

CORRECTION

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Correction: An integrated microbiome- and metabolome-genome-wide association study reveals the role of heritable ruminal microbial carbohydrate metabolism in lactation performance in Holstein dairy cows

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Following publication of the original article [1], the author reported that the content of the Funding should be for the Data availability section and the Funding information is missing. The sections should read as follows:

The original article can be found online at <https://doi.org/10.1186/s40168-024-01937-3>.

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Data availability

The raw sequencing data used and described in this study have been deposited into CNGB Sequence Archive (CNSA) (<https://db.cngb.org/cnsa/>) of China National GeneBank DataBase (CNGBdb) with accession number CNP0005323 (Metagenome data), CNP0005324 (whole-genome resequencing data), and CNP0005479 (Metabolome data). All data have now been publicly available since 21st March 2024.

The private link that the reviewers can use to access data is provided as follows:

Metagenome data:

http://db.cngb.org/cnsa/project/CNP0005323_2afb08a6/reviewlink/

Whole-genome resequencing data:

http://db.cngb.org/cnsa/project/CNP0005324_1354668f/reviewlink/

Metabolome data:

http://db.cngb.org/cnsa/project/CNP0005479_d4c88f7b/reviewlink/



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All information is included in the manuscript or supporting files.

The original article has been updated.

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Reference

1. Zhang C, Liu H, Jiang X, et al. An integrated microbiome- and metabolome-genome-wide association study reveals the role of heritable ruminal microbial carbohydrate metabolism in lactation performance in Holstein dairy cows. *Microbiome*. 2024;12:232. <https://doi.org/10.1186/s40168-024-01937-3>.