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Dear Editor of Genome Biology,

Please find enclosed revision for our manuscript entitled “Identification of Enriched Regions in ChIP-Seq Experiments using a Mappability Corrected Multiscale Signal Processing Framework” with manuscript ID 6182901821250031. We have included a response letter with itemized responses to each reviwer’s comments and exceprts from the manuscript, the updated manuscript, and the updated set of figures. In the revision, we addressed all the reviewers comments, which were primarily focused on extending the benchmarks of our method, MUSIC, with additional ChIP-Seq datasets corresponding to more punctate marks and with additional methods. We updated the manuscript to clarify the parameter selection and also listed the parameters used while running other methods. We show that MUSIC performs favorably in the extended benchmark. We also updated and highlighted the manuscript at the places where there were revisions. Finally, we added one new feature to MUSIC, as the first reviewer commented, for saving the smoothed tracks for visualization. The source code is available online.

Yours sincerely,

Mark Gerstein

Albert L. Williams Professor

of Biomedical Informatics