Reviewer’s report

Title: Microarray profiling shows distinct differences between primary tumors and commonly used preclinical models in hepatocellular carcinoma

Version: 2 Date: 15 April 2015

Reviewer: shigeki nakagawa

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Major Compulsory Revisions
1. First of all, it is not possible to see these figures (especially figure 1 and 3) at all. We cannot see anything from these figures.

2. It is too intemperate to conclude that the xenograft is not useful as HCC model. HCC has much multiplicity between patients and even in the same tumor, and authors used only HepG2 cell line. To consider about the validation of HCC is needed, such as the experiment using other cell lines, or analyze the HCC classification by gene expression (Lee et al, Ye et al, Hoshida et al, …)

3. Please clarify the change of gene expression between original tumor and PMX. (again, we cannot see the figure..)

Level of interest: An article of limited interest

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