

CORRECTION

Correction: Unified inference of missense variant effects and gene constraints in the human genome

The *PLOS Genetics* Staff

Notice of republication

This article was republished on January 14, 2021, to replace an incorrect Fig 4 image included in the article PDF file. The publisher apologizes for the errors. Please download this article again to view the correct version. The originally published, uncorrected article and the republished, corrected articles are provided here for reference.

Supporting information

S1 File. Originally published, uncorrected article.

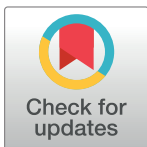
(PDF)

S2 File. Republished, corrected article.

(PDF)

Reference

1. Huang Y-F (2020) Unified inference of missense variant effects and gene constraints in the human genome. *PLoS Genet* 16(7): e1008922. <https://doi.org/10.1371/journal.pgen.1008922> PMID: [32667917](https://pubmed.ncbi.nlm.nih.gov/32667917/)



OPEN ACCESS

Citation: The *PLOS Genetics* Staff (2021) Correction: Unified inference of missense variant effects and gene constraints in the human genome. *PLoS Genet* 17(1): e1009348. <https://doi.org/10.1371/journal.pgen.1009348>

Published: January 28, 2021

Copyright: © 2021 The PLOS Genetics Staff. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.