

CORRECTION

Open Access



Correction to: The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle

Marc D. Auffret^{1*}, Richard J. Dewhurst¹, Carol-Anne Duthie¹, John A. Rooke¹, R. John Wallace², Tom C. Freeman³, Robert Stewart⁴, Mick Watson^{3,4} and Rainer Roehe¹

Correction to: *Microbiome* (2017) 5: 159
<https://doi.org/10.1186/s40168-017-0378-z>

Following publication of the original article [1], the authors reported an error in the Additional file 1. The revised manuscript was mistakenly uploaded as the Additional file 1. The correct file that includes Supplementary Figures and Tables is available here.

The publishers apologise for this error.

Supplementary information

Supplementary information accompanies this paper at <https://doi.org/10.1186/s40168-019-0764-9>.

Additional file 1: Figure S1. Relative abundance (%) of 20 groups of functional genes representing 204 selected genes (number of animals, $n = 50$ samples). The sum of the relative abundance (%) of genes grouping within the same function is shown in this figure. **Figure S2A.** Total abundance of 204 selected genes based on diet treatments ($n = 50$). * P value < 0.05 . **Figure S2B.** Shannon index diversity of 204 selected genes based on diet treatments ($n = 50$). * P value < 0.05 , $^{\circ}P$ value < 0.1 . **Figure S3.** Canonical Variate analysis (CVA) on the structure of 204 genes selected based on breed, age, weight, *Proteobacteria* ratio, FCR and methane grouping ($n = 50$). **Figure S4.** Factors explaining the significant differences observed for *Proteobacteria* ratio ($n = 50$). **Figure S5.** Microbial community composition at the phylum level ($n = 50$). **Table S1.** Characteristics of the cattle used in the experiment. **Table S2.** Groups of AMR genes significantly correlated with abundance of the *Proteobacteria* phylum and *Proteobacteria* ratio. **Table S3.** The relative abundance of AMR genes. **Table S4.** *Proteobacteria* populations strongly correlated with the *Proteobacteria* ratio. **Table S5.** Functional genes significantly correlated with *Proteobacteria* ratio (PLS). **Table S6.** Cluster distribution of functional genes significantly different between diets.

Author details

¹SRUC, Edinburgh EH25 9RG, UK. ²Rowett Institute, University of Aberdeen, Aberdeen AB25 2ZD, UK. ³Division of Genetics and Genomics, The Roslin Institute and R(D) SVS, University of Edinburgh, Edinburgh EH25 9RG, UK. ⁴Edinburgh Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh EH25 9RG, UK.

Published online: 18 November 2019

Reference

1. Auffret MD, Dewhurst RJ, Duthie C-A, Rooke JA, Wallace RJ, Freeman TC, Stewart R, Watson M, Roehe R. The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle. *Microbiome*. 2017;5:159. <https://doi.org/10.1186/s40168-017-0378-z>.

The original article can be found online at <https://doi.org/10.1186/s40168-017-0378-z>

* Correspondence: Marc.Auffret@sruc.ac.uk

¹SRUC, Edinburgh EH25 9RG, UK

Full list of author information is available at the end of the article



© The Author(s). 2019 **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated.