Reviewer’s report

Title: Lineage relationship of prostate cancer cell types based on gene expression

Version: 3 Date: 21 January 2011

Reviewer: Samuel Denmeade

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Discretionary

The paper is acronym and abbreviation rich and as such it is a tough read. It might benefit form a small table with the various lines and their corresponding derivation/characteristics.

Minor Essential

In the first set of results and figure1 the authors create a 3-dimensional plot using transcriptomes from basal B, luminal L, stromal S and endothelial E. They never really describe what these are, how these cells were isolated, etc in the Results or the Methods.

Major Compulsory

The conclusion of the paper is that transcriptomics can identify luminal-like and non-luminal-like prostate cancer cell types. The authors don’t ever define what they mean by the term “luminal” but one can infer this means the ability to form glandular structures. It would appear that the transcriptome analysis is not much of an improvement over the Gleason score in terms of predicting aggressive vs. non-aggressive tumors. Some analysis of other tumors showing that this analysis could tease out the “bad” Gleason 3 tumors from the “good” Gleason 3 tumors would make a more convincing argument that this type of transcriptome analysis is useful.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

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'