

## CORRECTION

# Correction: Using HSV-1 Genome Phylogenetics to Track Past Human Migrations

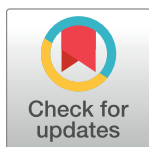
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## Notice of Republication

An incorrect version of Figure 4 was published in error. This article was republished on May 20, 2019 to correct for this error. Please download this article again to view the correct version.

## Reference

1. Kolb AW, Ané C, Brandt CR (2013) Using HSV-1 Genome Phylogenetics to Track Past Human Migrations. PLoS ONE 8(10): e76267. <https://doi.org/10.1371/journal.pone.0076267> PMID: 24146849



## OPEN ACCESS

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