Reviewer’s report

Title: Family-specific, novel, deleterious germline variants provide a rich source to identify genetic predispositions for BRCAx familial breast cancer

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Reviewer: Steven Narod

Reviewer’s report:

The authors have performed whole exome sequencing on three large multiply affected families with breast cancer. In each family a putative cancer susceptibility gene was identified.

Each assignment is probabilistic but in no family was the evidence sufficiently compelling to conclude with certainty that this was the responsible allele. As a result, the data are not strong enough to counsel families. This is a shortcoming. In particular this will be very difficult in the cases where there are only two or three cases of cancer in the family.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Not suitable for publication unless extensively edited

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests: i have no competing interests