

Corrigendum

A map of direct TF–DNA interactions in the human genome

Marius Gheorghe¹, Geir Kjetil Sandve², Aziz Khan¹, Jeanne Chèneby³, Benoit Ballester³ and Anthony Mathelier^{1,4,*}

¹Centre for Molecular Medicine Norway (NCMM), University of Oslo, Oslo, Norway, ²Department of Informatics, University of Oslo, Oslo, Norway, ³Aix Marseille Université, INSERM, TAGC, Marseille, France and ⁴Department of Cancer Genetics, Institute for Cancer Research, Radiumhospitalet, Oslo, Norway

Nucleic Acids Research, 2019, 47(4): e21, <https://doi.org/10.1093/nar/gky1210>

The Authors wish to make the following corrections to their article.

Due to a bug in the code used to compute the genome coverage of the predicted TFBSs, an error was introduced in the article. The current text states that the authors' predictions cover >4% of the human genome while it covers >2% instead. The article has been corrected as described below. This error was found in the code computing the genome coverage and does not impact the results and conclusions of the article.

ABSTRACT

... Our work culminated with predicted interactions covering >2% of the human genome, obtained by uniformly processing 1983 ChIP-seq peak data sets from the ReMap database for 232 unique TFs ...

INTRODUCTION (middle of the last paragraph)

... The set of predicted direct TF–DNA interactions derived from PWMs covers >2% of the human genome ...

RESULTS

Predicting direct TF–DNA interactions in the human genome from ChIP-seq data (last sentence)

... This set of direct TF–DNA interactions (TFBSs) extracted from the enrichment zones covers >2% of the human genome, encompassing 8 304 135 distinct TFBS locations.

*To whom correspondence should be addressed. Tel: +47 228 40 561; Email: anthony.mathelier@ncmm.uio.no