Reviewer’s report

Title: Computational identification and characterization of glioma candidate biomarkers through multi-omics integrative profiling

Version: 0 Date: 23 Mar 2020

Reviewer: Roland Huber

Reviewer's report:

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An article of importance in its field

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Needs some language corrections before being published

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**Reviewer summary**
Please provide a brief overview of your review, stating plainly your opinion of the manuscript’s overall validity, significance and originality.

The authors collected and analyzed a variety of multi-omics datasets on glioma. First, they identify brain tissue-specific genes and cross-reference the resulting list with genes detectable in the cerebrospinal fluid. They identify 2 genes in particular and show that they are well suited as biomarkers for grading gliomas. The analysis is conducted across various datasets that the relative regulation and methylation of these genes predicts survival rates. Data selection, statistical analysis and the authors interpretation of the data appears well justified to me. The study discusses previously identified markers included in the current WHO diagnostics recommendations. The manuscript identifies valuable additional biomarkers that could assist in guiding prognosis and treatment. Additionally, the large-scale analysis of public omics information is an excellent approach to make use of data that has been collected at great expense for additional research. In my opinion this is a well-executed study and should be published.

**Reviewer recommendations to authors**
Please make your report as constructive as possible, if necessary, recommending specific improvements so that the authors have the opportunity to overcome any serious deficiencies that you find. Please divide your comments into major and minor recommendations.

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