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Supplemental Data

for eQTL Studies that Accounts for Linkage Disequilibrium between Variants

Joe R. Davis, Laure Fresard, David A. Knowles, Mauro Pala, Carlos D. Bustamante, Alexis Battle, and Stephen B. Montgomery

Supplementary Data

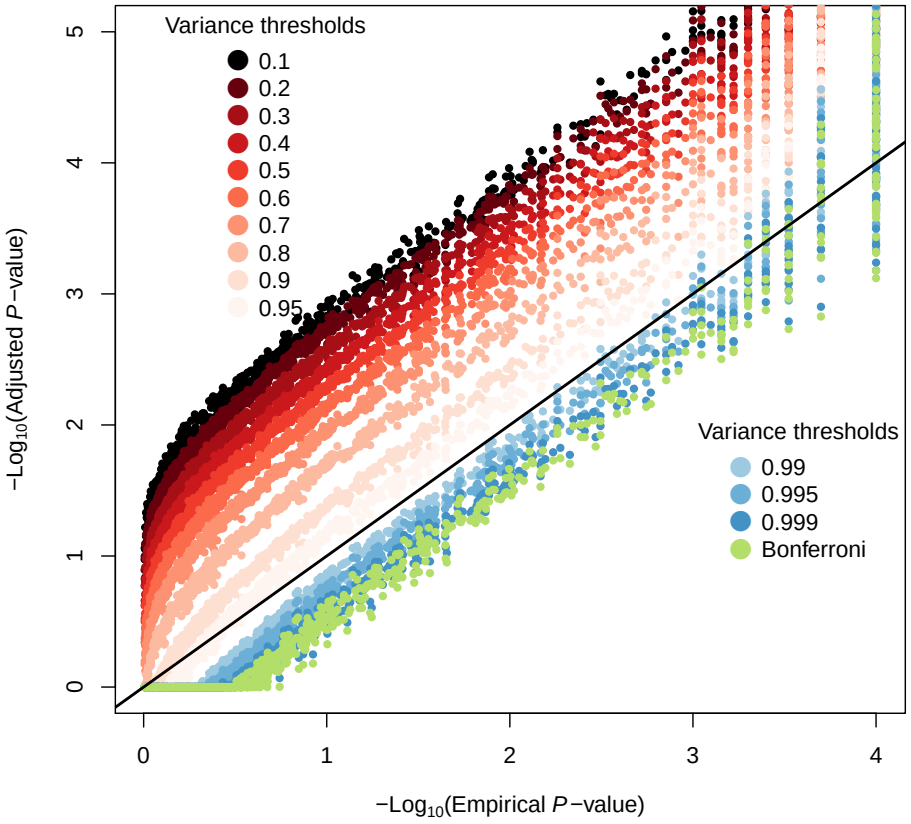

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Figure S1: Comparison of empirical P-values to Bonferroni and eigenMT adjusted P-values at various variance thresholds - GEUVADIS data. Below a certain level of variance explained, we are becoming more and more anti-conservative. We thus advice to at least set the variance parameter at 0.99 (default).

