Reviewer's report

Title: Clinicopathological and Gene Expression Parameters Predicts Liver Cancer Prognosis

Version: 1 Date: 24 May 2011

Reviewer: Cheng Li

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The authors used gene expression profiles of normal and tumor tissues to improve the prognosis power of clinical biomarkers in liver cancer. They showed expression profiles can further divide good and poor survival groups into subgroups with differential survival outcomes. The resulting gene signatures overlapped significantly with previously published survival signatures, and with the SNPs from eQTL studies of liver cancer.

Major Compulsory Revisions

1. The improvement of expression profiles was assessed within the good and poor prognosis groups of clinical parameters (stratified model). Alternatively, one can build a single prediction model using both clinical biomarkers and expression profiles (both normal and tumor), and compare it to the stratified model and the models using only clinical parameters or only expression profiles.

Minor essential revisions

1. Fig S1 not included.

Level of interest: An article of importance in its field

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