SCIENTIFIC REPORTS

OPEN

Author Correction: Direct RNA Sequencing of the Coding Complete Influenza A Virus Genome

Published online: 19 October 2018

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Correction to: *Scientific Reports* https://doi.org/10.1038/s41598-018-32615-8, published online 26 September 2018

In the original version of this Article, Matthew W. Keller and Benjamin L. Rambo-Martin were omitted as equally contributing authors.

The original version of this Article also contained typographical errors.

In the legend of Table 1 where:

"Influenza A/Florida/20/2018 (H1N1pdm09), A/Texas/50/2012 (H3N2), A/chicken Ghana/20/2017 (HPAI H5N1) and A/British Columbia/1/2015 (LPAI H7N9) viruses were used to demonstrate this method's broad utility across contemporary influenza A viruses of current clinical significance".

now reads:

"Influenza A/Florida/20/2018 (H1N1pdm09), A/Texas/50/2012 (H3N2), A/chicken Ghana/20/2015 (HPAI H5N1) and A/British Columbia/1/2015 (LPAI H7N9) viruses were used to demonstrate this method's broad utility across contemporary influenza A viruses of current clinical significance".

Additionally, in the Results section under subheading 'Sequencing RNA from crude versus purified influenza rA/Puerto Rico/8/1934 (H1N1) virus' where:

"The read level accuracy was 86.3 ± 0.3%, and the consensus sequence was 98.97 ± 0.01% in concordance with consensus sequence generated using our standardized multi-segment reverse transcriptase polymerase chain reaction (M-RTPCR)[15,16], Nextera, and MiSeq approach (Tables 2 and S3)".

now reads:

"The read level accuracy was 86.2 ± 0.3%, and the consensus sequence was 98.97 ± 0.01% in concordance with consensus sequence generated using our standardized multi-segment reverse transcriptase polymerase chain reaction (M-RTPCR)[15,16], Nextera, and MiSeq approach (Tables 2 and S3)".

These errors have now been corrected in the PDF and HTML versions of the paper.

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