Reviewer’s report

Title: Candidate pathways and genes for prostate cancer: a meta-analysis of gene expression data

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Reviewer: Ronglai Shen

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This study performed a meta-analysis of previously published gene expression data sets in prostate cancer. They further performed a functional annotation analysis on the top 500 genes identified to be most differentially expressed in the course of prostate tumorigenesis. Integrin-based pathways were among the top enriched pathways. The authors therefore formulated a collagen hypothesis of prostate tumorigenesis.

Major comments

The major conclusion of this study is this collagen hypothesis in prostate tumorigenesis based on the meta-analysis findings. However, whether the meta-analysis strategy employed here has sound basis and valid ground is unclear at best in the following aspects: 1) despite the vast literature on meta-analysis in prostate cancer and other types of cancer as well, there was virtually no mention about any one of them in the background. Neither is there discussion on how their results compare to other meta-analysis study findings; 2) despite much advancement in meta-analysis methods in gene expression data setting, the authors used an outdated approach (Stouffer’s method) where its applicability to microarray data is basically unclear. Unless the study undertakes a major effort to do a thorough investigation of meta-analysis and revamp the entire analysis either using up-to-date methods or justify the validity of the current approach via comparison, the article is unacceptable in the current form.

Level of interest: An article of limited interest

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

Statistical review: Yes, and I have assessed the statistics in my report.

Declaration of competing interests:

I declare that I have no competing interests.