

Correction

Correction: Domrazek et al. Application of Next-Generation Sequencing (NGS) Techniques for Selected Companion Animals. *Animals* 2024, 14, 1578

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The authors would like to make the following corrections in the original publication [1]. The changes are as follows:

(1) Replacing the following sentence in “Section 5. Veterinary Parasitology”.

“Huggings et al. developed and validated a long-read metabarcoding platform for the detection of filarial worm pathogens of animals and humans [68]. They demonstrated that NGS could be a specific and sensitive method for diagnosing filarial worms, but on the other hand, they also showed that this method is not ideal. In one case, genomic tools showed false-negative results [68]. This method might be refined through further research”.

with

“Kattor et al. used Targeted Next-Generation Sequencing for comprehensive testing for selected vector-borne pathogens in canines [68]. Their results showed false-negative results in two samples [68]. This method might be refined through further research”.

(2) Replacing the reference [68].

68. Huggins, L.G.; Atapattu, U.; Young, N.D.; Traub, R.J.; Colella, V. Development and Validation of a Long-Read Metabarcoding Platform for the Detection of Filarial Worm Pathogens of Animals and Humans. *BMC Microbiol.* **2024**, *24*, 28.

with

68. Kattoor, J.J.; Nikolai, E.; Quorllo, B.; Wilkes, R.P. Targeted Next-Generation Sequencing for Comprehensive Testing for Selected Vector-Borne Pathogens in Canines. *Pathogens* **2022**, *11*, 964. <https://doi.org/10.3390/pathogens11090964>.

The authors state that the scientific conclusions are unaffected. This correction was approved by the Academic Editor. The original publication has also been updated.

Reference

1. Domrazek, K.; Jurka, P. Application of Next-Generation Sequencing (NGS) Techniques for Selected Companion Animals. *Animals* **2024**, *14*, 1578. [[CrossRef](#)] [[PubMed](#)]

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Received: 23 January 2025
Accepted: 29 January 2025
Published: 19 February 2025

Citation: Domrazek, K.; Jurka, P. Correction: Domrazek et al. Application of Next-Generation Sequencing (NGS) Techniques for Selected Companion Animals. *Animals* **2024**, *14*, 1578. *Animals* **2025**, *15*, 606. <https://doi.org/10.3390/ani15040606>

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