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CORRIGENDUM

Correction to: High-coverage genomes to elucidate the evolution of penguins

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In the original version of the article "High-coverage genomes to elucidate the evolution of penguins" by Hailin Pan et al. [1], the authors received a request to make some clarifications and changes in the acknowledgements, the following is the modified version:

"We thank the following: John Cockrem, Scott Flemming, Helen McConnell, Chris Rickard, Sarah Fraser, Otto Whitehead, Kyle Morrison, and Amy Van Buren for help collecting samples; Jonathan Banks, Kirsten Rodgers, and Jo Hiscock for sample information; Manuel Paredes Oyarzún and Hernán Rivera Meléndez for facilitating permits and sample collection; Lauren Tworkowski, Richard O'Rorke, and Joanna Sumner for facilitating sample collection; Adrian Smith for providing laboratory support to extract 2 DNA samples; Peter Dearden, Neil Fowke, Michael Knapp, Hoani Langsbury, Claire Porima, Nic Rawlence, Paul Scofield, Jonathan Waters, Janet Wilmshurst, and Jamie Wood for informal discussions regarding the New Zealand indigenous consultation; The New Zealand Department of Conservation for facilitating New Zealand indigenous consultation and approving permits, particularly Neil Fowke and Jesse Mason for facilitating permits and/or obtaining past permit details; Brett Gartrell and Pauline Nijman for providing animal ethics details; and the China National Genebank for contributing the sequencing resources for this project. The Penguin Genome Consortium welcomes participation and collaboration for our ongoing work regarding comparative and evolutionary genomics of penguins."

References

1. Pan H, Cole T L, Bi X et al. High-coverage genomes to elucidate the evolution of penguins. GigaScience 2019;8(9):1-17.