

CORRECTION

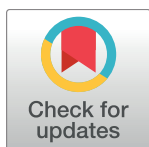
# Correction: Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe

François Blanquart, Chris Wymant, Marion Cornelissen, Astrid Gall, Margreet Bakker, Daniela Bezemer, Matthew Hall, Mariska Hillebregt, Swee Hoe Ong, Jan Albert, Norbert Bannert, Jacques Fellay, Katrien Fransen, Annabelle J. Gourlay, M. Kate Grabowski, Barbara Günsenheimer-Bartmeyer, Huldrych F. Günthard, Pia Kivelä, Roger Kouyos, Oliver Laeyendecker, Kirsi Liitsola, Laurence Meyer, Kholoud Porter, Matti Ristola, Ard van Sighem, Guido Vanham, Ben Berkhout, Paul Kellam, Peter Reiss, Christophe Fraser, BEEHIVE collaboration

The affiliation for the 25th author is incorrect. Matti Ristola is not affiliated with #19 but with #17 Department of Infectious Diseases, Helsinki University Hospital, Helsinki, Finland. Please see the full, correct byline and affiliations below.

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## Reference

1. Blanquart F, Wymant C, Cornelissen M, Gall A, Bakker M, Bezemer D, et al. (2017) Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. *PLoS Biol* 15(6): e2001855. <https://doi.org/10.1371/journal.pbio.2001855> PMID: 28604782