Comparing SUGEN and GENESIS

Results from both Imputed and Genotyped data for 7 traits

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Background

- All study comparisons were made in PAGE HCHS/SOL data (Population Architecture using Genomics and Epidemiology study (https://www.pagestudy.org/).

- 53,424 participants in the PAGE study were genotyped for 1.7 million SNPs on the Illumina MEGA array.

- Genome-wide association studies of the PAGE data require statistical methods to control for hidden population stratification, admixture, and relatedness.

- Two adjustment methods, one based on linear mixed models (LMM)and another on generalized estimating equations (GEE) were compared.

Methods

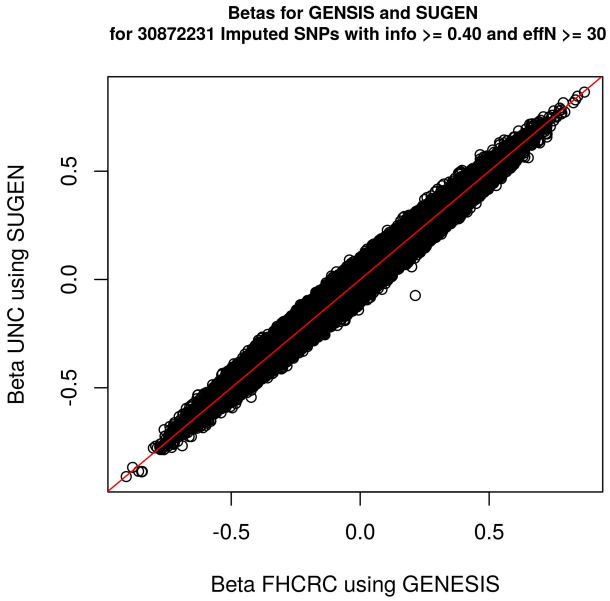
LMM is implemented in the R package GENESIS.

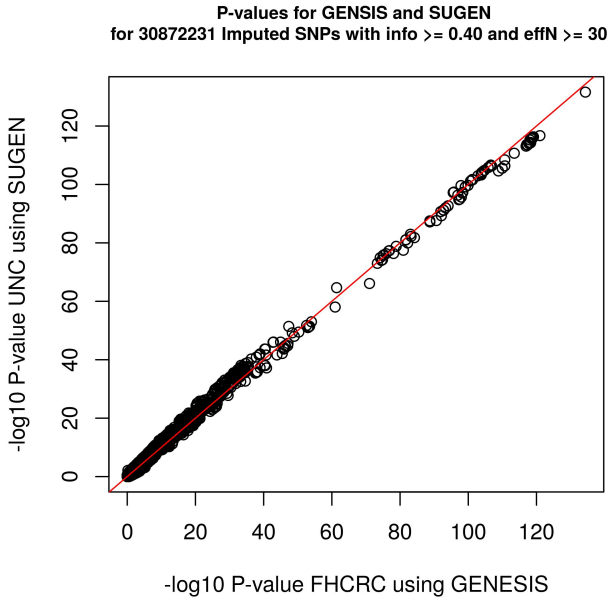
GEE is implemented in the standalone software program SUGEN.

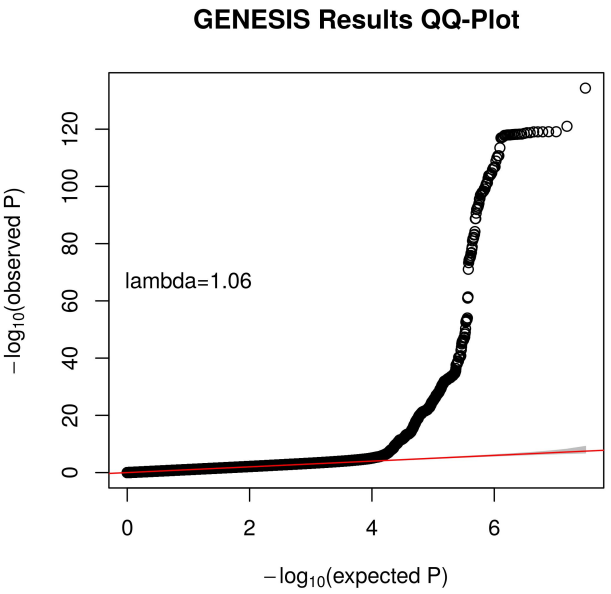
Markers with MAF > ½ % were used in the analysis.

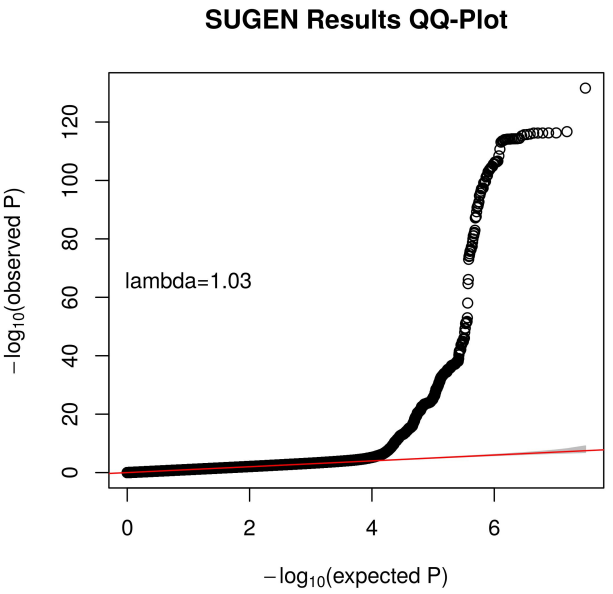
All analyses included principal components, age, sex, ancestry group, and study as adjustment variables.

CRP Imputed Data









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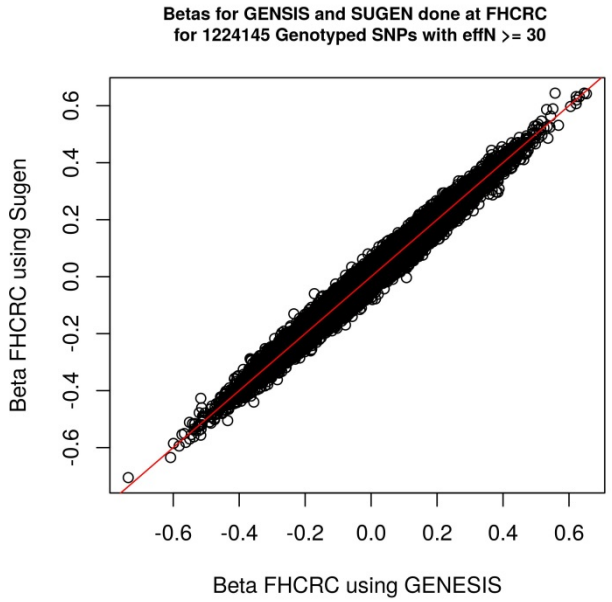

