Author's response to reviews

Title: A Detailed Hapmap of the STSL locus spanning 69kb; Differences between Caucasians and African-Americans

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Author's response to reviews: see over
Response to Reviewers

We would like to thank both reviewers for their inciteful and helpful comments. We have addressed all of the issues, and indicated our responses as below.

Reviewer 1.

Major Revisions

1. Since the HapMap has been published….compare and contrast…

We point out that we had completed our manuscript and possibly submitted it, prior to the publication and availability of the HapMap data. However, we have downloaded and analyzed the HapMap data with ours. Two new figures are provide (Figs 3 and 4) and a comment about this is now included in the Discussion, together with a reference to this paper. While the HapMap consortium used many more SNPs than we did, many of their SNPs are located in the intronic areas. Furthermore, while we share some of the SNPs analyzed, SNPs are unique to our analyses. Of these, 4 are cSNPs. Despite these differences, the overall analytical patterns are similar; the African origin samples have smaller haploblocks and have the greatest range of SNP variations. Additionally, despite the increased SNPs in the ABCG5 gene, overall, more SNPs are still located in ABCG8 compared to ABCG5. Thus, our overall conclusions are correct.

Minor Essential Revisions

1. Capitalize human genes
Done
2. Background, line 17, change ‘man’ to ‘humans’
Done
3. Haplotype Analyses, line 3, no need to capitalize ‘Diequilibrium’
Done
4. Discussion, line 13, no need to capitalize ‘Schizophrenia’
Done

Discretionary Revisions

5. Background, line 24, LDL-R LD paper could be cited
Done and we are grateful to this reviewer for drawing our attention to this paper.

Reviewer 2.

Major compulsory revisions

1. First Section of Discussion is not focussed..
We have revised this and made this more focused on the topic.

2. Page 5 methods, define the Caucasian study group
We apologize for this error. All the subjects in this group are self-identified as ‘Caucasian’.

Minor Essential Revisions

3. Page 11 (?12) Hardy-Weinberg…’smaller than what’  
The phrase has been edited to read ‘small sample size’, in keeping with our meaning.

4. Page 12, using the term ‘private’, ‘….polymorphism’, …‘mutation’  
We agree that we may have caused some confusion with our liberal use of these terms. We have stuck to the more accurate and rigorous definition and the term ‘private’ has been replaced with polymorphism that may be ‘race-specific’ to indicate our meaning.

5. Omission of some of the SNPs, and replace these to avoid confusion  
We have revised this figure and included all 14 SNPs, variant or other-wise that were chosen for analyses.

6. G575R is mentioned in Abstract, but omitted on page 7  
Error corrected

7. Page 9, Fig 2A and B referred to as 3 and 4  
Apologize for this, but we consolidated the figures and missed this change in our proof-reading.

8. Page 3 (Background) Zhang ref missed.  
Ah, the joys of Endnote. We have corrected this over-sight.

9. Page 5 (methods) PCR vs. primer extension…  
The reviewer is absolutely correct and we have replaced ‘PCR’ with ‘primer extension’, where we mean primer extension.

10. Ref to Table 1 nucleotide should be given  
We have included the GenBank ID number in the legend.

Discretionary Revisions

11. The authors should use the widely accepted guideline for nomenclature for each SNP etc.  
We agree and follow this for most of our publications. However, in this case, we tried to simplify the paper and allow the reader some facile way to appreciate the SNPs used. However, to ensure that no information is lost, all the SNPs we have used will be assigned the SNP ID number and Table 1 will be edited prior to publication. This should ensure both accuracy as well as allow for cross-referencing of databases.