

## CORRECTION

# Correction: The sockeye salmon genome, transcriptome, and analyses identifying population defining regions of the genome

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This article [1] cites a *PLOS ONE* article that was retracted on February 9, 2021 [2, 3] because the sample used for genome analysis was found to have been misidentified. The genomic assembly reported in [2] is still available at GenBank, but it has been relabelled as an unclassified species in the *Salvelinus* genus, or *Salvelinus sp.* (GenBank accession: GCF\_002910315.2).

The draft genome reported in [2] was one of six reference species used to confirm synteny placement of scaffolds during assembly of the sockeye salmon genome in this 2020 article [1]. The authors and an Academic Editor concluded that the retraction [3] and the species identity of the genome reported in [2] do not impact the validity or reliability of this article's [1] results and conclusions as multiple species and multiple lines of evidence were used to confirm synteny assessments.

The retracted article [2] was also cited as a source for methods used in the 2020 article [1]. As a result, the authors have provided the relevant Python scripts via GitHub and the Data Availability statement for this article [1] is as follows: Raw data has been deposited to the National Center for Biotechnology Information (NCBI) under BioProject PRJNA530256 (<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA530256/>). Custom scripts and sample information can be found in supplemental files and via GitHub: <https://github.com/KrisChristensen/OrthologyBetweenSpecies>.



## OPEN ACCESS

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## References

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2. Christensen KA, Rondeau EB, Minkley DR, Leong JS, Nugent CM, et al. (2018) The Arctic charr (*Salvelinus alpinus*) genome and transcriptome assembly. *PLOS ONE* 13(9): e0204076. <https://doi.org/10.1371/journal.pone.0204076> PMID: 30212580
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