Reviewer’s report

Title: Targeted next-generation sequencing identifies novel variants in candidate genes for Parkinson’s disease in Black South African and Nigerian patients

Version: 0 Date: 25 Apr 2019

Reviewer: Ana Gorostidi

Reviewer's report:

This work is interesting both for the clinical-genetic aspect of PD and for the methods and analysis shown. It is friendly and easy to read and should be published as it is an interesting contribution to the research of PD in the African population.

The following are some minor suggestions and questions I would like to do to the authors.

# All coding regions of the genes targeted in the panel are meant to be covered. My question is about the exonic flanking region. How many bases are targeted in the design?

# The link to the BMC website of figure1, to the interactive html-version, needs to be reviewed as it is not working.

# It is suggested in the discussion that common mutations could have not been detected because of a probable low quality of these loci. It would be interesting to show these data and to independently genotype these variants by other methods. Even if the main objective of the study seems to identify putative rare variants, there is much discussion and work around more common mutations and therefore, these will help to reinforce both results and discussion.

# The commercially available gene panel is mentioned as a limitation for the lack 18 genes previously identified to be related to PD. This is ended something that could have been solved designing a custom panel. Actually, the authors should make clear if analyzing these 34 PD related genes is more important than analyzing the rest of the genes included in the commercial "Neurological Research" panel. Other limitations like coverage and reed depth could have been avoided this way.

# Another limitation of the study is mentioned to be the lack of analysis for the variants in ethnicity-matched control samples. In the absence of previous studies, an analysis of the rare variants found in this study should have been performed. And mostly for the ones not found in the PDmutDB database. Previous to functional studies, a substantial number of ethnicity-matched control chromosomes should be genotyped.
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.

Not relevant to this manuscript

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