

A comprehensive evaluation of polygenic score and  
genotype imputation performances of human SNP  
arrays in diverse populations  
[Supplementary documents]

By Dat Thanh Nguyen, et al

July 4, 2022

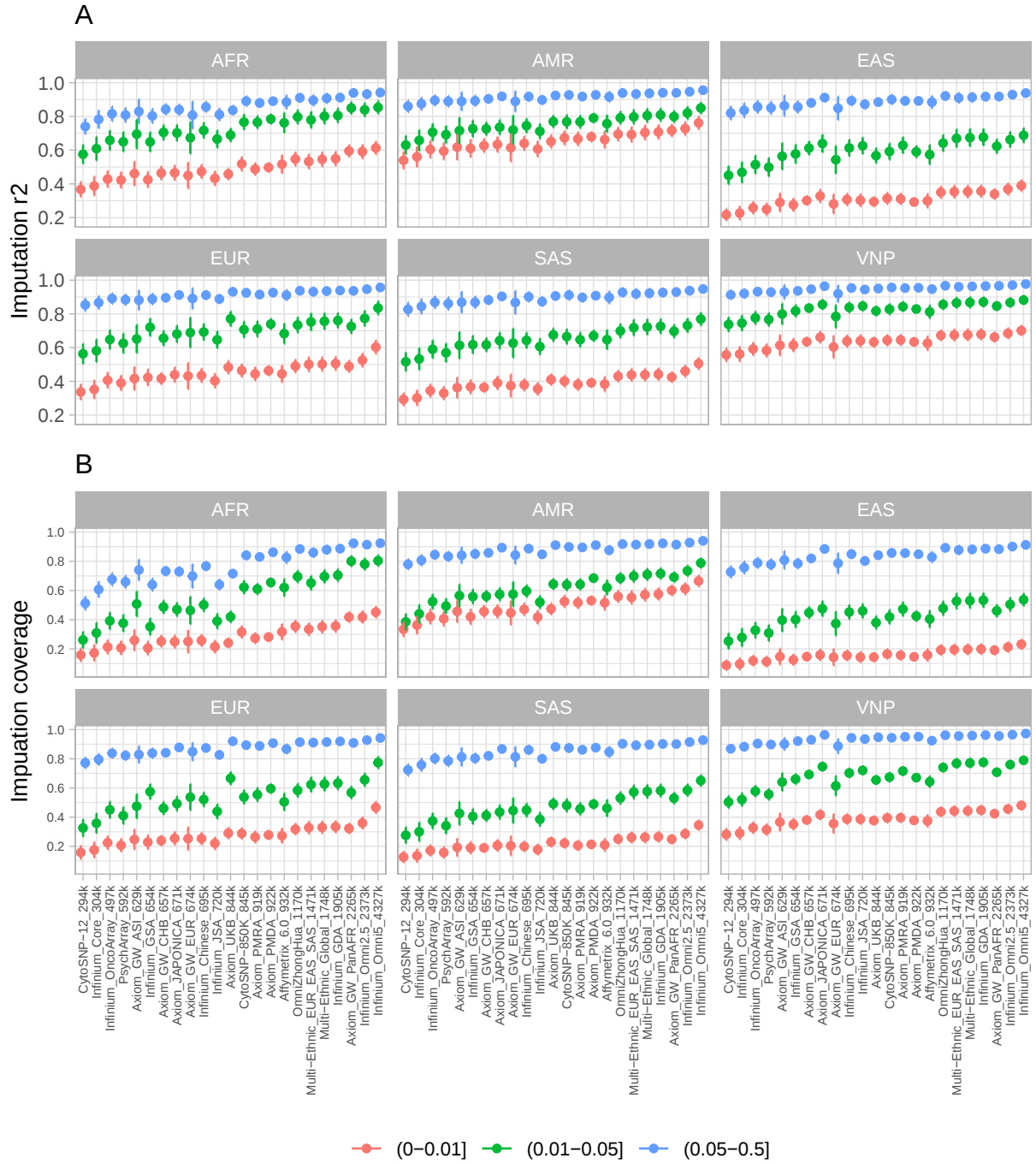


Figure S. 1: A. Mean imputation  $r^2$ , and B. Imputation coverage across 22 autosomes of 23 SNP arrays in three MAF bins including (0-0.01], (0.01-0.05], and (0.05-0.5]. The dots and the vertical lines present the mean and the standard deviation of imputation/ coverage values in 22 autosomes respectively.











