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Dear Editor of Genome Biology,

Please find enclosed our revision of the 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 point by point responses to each reviwer’s comments and excerpts from the revised text, the updated manuscript, and an 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 methods. We also included more ChIP-Seq datasets for a more comprehensive set of benchmarks. 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.

 Yours sincerely,

 Mark Gerstein

 Albert L. Williams Professor

 of Biomedical Informatics