

## Cover Letter

Dear Editor,

Our manuscript “A quantitative analysis about the impact on chromatin accessibility by histone modifications and binding of transcription factors in DNase I hypersensitive sites” is under submission to “BioMed Research International”.

It is known that chromatin features such as histone modifications and the binding of transcription factors exert a significant impact on the “openness” of chromatin. In this study, we present a quantitative analysis of the genome-wide relationship between chromatin features and chromatin accessibility. We derived quantitative models to directly predict the “openness” of chromatin using histone modification features and transcription factor binding features respectively. We show that both these two types of features are highly predictive for chromatin accessibility in a statistical viewpoint. Our study provides new insights into the combinatorial effects of different chromatin features to chromatin accessibility.

Your favorable consideration would be highly appreciated.

Yours sincerely,

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