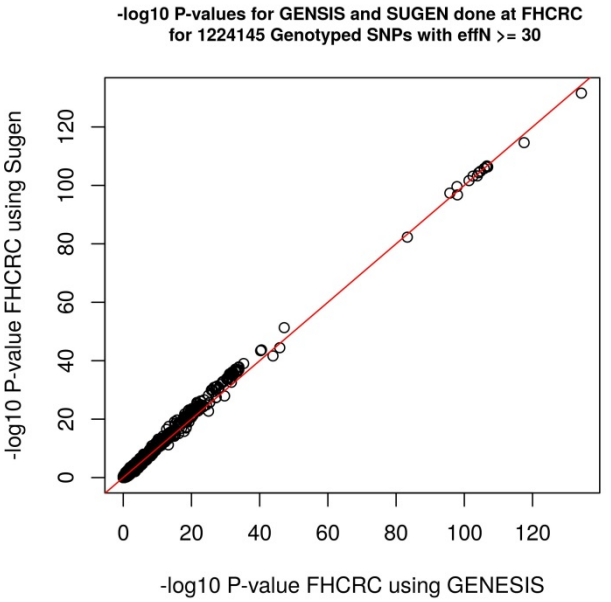

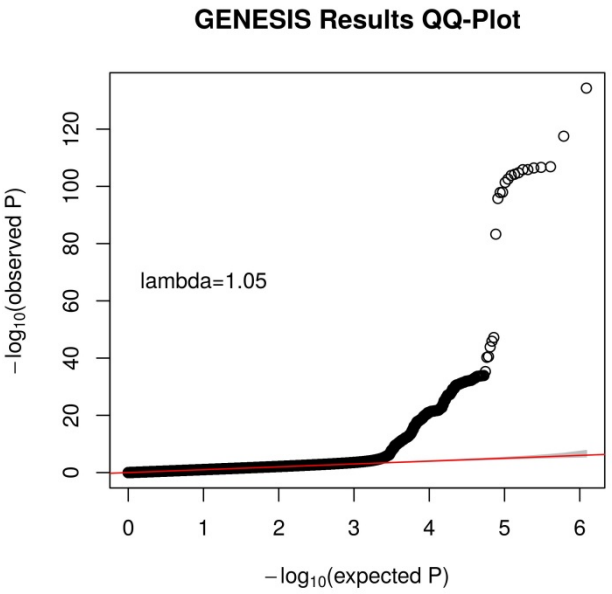

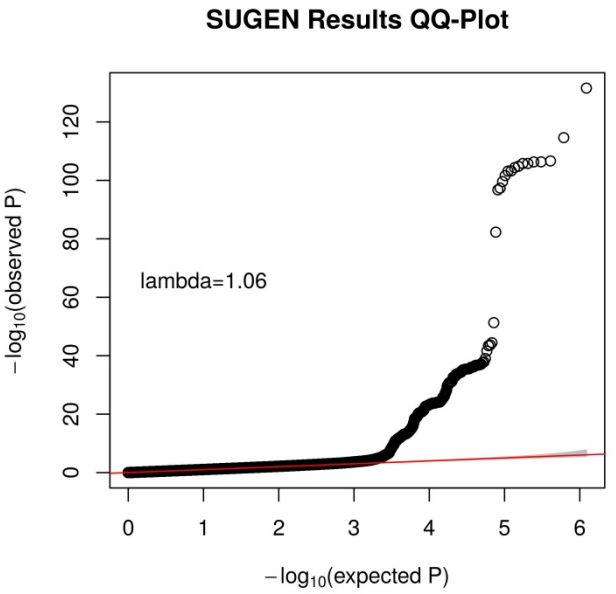

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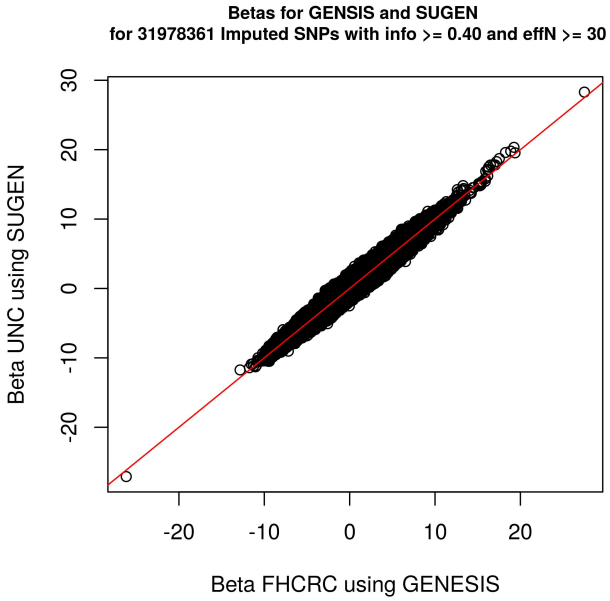

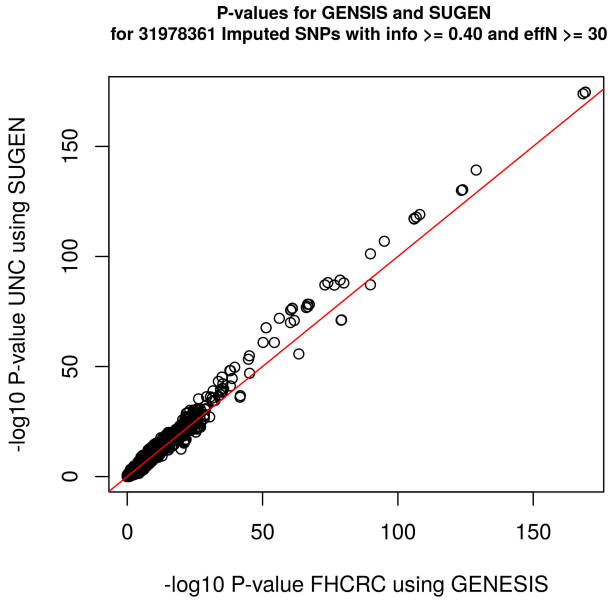

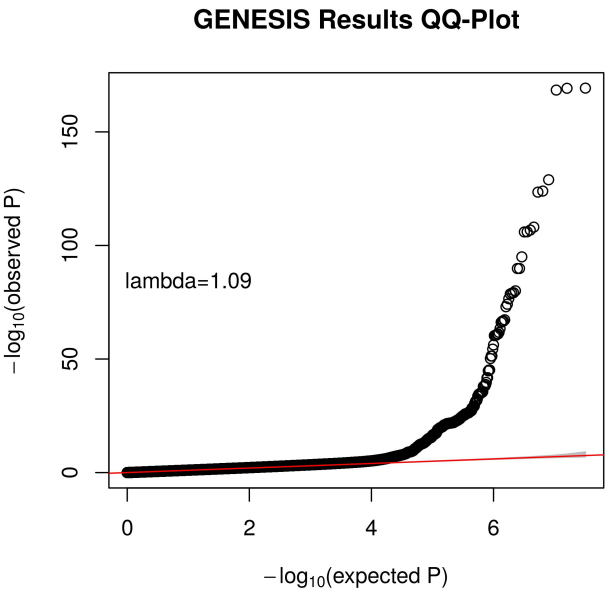

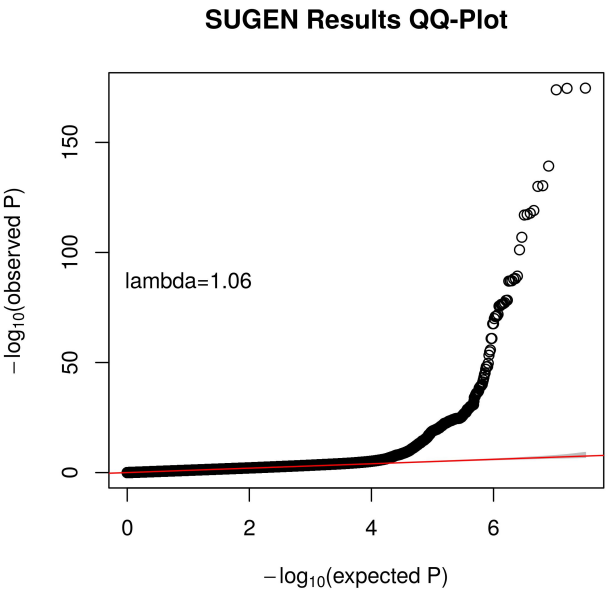

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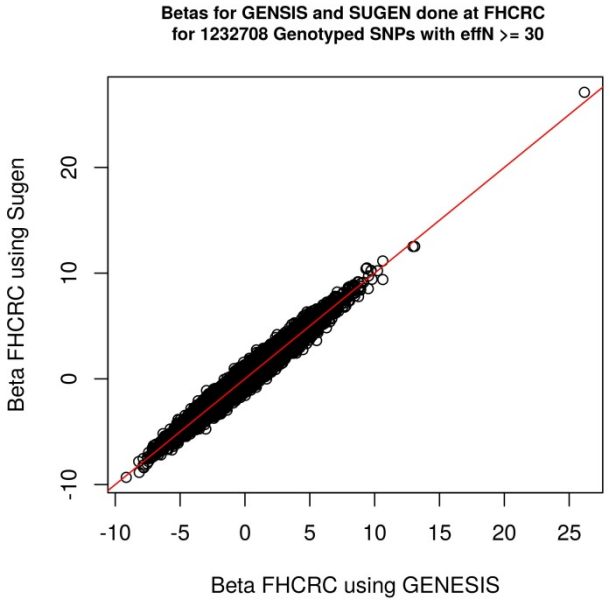