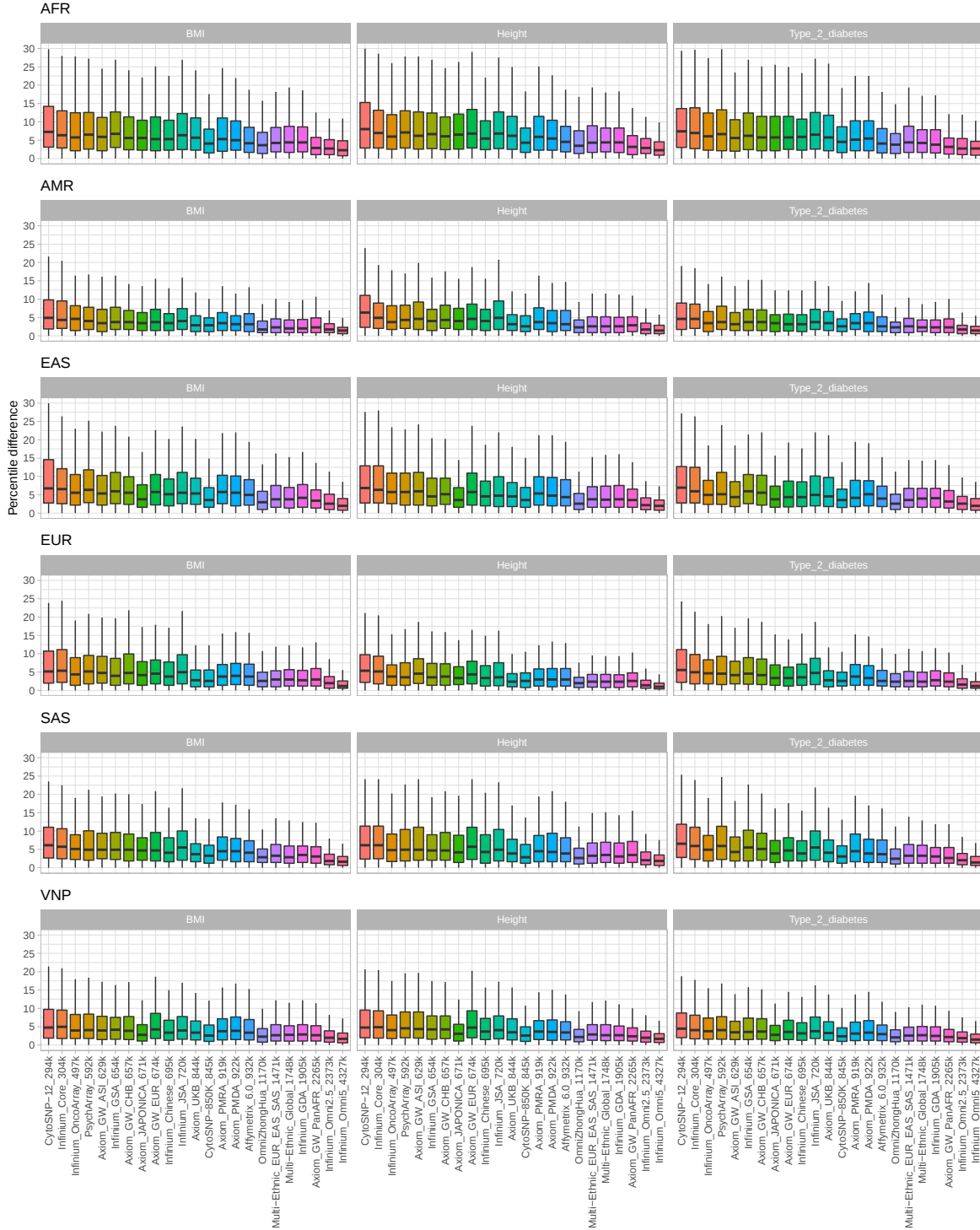


Figure S. 7: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 0.01.

