Reviewer's report

Title: Application of Affymetrix Array and Massively Parallel Signature Sequencing for Identification of Genes Involved in Prostate Cancer Progression

Version: 1 Date: 15 April 2005

Reviewer: Yiwei Li

Reviewer's report:

General

The authors of this paper investigated the genes involved in prostate cancer progression using Affymetrix microarray and massively parallel signature sequencing (MPSS). They found that both gene profiling technologies detected genes the other did not. They concluded that a combination of transcription profiling technologies will provide a more robust means to assess the gene expression profile of an RNA sample. They also found some genes that might be involved in the progression of prostate cancer. The understanding of gene expression profile and novel genes involved in cancer progression may be of value for further research and treatment of prostate cancers. The experimental design of the study is straightforward, the experiments were carefully conducted, and the data are clearly presented. Overall, I believe that the results could be of interest to researchers involved with gene expression profiling and prostate cancer.

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

1. Authors identified some genes which they believed to be involved in cancer progression. However, only mRNA data was presented. Since protein expression is more critical, it would be worthwhile to check the difference in protein expression.
2. In Fig. 4, 5 and 6, authors showed the different expressions of genes in prostate cell lines and tissues tested by RT-PCR. However, no internal control such as actin or GAPDH was included. Authors should include such control in RT-PCR data.
3. Authors compared the numbers of expressed genes in prostate cancer cell lines by two different methods. However, authors did not describe how many times they repeated the microarray and MPSS assays for a single sample. The differences in the expression of genes in two experiments will be observed even using same sample and same method. Lacking of statistical analysis made the data less significant.

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

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.