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Author Correction: MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants

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Correction to: *Nature Communications* https://doi.org/10.1038/s41467-022-29438-7, published online 07 April 2022.

The original version of this Article included the following errors in reference citations:

It incorrectly cited 'Thompson, L. R. et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* **551**, 457–463 (2017)' and 'Peterson, J. et al. The NIH Human Microbiome Project. *Genome Res.* **19**, 2317–2323 (2009)' as Refs 18 and 19 in the Introduction, at 'In the MiDAS project, we have thoroughly evaluated different wet-lab protocols, e.g., DNA extraction methods, and choice of amplicon primers and amplicon library preparation[17-19].' The two references have been removed from the correct version.

It incorrectly cited 'Zheng, M. et al. Active ammonia-oxidizing bacteria and archaea in wastewater treatment systems. *J. Environ. Sci.* **102**, 273–282 (2021)' and 'Thompson, L. R. et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* **551**, 457–463 (2017)' as Refs 42 and 18 in the last paragraph of Results and Discussion, at 'In the Danish WWTPs, we have successfully done this for groups in the Acidobacteriota[42] based on the MiDAS 3 database[18].' The correct version replaces the first reference with 'Kristensen, J. M., Singleton, C., Clegg, L.-A., Petriglieri, F. & Nielsen, P. H. High diversity and functional potential of undescribed "Acidobacteriota" in Danish wastewater treatment plants. *Front. Microbiol.* **12**, 906 (2021)' and the second reference with Ref. 16.

It incorrectly cited 'Rosselló-Mora, R. A., Wagner, M., Amann, R. & Schleifer, K. H. The abundance of *Zoogloea ramigera* in sewage treatment plants. *Appl. Environ. Microbiol.* **61**, 702–707 (1995)' as Ref. 43 in the last paragraph of Results and Discussion, at 'Our recent retrieval of more than 1000 high-quality MAGs from Danish WWTPs with advanced process design is also an important step to link identity to function[43].' The correct version replaces this reference with 'Singleton, C. M. et al. Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. *Nature Communications* **12**, 2009 (2021)'.

It incorrectly cited 'Nierychlo, M. et al. *Candidatus* Amarolinea and *Candidatus* Microthrix are mainly responsible for filamentous bulking in Danish municipal wastewater treatment plants. *Front. Microbiol.* 11, 1214 (2020)', 'Klindworth, A. et al. Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Res.* **41**, 1–11 (2013)' and 'Lane, D. J. 16S/23S rRNA sequencing In *Nucleic Acid Techniques in Bacterial Systematics* (eds Stackebrandt, E. & Goodfellow, M.) (Wiley, 1991)' as Refs 44–46 in the last paragraph of Results and Discussion, at 'These MAGs may also form the basis for further studies to link identity and function, e.g., by applying metatranscriptomics[44] and other in situ techniques such as FISH combined with Raman[45,46].' The correct version replaces these references with 'Herold, M. et al. Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. *Nature Communications* **11**, 5281 (2020)', 'Fernando, E. Y. et al. Resolving the individual contribution of key microbial populations to enhanced biological phosphorus removal with Raman–FISH. *ISME J.* **13**, 1933–1946 (2019)' and 'Petriglieri, F. et al. Quantification of Biologically and Chemically Bound Phosphorus in Activated Sludge from Full-Scale Plants with Biological P-Removal. *Environ. Sci. Technol.* **56**, 5132–5140 (2022)'.

The errors have been corrected in the PDF and HTML versions of the Article.

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