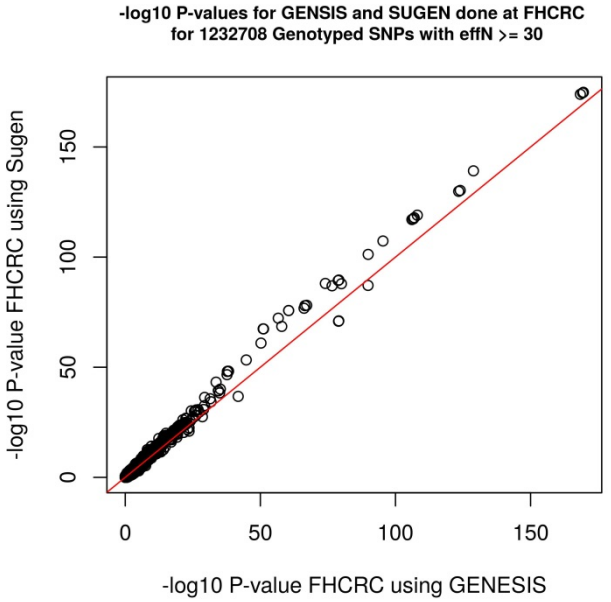

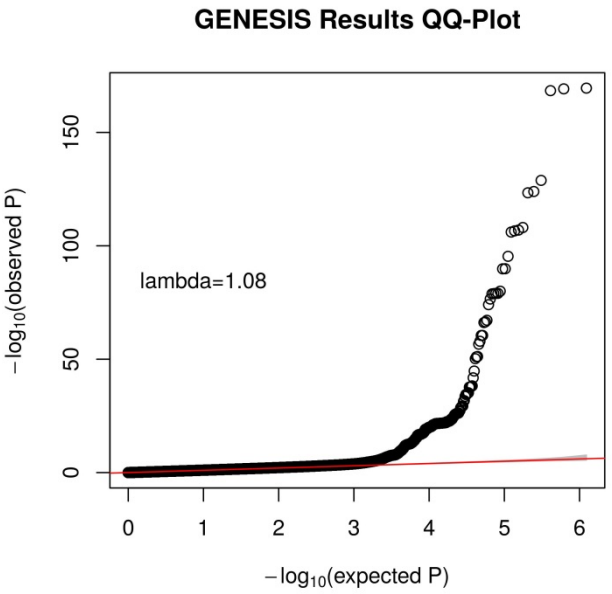

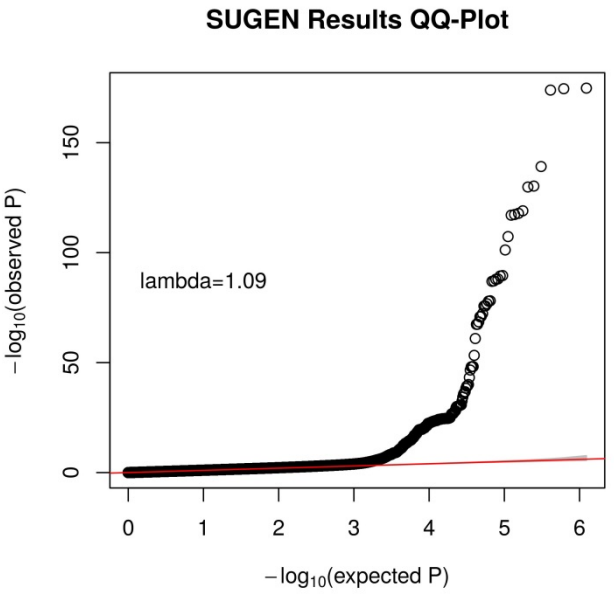

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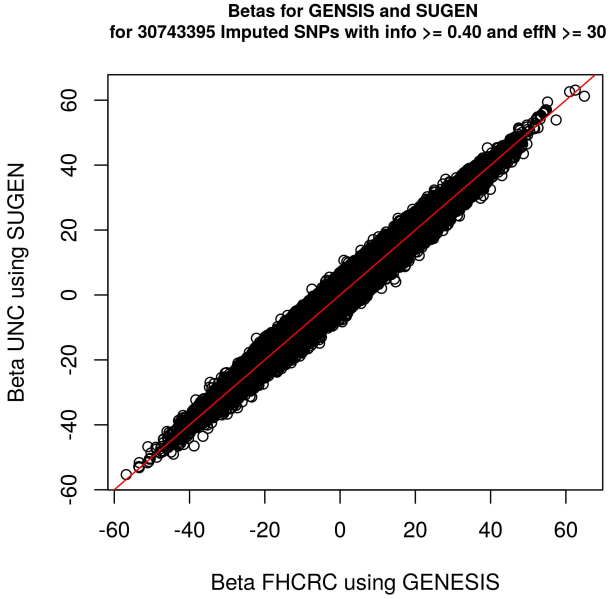

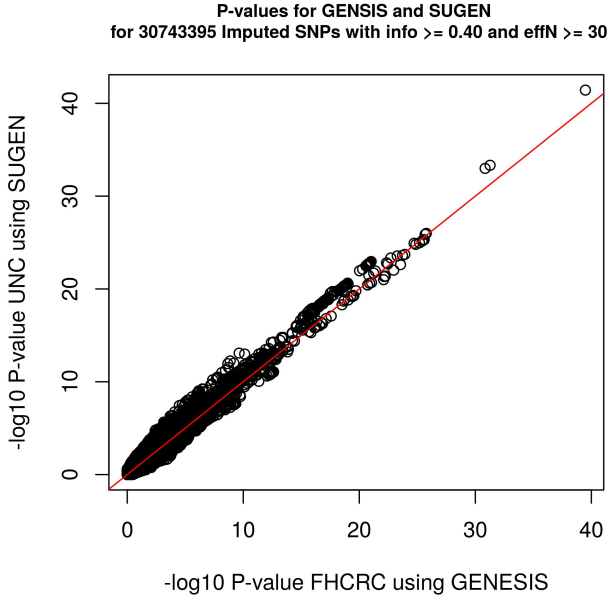

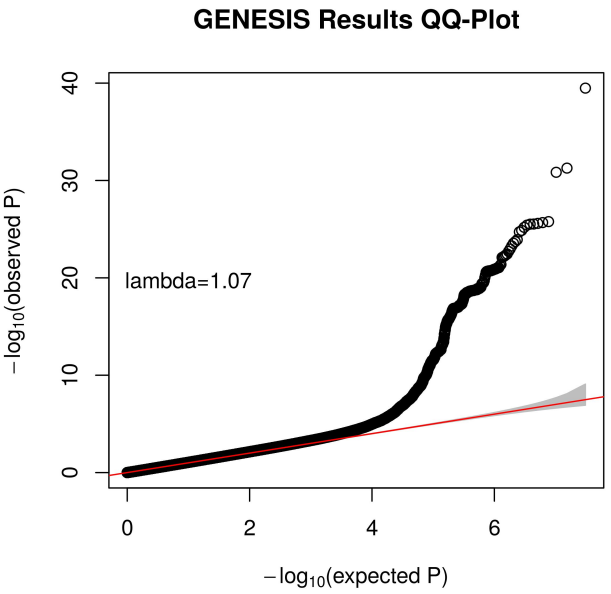

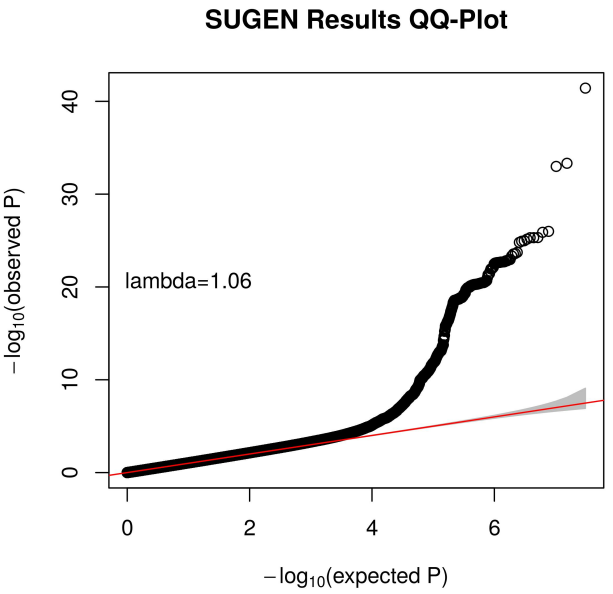

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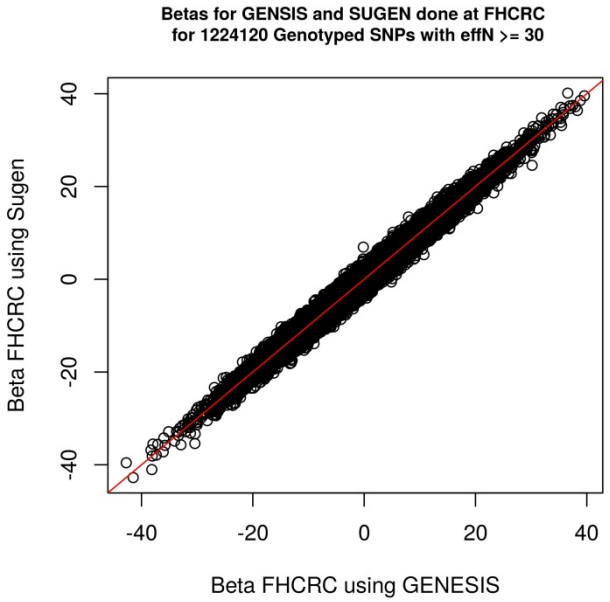

