

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: Ettore Mosca

Reviewer Comments to Author:

The authors responded appropriately to my comments. The manuscript still requires some editing for language and clarity, such as:

- 417. "The sensitivity and accuracy of multi-omics profile matching 418 methods needs further improvement" should be "The sensitivity and accuracy [...] need further improvement".
- 421. "The proMODMatcher depends on a set of biological cis-associations and the information content (Shannon entropy) of each cis-association depends on the randomness of each locus or gene". Here, the "randomness" attributed to "each locus or gene" is unclear and requires further explanation.

Methods

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

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

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