






Publisher Correction: Ancient hybridization and strong adaptation to viruses across African vervet monkey populations

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Correction to: *Nature Genetics* <https://doi.org/10.1038/ng.3980>, published online 30 October 2017.

In the version of this article published, in the Online Methods eight citations to supplementary material refer to the wrong supplementary items.

Published text: We therefore repeated the entire selection analysis (**Figs. 3–5** and **Supplementary Figs. 15–31**) using the updated call set. Correct supplementary citation: Supplementary Figs. 17–33.

Published text: We found 16–27 million SNPs segregating within taxa, corresponding to an average number of pairwise differences per site (nucleotide diversity) of 0.17–0.22% (**Fig. 1c** and **Supplementary Fig. 7**) and effective population sizes generally above 35,000 (except for *aethiops*, for which we estimated ~29,000).

Correct supplementary citation: Supplementary Fig. 10

Published text: Two taxon site-frequency spectra (**Supplementary Fig. 9**) generally showed fixed differences as well as shared and private variation, except for *hilgerty-cynosorus-pygerythrus*, which showed few fixed differences and highly correlated allele frequencies.

Correct supplementary citation: Supplementary Fig. 8

Published text: Next, for each of the six principal components we performed likelihood-ratio tests in R (function `anova` with option `test = 'LRT'`) to test whether a linear model “PC ~ latitude + longitude + taxon label” gave a significantly better fit than a model using either only geography or only taxon (**Supplementary Table 4**).

Correct supplementary citation: Supplementary Table 2

Published text: For each pairwise comparison, we summarized F_{ST} values in minor allele frequency (MAF) bins (**Supplementary Fig. 8**; the maximum across MAFs is shown in **Fig. 1c**).

Correct supplementary citation: Supplementary Fig. 11

Published text: The software Admixture 1.23 (ref. 22) was run on autosomal SNPs filtered for MAF >5%, converted to binary .bed format using GATK VariantToBinaryPed and LD pruned using the plink flag `--indep 50 10 2` (**Fig. 3a** and **Supplementary Fig. 11**).

Correct supplementary citation: Supplementary Fig. 13

Published text: Cross-coalescent rate was calculated as $2 \times \text{between}/(\text{within}_1 + \text{within}_2)$ (**Fig. 2b,c**, **Supplementary Figs. 12** and **13**, and **Supplementary Note**).

Correct supplementary citation: Supplementary Figs. 15 and 16, and Supplementary Note










Published text: To test whether these scores capture biological signal, we confirmed that scores were significantly higher in genic (introns + exons) than in intergenic regions (one-sided Mann–Whitney U test, $P < 10^{-300}$; **Supplementary Fig. 21**).

Correct supplementary citation: Supplementary Fig. 23

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Publisher Correction: The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution

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When published, this article did not initially appear open access. This error has been corrected, and the open access status of the paper is noted in all versions of the paper. Additionally, affiliation 16 denoting equal contribution was missing from author Robb Krumlauf in the PDF originally published. This error has also been corrected.

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