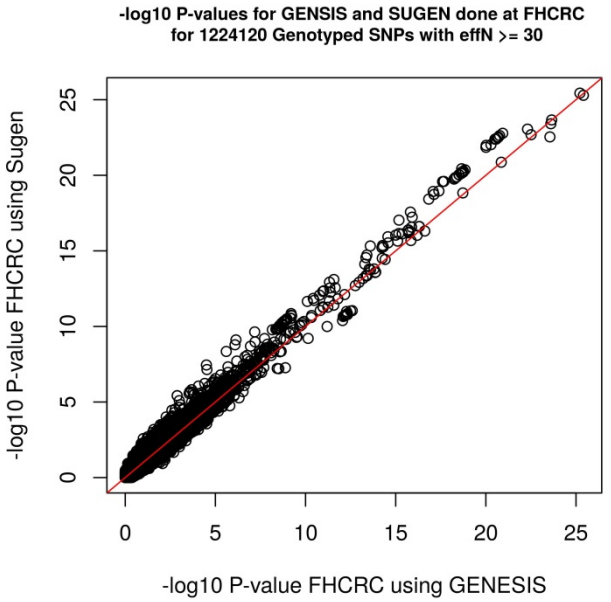

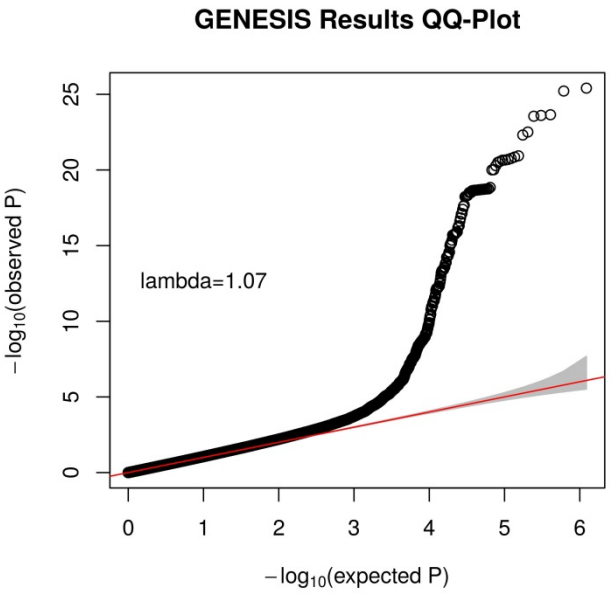

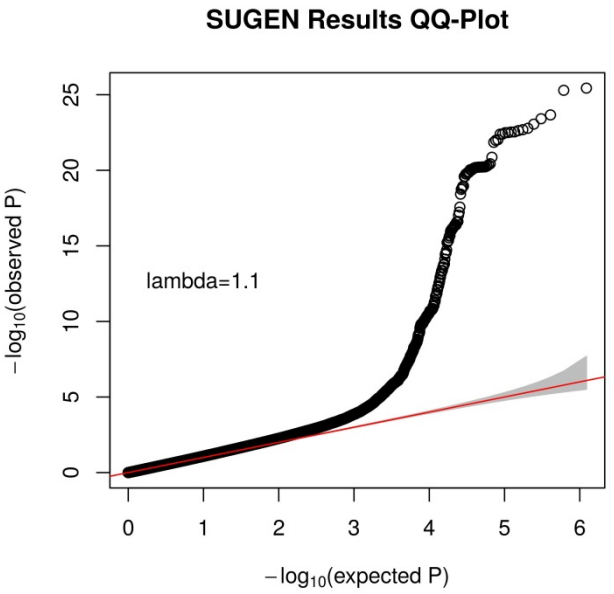

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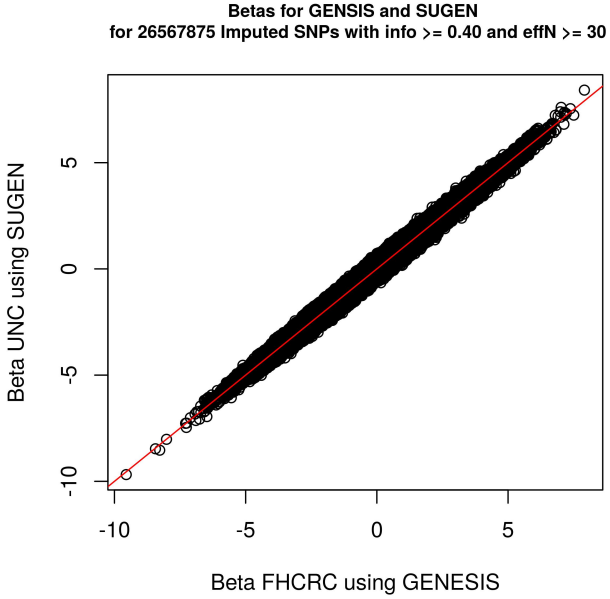

