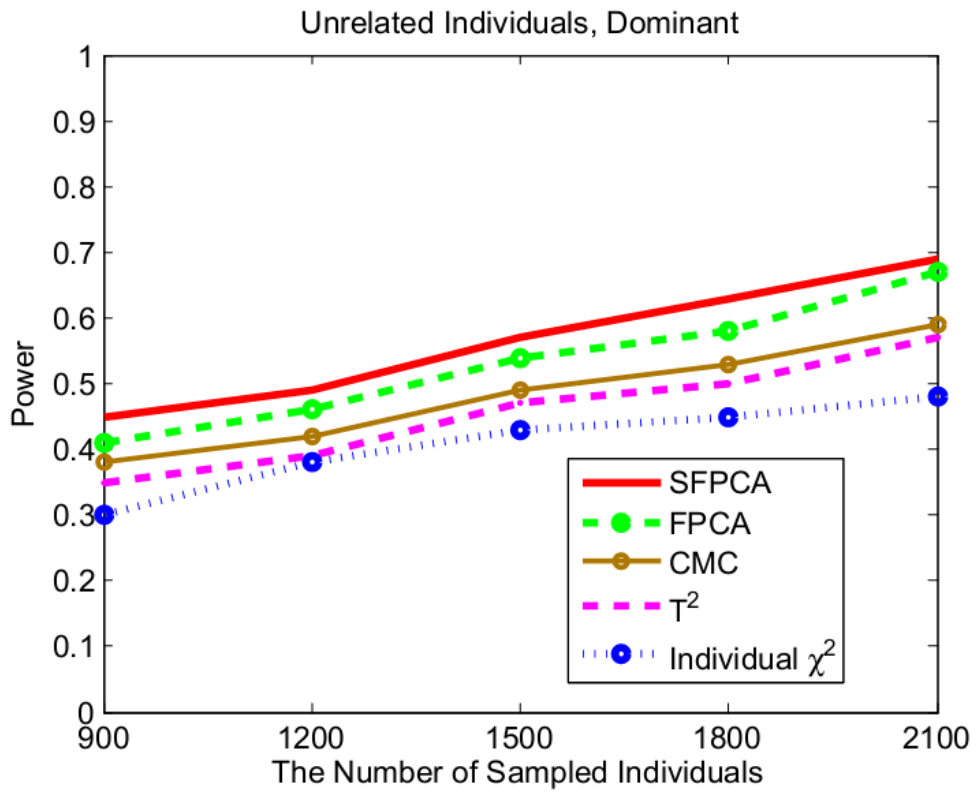
Figure S2. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for sib-pair group 2 as a function of the total number of individuals at the significance level $\alpha = 0.05$ under the dominant model, assuming 20% of risk variants and a baseline penetrance of 0.01.
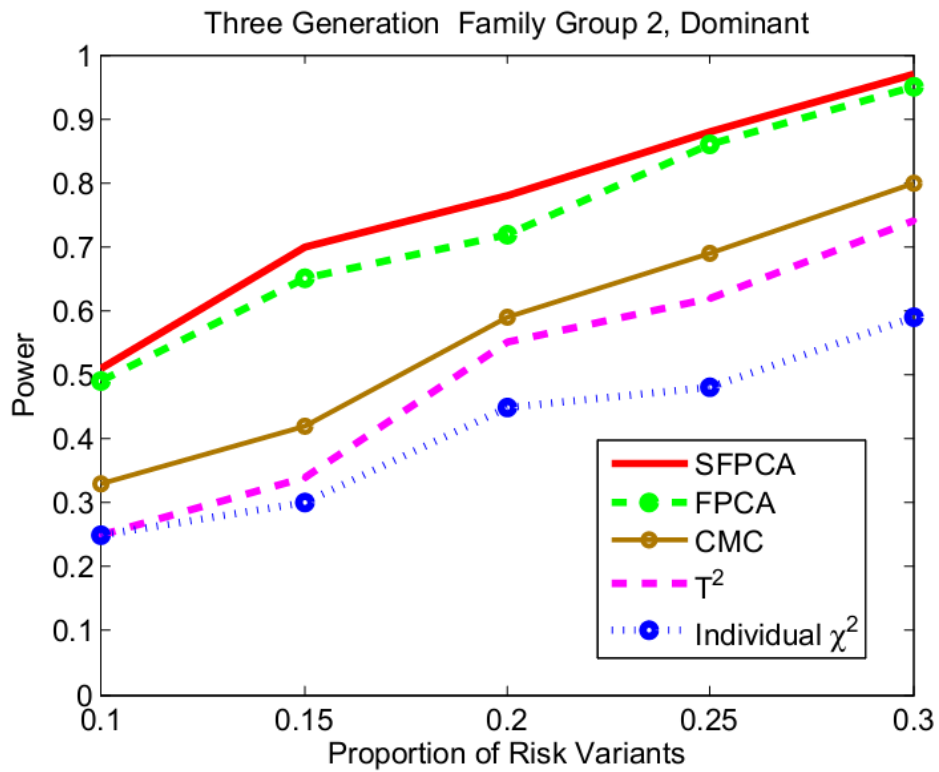
