

CORRECTION

Correction: Implications of the circumpolar genetic structure of polar bears for their conservation in a rapidly warming Arctic

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The following sentence was omitted and should have been included as the last sentence of the first paragraph in the Estimation of Gene Flow section of <u>S1 Supporting Information</u>:

Because we wanted input dataset for the gene flow analyses of microsatellite data to 1) be comparable for both MIGRATE and BayesAss analyses; 2) avoid as much as possible the use of individuals with large amounts of missing data; and because 3) 15 individuals are recommended (for efficiency) for the MIGRATE analyses (P. Beerli and M. Kuhner, pers. comm. to SAS), and we wanted each area to be fairly equally represented, we randomly sampled individuals from strata (geographic areas) within each subpopulation, selecting from 26 (WP), 34 (EP) and 60 (CA and SC), depending on the number available for analysis.

Please see the correct, complete <u>S1 Supporting Information</u> here.

Supporting Information

S1 Supporting Information. Detailed materials and methods. (DOCX)

Reference

Peacock E, Sonsthagen SA, Obbard ME, Boltunov A, Regehr EV, Ovsyanikov N, et al. (2015) Implications of the Circumpolar Genetic Structure of Polar Bears for Their Conservation in a Rapidly Warming Arctic. PLoS ONE 10(1): e112021. doi:10.1371/journal.pone.0112021 PMID: 25562525





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