Author's response to reviews

Title: SNP selection for genes of iron metabolism: in a study of genetic modifiers of hemochromatosis

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Author’s response to reviews: see over
Dear Dr Graham,

Thank you for accepting our manuscript subject to minor revisions. The reviewers revision requests are in italics with our responses below.

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Reviewer 2

1. Marker density (number of snps per kilobase) for each gene is very useful so that readers are clearer about questions such as whether a low capability of capturing untyped variants was due to lower than average coverage in the initial map. This can be done by inserting a column in relevant tables.

We have added a column to Table 7 showing the region included which allows the calculation of marker density. Adding marker density for each chip set would double the size of the table so we have elected not to do this. The marker density is relevant to HapMap and chip sets, not to re-sequencing data, so it was not clear to us that there are other tables to which this reviewer’s comment applies. We assume therefore that we are safe to interpret “relevant tables” as “the relevant table”, namely Table 7.

2. The authors described that for transferrin gene, using the SeattleSNPs database 45% of SNPs with MAF>=3% were captured by HapMap tagSNPs. This need some clarification, e.g. how the tagSNPs were identified? how much would be captured if all SNPs in the tranferrin gene genotyped by HapMap were used? how much if a multiPopTagSNP set was used instead?

We have added some clarification to the table and text, in particular that we used “Tagger” and it is a single population (Caucasian) so multiPopTagSNP is not directly relevant. We have also added the most up-to-date data from HapMap to show the coverage is much improved from phase 1.