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: 30 Apr 2019

Reviewer: Pyotr A. Slominsky

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Line 149

More detail description of patients is necessary. "Familial" and "sporadic" - what if familial? Clear mendelian inheritance or familial history of PD?

Table 2 - It is necessary to translate the coding of mutations into a common format. In the presented data is difficult to analyze. And add data on population frequencies and estimates from MetaLR and MetaSVM.

Table 3 - Many possible mutations in one patients. You must to solve a problem of most significant from them and discuss this situation.

Figure 1 - repeats the text of the article in an unsuccessful form. It must be removed.

Figure 2 is also an unsuccessful and poorly readable form. This is about comparing samples from SA and Nigeria - and not about PD. It is also better to remove, leaving a comparison in the text. Although there

Figure 3 and Line 297 - "Blind" drawing. Replace with a table with cut-off values for falling into the "deleterious" category

Line 168, 211 - cut the whole section by removing the standard methods

Line 294 - Why do you use different values for cutting in the case of known genes PD and new genes? These parameters relate to mutations - not genes. And what are your cut-off parameters in the further actively discussed mutations in the genes of familial forms of PD?

Line 319 - remove the entire section on modeling. You do not model a protein with a mutation - you just show the location of its localization on the model. The location of a mutation in a particular functional domain of a protein can simply be said in the text.

Line 416, frameshift mutations. Further, nothing is said about these mutations - although they may be pathogenetically highly significant.
We focused on identifying rare (MAF ≤ 0.01) or novel - but some your possibly deleterious variants are very frequent (Line 489-497). A population frequency of this variants?

GENERAL REMARK - the article should be radically reduced with a clear emphasis on key results.

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.
Unable to assess

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 am able to assess the statistics

Quality of written English
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