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Supplemental Data

Genetic Association Analysis under Complex Survey

Sampling: The Hispanic Community

Health Study/Study of Latinos

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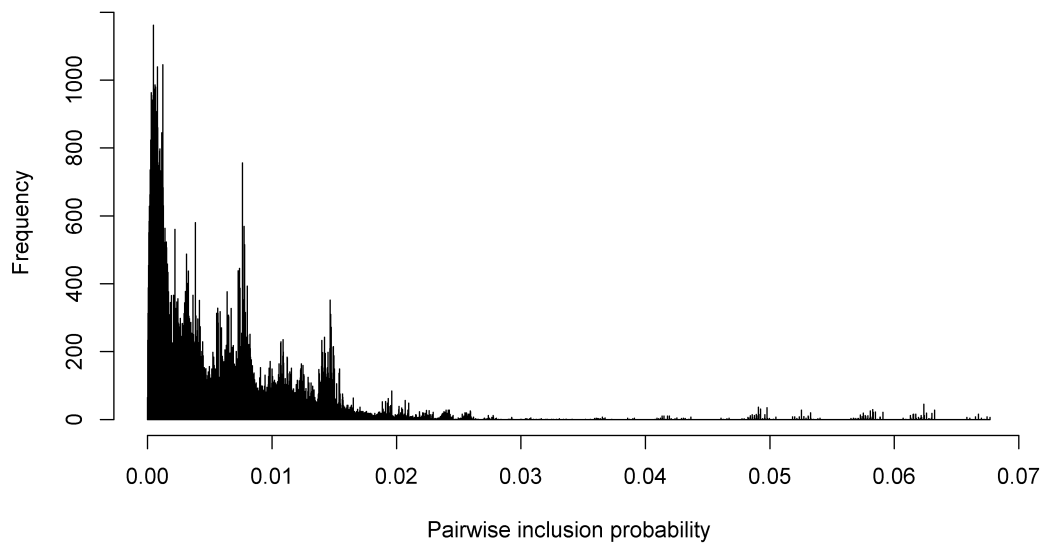
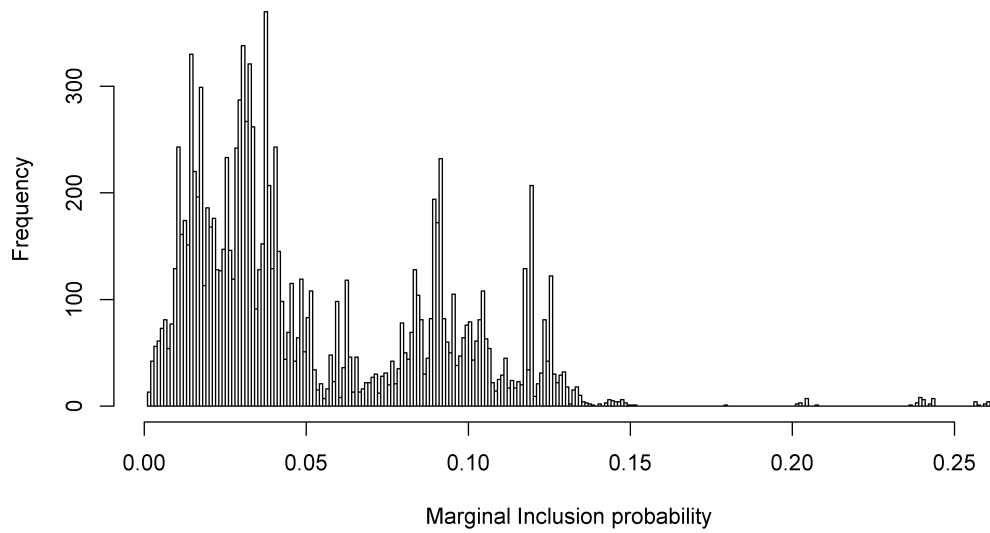


Figure S1. Marginal and pairwise inclusion probabilities in the HCHS/SOL.