Figure S3. The power curve of five family-based statistics: the smoothed FPCA,
FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for
nuclear family group 2 as a function of the total number of individuals at the
significance level $\alpha = 0.05$ under the dominant model, assuming 20% of risk variants
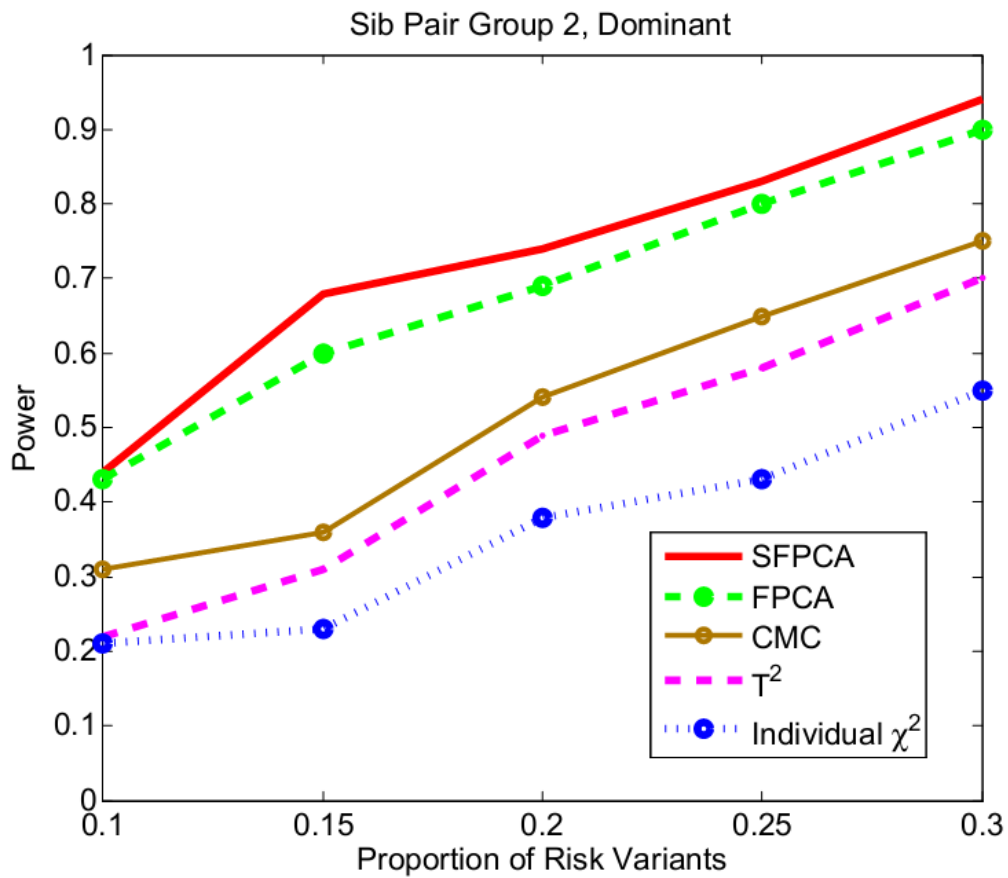and a baseline penetrance of 0.01.

