

CORRECTION

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Correction: Enhancing SNV identification in whole-genome sequencing data through the incorporation of known genetic variants into the minimap2 index

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The original article can be found online at <https://doi.org/10.1186/s12859-024-05862-y>.

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Following the publication of the original article [1], the authors identified errors in the authors names. The given names and family names were erroneously transposed.

The incorrect authors names are:

Guguchkin Egor, Kasianov Artem, Belenikin Maksim, Zobkova Gaukhar, Kosova Ekaterina, Makeev Vsevolod and Karpulevich Evgeny

The correct authors names are:

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The author group has been updated above and the original article [1] has been corrected.

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Reference

1. Guguchkin, et al. Enhancing SNV identification in whole-genome sequencing data through the incorporation of known genetic variants into the minimap2 index. *BMC Bioinformatics*. 2024;25:238. <https://doi.org/10.1186/s12859-024-05862-y>.

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