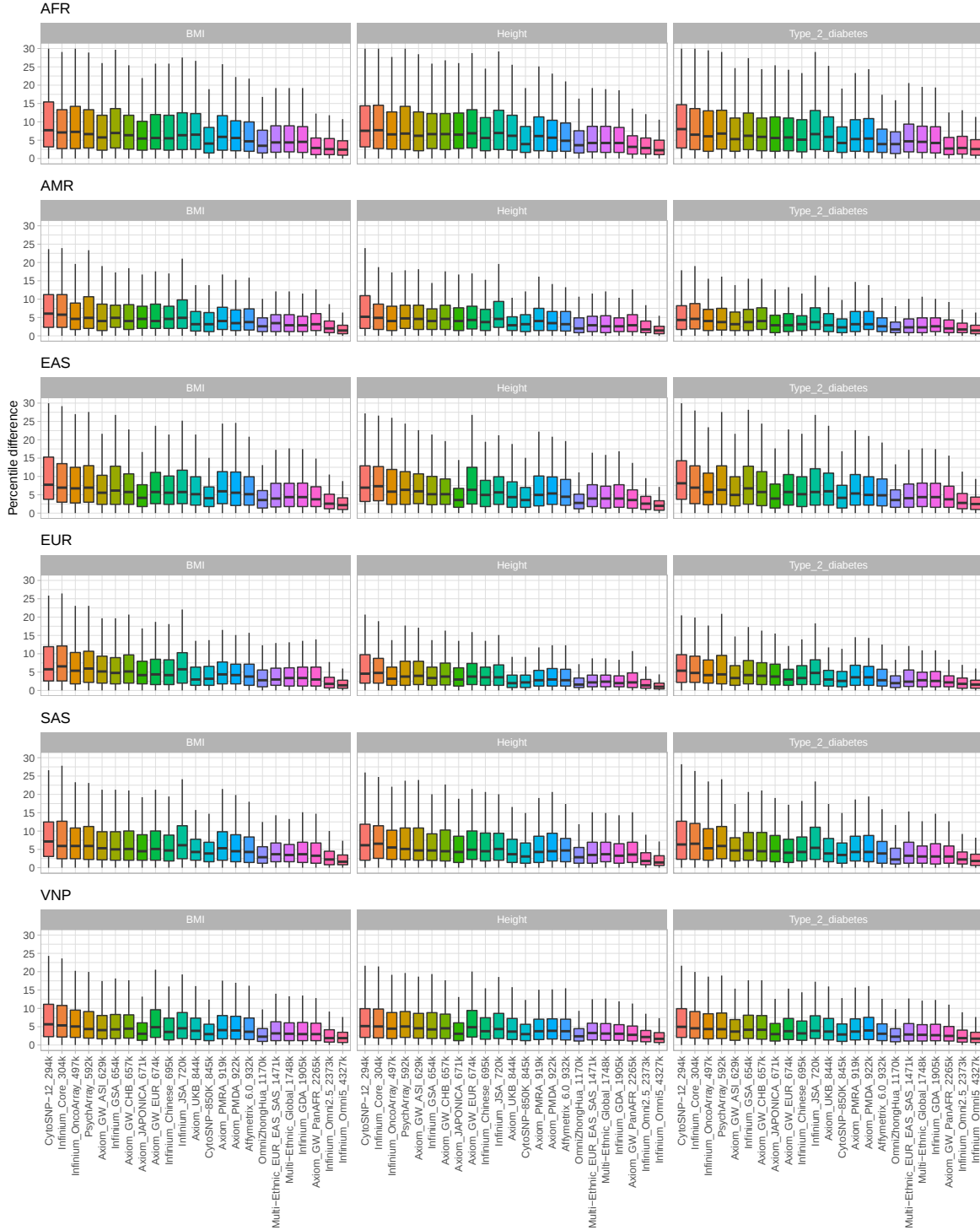


Figure S. 8: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 0.1.

