

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} $\geq 6.5\%$ 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} $\geq 6.5\%$. 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.

ACKNOWLEDGMENTS

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REFERENCES

1. Corcoy R. 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 (Letter). *Diabetes* 2011;60:e10. DOI: 10.2337/db10-1368
2. Soranzo N, Sanna S, Wheeler E, et al. Common variants at 10 genomic loci influence hemoglobin A_{1c} levels via glycemic and nonglycemic pathways. *Diabetes* 2010;59:3229–3239
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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