#### **Reviewer Report**

Title: A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis

Version: Original Submission Date: 4/16/2019

**Reviewer name: Sijia Huang** 

### **Reviewer Comments to Author:**

Major comments:

1. It would be highly appreciated if the github or other open source (e.g. CRAN R-package) version of the tool can be provided with a user-friendly manual, this will help to make this tool available to a large enough community.

2. It is not very clear how the proteomics/ CNV/ methylation are mapped to gene expression data. From the result part, I can only see

RNAseq/microRNA/RPPA/microarray datasets. I didn't see the results of other multi-omics layers as introduced in the data description section of the results part.

3. Mapping database: I can just see a mapper file in the package which is between microRNA and gene expression. I don't know the resource of the mapping file, which should be described in the methods section. 4. This resource may also be updated regularly. The mapping file should also include methylation/gene expression, protein/gene expression etc. Currently this tool is not as what it declares to be, a "multi-omics tool".

TCGA datasets are mostly based on U.S. patients, I am wondering if you can look into ICGC datasets (https://dcc.icgc.org/projects) to look into other multi-omics datasets and see if this tool still holds on the other datasets?

Minor comments:

There were several instances in the manuscript where there were minor grammatical errors. I'd recommend just having a native English speaker give it a careful read before publication. Also there are some misspelling errors (eg. Figure 4E Correlation) in this paper.

There seems to be a bar omitted in Figure 3A first plot with nCis = 75, # sample =1000.

#### Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

#### Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

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Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

# **Quality of Written English**

Please indicate the quality of language in the manuscript: Choose an item.

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