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: 15 Jan 2019

Reviewer: Yuichiro Kikuchi

Reviewer’s report:

This is a manuscript describing a bioinformatic analysis of datasets GSE10334, GSE16134 and GSE23586, which were microarray analysis of gene expression of tissue sampled from patients with chronic periodontitis or normal healthy control. This study identified the key genes such as CSF3, CXCL12, IL1B, TAGLN, CD19, IL8, CD79A, TNF, and FGF2 as potential biomarkers for CP diagnosis. The experimental procedures seem to be sound. However, some changes are necessary to make this paper more clear and complete.

Major Compulsory Revisions

1. (Abstract: page4, line55-56)

Why did you choose only CSF3, CXCL12, IL1B, TAGLN, CD19, IL8, 55CD79A, TNF, and FGF2 as potential biomarkers for CP diagnosis? Are FCGR3B, SELL, FCGR2B, C3, CD53 and IL10RA not so important? Please explain this reason to readers in the results or discussion section.

2. (Methods: page9, line104 and Table 1)

The authors should provide information about the clinical diagnosis of the patients (healthy control or chronic periodontitis) with the GSE 10334, GSE16134 and GSE23586.

[The sampling time, aged, probing depth, clinical attachment loss, smoking history, and so on.]

3. (Discussion)

The discussion is very succinct. Since the explanations of this results for the majority, please increase the consideration of the results and restructure the discussion.
For example,

I. how about comparing to the results of other studies (especially reference No. 17 and 24)?


24. Song L, Yao J, He Z, Xu B.


II. Page 17, Line 252-253. The authors state 'Among biomarker candidates and hub genes, the association of CD53, CD79A, MS4A1, PECAM1, and TAGLN with CP has not been previously reported.' Readers might want some additional explanations of this reasons.

Minor Essential Revisions

4. (Abstract)
   Line 37. Change "Method" to "Methods".

Line 55. Change "Conclusion" to "Conclusions".

5. (Introduction)
   Line 62. Change "Introduction" to "Background".

6. (Methods)
   Page 10, Line 125-127. What parameters (combined score) were used in STRING to construct the PPI network?

7. (Table 4, 5, 6, 7)
   It is difficult to understand the Table 4-7 at a glance. Like a Table 8, depending on the item to the left side, please separate a line space between right each item and delimit it.

(For example, Table 6. Separate a line space between CD19 and IL8, IL8 and CD79A, CD79A and FCGR3B, ------------------)
8. (List of abbreviations)

Please add the lists of abbreviations.

9. (References)


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.

Yes

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

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:

Acceptable

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