

AUTHOR CORRECTION

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Author Correction: A benchmark of computational methods for correcting biases of established and unknown origin in CRISPR-Cas9 screening data

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The original article can be found online at <https://doi.org/10.1186/s13059-024-03336-1>.

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Following publication of the original article [1], the authors identified an omission in the completing interests section. The omitted text is given in bold below.

Competing interests

FI receives funding from Open Targets, a public-private initiative involving academia and industry and performs consultancy for the joint CRUK-AstraZeneca Functional Genomics Centre and for Mosaic TX. JD is a consultant for and holds equity in Jumble Therapeutics. CDC performs consultancy for Droplet Biosciences and is a shareholder of Novartis. **FV receives research support from the Dependency Map Consortium, Riva Therapeutics, Bristol Myers Squibb, Merck, Illumina, and Deerfield Management. FV is on the scientific advisory board of GSK, is a consultant and holds equity in Riva Therapeutics and is a co-founder and holds equity in Jumble Therapeutics.** All other authors declare that they have no competing interests.

The original article [1] is corrected.

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Reference

1. Vinceti A, Iannuzzi RM, Boyle I, et al. A benchmark of computational methods for correcting biases of established and unknown origin in CRISPR-Cas9 screening data. *Genome Biol.* 2024;25:192. <https://doi.org/10.1186/s13059-024-03336-1>.



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