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Supplemental Data

A Versatile Gene-Based Test

for Genome-wide Association Studies

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Figure S1. Comparison of type-I error rates from PLINK set-based test and VEGAS for 1000 permutations on 9 genes. For each gene, height in 3,611 unrelated individuals was permuted 1000 times. The PLINK set-based test (with parameters `--set-p 1 --set-r2 1 --maf 0.01 --mperm 1000`) and VEGAS was performed for each permutation. The straight diagonal lines indicate a 1-1 relationship.

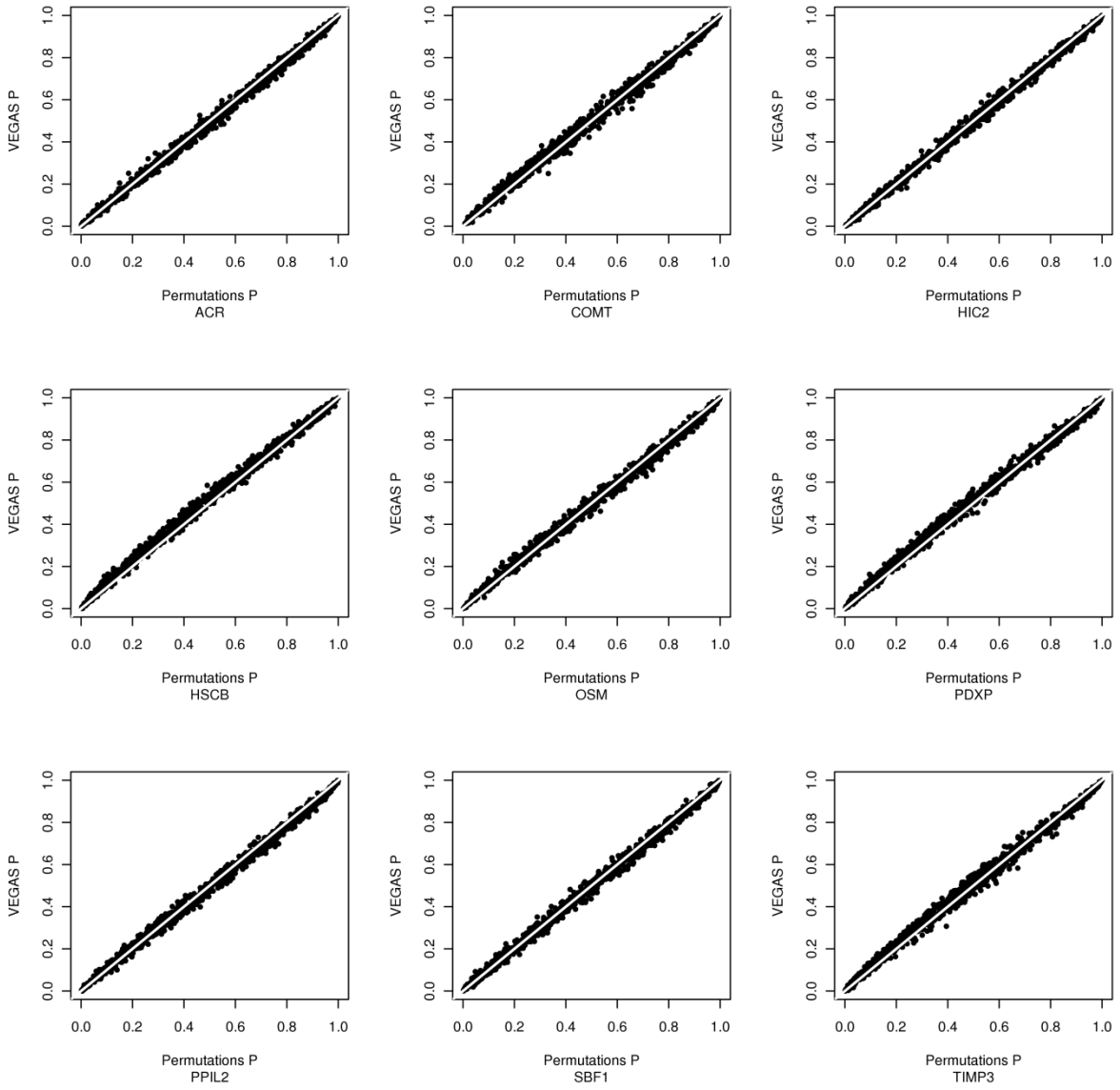

Figure S2. Comparison of the $-\log_{10}$ p-values from the PLINK set-based test and VEGAS on a GWAS of height in 3,611 individuals using (A) HapMap CEU and (B)

HapMap YRI as the reference population. The PLINK set-based test was performed on 413 genes on chromosome 22 with 10^4 permutations (circles) in addition to 7 genes on other chromosomes, selected on the basis of having the smallest p-values from using VEGAS, at 10^6 permutations (triangles). The p-values from VEGAS were obtained by running 10^3 to 10^6 multivariate normal simulations per gene. The straight diagonal lines indicate a 1-1 relationship.