Reviewer's report

Title: Significant Random Signatures Reveals New Biomarker for Breast Cancer

Version: 0 Date: 30 Jun 2019

Reviewer: Yanling Hu

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This paper proposes a computational method to extract signals that are embedded within significant random signatures. The results are even applied the method on the breast cancer data set to achieve a set of significant random signatures, then found the first one to suggest a role of TAT in breast cancer. The idea of this article is relatively novel, making this research important medical significance.

However, there are some unclear points as follow:

1. It is not clear how to ensure the accuracy of the computational method. It is suggested to increase the section of the discussion of accuracy to enhance the reliability of the results.

2. It is not clear how to complete statistical analysis through SPSS. And this section should have a clearer explanation.

3. Also, there are few explanations of selection of the number of patients for the study design. Can the number of patients support the conclusions of this study of TAT gene in breast cancer?

4. In the page 13, the sentence describes "sixteen genes are present in DMFS and RFS datasets data set". Is this sentence right?

In summary, this submission has been greatly improved and is worthy of publication.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

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

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Are the conclusions drawn adequately supported by the data shown?
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Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
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