Reviewer's report

Title: Breast Tumor Copy Number Aberration Phenotypes and Genomic Instability

Version: 1 Date: 19 March 2006

Reviewer: Markus Ringner

Reviewer's report:

General

Fridlyand and co-workers present a study of copy number aberrations in sporadic breast tumors. The study is nicely designed, results support conclusions, and the paper is clearly written. Although other work has been done using array-based CGH to investigate breast cancer, Fridlyand et al. add to other studies by investigating genes and pathways associated with genomic instability in these tumors.

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Major Compulsory Revisions (that the author must respond to before a decision on publication can be reached)

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Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)

1) Fridlyand et al. use a set of measures to quantify the genomic instability of a tumor, for example, by counting "copy number transitions". Are these measures likely to depend heavily on the coverage and resolution of the arrays? Arrays of 2464 genomic clones are used so the coverage is relatively low. Some discussion on the influence of the coverage and resolution of the arrays on the measures of genomic instability and also the results would benefit the manuscript.

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Discretionary Revisions (which the author can choose to ignore)

2) In the last paragraph on page 7, the middle branch of the dendrogram in Fig 1A is described. This branch is described with n=16, while the branch consists of 21 samples, of which 16 are sporadic. This description is confusing.

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What next?: Accept after minor essential revisions

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

Quality of written English: Acceptable

Statistical review: No
Declaration of competing interests:

I declare that I have no competing interests