

CORRECTION

Correction: Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans

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In [S2 Text](#), some reference numbers to equations in the second to last paragraph are misprinted and appear as question marks instead of numbers. Please view the correct [S2 Text](#) below.

Supporting Information

S2 Text. Probabilistic inference using BAM files. Explanation of methodology for inferring fragment-specific error parameters in the optional BAM mode of DICE. (PDF)

Reference

1. Racimo F, Renaud G, Slatkin M (2016) Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. *PLoS Genet* 12(4): e1005972. doi:[10.1371/journal.pgen.1005972](https://doi.org/10.1371/journal.pgen.1005972) PMID: [27049965](https://pubmed.ncbi.nlm.nih.gov/27049965/)



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