

Reviewer Report

Title: VaDiR: an integrated approach to Variant Detection in RNA

Version: Revision 1 **Date:** 6/19/2017

Reviewer name: Jiarui Ding

Reviewer Comments to Author:

For a), the authors added some experiment results. However, I still have major concerns about the validity of their analysis and the presentation of the results. 1, the authors presented the results in two supplementary tables (without any quantitative comparison), which are very difficult to interpret. Instead, the authors can present the results using figures such as ROC curves for better visualization and interpretation of the results. I suggest the authors quantitatively compare their original approach with the approach based on training classifiers and evaluate the results based on cross-validation analysis (below). Also, the authors can do a clustering analysis of the features (other algorithm outputs). 2, given that there were not many true mutations, I don't understand why the authors randomly choose a subset of 12 samples for this analysis and completely throw away the rest. Instead, the authors can do a cross-validation analysis on the whole dataset.

3, the authors did not present their detailed analysis. If there was not enough space, the authors can at least briefly talk about their analysis in the main text, and leave the details in supplementary materials.

Level of Interest

Please indicate how interesting you found the manuscript: An article of importance in its field

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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