Reviewer’s report

Title: Comparing gene expression data from formalin-fixed, paraffin embedded tissues and qPCR with that from snap-frozen tissue and microarrays for modeling outcomes of patients with ovarian carcinoma

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Reviewer: Deqin Ma

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The manuscript by Bradley et al, compared 1) gene expression measured by qPCR on snap-frozen and FFPE tissues; 2) two platforms, microarray and qPCR, for measurement of gene expression from snap-frozen tissues. They utilized the gene expression microarray data from the TCGA study and did extensive statistical analysis. The work is interesting; however, if the authors could address the following points, they could make it a better manuscript.

Major Compulsory Revisions

1. Although there is good correlation between the two test platforms, the sample size (10) is too small to draw a definitive conclusion.

2. Fourteen out of 91 genes (15%) were unexpressed in at least one TaqMan assay including two (AKT2 and DNTT) of the top 3 genes in the MAPK pathway (see reference 1) and other genes involved in multiple pathways. Figure 3 showed normal distribution of gene expression in all the pathways examined. It was also mentioned in the manuscript that these 14 genes were those that had lowest expression in TCGA microarray but it raises the concern that the qPCR assay may miss some of the low expressing yet important genes.

3. In Figure 2, could the author show the degree of correlation for the rest of the 10 samples?

Minor Essential Revisions

1. The running title is unclear: correlation of ovarian carcinoma tissue with ?-need to specify.

2. Several typos.

Level of interest: An article of limited interest

Quality of written English: Needs some language corrections before being published

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.
Declaration of competing interests:

I declare that I have no competing interests.