Figure S4. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for unrelated cases and controls as a function of the total number of individuals at the significance level $\alpha = 0.05$ under the dominant model, assuming 20% of risk variants and a baseline penetrance of 0.01.
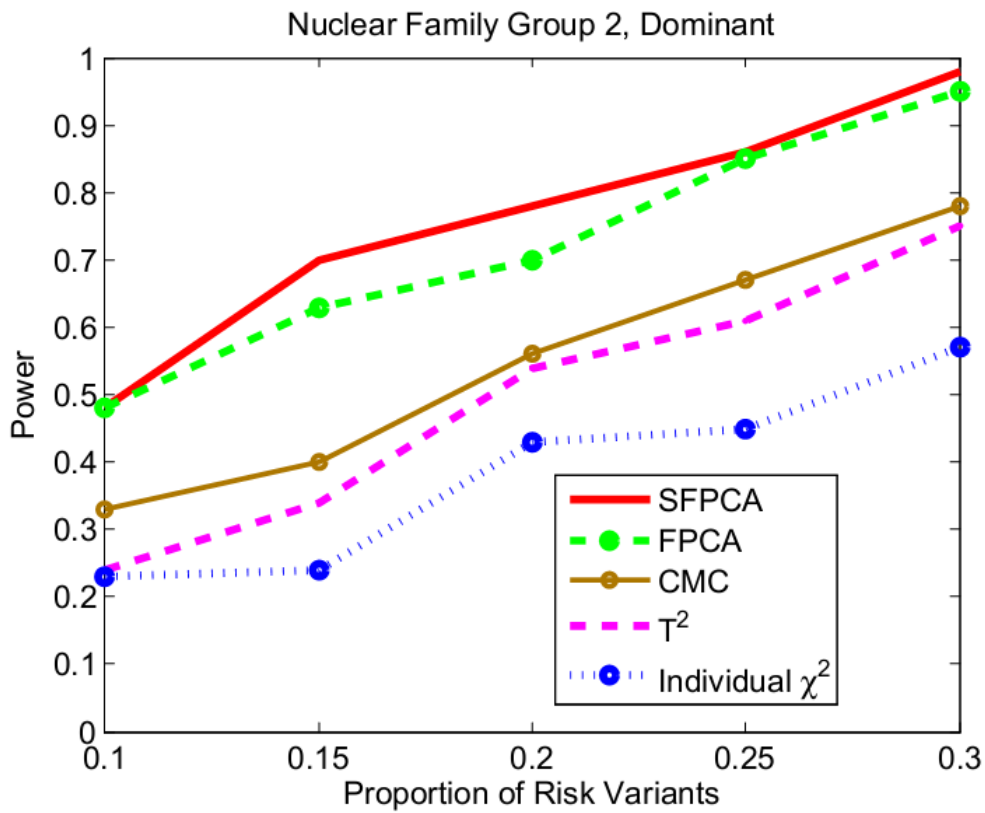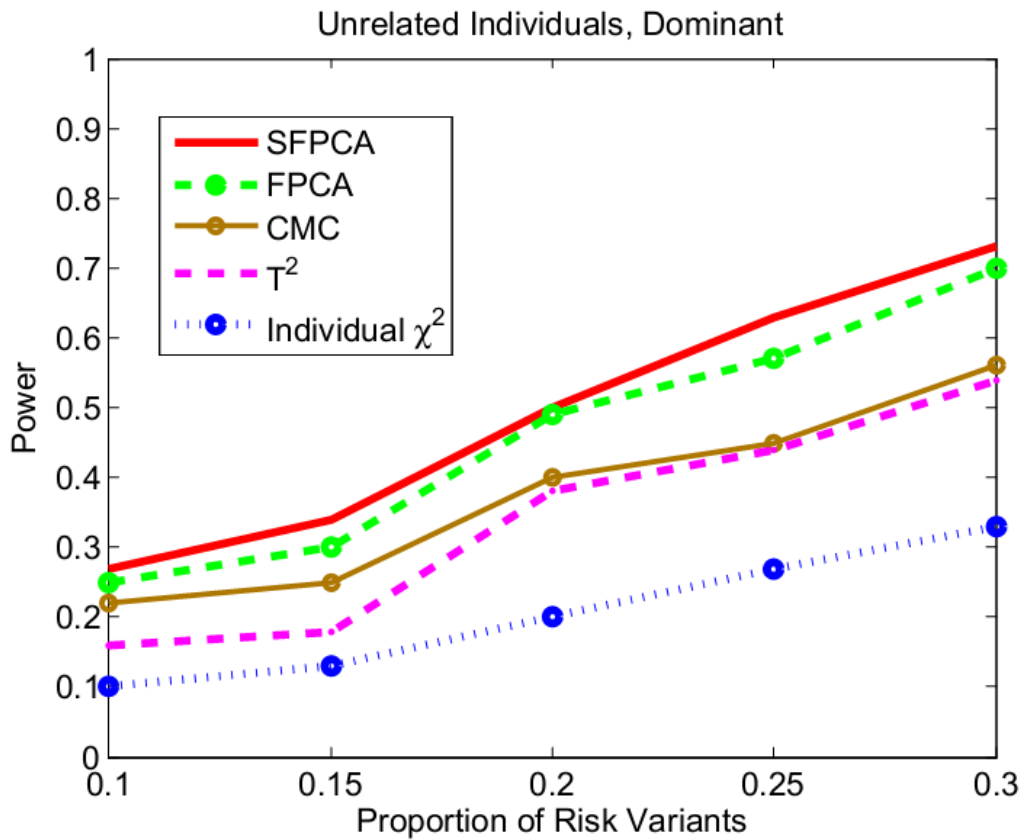
Figure S5. The power curve of five family-based statistics: the smoothed FPCA,

FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for

three generation family group 2 as a function of the proportion of risk variants at the

significance level $\alpha = 0.05$ under the dominant model, assuming a total of 1,800

sampled individuals and a baseline penetrance of 0.01.

Figure S6. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for sib-pair group 2 as a function of the proportion of risk variants   at the significance level $\alpha = 0.05$ under the dominant model, assuming a total of 1,800 sampled individuals   and a baseline penetrance of 0.01.

Figure S7. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for nuclear family group 2 as a function of the proportion of risk variants at the significance level $\alpha = 0.05$ under the dominant model, assuming a total of 1,800 sampled individuals and a baseline penetrance of 0.01.

Figure S8. The power curve of five family-based statistics: the smoothed FPCA, FPCA without smoothing, CMC, generalized T^2 and individual χ^2 statistic for unrelated cases and controls as a function of the proportion of risk variants at the significance level $\alpha = 0.05$ under the dominant model, assuming a total of 1,800 sampled individuals and a baseline penetrance of 0.01.
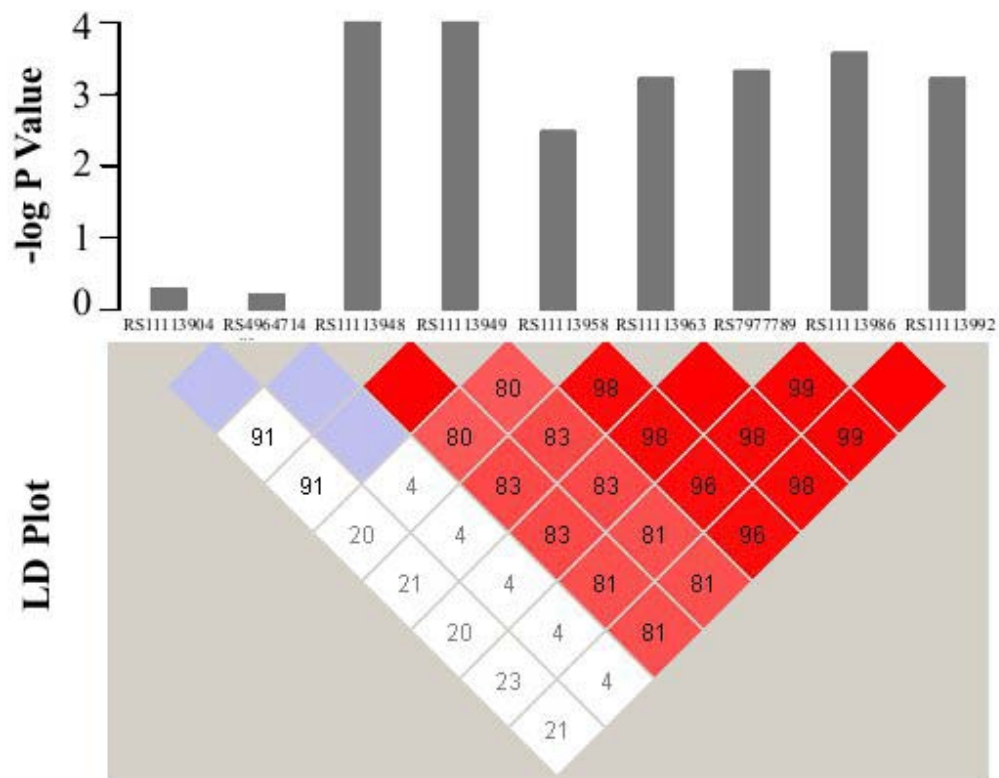
Figure S9. –log P-values of individual test for association of nine rare variants (MAF <0.05) by the family-based corrected single marker χ^2 test within gene *CRY1* and linkage disequilibrium pattern among them.