# 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)
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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
- 2 Liangzhu Laboratory, Zhejiang University, 1369 West Wenyi Road, Hangzhou 311121, China
- 10.1186/s13073-023-01274-4
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[^0][^1]gram of Zhejiang (No. 2021R01012) and the Starting Fund from Zhejiang University.

## 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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## References

1. 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.
2. 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/10.1 186/s13073-023-01269-1.

[^0]:    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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