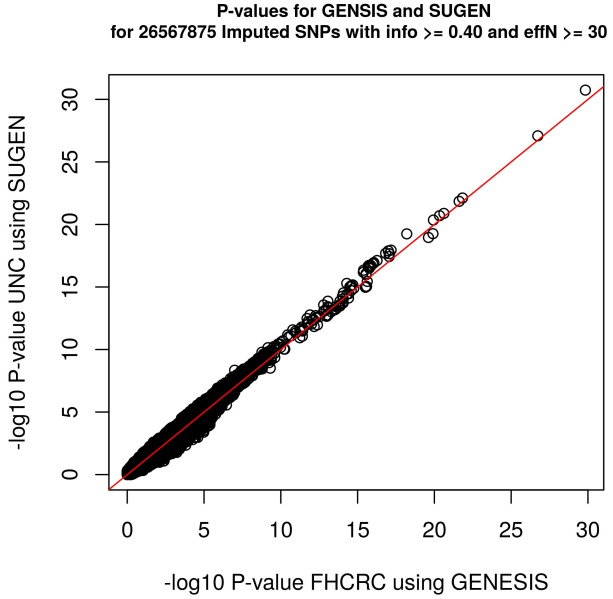

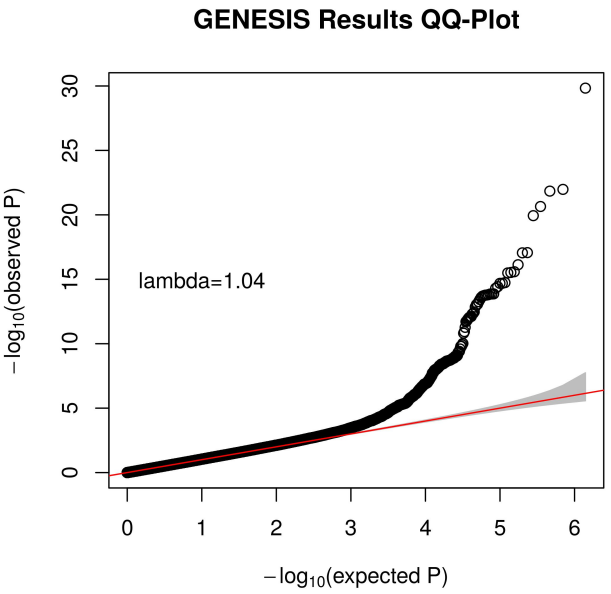

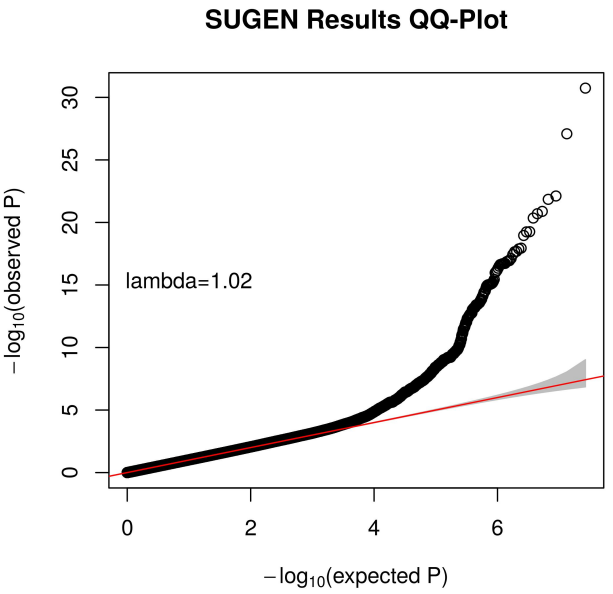

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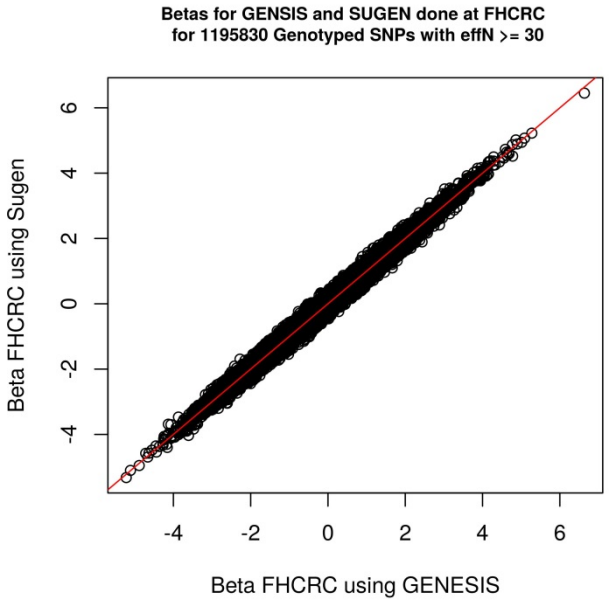
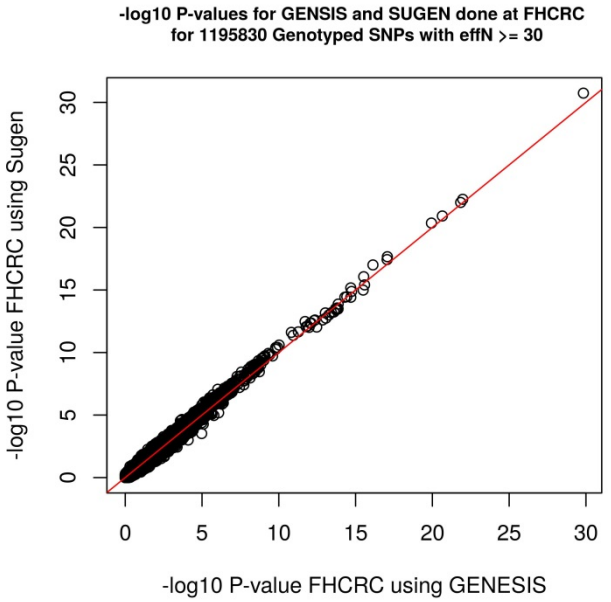
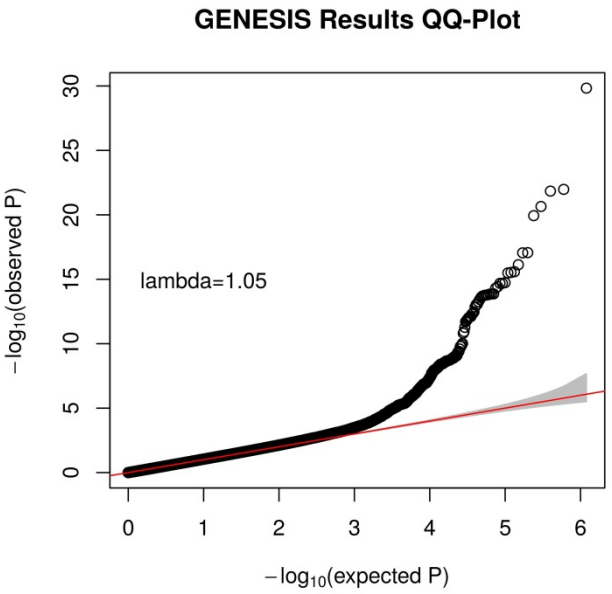
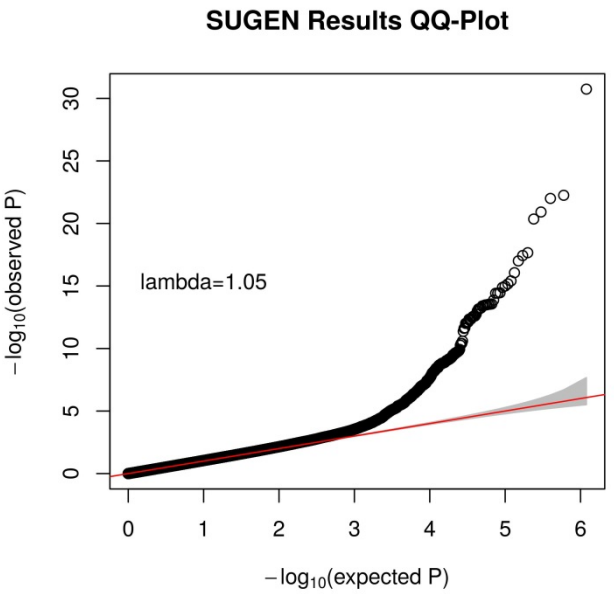
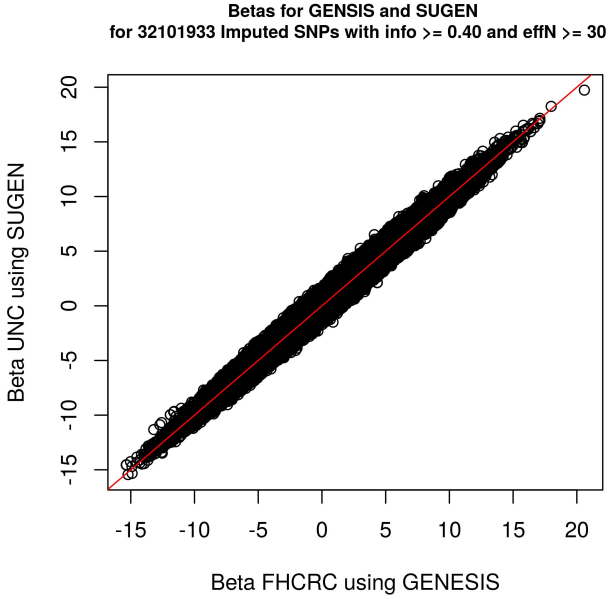


