Corrigendum: Precise genotyping of circular mobile elements from metagenomic data uncovers human-associated plasmids with recent common ancestors

Nitan Shalon, David A. Relman and Eitan Yaffe

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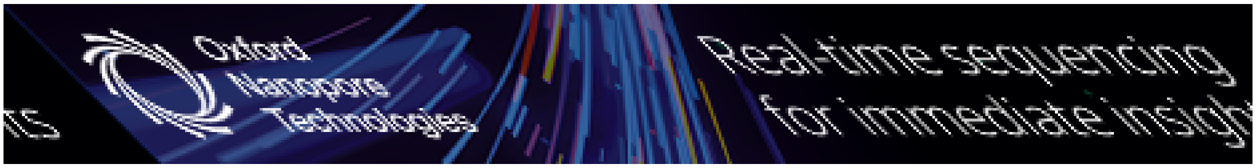

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Corrigenda

***Genome Research* 32:** 778–790 (2022)

Corrigendum: An association test of the spatial distribution of rare missense variants within protein structures identifies Alzheimer's disease–related patterns

Bowen Jin, John A. Capra, Penelope Benchek, Nicholas Wheeler, Adam C. Naj, Kara L. Hamilton-Nelson, John J. Farrell, Yuk Yee Leung, Brian Kunkle, Badri Vadarajan, Gerard D. Schellenberg, Richard Mayeux, Li-San Wang, Lindsay A. Farrer, Margaret A. Pericak-Vance, Eden R. Martin, Jonathan L. Haines, Dana C. Crawford, and William S. Bush

In the above-mentioned article, the authors would like to correct errors related to Figures 5 and 6. Figure 6 was a duplication of Figure 5, and the variant positions within Figure 5 were incorrect due to an inconsistency in the residue numbering of the PDB:6XDS with its corresponding UniProt entry. This error was isolated to the 6XDS structure only, and did not qualitatively change the results or conclusions of the analysis. Both Figures 5 and 6 have been updated in the revised article online.

The authors apologize for any confusion this might have caused.

doi: 10.1101/gr.276900.122

***Genome Research* 32:** 437–448 (2022)

Corrigendum: Enhancer–silencer transitions in the human genome

Di Huang and Ivan Ovcharenko

In the above-mentioned article, the authors would like to correct the citation of the prior studies of mesodermal silencers functioning as enhancers during *Drosophila* embryonic development and provide additional background information in the introductory section. Although the original citation was factually correct, the expanded citation provides a more accurate and extended description of the prior work on enhancer–silencer transitions in *Drosophila*. This correction has no impact on either the data, results, or conclusions reported in this article.

The corrected text (third paragraph, fourth sentence) reads as follows:

"…whereas 22 out of 29 (76%) identified mesodermal silencers were shown to act as DFREs in large enhancer screens (Gallo et al. 2011; Bonn et al. 2012) and were later augmented by additional six DFREs picked up by a targeted enhancer analysis (thus, bringing the total to 28/29 [Gisselbrecht et al. 2020])."

The additional references are as follows:

Bonn S, Zinzen RP, Girardot C, Gustafson EH, Perez-Gonzalez A, Delhomme N, Ghavi-Helm Y, Wilczyński B, Riddell A, Furlong EEM. 2012. Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. *Nat Genet* **44:** 148–156. doi:10.1038/ng.1064

Gallo SM, Gerrard DT, Miner D, Simich M, Des Soye B, Bergman CM, Halfon MS. 2011. REDfly v3.0: toward a comprehensive database of transcriptional regulatory elements in *Drosophila*. *Nucleic Acids Res* **39:** D118–D123. doi:10.1093/nar/gkq999

These changes have been updated in the article online. The authors apologize for any inconvenience.

doi: 10.1101/gr.276950.122

***Genome Research* 32:** 986–1003 (2022)

Corrigendum: Precise genotyping of circular mobile elements from metagenomic data uncovers human-associated plasmids with recent common ancestors

Nitan Shalon, David A. Relman, and Eitan Yaffe

The authors would like to correct the email of the corresponding author, Eitan Yaffe, to the following: eitan.yaffe@stanford.edu.

This correction has been updated in the revised article online.

doi: 10.1101/gr.276946.122

***Genome Research* 32:** 534–544 (2022)

Corrigendum: NicE-C efficiently reveals open chromatin–associated chromosome interactions at high resolution

Zhengyu Luo, Ran Zhang, Tengfei Hu, Yuting Zhu, Yueming Wu, Wenfei Li, Zhi Zhang, Xuebiao Yao, Haiyi Liang, and Xiaoyuan Song

The authors would like to correct the inadvertent omission of a funding source in the Acknowledgments section in the above-mentioned article. The corrected text is as follows and has been updated in the article online:

“This work was supported by the National Key Scientific Program of China (2016YFA0100502), the research project of the Joint Laboratory of University of Science and Technology of China and Anhui Mental Health Center (2019LH03), the Fundamental Research Funds for the Central Universities (WK2070210004), and China Postdoctoral Science Foundation (2021M703091).”

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