

AUTHOR CORRECTION

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Author Correction: The SEQC2 epigenomics quality control (EpiQC) study

Jonathan Foxx^{1,2†}, Jessica Nordlund^{3,4†}, Claudia Lalancette^{5†}, Ting Gong^{6†}, Michelle Lacey^{7†}, Samantha Lent^{8†}, Bradley W. Langhorst⁹, V. K. Chaithanya Ponnaluri⁹, Louise Williams⁹, Karthik Ramaswamy Padmanabhan⁵, Raymond Cavalcante⁵, Anders Lundmark^{3,4}, Daniel Butler¹, Christopher Mozsary¹, Justin Gurvitch¹, John M. Greally¹⁰, Masako Suzuki¹⁰, Mark Menor⁶, Masaki Nasu⁶, Alicia Alonso^{1,11}, Caroline Sheridan^{1,11}, Andreas Scherer^{4,12}, Stephen Bruinsma¹³, Gosia Golda¹⁴, Agata Muszynska¹⁵, Paweł P. Łabaj¹⁵, Matthew A. Campbell⁹, Frank Vos¹⁶, Amanda Raine^{3,4}, Ulrika Liljedahl^{3,4}, Tomas Axelsson^{3,4}, Charles Wang¹⁷, Zhong Chen¹⁷, Zhaowei Yang^{17,18}, Jing Li^{17,18}, Xiaopeng Yang¹⁹, Hongwei Wang²⁰, Ari Melnick¹, Shang Guo²¹, Alexander Blume²², Vedran Franke²², Inmaculada Ibanez de Caceres^{4,23}, Carlos Rodriguez-Antolin^{4,23}, Rocio Rosas^{4,23}, Justin Wade Davis⁸, Jennifer Ishii¹⁶, Dalila B. Megherbi²⁴, Wenming Xiao²⁵, Will Liao¹⁶, Joshua Xu²⁶, Huixiao Hong²⁶, Baitang Ning²⁶, Weida Tong²⁶, Altuna Akalin²², Yunliang Wang^{21*}, Youping Deng^{6*} and Christopher E. Mason^{1,2,27,28*}

The original article can be found online at <https://doi.org/10.1186/s13059-021-02529-2>.

* Correspondence:

wangyunliang81@163.com; dengyu@hawaii.edu; chm2042@med.cornell.edu

[†]Jonathan Foxx, Jessica Nordlund, Claudia Lalancette, Ting Gong, Michelle Lacey and Samantha Lent are co-first authors.

²¹Department of Neurology, the Second Affiliated Hospital of Zhengzhou University, Zhengzhou 450014, China

⁶Department of Quantitative Health Sciences, University of Hawaii John A. Burns School of Medicine, Honolulu, HI 96813, USA

¹Department of Physiology and Biophysics, Weill Cornell Medicine, New York, NY, USA

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

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Following publication of the original article [1], the authors identified the following errors:

- 1) Jonathan Foxx, Jessica Nordlund, Claudia Lalancette, Ting Gong, Michelle Lacey and Samantha Lent are co-first authors.
- 2) Affiliation 21 was incorrectly published. It should be: Department of Neurology, the Second Affiliated Hospital of Zhengzhou University. Zhengzhou, China, 450014.
- 3) Additional file 1 should contain the supplementary figures. The additional file 1 in this correction article has been updated accordingly.
- 4) Reference 9 in the original article has been updated to: Vaisvila R, Ponnaluri VKC, Sun Z, Langhorst BW, Saleh L, Guan S, Dai N, Campbell MA, Sexton BS, Marks K, Samaranyake M, Samuelson JC, Church HE, Tamanaha E, Corrêa IR Jr., Pradhan S, Dimalanta ET, Evans TC Jr., Williams L, Davis TB. Enzymatic methyl sequencing detects DNA methylation at single-base resolution from picograms of DNA. *Genome Res.* 2021 Jun 17;31(7):1280–9. doi: <https://doi.org/10.1101/g.266551.120>. Epub ahead of print. PMID: 34140313; PMCID: PMC8256858.

The original article [1] has been corrected.



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Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13059-021-02573-y>.

Additional file 1. Contains the supplementary figures (Supplementary Figure 1–14).

Author details

¹Department of Physiology and Biophysics, Weill Cornell Medicine, New York, NY, USA. ²The HRH Prince Alwaleed Bin Talal Bin Abdulaziz Alsaud Institute for Computational Biomedicine, Weill Cornell Medicine, New York, NY, USA. ³Department of Medical Sciences and Science for Life Laboratory, Uppsala University, Uppsala, Sweden. ⁴EATRIS ERIC-European Infrastructure for Translational Medicine, De Boelelaan 1118, 1081, HZ, Amsterdam, The Netherlands. ⁵BRCF Epigenomics Core, University of Michigan Medicine, Ann Arbor, MI 48109, USA. ⁶Department of Quantitative Health Sciences, University of Hawaii John A. Burns School of Medicine, Honolulu, HI 96813, USA. ⁷Tulane University, New Orleans, LA 70118, USA. ⁸AbbVie Genomics Research Center, 1 N. Waukegan Rd, North Chicago, IL 60036, USA. ⁹New England Biolabs, Ipswich, MA 01938, USA. ¹⁰Albert Einstein College of Medicine, Bronx, NY 10461, USA. ¹¹Division of Hematology/Oncology, Department of Medicine, Epigenomics Core Facility, Weill Cornell Medicine, New York, NY, USA. ¹²Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland. ¹³Illumina, Inc, Madison, WI 53705, USA. ¹⁴Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Krakow, Poland. ¹⁵Malopolska Centre of Biotechnology, Jagiellonian University, Krakow, Poland. ¹⁶New York Genome Center, New York, NY 10013, USA. ¹⁷Center for Genomics, School of Medicine, Loma Linda University, Loma Linda, CA 92350, USA. ¹⁸Department of Allergy and Clinical Immunology, State Key Laboratory of Respiratory Disease, Guangzhou Institute of Respiratory Health, the First Affiliated Hospital of Guangzhou Medical University, Guangzhou, Guangdong, China. ¹⁹Department of Neurology, The Second Affiliated Hospital of Zhengzhou University, Zhengzhou 450014, China. ²⁰Department of Medicine, the University of Chicago, Chicago, IL 60637, USA. ²¹Department of Neurology, the Second Affiliated Hospital of Zhengzhou University, Zhengzhou 450014, China. ²²Bioinformatics and Omics Data Science Platform, Berlin Institute for Medical Systems Biology, Max Delbrueck Center for Molecular Medicine, Berlin, Germany. ²³Cancer Epigenetics Laboratory, INGEMM, IdiPAZ, Madrid, Spain. ²⁴CMINDS Research Center, Francis College of Engineering, University of Massachusetts Lowell, Lowell, MA 01854, USA. ²⁵Center for Devices and Radiological Health, Food and Drug Administration, 10903 New Hampshire Ave, Silver Spring, MD 20993, USA. ²⁶Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, Food and Drug Administration, 3900 NCTR Road, Jefferson, AR 72079, USA. ²⁷The Feil Family Brain and Mind Research Institute, New York, NY, USA. ²⁸The WorldQuant Initiative for Quantitative Prediction, Weill Cornell Medicine, New York, NY, USA.

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