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May 15, 2018

Dear Editor,

I am writing to resubmit our manuscript, titled "RADAR: An integrative framework for variant annotation and prioritization in post-transcriptional regulome of RNA binding proteins" for the exclusive consideration of publication in Genome Biology as a **Companion Paper in the ENCODE3 package**.

While specific attention was paid to these points that the editor particularly emphasized, we have tried to fully address comments in a point by point fashion, and included relevant figures to support our responses. We want to highlight several main points regarding our revisions.

- We resubmit our revised manuscript as a software article and provided both online and command line versions of our software with relevant data and detailed documentation.
- We have tried to build RADAR scores based on only K562/HepG2 data and compared their performances on variants in liver. Results showed that RADAR can provide biologically relevant results when using matched data.
- We have additionally added FATHMM-MKL as another comparison method.
- We have tried to explain the binding peak weighting scheme more clearly and added more analyses to demonstrate that RADAR can capture the true biology of RBPs.
- We have added more text and supplementary figures to show the uniqueness and novelty of RADAR against previous efforts, such as FunSeq2.
- We have revised the methods section to better describe how we score variants using RADAR.

We also would like to emphasize that RADAR is unique due to its focus on the post-transcriptional level, while most current methods are focused on transcriptional level regulation. It can be used in conjunction with existing transcriptional-level variant impact evaluation tools. We make available all the results on our website (radar.gersteinlab.org) and the Gerstein lab GitHub (https://github.com/gersteinlab/RADAR). We appreciate you taking the time to review and respond to our manuscript. Please address all correspondence to pi@gersteinlab.org.

Many thanks,
Mark Gerstein