Reviewer's report

**Title:** Optimization of simultaneous screening of the main mutations involved in non-syndromic deafness using TaqMan(R) OpenArrayTM Genotyping Platform

**Version:** 1  **Date:** 26 August 2013

**Reviewer:** Camila Andréa CAO de Oliveira

Reviewer's report:

The paper describes a new screening strategy that leads the identification of known mutations in genes related with nonsyndromic hearing loss. The authors propose this methodology using a high-throughput genotyping technology based on real-time PCR named TaqMan® OpenArray™ Genotyping PCR as an initial screening approach in patients with deafness. Although the methodology proposed is new and worth it to publish there are few issues that should be considered before considering its publication.

- **Major Compulsory Revisions**

  1- In Abstract (Results): the authors have to describe the error rate (in percentage) that occurred during the validation of the results using the TaqMan® Open Array™ genotyping platform. Likewise in the results section (eighth paragraph).

  2- In Discussion (third paragraph): The phrase "These assays were not excluded from the selected layout, but will need, in new genotyping reactions, be validated by other techniques, in this case by direct sequencing" is confusing and needs to be rewritten. The authors state that the false positives mutations were validated by direct sequencing. Then they say that in new genotyping reactions will be validated by other techniques, the same direct sequencing.

  3- Conclusion: The section has to describe concisely and specifically the findings (and limitations) found in this study and do not redundantly repeat those that have been mentioned in the above sections.

  4- In authors’ contribution is expected to find the contribution of the each author’s manuscript and not only the first author. Therefore, this section should include the contribution of all the authors.

- **Minor Essential Revisions**

  1- In Abstract (Results): Remove the dot of the number 11656.

  2- In Background remove (Intro).

  3- Background (2nd paragraph): the term (both ears) is not necessary.
4- The authors could write the introduction of the manuscript more briefly. I suggest removing the fourth and the ninth paragraph.

5- A lower space between each symbol (> on name of the mutations has to be uniformly applied in the results and casuistic.

6- Results (1st paragraph): the number of the Table is 2.

7- Results (third paragraph): The information described in this paragraph has already been cited in casuistry.

8- Results (last paragraph): Replace the dot by comma in etc.

9- The entire discussion is without reference.

10- In Materials and Methods (Sample Preparation - 2nd paragraph): enter a space between the number and the word rpm.

11- Figures: in legend of Figure 1 replace 48 nano-wells by 64.

12- Table 1: Replace pós-natal by pos-natal or postnatal.

13- In table 3 (1st column, rows 4, 5 and 6): the authors should use the name of the genes and do not the name of the mutations.

- Discretionary Revisions

1- In conclusion, I suggest that it is writing more objectively. Most of the information described in this item has been cited in other sections. So use this topic to describe the information in a clear and concise as well as potential pitfalls and limitations of the assay.

2- Table: I suggest inversion between tables 3 and 4, that is, the information of table 4 is shown in table 3 and vice versa.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.