Correction

EVOLUTION

Correction for “Whole-genome comparison of endogenous retrovirus segregation across wild and domestic host species populations,” by Salvador Daniel Rivas-Carrillo, Mats E. Pettersson, Carl-Johan Rubin, and Patric Jern, which was first published October 8, 2018; 10.1073/pnas.1815056115 (*Proc Natl Acad Sci USA* 115:11012–11017).

The authors wish to note: “It has come to our attention that our paper includes findings that should be updated. A script error in candidate ERV–host junction peak calling summed ERV hits instead of chromosomal mapping hits for paired-end short reads. The read counts were inflated at chromosomal locations linked to common ERVs in the reference dataset and thus peaks were called at a lower confidence level. We note that all called ERV–host junctions have supporting reads, but for these candidate loci effective thresholds were as low as one read compared to the expected six to seven reads derived from the FDR correction described in the text.”

Published under the [PNAS license](#).

Published online December 17, 2018.

www.pnas.org/cgi/doi/10.1073/pnas.1820237116