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Correction to: Phenotate: crowdsourcing phenotype annotations as exercises in undergraduate classes (Genetics in Medicine, (2020), 22, 8, (1391-1400), 10.1038/s41436-020-0812-7)

Willie H. Chang
Hospital for Sick Children University of Toronto

Pouria Mashouri
Hospital for Sick Children University of Toronto

Alexander X. Lozano
Hospital for Sick Children University of Toronto

Brittney Johnstone
Hospital for Sick Children University of Toronto

Mia Husić
Hospital for Sick Children University of Toronto

See next page for additional authors

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Willie H. Chang, MSc, Pouria Mashouri, MSc, Alexander X. Lozano, MSc, Brittney Johnstone, MSc, CGC, Mia Husić, MSc, Annie Olry, PhD, Sylvie Maiella, PhD, Tugce B. Balci, MD, Sarah L. Sawyer, PhD, MD, Peter N. Robinson, MD, MSc, Ana Rath, MD and Michael Brudno, PhD

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The original version of this Article contained an incorrect supplementary file in the Excel file format. This has now been replaced in the HTML version of the Article.

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Correction: Alternative mRNA splicing can attenuate the pathogenicity of presumed loss-of-function variants in *BRCA2*

Romy L. S. Mesman, MSc, Fabienne M. G. R. Calléja, MSc, Miguel de la Hoya, PhD, Peter Devilee, PhD, Christi J. van Asperen, MD, PhD, Harry Vrieling, PhD and Maaike P. G. Vreeswijk, PhD

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Correction to: *Genetics in Medicine* 2020; https://doi.org/10.1038/s41436-020-0814-5, published online 13 May 2020

The original version of this Article omitted an essential reference ("Meulemans L, Mesman RLS, Caputo SM, et al. Skipping nonsense to maintain function: the paradigm of BRCA2 exon 12. Cancer Res. 2020;80(7):1374–1386. DOI: 10.1158/0008-5472.CAN-19-2491"). This has now been added in both the PDF and HTML versions of the Article.

In addition, the original version of this Article contained a typo in the sentence "However, two variants in respectively the splice acceptor site (c.517–2A>G) and donor site (c.631+2T>G) of exon 7 were classified as pathogenic based..." that was incorrectly given as "However, two variants in respectively the splice donor site (c.517–2A>G) and acceptor site (c.631+2T>G) of exon 7 were classified as pathogenic based...". Where "donor" should be "acceptor" and vice versa. This has now been corrected in both the PDF and HTML versions of the Article.