Reviewer’s report

Title: Identification of differentially expressed lncRNAs and mRNAs in luminal-B breast cancer by RNA-sequencing

Version: 1 Date: 30 Sep 2019

Reviewer: Adriana Aguilar-Lemarroy

Reviewer's report:

The manuscript is very interesting, and I consider it very valuable, however, there are some points that need to be reviewed:

-In the methods section, in patients and samples, the description of the patients is poorly detailed, authors should include if the patients were under any treatment or were free of treatment. In Table 1, one of the patients is HER2 positive, under which selection criteria they considered this sample as Luminal? The percentage found of each of the receptors should be included in Table 1, as also age of each patient. Additionally, how adjacent was the sample taken without a tumor? Why were tumor-free breast samples not included?

In the method sections, it is necessary to include several details such as:
- what conditions and what software were used to filter the data and the quality of the readings?
- what were the trimming data conditions? which phred was used?
- the sequencing was done with paired-ends or single ends? and the depth?
- It is important to mention what kind of normalization was used with String Tie.
- Did authors performed post hoc tests to get the padj? or Q value? and why authors did not take that value instead of the p?
- In the analysis of functional annotations authors need to describe what parameters they used for enrichment.
- In protein-protein interaction networks it is necessary to include that confidence cut-off selected.

- I'm curious to know why authors included in their analysis of DelncRNA-DEmRNA co-expression networks all the genes and not only those found in the Cis-nearby-targeted DEmRNAs of DElncRNAs analysis?

- In the figure 1c, I do not see the pink and light blue inner layer that authors described (that represents the distribution of up- and down-regulated DElncRNAs on different chromo-some).

- I consider that the work is based on the analysis of very few samples, a larger number of samples would be necessary to strengthen the conclusions.

- Authors do not include if they have deposited their datasets in a publicly available repository, BMC Cancer strongly encourages that all datasets on which the conclusions of the paper rely should be
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.

No

Are the conclusions drawn adequately supported by the data shown?
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