Reviewer’s report

Title: Investigation of molecular biomarker candidates for diagnosis and prognosis of chronic periodontitis by bioinformatics analysis of pooled microarray gene expression datasets in Gene Expression Omnibus (GEO)

Version: 0 Date: 23 Jan 2019

Reviewer: Ulvi Gursoy

Reviewer’s report:

This is a well planned and well-written study on the search of periodontitis biomarkers using pooled microarray gene expression datasets. On the era of big data, I agree with the authors that it is time to understand the available data instead of producing new ones continously.

I will have criticisms and I will put them below in the order of text:

- Abstract: Authors state that "for the diagnosis of CP and the associated systemic diseases...", the present study protocol does not allow them to evaluate anything from associated systemic diseases. Same statement is also in introduction, which gives a false expectation.

- Abstract: Conclusion is the repetition of results

- Main text: Use of abbreviations is too much. This is a gene expression study and the need to use abbreviations is understandable. However, it is getting very difficult when authors use abbreviations also for chronic periodontitis (CP), molecular function (MF), biological process (BP, etc..)

- Data sets: GSE10334 included 63 GP and 27 AP patients, GSE 16134 included 120 periodontitis patients, and GSE23586 included 3 periodontitis and 3 periodontally healthy participants. Number of healthy control are very low. I see that the first dataset also took samples from periodontally healthy sites, but at the end those were periodontitis patients. Is the outcome reliable?

-There are unclear expressions, such as: "...positive regulation of the biosynthetic process, the biosynthetic process, and... (page 14 line 197)"

- Discussion is a repetition of results and needs to be rewritten. There are several studies that can be discussed: PMID:26793622, PMID: 27924602, PMID: 26334995. Basically I would expect to see a wider description of the candidate biomarkers and their interactions in disease pathogenesis. Limitations of this approach is also missing.

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.

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 recommend additional statistical review

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Please indicate the quality of language in the manuscript:

Acceptable

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