CORRECTION Open Access



Correction: Genome Med 15, 115 & Genome Med 16, 3

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Correction: Genome Med 16, 3 (2024) https://doi.org/10.1186/s13073-023-01274-4 Correction: Genome Med 15, 115 (2023) https://doi.org/10.1186/s13073-023-01269-1

The original publications of the below articles [1, 2] contained 2 errors. The incorrect and correct information is listed below. The original articles have been updated.

Incorrect

- 10.1186/s13073-023-01274-4 & 10.1186/s13073-023-01269-1
 - 1 Department of Hepatobiliary and Pancreatic Surgery, First Affiliated Hospital, Zhejiang University School of Medicine, Hangzhou 311121, China
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- 10.1186/s13073-023-01274-4
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The original articles can be found online at https://doi.org/10.1186/s13073-023-01274-4 and https://doi.org/10.1186/s13073-023-01269-1.

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Correct

- 10.1186/s13073-023-01274-4 & 10.1186/s13073-023-01269-1
 - 1 Department of Hepatobiliary and Pancreatic Surgery of the First Affiliated Hospital & Liangzhu Laboratory, Zhejiang University School of Medicine, Hangzhou, 311121, China
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- Liu Y, Zhang T, You N, et al. MAGPIE: accurate pathogenic prediction for multiple variant types using machine learning approach. Genome Med. 2024;16:3. https://doi.org/10.1186/s13073-023-01274-4.
- Zhang T, Jia H, Song T, et al. De novo identification of expressed cancer somatic mutations from single-cell RNA sequencing data. Genome Med. 2023;15:115. https://doi.org/10.1186/s13073-023-01269-1.



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