Correction to: Proteomic profiling identifies novel proteins for genetic risk of severe COVID-19: the Atherosclerosis Risk in Communities Study

This is a correction to: Brian T Steffen, James S Pankow, Pamela L Lutsey, Ryan T Demmer, Jeffrey R Misialek, Weihua Guan, Logan T Cowan, Josef Coresh, Faye L Norby, Weihong Tang, Proteomic profiling identifies novel proteins for genetic risk of severe COVID-19: the Atherosclerosis Risk in Communities Study, *Human Molecular Genetics*, Volume 31, Issue 14, 15 July 2022, Pages 2452–2461, https://doi.org/10.1093/hmg/ddac024

Since the original publication of this paper the authors have identified a minor error in one of the associations reported. A new paragraph (reproduced below) has been added to the results section of the article to address this:

"Upon further investigation, it was found that the ABO protein has a distinct bimodal distribution. Since the linear regression model assumes a normal distribution—particularly for the dependent variable—the association between rs657152 and ABO protein levels became dubious. To better assess whether rs657152 is associated with the bimodally-distributed ABO protein, we first dichotomized protein levels into high and low values (using the 11.5 as the cutpoint); next, we used linear regression to examine the relationship between rs657152 and ABO levels in Black and white participants with adjustments for age, sex, field center, ten principal components of ancestry, and estimated glomerular filtration rate. Significant associations were observed between rs657152 and plasma levels of the ABO protein, but only for those in the 'high' category in Black ($\beta = 0.323$; p = 3.0E-17) and white participants ($\beta = 0.484$; p = 5.0E-172)."