

Reviewer Report

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

Version: Revision 1 **Date: 5/31/2019**

Reviewer name: Sijia Huang

Reviewer Comments to Author:

Most of the issues have been addressed.

One question regarding the package is regarding the resource of these mapping files, where are they coming from? Are they up-to-date? Are they all experiment validated?

It will be much better if you can provide the links for these files and offer an automatic way of updating, with standardized IDs for each category (gene expression, methylation, CNV, proteins etc.)

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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Does the manuscript adhere to the journal's guidelines on [minimum standards of reporting?](#) Choose an item.

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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