Reviewer's report

Title: Analysis of gene expression in prostate cancer epithelial and interstitial stromal cells using laser capture microdissection

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Reviewer: Tomohiko Ichikawa

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The present study was performed to examine differences in gene expression between microdissected tumor epithelial cells and adjacent stromal cells within the neoplastic prostate. The authors have concluded that LCM and microarray analysis are able to identify distinct gene expression patterns in prostate cell populations. They also showed that these tools identified genes of potential significance in prostate cancer, such as WT1.

In order to make sure the microarray data, the authors re-examined expression levels of 10 representative genes as shown in the figure 2. As mentioned by the authors, one of the 10 genes (i.e. EGR1), did not show the consistent data. Although the reason of this disconcordance has been discussed in the text, additional data such as immunohistochemical data of clinical samples would be helpful to show the significance of the higher expression of EGR1 observed in the microarray analysis.

Level of interest: An article of outstanding merit and interest in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.