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Publisher Correction: Comparison of the Hi-C, GAM and SPRITE methods using polymer models of chromatin

Luca Fiorillo, Francesco Musella, Mattia Conte, Rieke Kempfer, Andrea M. Chiariello, Simona Bianco, Alexander Kukalev, Ibai Irastorza-Azcarate, Andrea Esposito, Alex Abraham, Antonella Prisco, Ana Pombo and Mario Nicodemi

Correction to: *Nature Methods* https://doi.org/10.1038/s41592-021-01135-1, published online 7 May 2021.

This paper was originally published under standard Springer Nature license (© The Author(s), under exclusive licence to Springer Nature America, Inc.). It is now available as an Open Access paper under a Creative Commons Attribution 4.0 International license, © The Author(s). The error has been corrected in the HTML and PDF versions of the article.

https://doi.org/10.1038/s41592-021-01251-y

Publisher Correction: Towards resolving proteomes in single cells

Arunima Singh

Correction to: *Nature Methods* https://doi.org/10.1038/s41592-021-01243-y, published online 5 August 2021.

In the version of this Research Highlight initially published, the third paragraph, first sentence was unclear. The original sentence read, in part, "Nikolai Slavov and his research group at Northeastern University previously developed SCoPE-MS"; this sentence has been amended to read: "Nikolai Slavov of Northeastern University, along with Bogdan Budnik of Harvard University, and their colleagues, previously developed SCoPE-MS (Single-Cell ProtEomics by Mass Spectrometry)—a single-cell proteomics method that originally made use of carrier cells with isobaric labeled proteins mixed with single cells of interest to reduce sample loss."

The original Research Highlight has been corrected in the online version of the paper.

https://doi.org/10.1038/s41592-021-01298-x