UC San Diego
Jacobs School of Engineering

Shicheng Guo <shg047@eng.ucsd.edu>

Review of BMC Medical Genomics manuscript - Biomarker discovery: Quantific...

2 messages

BioMed Central Editorial Editorial <editorial@biomedcentral.com> Mon, May 18, 2015 at 3:37 AM
To: Dr Shicheng Guo <scguo@ucsd.edu>

Re: Juan Pablo Lopez, Alpha Diallo, Cristiana Cruceanu, Laura M. Fiori, Sylvie Laboissiere, Isabelle Guillet, Joelle Fontaine, Jiannis Ragoussis, Vladimir Benes, Gustavo Turecki and Carl Ernst
Biomarker discovery: Quantification of microRNAs and other small non-coding RNAs using next generation sequencing
BMC Medical Genomics

Dear Dr Guo,

This is just a quick note to confirm receipt of your review. In case it is helpful, you will find a copy of your review and any confidential comments at the end of this message. We will be sending your review to the authors as soon as we are able to come to a decision on the manuscript.

I would like to thank you for your assistance in reviewing the manuscript for one of our Open Access journals. You can also support Open Access publishing by submitting your next article to one of our journals: see http://www.biomedcentral.com/info/authors/ for more information.

Again, thank you for all your help.

With best wishes,

Mr Ervin Cenzon
on behalf of Dr Patrick Tan

Tel: +44 (0) 20 3192 2013
e-mail: editorial@biomedcentral.com
Web: http://www.biomedcentral.com/

****

Reviewer's report: Comments to the Authors,

This manuscript provided a comprehensive design to evaluate the influence of purification method, miRNA-seq method (Hiseq or Miseq), RNA quality or degradation and sequencing coverage to miRNA-seq. And the authors found RNA degradation, Hiseq or Miseq would not bring dramatically effect to miRNA-seq while purification method in library preparation would bring significantly change to miRNA-seq. The study was performed rigorously and the findings are interesting. However, the manuscript needs more careful editing since the design is very complicated which would make the reader confused without perfect and smooth manuscript. In general, I'd recommend publication if the authors can address the following concerns and prepare a more concise draft.

Major Compulsory Revisions

1, In the background section, The function of the miRNA, LincRNA, rRNA, piRNA and T-UCRs, however, please

provide some explicit evidences that they could be taken as biomarkers, or else, please shorten these comprehensive description. In addition, DNA methylation also has been considered to be a great biomarker for some complex disease. It should be mentioned in the background.
2, In the background section, large content were used to introduce miRNA, piRNA and so on. However, these information is non-informative for the manuscript. However, the most important thing of Table 1 is lack of enough description. Please change the styles.
3, Please make sure about the GEO accession ID for the dataset is correct in the line 5 of page 11.
4, All the commas in the Tables should be replaced with points throughout Tabel 2,4,5 and 6
5, In the section of “Bioinformatic output measures for small RNA sequencing quality control”, the sentence of “was consistent with published results” and “was externally validated with **” was confusing. Please make this sentence clearer. What’s your conclusion for this section?
6, The authors should give some interpretation to the reason why PPS give so many raw reads than other methods in the table 2.
7, It would be perfect for authors to make a comprehensive comparison between different RNA purification method with a table in the supplementary.

Minor Essential Revisions
8, Please change all the points in “has.miR.485.5p” as “has-miR-485-5p”
9, How RIN was measured should be introduced in the background section. In addition, please define it when you use it at the first time.
10, Please provide the rank correlation of shared miRNAs in the Table 6. I assume the correlation of the rank between the identified miRNAs in Hiseq2500 and Miseq would be very strong.
11, Please provide a short eventual and explicit recommendation or highlight for the readers in the summary section as the main discovery in the study such as RIN would not affect the miRNA-seq and so on.
12, Please provide the detailed numbers of the miRNAs in Figure 6, except the proportions.
13, Please provide corresponding heatmap plot based on the data of Figure 4 and Figure 7, respectively, as the supplementary or in the main body.
14, Which factors in the RNA-seq would affect “Surviving Reads” as mentioned in Table 2,4,5,6?
15, Table 3, specific values would be prefer than relative description.
16, Figure 1 should provide more information. For example, the purification method can be labelled in Figuare 1B and so on.
17, it seems there is no any difference between AMPure and control group with the data of Table 2. Why?
18, In the table 1, what does it mean “we removed reads with a quality scores<30”? Any reads which have any base score <30 will be filter out?

Level of interest: An article of importance in its field

Quality of written English: Needs some language corrections before being published

Statistical review: Yes, and I have assessed the statistics in my report.

Declaration of competing interests: I declare that I have no competing interests

****

Confidential comments to editors: This manuscript provided a comprehensive design to evaluate the influence of purification method, miRNA-seq method (Hiseq or Miseq), RNA quality or degradation and sequencing coverage to miRNA-seq. And the authors found RNA degradation, Hiseq or Miseq would not bring dramatically effect to miRNA-seq while purification method in library preparation would bring significantly change to miRNA-seq. The study was performed rigorously and the findings are interesting. However, the manuscript needs more careful editing since the design is very complicated which would make the reader confused without perfect and smooth

manuscript. In general, I'd recommend publication if the authors can address the following concerns and prepare a more concise draft.

Quality of Figures: Acceptable.

What next?: Unable to decide on acceptance or rejection until the authors have responded to the major compulsory revisions

---

BioMed Central Editorial Editorial <editorial@biomedcentral.com> Mon, May 18, 2015 at 3:37 AM
To: Dr Shicheng Guo <scguo@ucsd.edu>

[Quoted text hidden]