Reviewer’s report

Title: Genetic and epigenetic characteristics of human multiple hepatocellular carcinoma

Version: 1 Date: 27 October 2009

Reviewer: Yujin Hoshida

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Major Comments
(1) Is there any speculation on the higher similarity in the pattern of methylation levels from the same patients, e.g., there may be individual difference in susceptibility for specific promoter methylation?

(2) It would be better to clarify that the very high similarity (i.e., r>0.8), not the relatively higher r associated with the individual difference, is a potential indicator of IM to avoid confusion.

(3) It would be informative to include clinical variables (e.g., tumor size, histological differentiation, encapsulation, presence of nodule-in-nodule structure, presence of cirrhosis,….) in Table 1. It will provide clue to have a sense about clinical likelihood of IM or MC and its correlation to r for each case. Instead, the results for mutation and chromosomal aberration in Table 1 can be moved to Table 2.

(4) The negative results for mutation and chromosomal aberration analysis are likely due to small sample size, rather than technical limitation of the assays as mentioned in the last paragraph of Discussion, given the huge clinical and molecular heterogeneity in HCC.

Minor comments
(1) It would be better to rephrase "adjacent normal liver" to "adjacent non-tumor liver" to avoid confusion.

(2) Results, Chromosomal aberration, "nucleotide resolution": More precisely, "probe-level resolution" would be better because the data were generated on CGH array.

(3) It would be ideal to deposit the datasets to public database like NCBI’s Gene Expression Omnibus.

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

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.