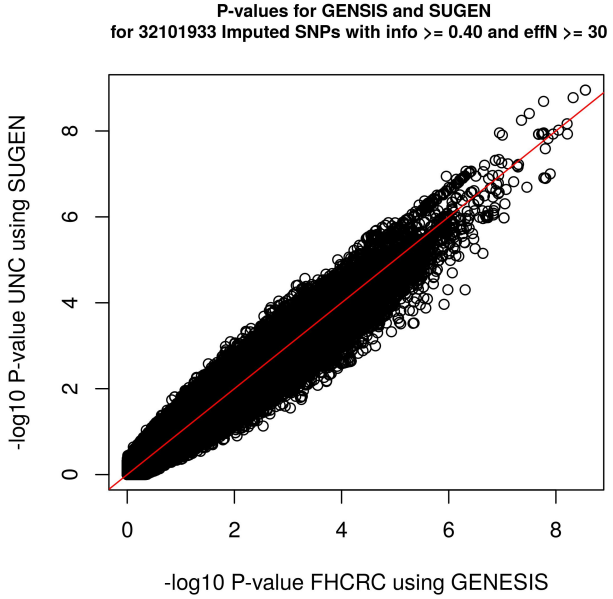


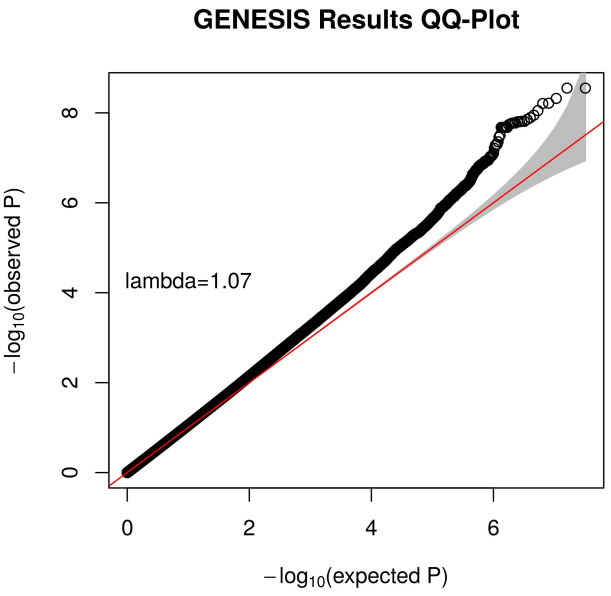


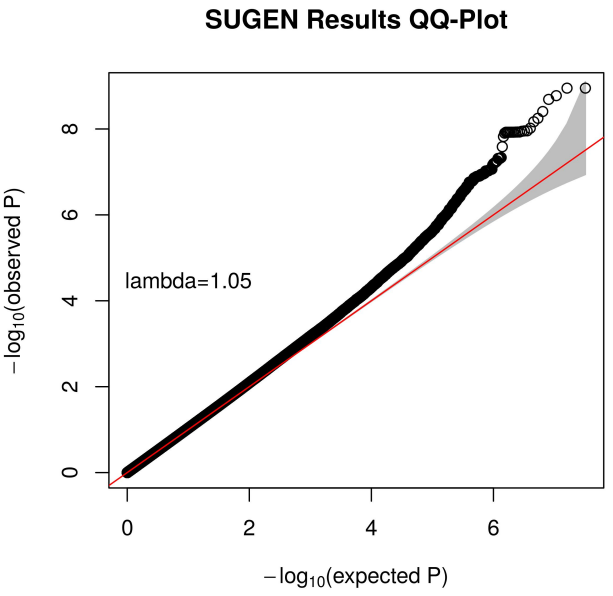


SBP Imputed Data









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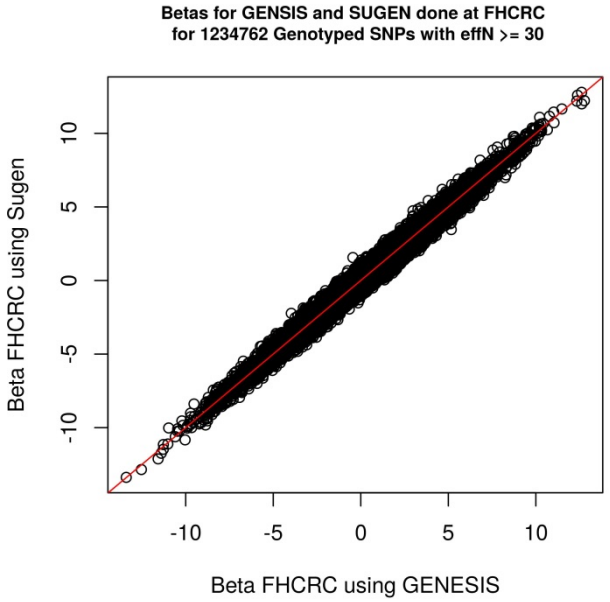
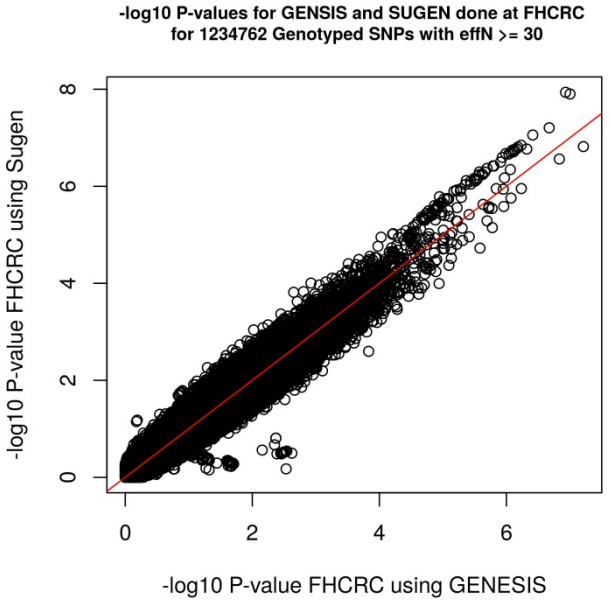
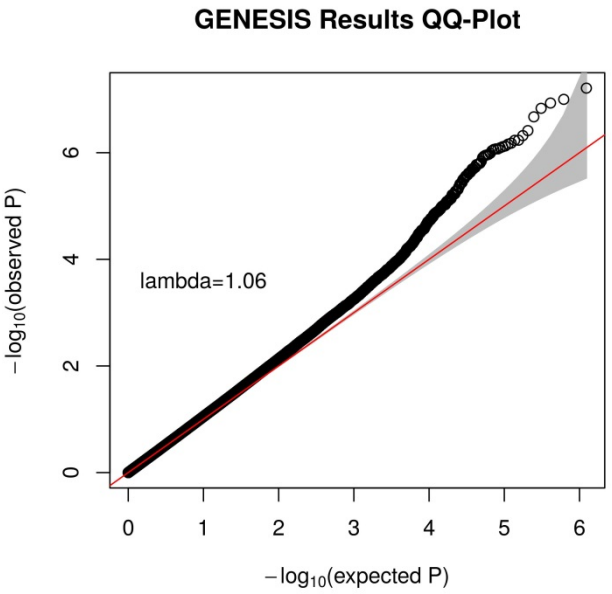
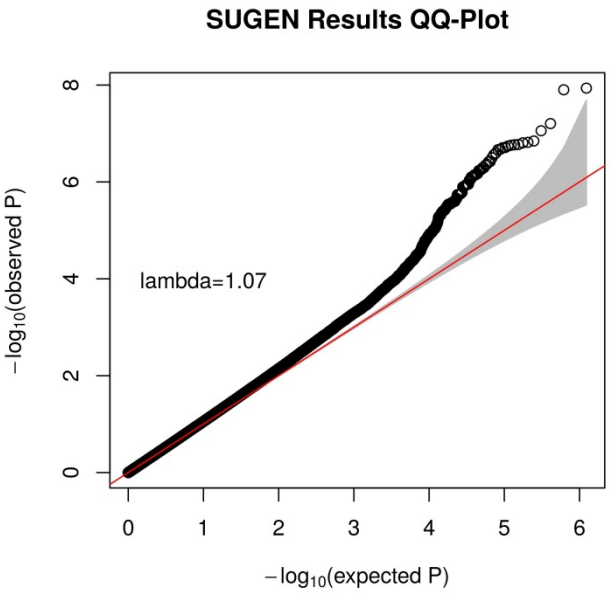
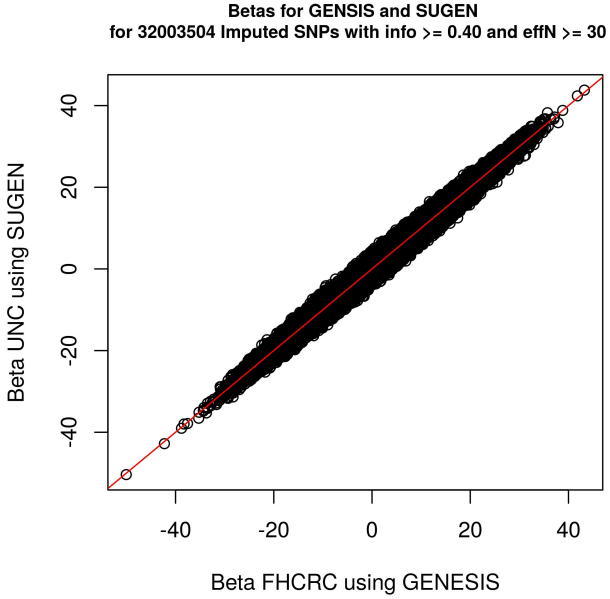


