CORRECTION

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

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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
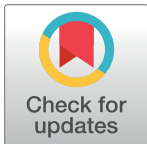
Reference

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