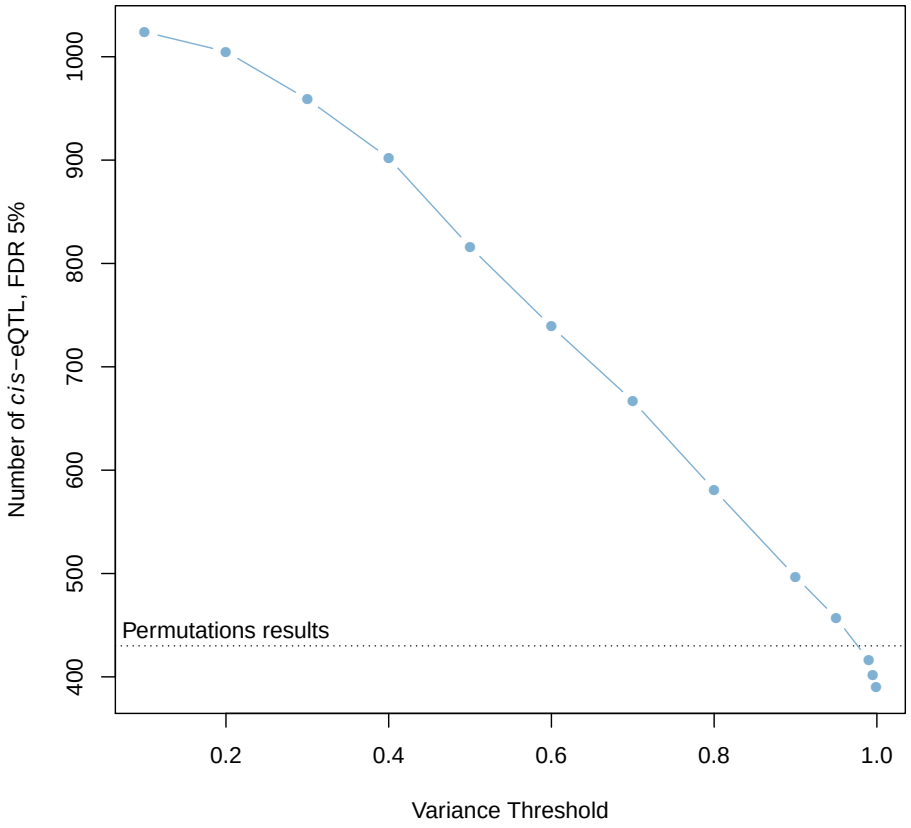

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Figure S2: *cis*-eQTL discoveries at various variance thresholds - GEUVADIS data. In terms of number of discoveries, we confirm what we expect on Figure S1, a variance threshold inferior smaller than 0.99 leads to more *cis*-eQTL discoveries than permutation approach does (dotted line).

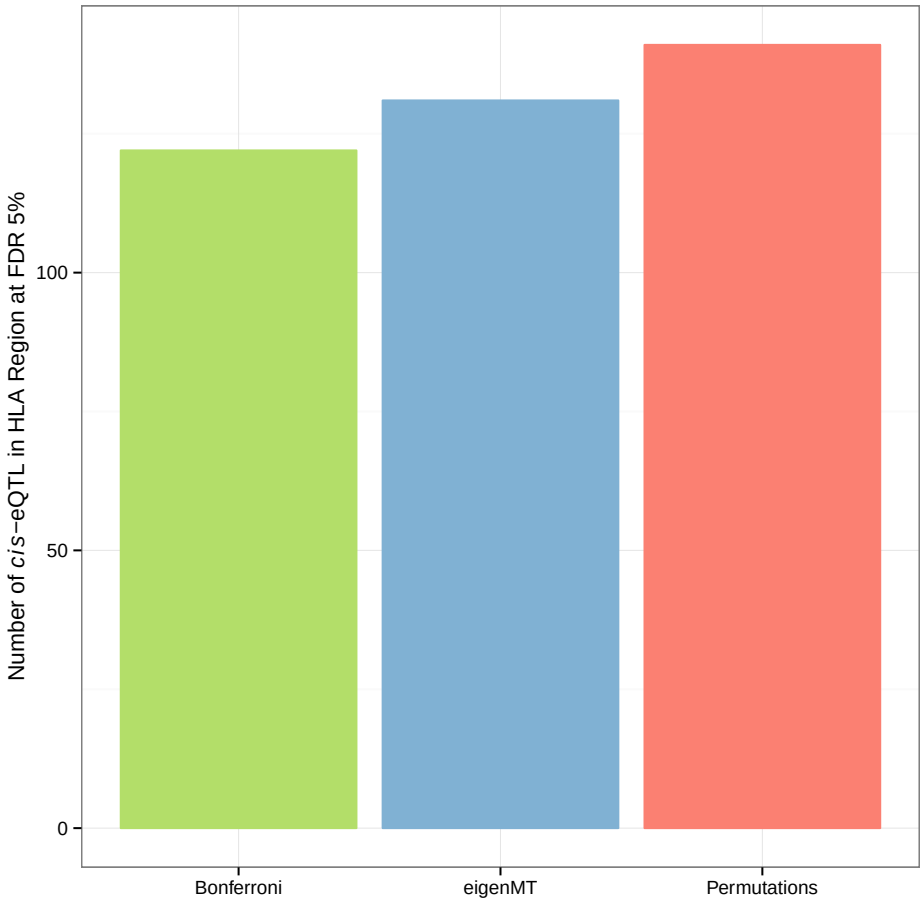

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Figure S3: *cis*-eQTL discoveries for the HLA region by correction method - GEUVADIS data. We demonstrate that eigenMT increases the number of discoveries relative to the Bonferroni correction on the HLA region, known to be computationally challenging.

