Reviewer's report

Title: Expression of aurora kinase A is associated with metastasis-free survival in node-negative breast cancer patients

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Reviewer: Benjamin Haibe-Kains

Reviewer's report:

In the manuscript Siggelkow and colleagues reported the strong and independent prognostic value of Aurora Kinase A, a well-known proliferation gene. This is not new as there are plenty of publication reporting this, however the paper is easy to read and provide a nice overview of the accumulated evidence regarding the prognostic value of AURKA. I would then suggest the authors to enrich the introduction by describing more of the literature available on AURKA.

please see my major and minor comments below.

Major Compulsory Revisions

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Page 6: AURKA has been identified as a good predictor of survival in breast cancer in numerous studies (see references below). Description of these papers is insufficient and the introduction should be updated to reflect their findings.

Refs:
- and references 24 and 27 in the text.

Actually AURKA has also been selected in at least 182 microarray gene signatures as reported in GeneSigDB (http://compbio.dfci.harvard.edu/genesigdb); among these signatures, one can cite the extended mammaprint signature (231 genes) published by van't Veer et al., the Gene expression Grade Index (GGI) published by Sotiriou et al., and the 72 proliferation genes published by Reyal et al.
Page 6: The authors wrote "seemingly contradictory results on the role of AURKA in breast cancer prognosis". There is plenty of evidence that AURKA expression is highly prognostic and is negatively correlated with survival in ER+ breast cancer patients. Why do the authors think the published results are contradictory?

Page 11: If the authors refer to ref 16 as the discrepancy, it is only one paper among the plethora of publications consistently identifying AURKA as a strong prognostic factor.

Page 10: Given the high correlation of AURKA and histological grade it is unclear whether there is a real benefit of considering AURKA expression in addition to the traditional clinical parameters. I would suggest the authors to perform an analysis similar to Figure 1 of the last paper of Prat et al.


Minor Essential Revisions
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Page 7: Because the gene expression data come from three different patients cohorts and datasets, one should check for batch effect. Batch effect correction could be performed if necessary. Frozen RMA could also be used in place of RMA to reduce batch effects.

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: Yes, and I have assessed the statistics in my report.

Declaration of competing interests:

I declare that I have no competing interests