







Author Correction: Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance

Xianding Deng, Asmeeta Achari, Scot Federman, Guixia Yu, Sneha Somasekar, Inês Bártolo, Shigeo Yagi, Placide Mbala-Kingebeni, Jimmy Kapetshi, Steve Ahuka-Mundeke, Jean-Jacques Muyembe-Tamfum, Asim A. Ahmed, Vijay Ganesh, Manasi Tamhankar, Jean L. Patterson, Nicaise Ndembi, Dora Mbanya, Lazare Kaptue, Carole McArthur, José E. Muñoz-Medina , Cesar R. Gonzalez-Bonilla , Susana López , Carlos F. Arias , Shaun Arevalo, Steve Miller, Mars Stone, Michael Busch, Kristina Hsieh, Sharon Messenger, Debra A. Wadford, Mary Rodgers, Gavin Cloherty, Nuno R. Faria , Julien Thézé, Oliver G. Pybus, Zoraima Neto, Joana Morais, Nuno Taveira, John R. Hackett Jr. and Charles Y. Chiu 

Correction to: *Nature Microbiology* <https://doi.org/10.1038/s41564-019-0637-9>, published online 13 January 2020.

In the version of this Article originally published, the sentence beginning “We also used MPSSE to enrich...” should have stated that the samples were from a patient who developed a fatal viral encephalitis following a ‘mosquito bite’ rather than a ‘tick bite’. The sentence has now been corrected to read: “We also used MSSPE to enrich for Jamestown Canyon virus (JCV) in post-mortem brain tissue samples from a patient who developed a fatal viral encephalitis following a mosquito bite”.

Published online: 21 January 2020

<https://doi.org/10.1038/s41564-020-0671-7>

© The Author(s), under exclusive licence to Springer Nature Limited 2020