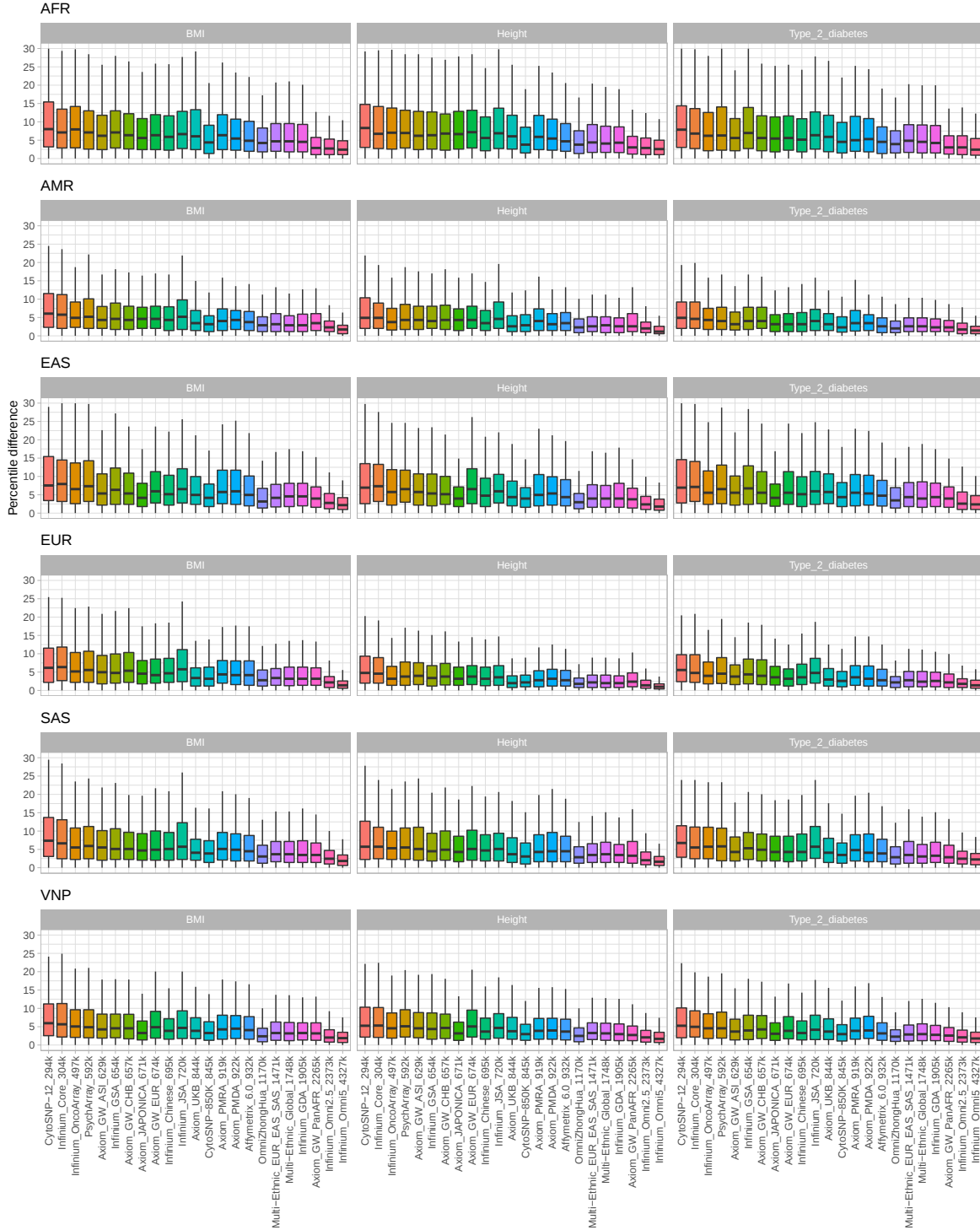


Figure S. 9: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 0.2.

