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## Erratum to: The advantages of SMRT sequencing

Richard J. Roberts<sup>1\*</sup>, Mauricio O. Carneiro<sup>2</sup> and Michael C. Schatz<sup>3</sup>

## **Erratum**

It has been highlighted that the original manuscript [1] has been published in duplicate and indexed on the SpringerLink platform. The duplicate article [2] is not the official version of this manuscript. We apologise for any confusion caused by this discrepancy and acknowledge the former, original manuscript [1], also indexed on the PubMed platform, as the official version of this work on behalf of the author.

The publisher apologises for these errors.

## **Author details**

<sup>1</sup>New England Biolabs, 240 County Road, Ipswich, MA 01938, USA. <sup>2</sup>Broad Institute of Harvard and MIT, Cambridge, MA 02142, USA. <sup>3</sup>Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11743, USA.

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## References

- Roberts RJ, Carneiro MO, Schatz MC. The advantages of SMRT sequencing. Genome biology. 2013;14(6):405.
- Roberts RJ, Carneiro MO, Schatz MC. The advantages of SMRT sequencing. Genome biology. 2013;14(7):405.

<sup>&</sup>lt;sup>1</sup>New England Biolabs, 240 County Road, Ipswich, MA 01938, USA



<sup>\*</sup> Correspondence: roberts@neb.com