Reviewer’s report

Title: Survival analysis of immune-related lncRNA in low-grade glioma

Version: 0 Date: 22 Jul 2019

Reviewer: Stefano Barbi

Reviewer's report:

The authors report a study on low-grade glioma aimed at identifying immunity related lncRNAs that affect survival. However, the study is poorly conducted and described and my recommendation is to reject it.

Below there are some suggestions that, in my opinion, may improve the study.

* Materials and methods

- The authors should better specify and provide direct links to the dataset they used. Specifically, they should mention that it was a RNA-Seq dataset and whether it was already normalized. The authors should also specify whether the limma analysis has been applied to the whole dataset or just the genes annotated as lncRNAs.

- I don’t understand how the authors characterized lncRNAs as being immune-related. Specifically, what does the sentence "correlation between molecules was calculated" mean in that context.

- In the last paragraph of materials and methods, variants of parametric and non-parametric two-sample tests are mentioned but never used in the paper. Moreover, I don't think that "the abnormal distribution" is the correct wording to indicate a non normal distribution.
**Results**

- The authors report that at the first stage of their screening, they looked for differentially expressed lncRNAs but they do not specify how they contrasted the samples (e.g., tumor vs normal, dead vs alive).

- According to the characterization based on innatedb, there is a significant enrichment of immuno-related lncRNA in the set of overexpressed lncRNAs, that is never mentioned or discussed.

- In the univariate Cox regression series, multiple testing was not addressed.

- No technique to address overfitting has been used, such as, for example, the division of the dataset into a discovery and a validation set. Therefore, there is no evidence that these results can be generalized.

- The authors report that, based on multivariate survival model, they divided samples into high-risk and low-risk, but there is no mention of the threshold used (e.g., median, zero etc.).

- The authors specify that besides the 10 lncRNAs in the survival model, there were other 7 lncRNAs that were "independent prognostic risk factors". However, I cannot find any description of these 7 lncRNAs and the respective multivariate models, which supposedly, would have included clinical covariates.

- The authors subsequently identify genes that are differentially expressed between the high-risk and low-risk groups. However, these genes are never reported. Instead, they present a gene enrichment analysis that identifies mostly broad functional categories (e.g., extracellular region) and is poorly informative.
* Figures 1a,2a,3a

- The color legend doesn't read well (at all). Usually, before clustering, gene expression values are centered by mean, so that the (unspecified in the paper) distance between samples, does not incorporate the scale differences between gene expression baselines but just their differential expression. This also can help to generate a visually interpretable heatmap. In addition, the samples dendrogram, does not show any feature associated with samples (like for instance a bar with color codes) and axis labels (gene names and sample names) are not readable.

**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?**
If not, please explain in your comments to the authors.

No

**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:

Not suitable for publication unless extensively edited
Declaration of competing interests
Please complete a declaration of competing interests, considering the following questions:

1. Have you in the past five years received reimbursements, fees, funding, or salary from an organisation that may in any way gain or lose financially from the publication of this manuscript, either now or in the future?

2. Do you hold any stocks or shares in an organisation that may in any way gain or lose financially from the publication of this manuscript, either now or in the future?

3. Do you hold or are you currently applying for any patents relating to the content of the manuscript?

4. Have you received reimbursements, fees, funding, or salary from an organization that holds or has applied for patents relating to the content of the manuscript?

5. Do you have any other financial competing interests?

6. Do you have any non-financial competing interests in relation to this paper?

If you can answer no to all of the above, write 'I declare that I have no competing interests' below. If your reply is yes to any, please give details below.

I declare that I have no competing interests.

I agree to the open peer review policy of the journal. I understand that my name will be included on my report to the authors and, if the manuscript is accepted for publication, my named report including any attachments I upload will be posted on the website along with the authors' responses. I agree for my report to be made available under an Open Access Creative Commons CC-BY license (http://creativecommons.org/licenses/by/4.0/). I understand that any comments which I do not wish to be included in my named report can be included as confidential comments to the editors, which will not be published.

I agree to the open peer review policy of the journal.