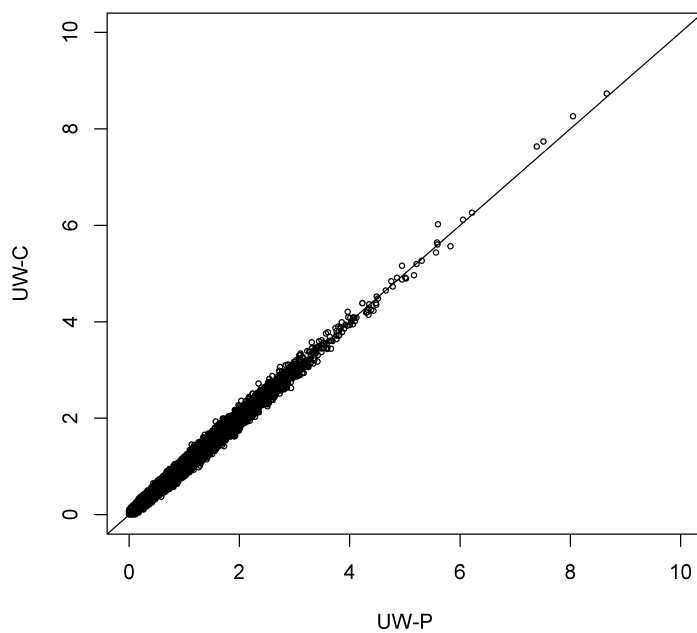


Figure S2. Plot of the $-\log_{10}(p\text{-values})$ for the UW-C versus UW-P methods (with model-based variance estimators) from the genome-wide association analysis of BMI in the HCHS/SOL . The log-transformation was applied to BMI. SNPs with $\text{MAF} < 1\%$ were excluded.

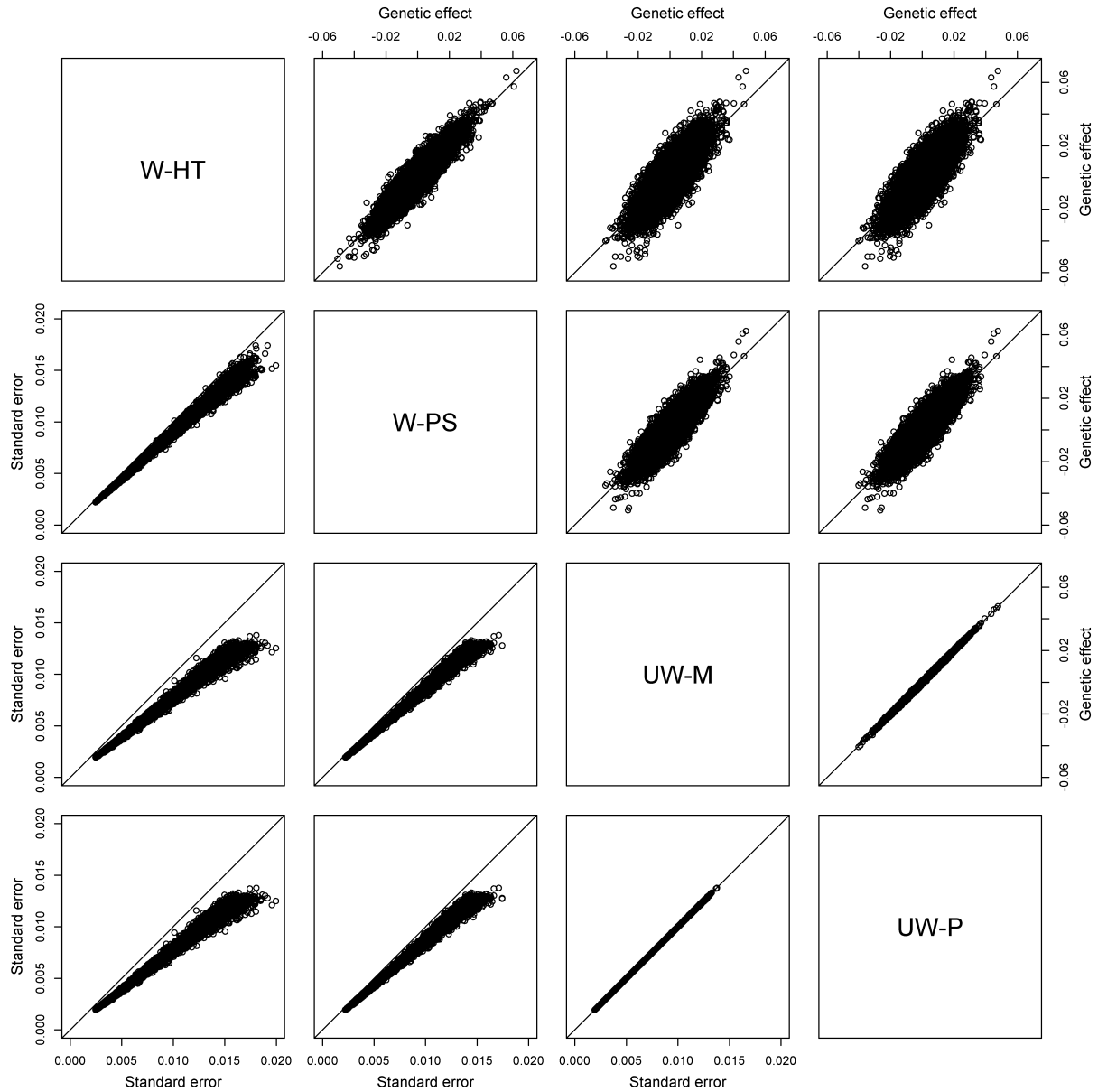


Figure S3. Effect estimates (upper right triangle) and standard error estimates (lower left triangle) from the genome-wide association analysis of BMI in the HCHS/SOL under weighted and unweighted methods with model-based variance estimators. The log-transformation was applied to BMI. SNPs with $MAF < 1\%$ were excluded.

