Reviewer’s report

Title: Treatment recommendations to cancer patients in the context of FDA guidance for next generation sequencing

Version: 1 Date: 20 Nov 2018

Reviewer: Takahiko Koyama

Reviewer's report:

1. What is the coverage of sequencing?

2. Did you use matching normal sample to remove germline mutations?

3. In table 4, BRCA1, BRCA2, NF1 have very vague definitions of actionable mutations. Do you consider any mutations in these genes actionable or just inactivating such as stop gain, splicing, and frameshift? How do you evaluate SNVs with no evidence of low activity?

Are the methods appropriate and well described?  
If not, please specify what is required in your comments to the authors.

No

Does the work include the necessary controls?  
If not, please specify which controls are required in your comments to the authors.

Yes

Are the conclusions drawn adequately supported by the data shown?  
If not, please explain in your comments to the authors.

Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?  
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics
Quality of written English
Please indicate the quality of language in the manuscript:

Acceptable

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