Reviewer's report

**Title:** Histotype-specific copy-number alterations in ovarian cancer

**Version:** 1  **Date:** 16 May 2012

**Reviewer:** Åslaug Helland

**Reviewer's report:**

Review

The authors state in the abstract that they have aimed at dissecting the heterogeneity of ovarian cancer and to identify histotype-specific alterations by doing in silico analyses on multiple datasets. This is an excellent approach since data produced in such (expensive) studies have extensive information that could and should be used in different settings to produce as much as possible information, and to give more power to the results. By doing this, the authors have provided results on the different histological subtypes of ovarian cancer. However, I have some comments.

- **Major Compulsory Revisions.** The author must respond to these before a decision on publication can be reached. For example, additional necessary experiments or controls, statistical mistakes, errors in interpretation.

The choice of data to include in this study:

The study has tried to find aberrations characteristic of the more rare histologies, and by analysing all three selected cohorts, the number of for instance clear cell ovarian cancer amount to 29 samples. There are other studies with substantially more samples which also could have been used. For instance, I find it strange that they have not used the data published by Anglesio M et al, 2011, which have data on 59 clear cell tumours for instance. The TCGA data are also available for analyses.

The published cohorts analysed are two by Gorringer et al. Are some of the same samples analysed twice?

As the abstract describes in silico analyses of datasets, the method chapter describes two datasets which seem to have been analysed in the lab and used as different datasets. Are this in the public domain, or are the lab-analyses performed for this particular study?

The other aim of the study is to identify drivers. They report several possible drivers, by investigating the concordance between copy-number alterations and expression of the genes in specific altered regions of the genome. Many would say that this is a weak indication of driver-characteristics of an alteration. Some of the identified genes are known oncogenes, while others (like TP53) are tumour-suppressor genes. Other, more functional studies could be performed to validate the more unknown genes as actual drivers.
• Minor Essential Revisions
The abovementioned comments should be addressed before minor revision.

The author can be trusted to make these. For example, missing labels on figures, the wrong use of a term, spelling mistakes.

• Discretionary Revisions
These are recommendations for improvement which the author can choose to ignore. For example clarifications, data that would be useful but not essential.

Please note that both the comments entered here and answers to the questions below constitute the report, bearing your name, that will be forwarded to the authors and published on the site if the article is accepted.

**Level of interest:** An article of limited interest

**Quality of written English:** Acceptable

**Statistical review:** Yes, but I do not feel adequately qualified to assess the statistics.