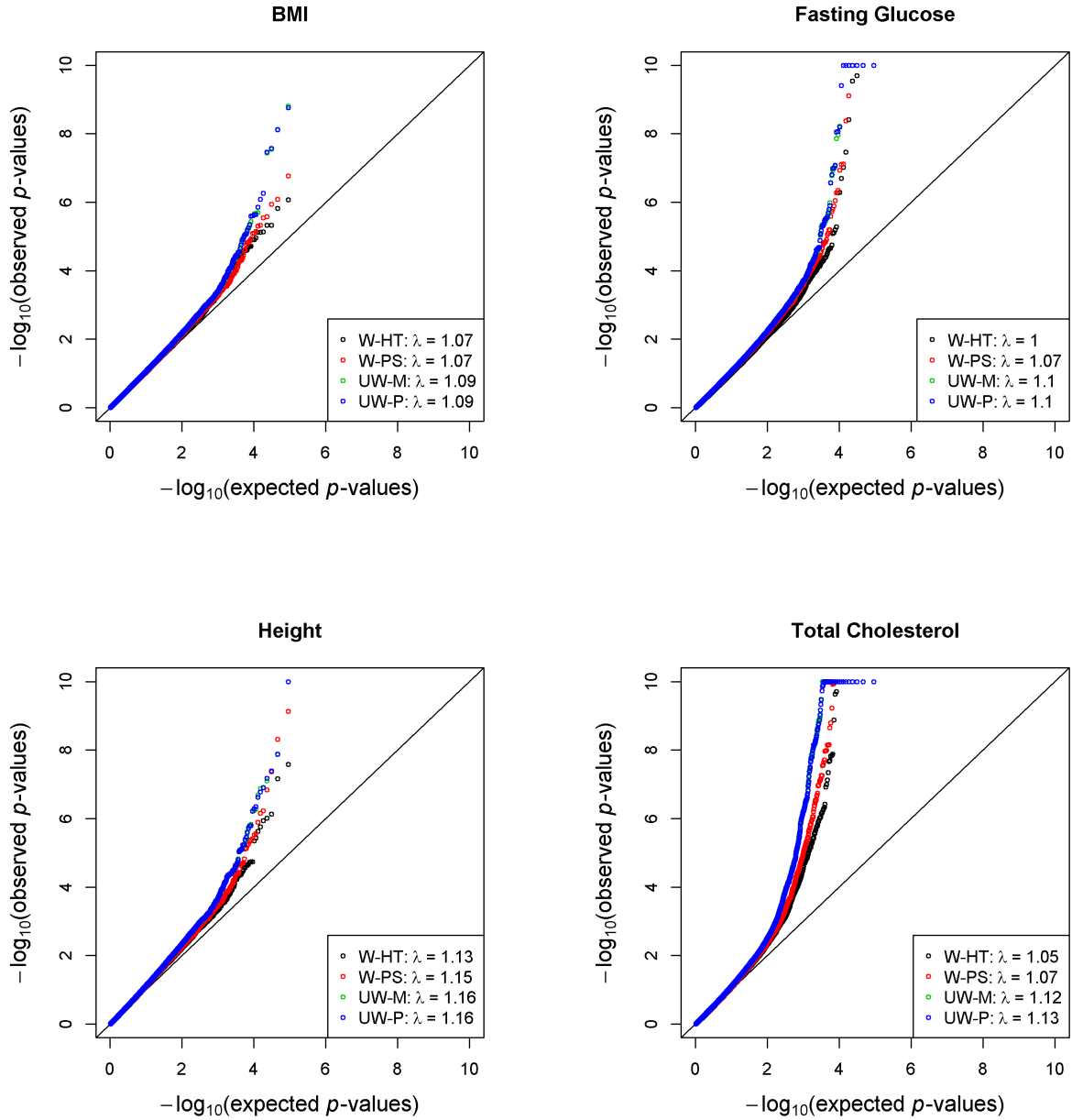


Figure S4. Quantile-quantile plots of $-\log_{10}(p\text{-values})$ from the genome-wide association analysis of BMI, fasting glucose, height, and total cholesterol in the HCHS/SOL under weighted and unweighted methods with model-based variance estimators when the relatedness beyond the original households is disregarded. The log-transformation was applied to BMI and total cholesterol, and the inverse normal transformation was applied to fasting glucose. SNPs with $\text{MAF} < 1\%$ were excluded. Most of the p -values are indistinguishable between UW-M and UW-P.

