

CORRECTION

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Correction to: Characterization of the chicken T cell receptor γ repertoire by high-throughput sequencing

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Correction to: BMC Genomics 22, 683 (2021)
<https://doi.org/10.1186/s12864-021-07975-7>

Following publication of the original article [1], an error was identified in the Methods section.

It currently reads:

In “Library preparation, HTS and data analysis” in the Methods section, the description “Overlapping paired-end reads from the 5’ RACE-based library were merged with FLASH [20], and these merged sequences were aligned to the germline V γ and J γ segments identified above using a local BLAST program (version 2.2.30) and each sequence was assigned an optimal germline V γ and J γ segments” is wrong. Actually, the authors used the 3’ end reads which contain the C γ -specific reverse primer for 5’ RACE and 250 bp in length to analyze the optimal germline V γ and J γ segments that participated in V γ -J γ rearrangement. This error does not influence any conclusion of this paper.

It should read:

In “Library preparation, HTS and data analysis” in the Methods section, use “The 3’ end reads which contain the C γ -specific reverse primer for 5’ RACE and 250 bp in length were aligned to the germline V γ and J γ segments identified above using a local BLAST program

(version 2.2.30) and each sequence was assigned an optimal germline V γ and J γ segments.”

All the changes requested are implemented in this correction and the original article [1] has been corrected.

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Reference

1. Zhang T, Li Q, Li X, et al. Characterization of the chicken T cell receptor γ repertoire by high-throughput sequencing. *BMC Genomics*. 2021;22:683. <https://doi.org/10.1186/s12864-021-07975-7>.

The original article can be found online at <https://doi.org/10.1186/s12864-021-07975-7>.

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