Author's response to reviews

Title: Association between paraoxonase gene and stroke in the Han Chinese Population

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Author's response to reviews: see over
Dear Editors and reviewers,

Thank you for your careful review of our manuscript entitled as “Association between Paraoxonase gene and stroke in the Han Chinese Population”. Those comments are very valuable and helpful for improving our manuscript. We have carefully revised the manuscript according to the comments. We hope this revision can be accepted by your journal.

Sincerely yours,
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The following is a point-to-point response to the reviewer’s comments.

Reviewer #2:

MAJOR COMPULSORY REVISIONS

Q1: It is clear that the authors and I are not on the same page on this matter. Thus I would urge the authors to add a sentence along the lines of: "It is unclear to us whether adjusted or unadjusted analyses are preferable in this particular application. In other settings, authorities have discouraged the use of adjustments when obtaining the total genetic effect. [ref 1]"

Answer: Thank you very much for the comment. We have added a sentence according to your suggestion, which is marked as red, in the discussion part of the
Q2: Thanks for clarifying the haplotype analyses. I think that a preferable analysis would be an ANOVA in which the factors are the haplotypes. This can be done also in a regression context, where all haplotypes are considered jointly. The analyses you have performed take a haplotype (I presume present either as one copy or as two copies (a diplotype) versus being absent. However, all these analyses are non-independent and are best performed jointly as per my suggestion above. Again, I leave this to the editor to decide how to handle (demand a re-analysis, as I am inclined to suggest, or allow the current analysis with a mention in the discussion that it is a suboptimal approach, as per my comment above.)

**Answer:** Thank you very much for the valuable comment. As suggested, we have re-performed all haplotypes jointly for each block by ANOVA analysis for including or not including the haplotype information in a likelihood ration test of nested model.

Q3: Finally, please seek the help of an editor. Some additions in the abstract and the text read awkwardly.

**Answer:** Thank you very much. We did it. We hope the language is acceptable now.