Reviewer’s report

Title: Automated array-CGH optimized for archival formalin-fixed, paraffin-embedded tumor material

Version: 1 Date: 8 November 2006

Reviewer: Markus Ringner

Reviewer’s report:

General

Joosse et al present an array CGH protocol optimized for automated hybridization of formalin-fixed paraffin-embedded (FFPE) tissue. The possibility to use paraffin-embedded material for array CGH is an advantage for this technology compared to for example gene expression arrays. An important step in this direction is to develop methods to obtain reproducible data with low-noise levels from FFPE samples. As the authors mention there has been earlier reports on array CGH of FFPE samples. There has also been reports showing that, although FFPE tissue results in more noisy array CGH data than freshly frozen tissue, array CGH profiles of both these tissue types are highly similar (see e.g. Cancer Cancer Res 2005; 65:7612). This report by Jossee et al adds to previous reports by combining array CGH of FFPE tissue with automated hybridization and their results show that high quality results can be obtained using their propose protocol.

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

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

*) Page 8, section "Hybridization buffer composition". It is written "Of these four hybridizations, the best profile ..., this is at 37 C using 15% dextran sulphate". It is not clear to me that this conditions give the best result based on the data presented in the text. It seems to me that 10% dextran sulphate resulted in a lower (=better) standard deviation. Could the authors clarify why the selected profile is the best?

Discretionary Revisions (which the author can choose to ignore)

*) Earlier investigations of qualities of array CGH technologies have indicated that automated hybridization stations were less effective for array CGH than using simple wells for hybridization. See for example, Cytometry. 2002 Oct 1;49(2):43-8. Could the authors comment on the most likely cause why their findings are different? Have hybridization stations improved or is the development of an optimized protocol more important?

*) Page 8, section 'Hybridization buffer composition'. It is written "variances were 0.02" it is not clear the this refers to two identical values for dextran sulphate concentration 7% and 15%, respectively. It is similarly unclear in some following sentences describing results where the variances were also identical.

What next?: Accept after minor essential revisions

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: No

Declaration of competing interests:

I declare that I have no competing interests