

CORRECTION

Open Access



Correction to: Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) Study

Yao Hu^{1†}, Stephanie A. Bien^{1†}, Katherine K. Nishimura^{1†}, Jeffrey Haessler¹, Chani J. Hodonsky², Antoine R. Baldassari², Heather M. Highland², Zhe Wang³, Michael Preuss³, Colleen M. Sitlani⁴, Genevieve L. Wojcik⁵, Ran Tao^{6,7}, Mariaelisa Graff², Laura M. Huckins⁸, Quan Sun⁹, Ming-Huei Chen^{10,11}, Abdou Mousas¹², Paul L. Auer¹³, Guillaume Lettre^{12,14}, the Blood Cell Consortium, Weihong Tang¹⁵, Lihong Qi¹⁶, Bharat Thyagarajan¹⁷, Steve Buyske¹⁸, Myriam Fornage¹⁹, Lucia A. Hindorff²⁰, Yun Li^{9,21}, Danyu Lin⁹, Alexander P. Reiner^{1,4}, Kari E. North², Ruth J. F. Loos^{3,8}, Laura M. Raffield²¹, Ulrike Peters¹, Christy L. Avery² and Charles Kooperberg^{1*}

Correction to: *BMC Genomics* 22, 432 (2021)
<https://doi.org/10.1186/s12864-021-07745-5>

Following publication of the original article [1], it was reported that a number of authors were missing from the authorship list. The following fourteen authors were mistakenly captured as members of the Blood Cell Consortium instead of full authors: Weihong Tang, Lihong Qi, Bharat Thyagarajan, Steve Buyske, Myriam Fornage, Lucia A Hindorff, Yun Li, Danyu Lin, Alexander P Reiner, Kari E North, Ruth J F Loos, Laura M Raffield, Ulrike Peters, Christy L Avery.

They have been added as full authors and the original article has been updated.

Author details

¹Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, USA. ²Department of Epidemiology, Gillings School of Public Health, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ³The Charles Bronfman Institute for Personalized Medicine, Icahn School of Medicine at Mount Sinai, New York, NY, USA. ⁴Cardiovascular Health Research Unit, University of Washington, Seattle, WA, USA. ⁵Stanford University School of Medicine, Stanford, CA, USA. ⁶Department of Biostatistics, Vanderbilt University Medical Center, Nashville, TN, USA. ⁷The Vanderbilt Genetics Institute, Division of Genetic Medicine, Vanderbilt University Medical Center, Nashville, TN, USA. ⁸Pamela Sklar Division of Psychiatric Genomics, Icahn School of Medicine at Mount Sinai, New York, NY, USA. ⁹Department of Biostatistics, Gillings School of Public Health, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ¹⁰The Framingham Heart Study, National Heart, Lung and Blood Institute, Framingham, MA, USA. ¹¹Population Sciences Branch, Division of Intramural Research, National Heart, Lung and Blood Institute, Framingham, MA, USA. ¹²Montreal Heart Institute, Montreal, Quebec, Canada. ¹³School of Public Health, University of Wisconsin–Milwaukee, Milwaukee, WI, USA. ¹⁴Department of Medicine, Faculty of Medicine, Université de Montréal, Montreal, Quebec, Canada. ¹⁵School of Public Health, University of Minnesota, Minneapolis, MN, USA. ¹⁶School of Medicine, University of California Davis, Davis, CA, USA. ¹⁷Medical School of University of Minnesota, Minneapolis, MN, USA. ¹⁸Department of Statistics and Biostatistics, Rutgers University, Piscataway, NJ, USA. ¹⁹Brown Foundation Institute for Molecular Medicine, the University of Texas Health Science Center, Houston, TX, USA. ²⁰Division of Genomic Medicine, NIH National Human Genome Research

The original article can be found online at <https://doi.org/10.1186/s12864-021-07745-5>.

* Correspondence: clk@fredhutch.org

[†]Yao Hu, Stephanie A. Bien and Katherine K. Nishimura contributed equally to this work.

¹Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, USA

Full list of author information is available at the end of the article



© The Author(s). 2021 **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

Institute, Bethesda, MD, USA. ²¹Department of Genetics, Gillings School of Public Health, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA.

Published online: 13 September 2021

Reference

1. Hu Y, Bien SA, Nishimura KK, Haessler J, Hodonsky CJ, Baldassari AR, et al. Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the population architecture using genomics and epidemiology (PAGE) study. *BMC Genomics*. 2021;22(1):432. <https://doi.org/10.1186/s12864-021-07745-5>.