Author's response to reviews

Title: Comparing the frequency of common genetic variants and haplotypes between carriers and non-carriers of BRCA1 and BRCA2 deleterious mutations in Australian women diagnosed with breast cancer before 40 years of age

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Author's response to reviews: see over
Dear Editor,

I have made the changes that you requested. All the changes have been highlighted in both, this letter and the manuscript. I have also addressed your concerns in point by point format below.

a) Please clarify what consent you obtained from the participants in your study and add this to you methods section.

I have added the following two sentences to the study methods section of the paper:

All patients provided written informed consent for participation in all aspects of the study. Details of recruitment strategy, participation, and data collection methods have previously been described [6].

Reference 6 was already in the reference section of the manuscript.

b) Authors' contributions: Please review your authorship list and re-format it appropriately as outlined below. We think that it may be more appropriate to list author MB in the acknowledgements.

We would like to retain MB as author as we understated her role. She was involved in co-design including writing methods section and genetics background of the competitive grant application that funded some of this work as well as doing critical edits of the manuscript including statistical methods.

I have re-formatted author’s contribution section as requested:

JLH conceived the idea of the ABCFS and co-designed the current study. LCG assisted with statistical analysis and writing the manuscript. GSD designed and maintained the database for ABCFS, conceptualized the structure of data extracts for the current study and assisted with data formatting for current analysis. MCS supervised and in some cases performed the sequencing and genotyping of variants used in this study and is responsible for the biospecimen repository from which samples were drawn. MB co-designed the current study, advised on haplotype analysis and statistical analysis of genetic variants and did critical edits of the statistical methods section of the manuscript. LT collated data into required format for genetic association analysis, performed analysis and wrote the draft of the paper. All authors read and approved the final manuscript.

We look forward to hearing from you.

Regards,

Lidija