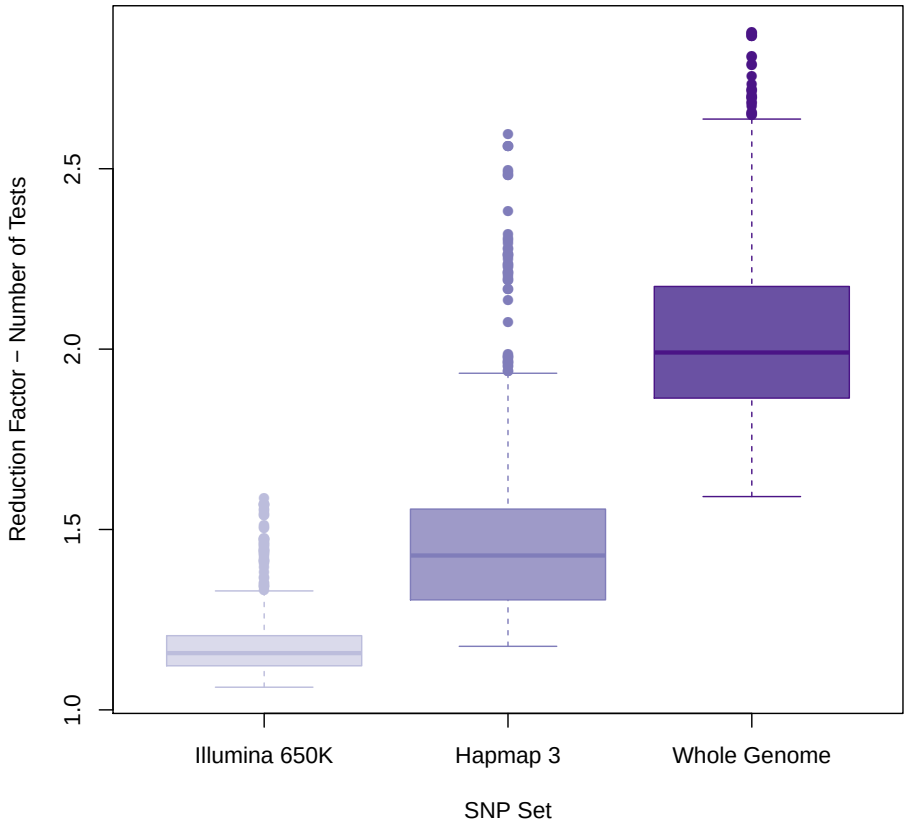

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Figure S4: Fold reduction in effective number of tests from eigenMT across genotyping platforms - GEUVADIS data. As variant density increases (left to right), the reduction factor increases. The increase in number of discoveries from eigenMT will be the greatest for higher densities.

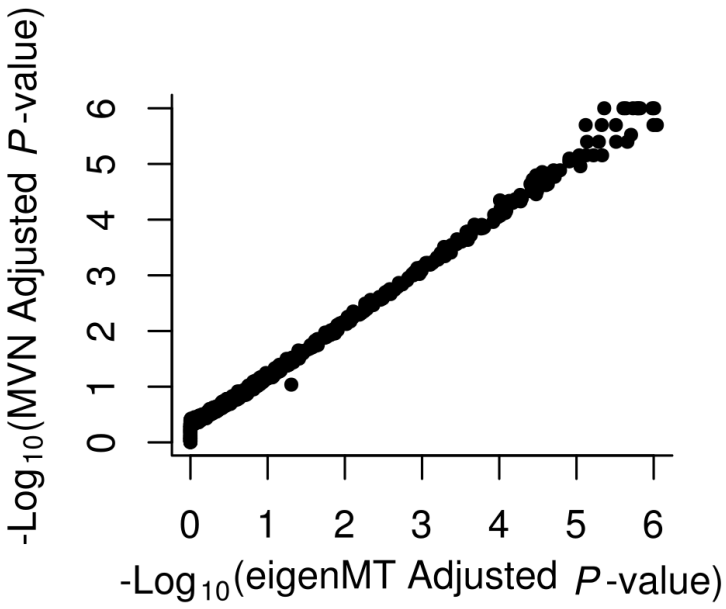

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Figure S5: Comparison of eigenMT and MVN adjusted P-values. We observe a strong correlation between P-values from both methods. Comparison was performed on P-values >10e-6 on GEUVADIS data at sample size 373

