

Correction

PSYCHOLOGICAL AND COGNITIVE SCIENCES, GENETICS

Correction for “Common genetic variants associated with cognitive performance identified using the proxy-phenotype method,” by Cornelius A. Rietveld, Tõnu Esko, Gail Davies, Tune H. Pers, Patrick Turley, Beben Benyamin, Christopher F. Chabris, Valur Emilsson, Andrew D. Johnson, James J. Lee, Christiaan de Leeuw, Riccardo E. Marioni, Sarah E. Medland, Michael B. Miller, Olga Rostapshova, Sven J. van der Lee, Anna A. E. Vinkhuyzen, Najaf Amin, Dalton Conley, Jaime Derringer, Cornelia M. van Duijn, Rudolf Fehrmann, Lude Franke, Edward L. Glaeser, Narelle K. Hansell, Caroline Hayward, William G. Iacono, Carla Ibrahim-Verbaas, Vincent Jaddoe, Juha Karjalainen, David Laibson, Paul Lichtenstein, David C. Liewald, Patrik K. E. Magnusson, Nicholas G. Martin, Matt McGue, George McMahon, Nancy L. Pedersen, Steven Pinker, David J. Porteous, Danielle Posthuma, Fernando Rivadeneira, Blair H. Smith, John M. Starr, Henning Tiemeier, Nicholas J. Timpson, Maciej Trzaskowski, André G. Uitterlinden, Frank C. Verhulst, Mary E. Ward, Margaret J. Wright, George Davey Smith, Ian J. Deary, Magnus Johannesson, Robert Plomin, Peter M. Visscher, Daniel J. Benjamin, David Cesarini, and Philipp D. Koellinger, which appeared in issue 38, September 23, 2014, of *Proc Natl Acad Sci USA* (111:13790–13794; first published September 8, 2014; 10.1073/pnas.1404623111).

The authors note that on page 13790, in the Abstract, line 15, “*KNCMA1*, *NRXN1*, *POU2F3*, and *SCRT*” should instead appear as “*KCNMA1*, *NRXN1*, *POU3F2*, and *SCRT*.” Also, on page 13793, left column, first full paragraph, lines 8–9, “*KNCMA1*, *NRXN1*, *POU2F3*, and *SCRT*” should instead appear as “*KCNMA1*, *NRXN1*, *POU3F2*, and *SCRT*.”

The authors also note that on page 13792, left column, first full paragraph, line 8, the following sentences should be added after “analyses in ref. 11”: “However, one of the SNPs that is significantly associated with cognitive performance after Bonferroni correction (rs1487441) is in linkage disequilibrium with rs9320913, which is one of the genome-wide significant SNPs reported in ref. 11 in their GWAS of educational attainment. The distance between the two SNPs is 30,839 base pairs and the $R^2 = 0.905$ according to the 1,000 Genomes Pilot 1 CEU reference panel (25).”

25. Johnson AD, et al. (2008) SNAP: A web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics* 24(24):2938–2939.

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