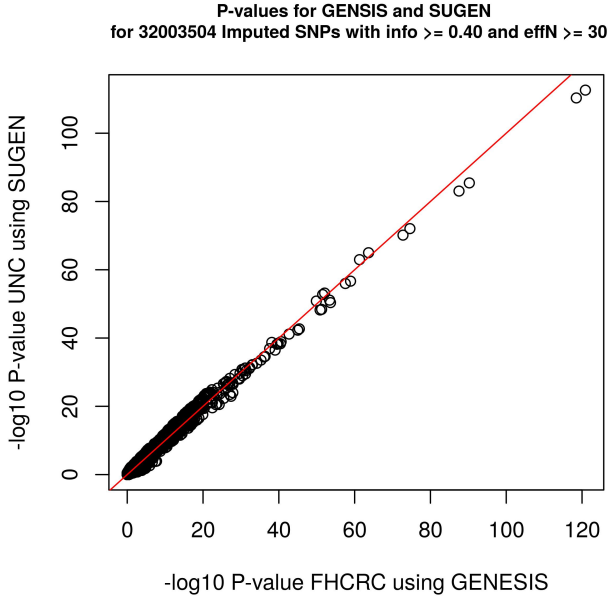


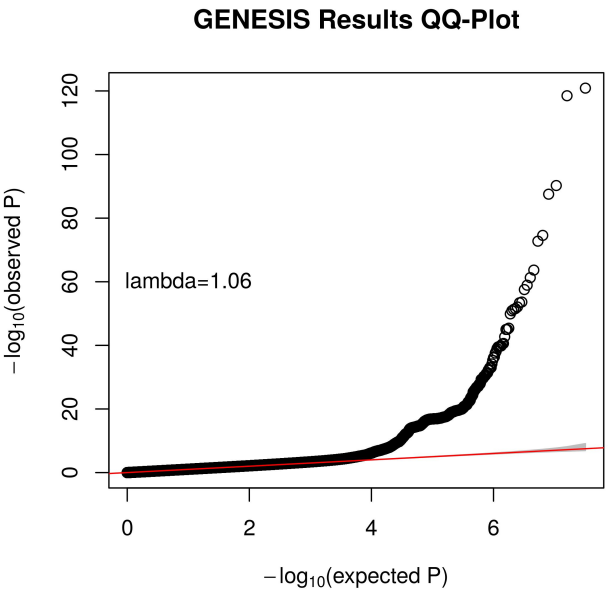


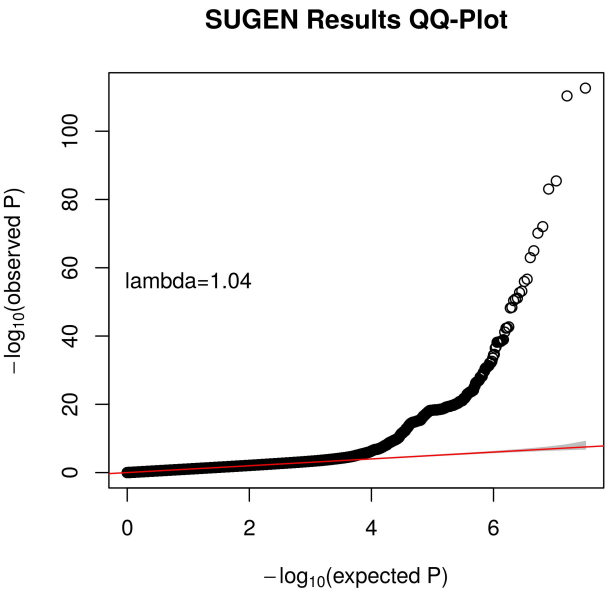


Total Cholesterol Imputed Data









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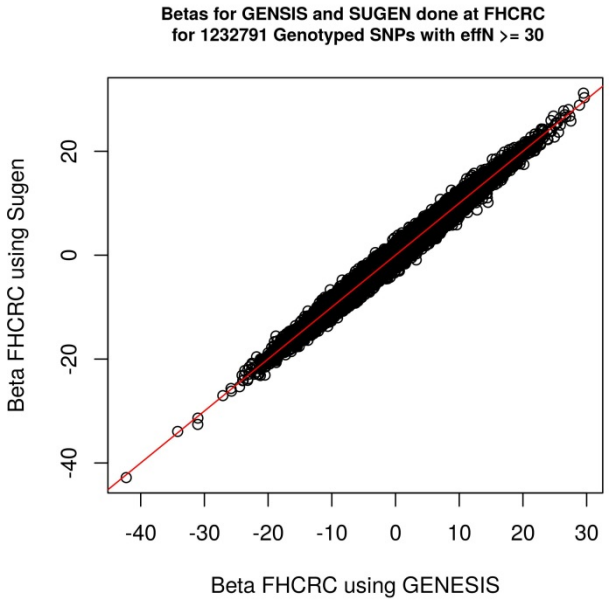
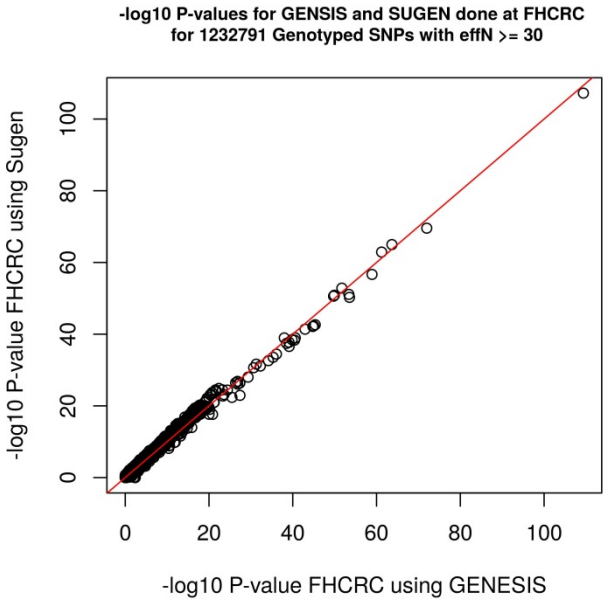
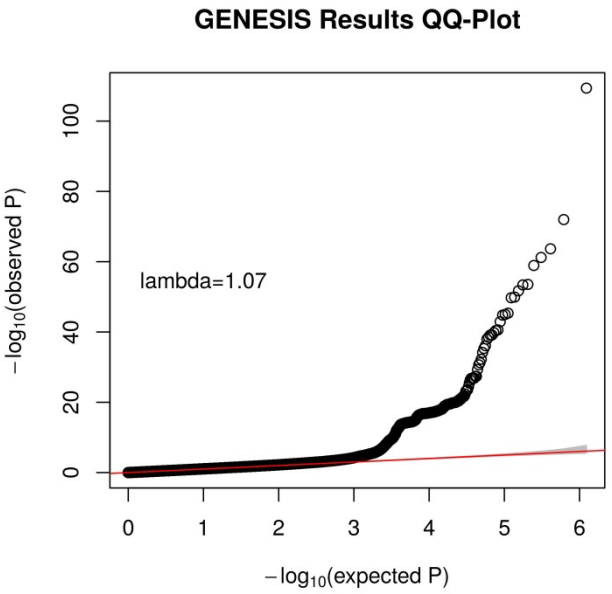
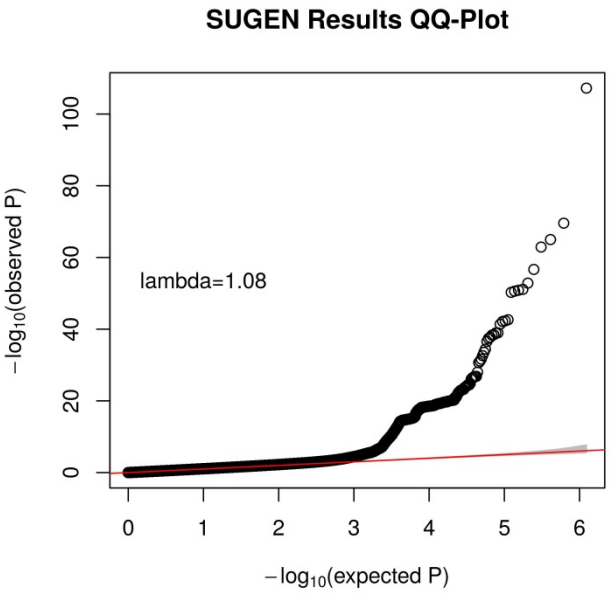
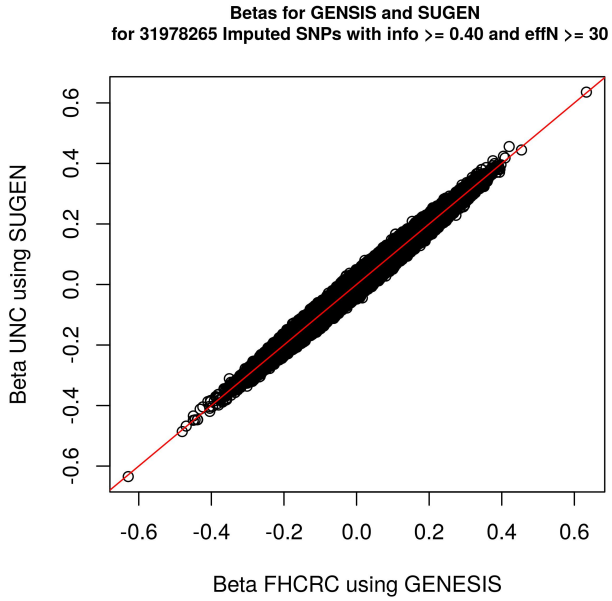