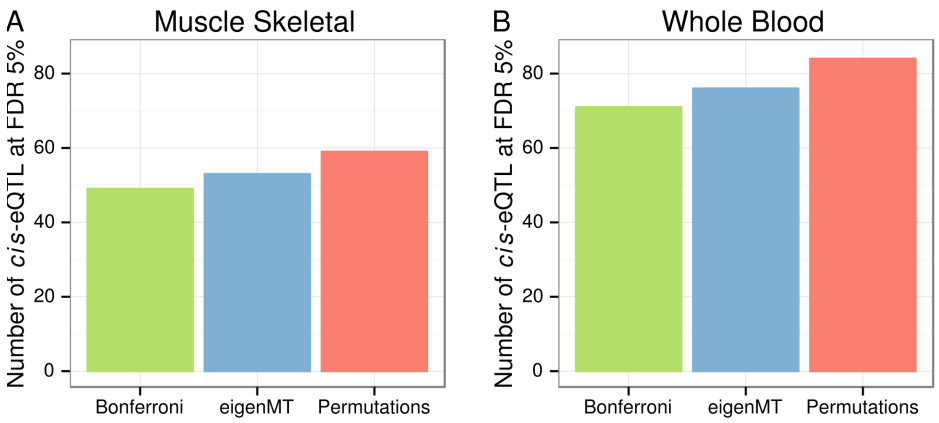

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Figure S6: Number of *cis*-eQTL Discoveries at FDR 5% - GTEx pilot data. (A) Skeletal Muscle. (B) Whole blood. eigenMT is less conservative than Bonferroni correction, independentely of the tissue. eigenMT can be applied with the same genotype matrix on variable phenotypes (different expression in two tissues in this example).

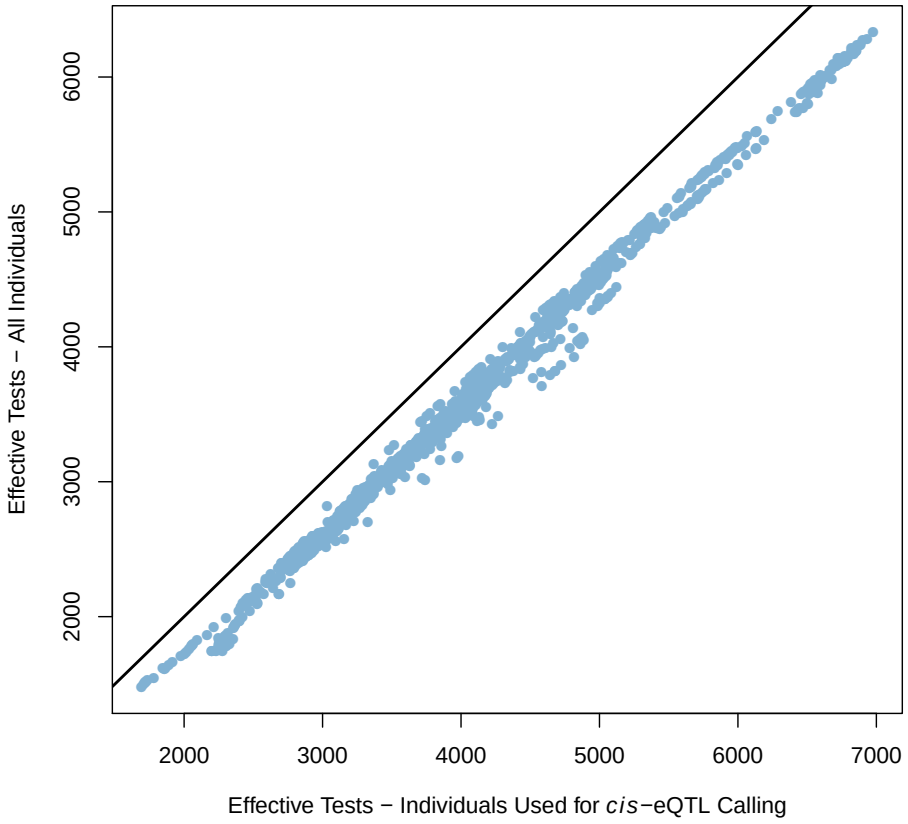

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Figure S7: Comparison of M_{eff} estimates from limited (N = 122) and entire (N = 175) genotype matrices - GTEx pilot data. Incorporating additional individuals in the genotype matrix decreases the estimated number of effective tests due to improved estimation of the genotype correlation matrix.