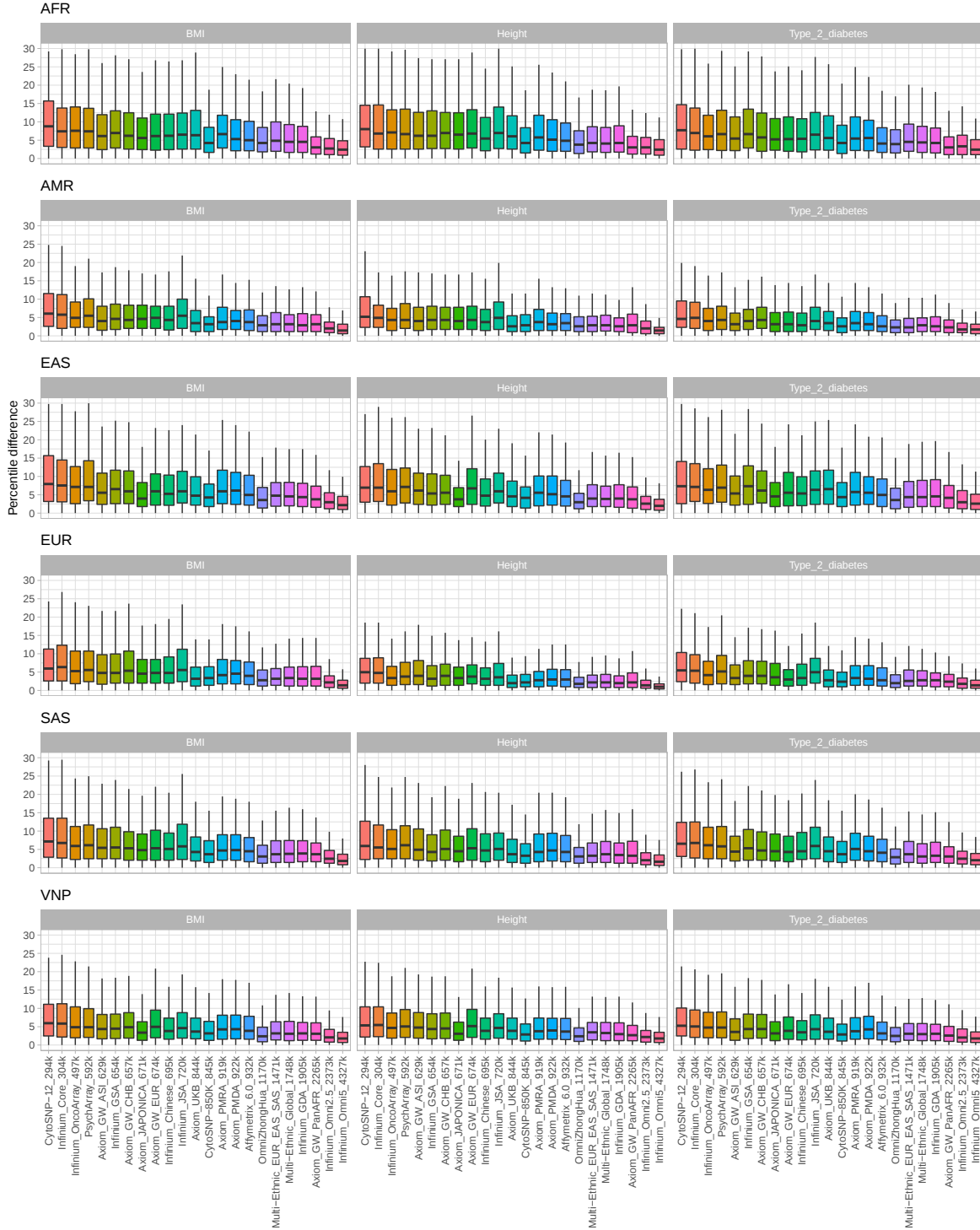


Figure S. 10: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 0.3.

