Response to Comment on: Soranzo et al. Common Variants at 10 Genomic Loci Influence Hemoglobin A$_{1C}$ Levels via Glycemic and Nonglycemic Pathways. Diabetes 2010;59:3229–3239

James B. Meigs for Nicole Soranzo and the rest of the MAGIC HbA$_{1c}$ GWAS co-authors

We read with interest the letter by Corcoy (1) with regards to our recent article in *Diabetes* (2). In this article, we calculated net reclassification using the approach of Pencina et al. (3). We counted the proportion of undiagnosed diabetic individuals with unadjusted HbA$_{1c}$ ≥6.5% who had a 7-single nucleotide polymorphism (SNP)-adjusted HbA$_{1c}$ <6.5%, and the proportion of nondiabetic individuals with unadjusted HbA$_{1c}$ <6.5% who had a 7-SNP-adjusted HbA$_{1c}$ ≥ 6.5%. The difference between these proportions is called "net reclassification" and in this instance indicates the overall proportion of a population whose diagnostic status would change based on the influence of the seven nonglycemic genetic variants that we identified.

REFERENCES

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3. Pencina MJ, D'Agostino RB Sr, D'Agostino RB Jr, Vasan RS. Evaluating the added predictive ability of a new marker: from area under the ROC curve to reclassification and beyond. Stat Med 2008;27:157–172; discussion 207–112

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