

Dear Dr. Rusk,

Thank you for sending the reviewer report for our paper titled "Analysis of Sensitive Information Leakage in Functional Genomics Signal Profiles through Genomic Deletions". We greatly appreciate your reviewing our manuscript. We were, however, disappointed by the decision. We are wondering if it is at all possible for you to reconsider the manuscript and perhaps let us submit a rebuttal.

Our reason for asking for a reconsideration is that we think the referee reports do not reveal any major weakness in our manuscript. We believe that much of the referees' concerns are caused by unclear explanation of methods and results. We believe these can be addressed by clarification and reorganization of the main text.

We understand that you have two main concerns:

First is about the reviewers' doubts on RNA-seq data revealing underlying genomic deletions. We can clarify this by giving solid examples about how RNA-seq signal profiles do reveal genomic deletions. In addition, we do agree with the fact that RNA-seq is a much more prevalent in clinical setting than ChIP-Seq. This claim already supports our manuscript: This is exactly why our anonymization strategy focuses on protecting RNA-seq signal profiles.

Second is about the fact that although Reviewer 2 finds the attacks convincing, Reviewer raised concerns about anonymization procedure.

These are specifically about that there can be other leakages than the ones we study in our manuscript. We think this is a miscommunication that can be

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solved by clarification: We do not claim that we are anonymizing all the sensitive information leakage from the signal profiles. As the reviewer points out, there are other leakages that can lead to breaches of privacy. We show that there is a very obvious source of leakage that needs to be immediately patched. We believe we demonstrate well that the proposed anonymization procedure is effective in closing this source. We do realize that there can be other sources of information leakage that the Reviewer 2 rightfully mentions, and our anonymization procedure may not be effectively protecting against these leakages. We can highlight and discuss this point in the Discussion section of the manuscript.

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Finally, given the timeframe and concerns in the reviews, we think that the referee's questions would not warrant rejection of our manuscript. In addition, we think that privacy is a very important topic and our paper would be a perfect complement to the ENCODE rollout as it deals with the privacy of functional genomics data. It would be great if it is possible to have a phone call to go over these. We will be looking forward to hearing from you soon.

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Yours Sincerely,

Mark Gerstein.