Reviewer’s report

Title: Non-Familial Cardiomyopathies in Lebanon: Exome Sequencing Results for Five Idiopathic Cases

Version: 0 Date: 02 Aug 2018

Reviewer: Oscar Campuzano Larrea

Reviewer’s report:

The study is well design and technically performed.

The conclusions are according to the results.

However, there are some points that should be clarified:

1.- ARVC or ARVD are term not currently used. Now, the disease is named ACM (Arrhyhtmogenic Cardiomyopathy).

2.- After exome analysis and posterior re-analysis of 86 genes, all exons of all genes were amplified? At least at 30x?

3.- All rare variants were confirmed by Sanger method?

4.- Exons not amplified at least at 30x, were amplified using Sanger?

5.- Why not use global data of gnomeAD? It is more specific that ExAC or EVS.

6.- Concerning in silico prediction, only Mutation Taster was used? Nowadays, at least 3 to 5 in silico methods are required in order to supor the prediction.

7.- The classification of pathogenicity follows ACMG recommendations? This is the oficial classification in genètic field to date. A previous report of a variant do not suppose its pathogenic role.

8.- What about CNV (Copy Number Variants)? Do you analyse these kind of alterations? Any result?

9.- Finally, the main limitation of the manuscrit is family segregation. It is a crucial point in order to clarify the role of variants. Why not analysis of relatives?

Please, could you include all mentioned data in the manuscrit?
Thanks,

**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?**
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