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CORRECTION

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# Correction to: Whole genome sequencing *Mycobacterium tuberculosis* directly from sputum identifies more genetic diversity than sequencing from culture

Camus Nimmo<sup>1,2\*</sup> , Liam P. Shaw<sup>3,4</sup>, Ronan Doyle<sup>1,5</sup>, Rachel Williams<sup>1</sup>, Kayleen Brien<sup>2</sup>, Carrie Burgess<sup>1</sup>, Judith Breuer<sup>1</sup>, Francois Balloux<sup>3</sup> and Alexander S. Pym<sup>2</sup>

**Correction to: BMC Genomics (2019) 20:389**  
**DOI: 10.1186/s12864-019-5782-2**

Following the publication of this article [1], the authors reported that one of the authors' names was type-set incorrectly in the authorship list.

In this Correction article the incorrect and correct author name are shown. The original publication of this article has been corrected.

Originally the author name was published as:

- Rona Doyle

The correct author name is:

- Ronan Doyle

The publisher apologizes to the authors and readers for any inconvenience caused by this error.

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1. Nimmo C, et al. Whole genome sequencing *Mycobacterium tuberculosis* directly from sputum identifies more genetic diversity than sequencing from culture. *BMC Genomics*. 2019;20:389 <https://doi.org/10.1186/s12864-019-5782-2>.

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