Reviewer's report

Title: Molecular Risk Assessment of BIG 1-98 Participants by Expression Profiling using RNA from Archival Tissue

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Reviewer: Giorgio Stanta

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COMMENT TO AUTHORS
This study describes a new gene expression method for assessing risk score in post menopausal breast cancer women. Albeit the study is well organised it is not original, since a similar test was developed in the past (J Clin Oncol, 2006 24: 3726-3734).

Major criticisms:
1. The organisation and the set up of the method are very good, but it is not original. This is the major criticism of this study, but the comparison could be very interesting to validate both methods. The authors did not compare the two methods, but this should be done at least as a comment of the published results.

2. The RS described in the study is very similar to Oncotype DX. The proposed test analyses 25 genes involved in breast cancer progression and 3 reference genes for a total of 28 genes. The oncotypeDX is based on 21 genes, 5 of these being reference genes. What is the reason to analyse more genes? Why did the authors create a new test using different genes, but belonging to the same group as the aforementioned kit? Do they hope to analyse other populations of breast cancers, not only ER+ postmenopausal women?

The authors should discuss these points along the article.

Level of interest: An article of importance in its field

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.