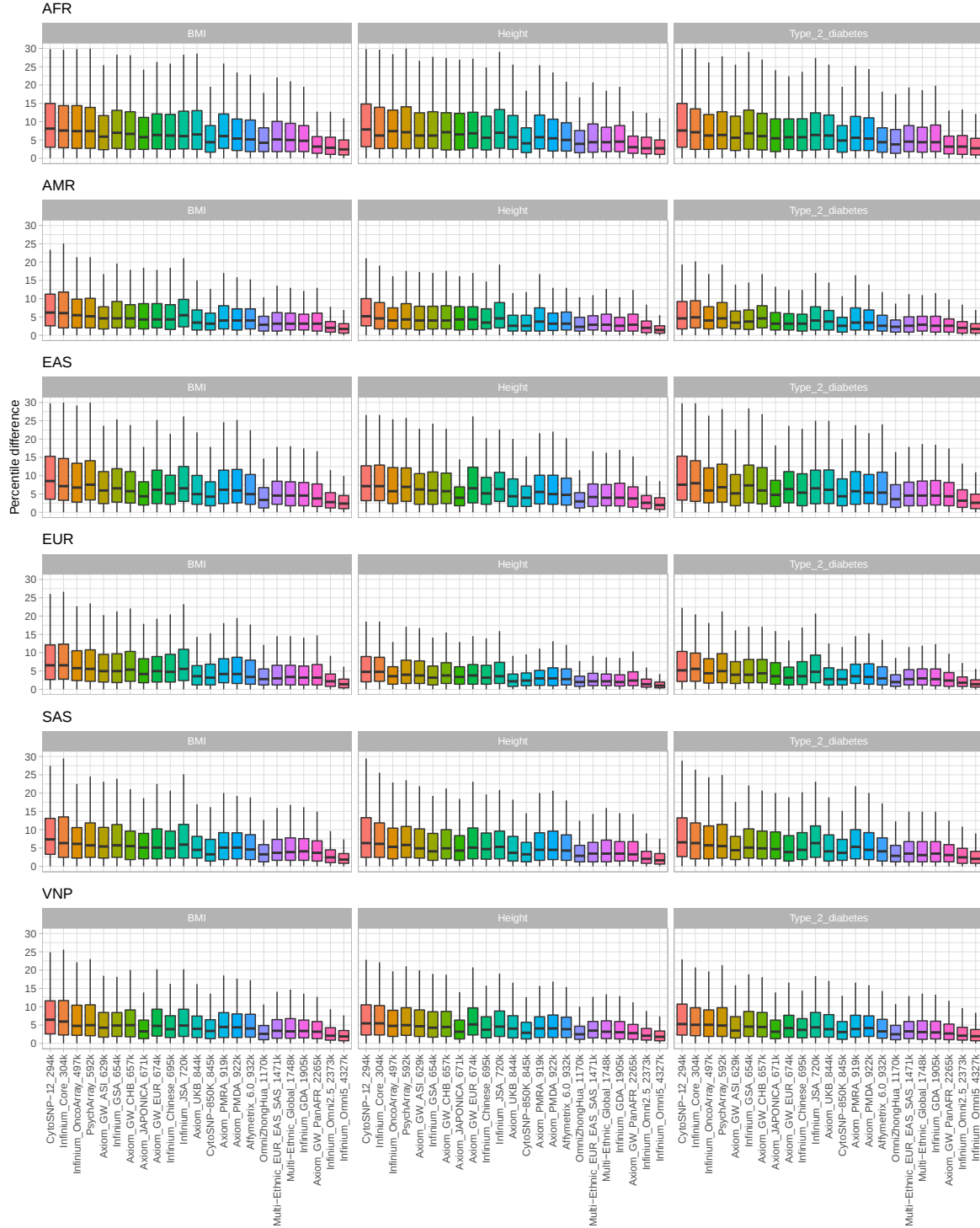


Figure S. 11: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 0.5.

