Author’s response to reviews

Title: Identification of candidate breast cancer predisposing variants by performing whole exome sequencing on index patients from BRCA1 and BRCA2-negative breast cancer families

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Version: 3 Date: 17 Mar 2019

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We would like to thank all the reviewers for their valuable and constructive comments and suggestions.

Here we provide a point-by-point reply to the comments made by REVIEWER 3.

4) Perhaps "...over-represented in BC patients. These over-represented genes were especially functional in the DNA double-strand break repair process" would read better as " over-represented in women with breast cancer and commonly involved in DNA double-strand break repair".

ANSWER: Done as suggested by the reviewer (see page 2, line 44/45).
9) I think the breast cancer penetrance estimates for pathogenic variants in PALB2 are now well established - I would cite Antoniou et al NEJM. Note: These are penetrance estimates - I do not think that "exact penetrance" figures are realistic.

ANSWER: Done as suggested by the reviewer (see page 3, line 51, reference no. 4).

Page 12, line 27. I suggest "more frequently tackle genes functionally" would read better as "more frequently identified in genes functionally".

ANSWER: Done as suggested by the reviewer (see page 12, line 26/27)