Reviewer's report

Title: Validation and simplification of microarray-based grading in breast cancer

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Reviewer: Andrew Sims

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Wennmalm and Bergh present a simplified method for grading breast cancer patients based upon gene expression data using an R script.

This work is essentially a minor extension of a previous study used to delineate breast tumours into high and low grade tumours based upon microarray data. Whilst the original studies focused on splitting grade 2 tumours from different datasets into grade 1 or 3 tumours, this study demonstrates a method to stratify individual tumours independently.

It is a little odd to stress that the method does not require any further information when histological grade was used to assess how well the method works.

I was able to use the R script provided to establish the molecular grade of some primary breast tumours processed on Affymetrix GeneChips using the instructions provided. However it might be clearer if the authors annotated the R script itself.

A heatmap demonstrating the separation might better illustrate the method.

The authors should state how many (if any) of the tumours in Sotoriou’s study were given a different genomic grade assignment when using their method?

I am not convinced that the current title appropriately reflects the content of the letter/method article? Perhaps something like this would be more appropriate; “A simple method for assigning genomic grade to individual breast tumours”

Minor changes:
3rd Sentence results: This resulted in bias toward low genomic grade calls, we THEREFORE removed 37 lowly expressed genes...

Level of interest: An article of limited interest

Quality of written English: Acceptable

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

Declaration of competing interests:
I declare that I have no competing interests