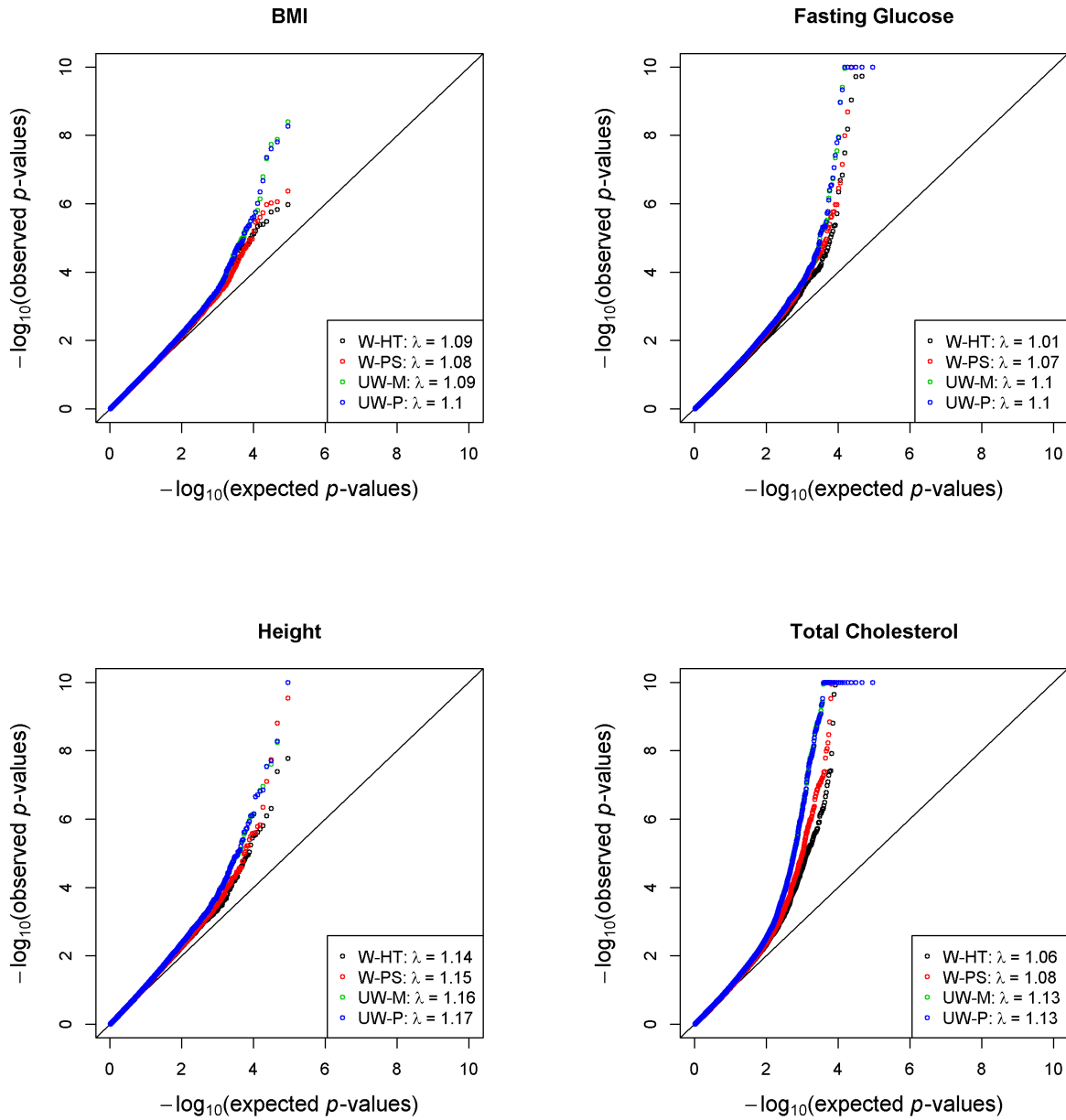


Figure S5. Quantile-quantile plots of $-\log_{10}(p\text{-values})$ from the genome-wide association analysis of BMI, fasting glucose, height, and total cholesterol in the HCHS/SOL under weighted and unweighted methods with model-based variance estimators when the relatedness beyond BGs is disregarded. The log-transformation was applied to BMI and total cholesterol, and the inverse normal transformation was applied to fasting glucose. SNPs with $\text{MAF} < 1\%$ were excluded. Most of the p -values are indistinguishable between UW-M and UW-P.