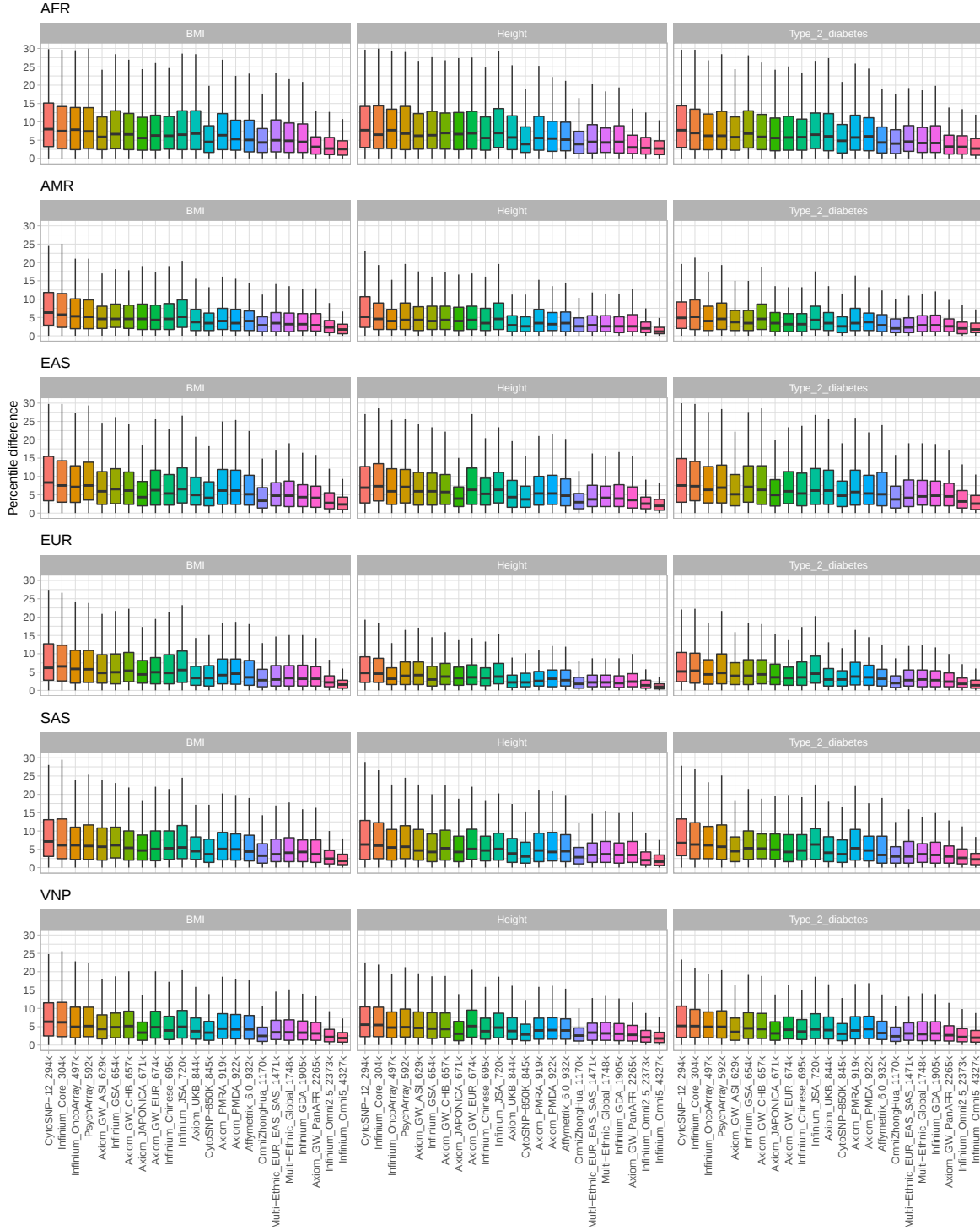


Figure S. 12: Absolute difference of percentile ranking between PGSs estimated from imputed genotyping data of 23 SNP arrays and PGSs estimated from WGS in 6 different populations. The figure shows results of 3 phenotypes including height, BMI, and type 2 diabetes with PRsice p-value setting of 1.