Epigenomics

Future Medicine fsg

Research Article Reporting Checklist for Bioinformatic and Data Re-analysis Studies

This is a submission requirement for Research Articles reporting the results of a bioinformatic study and/or re-analysis of available online data. The checklist is intended as an aid to authors to inform reviewers and readers of their methods and findings clearly, completely and transparently. This checklist will also be used as a tool to evaluate the suitability and novelty of manuscripts for publication in *Epigenomics*.

Please read the checklist below and indicate if the following information is available in your manuscript (or supplementary material). In cases where you have confirmed that the stipulated information is present in your article, please detail where it can be found by providing the page/paragraph/line number.

Criteria	**Information is located on page/paragraph/line of the manuscript**	**N/A**
Explain if and how you generated and analysed your own data (e.g. cell samples, tissue samples, mouse models, human models)	**Page 4,8,9 in MATERIALS & METHODS**	
Explain how you have adjusted for differences between data types (e.g. data derived from different cell, tissue and population types) and data sets (both own and previously published) **AND** Detail how you have processed the different datasets to make them comparable	**Page 8,9**	
Describe how you have identified a suitable tool for the data analysis **OR** description of the novel bioinformatic tool/technology developed in your study	**Page 8,9**	
Detailed comparison of your own new findings against the findings of the original study in which the data was first generated	**Page 16-22 in discussion**	
Explain in detail the impact of your findings within the field of epigenomics	Our data provide the first investigation regarding alterations of m6A modifications in AGEs-induced dermal fibroblasts and photoaging field.	
Clearly show that your study has implemented the FAIR principles on data management*	**F**indable: yes **A**ccessible:yse **I**nteroperable:yes **R**eusable:yes	

*In 2016, the 'FAIR Guiding Principles for scientific data management and stewardship' were published in *Scientific Data*. The authors intended to provide guidelines to improve the Findability, Accessibility, Interoperability, and Reuse of digital assets. Visit the GO FAIR website for more guidance on the FAIR Principles.

For more information on the journal, please visit our website. If you have any questions regarding the criteria listed above, please contact Storm Johnson, Commissioning Editor of *Epigenomics*: s.johnson@futuremedicine.com

Author print name: _____**blinded**_____
Date: _____2022-01-10_____