

Evaluation of height as a disease risk factor through a phenome-wide association study of genetically-predicted height

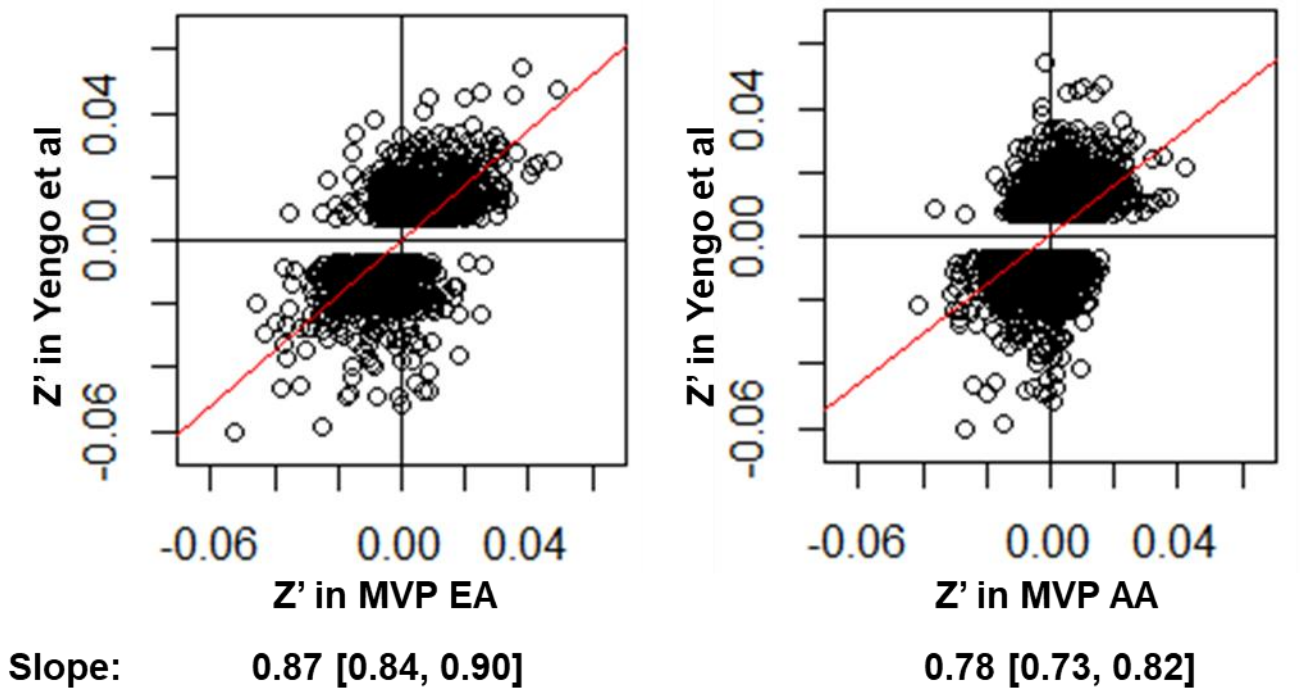
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Online Supplemental Figures

Supplemental Figure 1. Effect size comparison of height-associated variants from source European-ancestry GWAS meta-analysis and non-Hispanic White- and non-Hispanic Black MVP participants.

Supplemental Figure 2. Effect size comparison of associations of genetically-predicted height with clinical traits in MR-PheWAS without and with body mass index (BMI) as a covariate in non-Hispanic White (A) and non-Hispanic Black (B) individuals.

Supplemental Figure 1. Effect size comparison of height-associated variants from source European-ancestry GWAS meta-analysis and non-Hispanic White- and non-Hispanic Black MVP participants.



Supplemental Figure 1. Comparison of standardized effect sizes (Z') for associations with height of variants used in height genetic risk score for MR-PheWAS in Yengo et al (*Human Molecular Genetics* 2018;27(20):3641-3649) and MVP non-Hispanic White (EA, left) and non-Hispanic Black (AA, right) individuals.

Supplemental Figure 2. Effect size comparison of associations of genetically-predicted height with clinical traits in MR-PheWAS without and with body mass index (BMI) as a covariate in non-Hispanic White (A) and non-Hispanic Black (B) individuals.

