

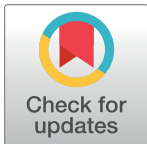
## CORRECTION

# Correction: Reproducible big data science: A case study in continuous FAIRness

Ravi Madduri, Kyle Chard, Mike D’Arcy, Segun C. Jung, Alexis Rodriguez, Dinanath Sulakhe, Eric Deutsch, Cory Funk, Ben Heavner, Matthew Richards, Paul Shannon, Gustavo Glusman, Nathan Price, Carl Kesselman, Ian Foster

The URLs in the Data Availability statement for this paper are incorrect. The correct URLs are:

- DNase-Seq has the unique identifier minid:b9dt2t and is available from <https://identifiers.org/minid:b9dt2t>
- Aligned BAM files have an identifier: minid:b9vx04 and are available from <https://identifiers.org/minid:b9vx04>
- The collection of BED files of footprints have an identifier: minid:b9496p and are available from <https://identifiers.org/minid:b9496p>
- The non-redundant Motifs database has an identifier: minid:b97957 and is available from <https://identifiers.org/minid:b97957>
- The motif intersected hits have an identifier: minid:b9p09p and are available from <https://identifiers.org/minid:b9p09p>
- The Transcription Factor Binding Sites generated from the study have an identifier: minid:b9v398 and are available from <https://identifiers.org/minid:b9v398>



## Reference

1. Madduri R, Chard K, D’Arcy M, Jung SC, Rodriguez A, Sulakhe D, et al. (2019) Reproducible big data science: A case study in continuous FAIRness. *PloS ONE* 14(4): e0213013. <https://doi.org/10.1371/journal.pone.0213013> PMID: 30973881

## OPEN ACCESS

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