

CORRECTION

Open Access



# Correction to: Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions

Indhu-Shree Rajan-Babu<sup>1,2\*</sup>, Junran J. Peng<sup>1</sup>, Readman Chiu<sup>3</sup>, IMAGINE Study<sup>1</sup>, CAUSES Study<sup>1</sup>, Chenkai Li<sup>3,4</sup>, Arezoo Mohajeri<sup>1</sup>, Egor Dolzhenko<sup>5</sup>, Michael A. Eberle<sup>5</sup>, Inanc Birol<sup>1,3</sup> and Jan M. Friedman<sup>1</sup>

**Correction to: *Genome Med* 13, 126 (2021)**

<https://doi.org/10.1186/s13073-021-00932-9>

It was highlighted that in the original article [1] the list of the authors belonging in the IMAGINE and CAUSES Study were erroneously interchanged. The original article has been updated.

## Acknowledgements

We would like to thank all the CAUSES and IMAGINE Study investigators. CAUSES Study investigators include Shelin Adam, Christele Du Souich, Alison Elliott, Anna Lehman, Jill Mwenifumbo, Tanya Nelson, Clara van Karnebeek, Rajan-Babu et al. *Genome Medicine* (2021) 13:126 Page 13 of 15 and Jan Friedman. The CAUSES Study is funded by Mining for Miracles, British Columbia Children's Hospital Foundation, and Genome British Columbia. IMAGINE Study investigators include Patricia Birch, Madeline Couse, Colleen Guimond, Anna Lehman, Jill Mwenifumbo, Clara van Karnebeek, and Jan Friedman. We thank Compute Canada for the Research Allocation Competitions allocation, which facilitated our analysis of the IMAGINE and EGA genomes, and Julia Handra for coordinating the STR molecular testing of the clinical samples.

## Author details

<sup>1</sup>Department of Medical Genetics, University of British Columbia and Children's & Women's Hospital, Vancouver, BC V6H3N1, Canada. <sup>2</sup>Department of Medical and Molecular Genetics, King's College London, Strand, London WC2R 2LS, UK. <sup>3</sup>Canada's Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, BC V5Z4S6, Canada. <sup>4</sup>Bioinformatics Graduate Program, University of British Columbia, Vancouver, BC V6T1Z4, Canada. <sup>5</sup>Illumina Inc., San Diego, CA 92121, USA.

Published online: 13 September 2021

## Reference

1. Rajan-Babu, et al. Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. *Genome Med.* 2021;13:126. <https://doi.org/10.1186/s13073-021-00932-9>.

The original article can be found online at <https://doi.org/10.1186/s13073-021-00932-9>.

\* Correspondence: [indhu.babu@bcchr.ca](mailto:indhu.babu@bcchr.ca)

<sup>1</sup>Department of Medical Genetics, University of British Columbia and Children's & Women's Hospital, Vancouver, BC V6H3N1, Canada

<sup>2</sup>Department of Medical and Molecular Genetics, King's College London, Strand, London WC2R 2LS, UK

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.