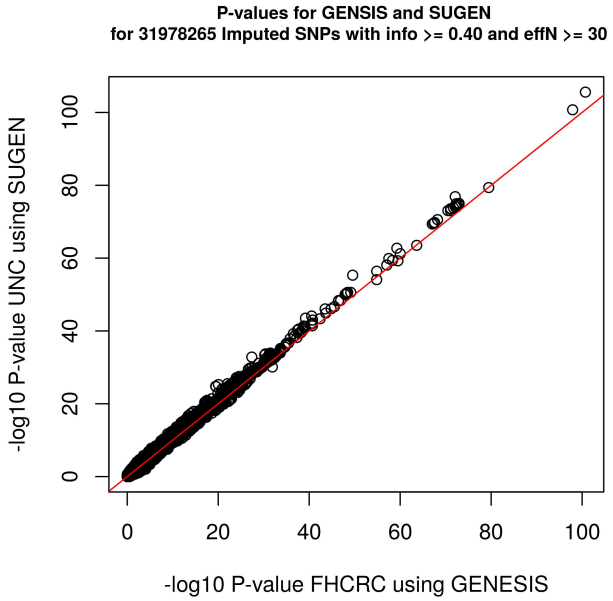


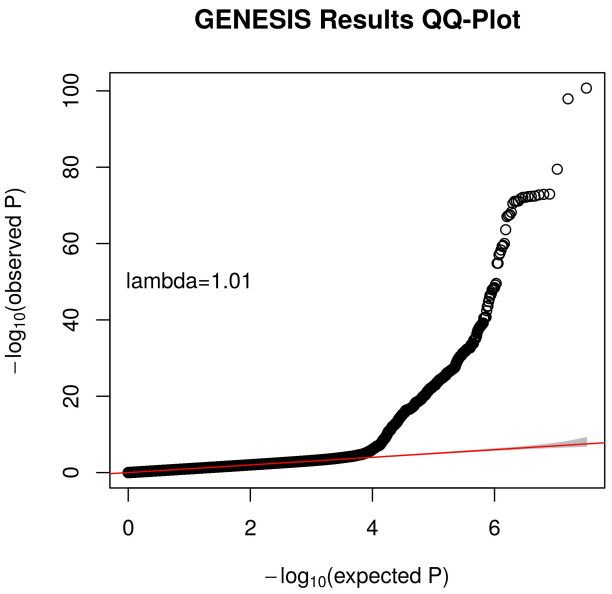


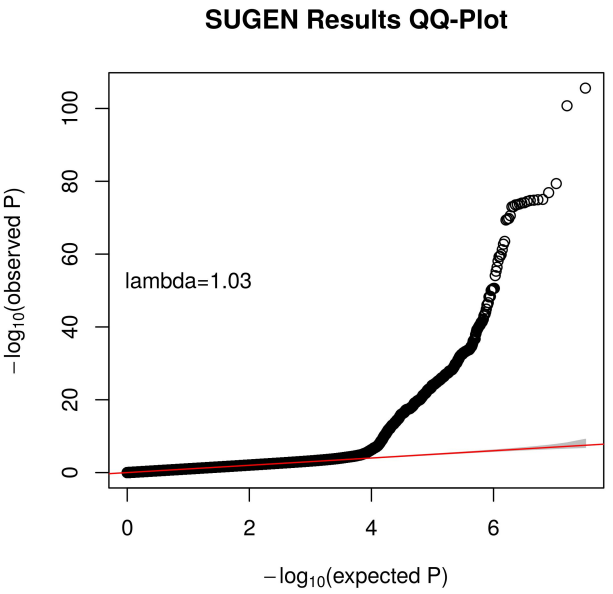


Triglycerides Imputed Data

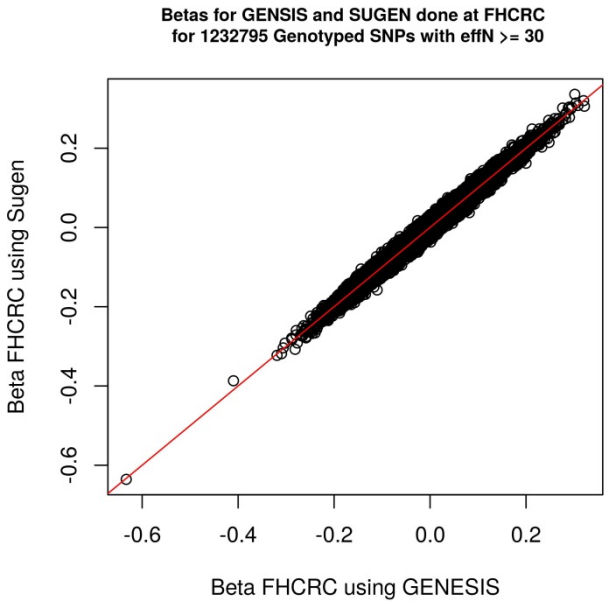


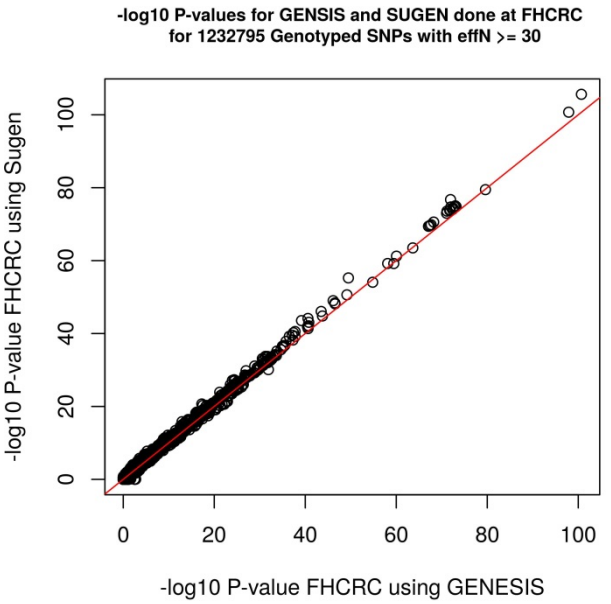


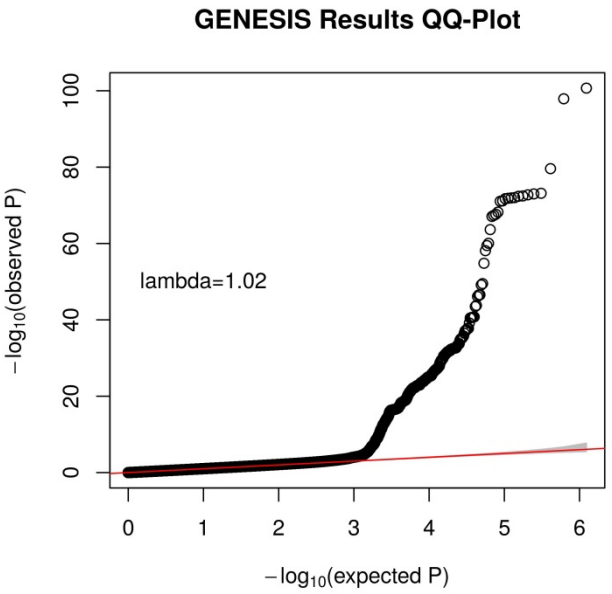


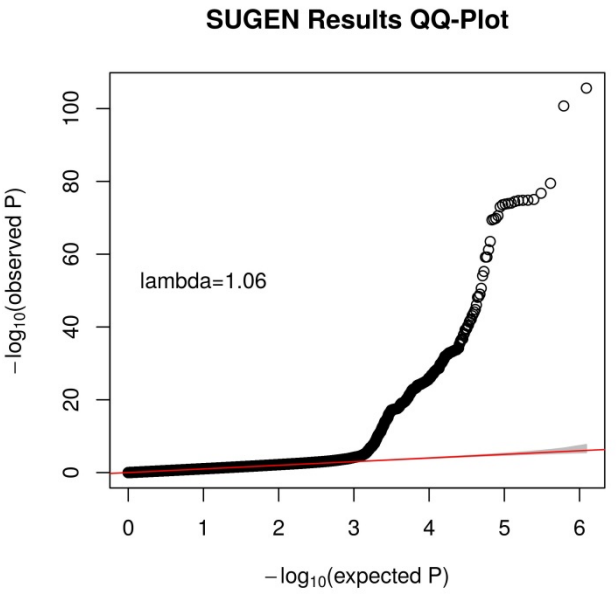


Triglycerides Genotyped Data









Conclusions

Proper control for hidden population stratification, admixture, and relatedness is paramount in the association analysis of the PAGE data.

The two adjustment methods, LMM and GEE, yield similar results.