

## Author Correction: A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease

Douglas P. Wightman , Iris E. Jansen, Jeanne E. Savage , Alexey A. Shadrin , Shahram Bahrami, Dominic Holland, Arvid Rongve , Sigrid Børte , Bendik S. Winsvold , Ole Kristian Drange, Amy E. Martinsen, Anne Heidi Skogholt, Cristen Willer , Geir Bråthen , Ingunn Bosnes, Jonas Bille Nielsen, Lars G. Fritsche , Laurent F. Thomas , Linda M. Pedersen , Maiken E. Gabrielsen, Marianne Bakke Johnsen, Tore Wergeland Meisingset, Wei Zhou , Petroula Proitsi , Angela Hodges , Richard Dobson , Latha Velayudhan , Karl Heilbron, Adam Auton, 23andMe Research Team\*, Julia M. Sealock , Lea K. Davis , Nancy L. Pedersen, Chandra A. Reynolds , Ida K. Karlsson, Sigurdur Magnusson , Hreinn Stefansson , Steinunn Thordardottir, Palmi V. Jonsson, Jon Snaedal, Anna Zettergren , Ingmar Skoog, Silke Kern, Margda Waern, Henrik Zetterberg, Kaj Blennow, Eystein Stordal , Kristian Hveem, John-Anker Zwart , Lavinia Athanasiu, Per Selnes, Ingvild Saltvedt , Sigrid B. Sando, Ingun Ulstein, Srdjan Djurovic , Tormod Fladby , Dag Aarsland, Geir Selbæk , Stephan Ripke , Kari Stefansson , Ole A. Andreassen , and Danielle Posthuma 

Correction to: *Nature Genetics* <https://doi.org/10.1038/s41588-021-00921-z>, published online 7 September 2021.

In the version of this article initially published, the Acknowledgements section omitted the text “European Research Council advanced grant (grant no. ERC-2018-AdG GWAS2FUNC 834057 (to D.P.)),” which has now been included in the HTML and PDF versions of the article.









\*A list of authors and their affiliations appears online.

Published online: 20 June 2022

<https://doi.org/10.1038/s41588-022-01126-8>

© The Author(s), under exclusive licence to Springer Nature America, Inc. 2022

## Publisher Correction: UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs

Malgorzata Gozdecka, Eshwar Meduri, Milena Mazan, Konstantinos Tzelepis , Monika Dudek, Andrew J. Knights, Mercedes Pardo , Lu Yu , Jyoti S. Choudhary, Emmanouil Metzakopian, Vivek Iyer, Haiyang Yun, Naomi Park, Ignacio Varela , Ruben Bautista, Grace Collord , Oliver Dovey, Dimitrios A. Garyfallos, Etienne De Braekeleer, Saki Kondo, Jonathan Cooper, Berthold Göttgens , Lars Bullinger, Paul A. Northcott, David Adams, George S. Vassiliou , and Brian J. P. Huntly 

Correction to: *Nature Genetics* <https://doi.org/10.1038/s41588-018-0114-z>, published online 7 May 2018.

In the Supplementary Information initially published online, there were numerous errors in the linking to files for Supplementary Tables 1–31. The correct versions of Supplementary Tables 1–31 and captions have been restored to the HTML version of the article.

### Additional information

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s41588-022-01060-9>.

Published online: 20 June 2022

<https://doi.org/10.1038/s41588-022-01060-9>

© The Author(s), under exclusive licence to Springer Nature America, Inc. 2022