Author's response to reviews

Title: Prevalence of Genetic Polymorphisms in the Promoter Region of the Alpha-1 Antitrypsin (SERPINA1) Gene in Chronic Liver Disease: a Case Control Study

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Author's response to reviews: see over
Dear T. Shipley,

Thank you for reviewing our revised manuscript, we have changed our manuscript following the suggestions made by the reviewers. Please find below our response to the reviewers’ comments.

**Reviewer 2: Michele Zorzetto**

This reviewer had no further comments and we wish to thank her for reviewing the revised manuscript.

**Reviewer 3: Sally Chappell**

The authors have addressed the majority of comments raised during the review process. The replacement of table 2 is a vast improvement on the previous version, although I would still like to see a little more detail on how the diplotypes/haplotypes were constructed. Was a software package (e.g., HPlus, Haplovew, Unphased) used for this analysis? If so, more detail needs to be given.

_Thank you for this comment, we used PLEM software to determine the diplo- and haplotypes. We have added this information to our manuscript._

Where individuals are either homozygous at all of the polymorphic sites, or only heterozygous at one site, it is straightforward to determine the haplotypes. However, this is more difficult with heterozygosity at 2 or more sites, and I would be interested to know how this was done. Values for linkage disequilibrium ($r^2$) would also be of interest, and could be added here for the controls and cases separately.

_We have included these values in the revised version of our manuscript. We have calculated the linkage disequilibrium ($R^2$) using Haplovew 4.0. This piece of information is now included in the manuscript._

We hope that you will reconsider our manuscript for publication, and are looking forward to your response.

Yours sincerely,

Karin F Kok, René H te Morsche, Martijn GH van Oijen and Joost PH Drenth