Reviewer's report

Title: Hepatic microRNA expression is associated with the response to interferon treatment of chronic hepatitis C

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Reviewer: Michael G Katze

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In this manuscript, Murakami et al described their approach to identify the cellular microRNAs associated with the response to the Interferon treatment against chronic hepatitis C infection. Using microRNA microarrays, the authors profiled the expression patterns of 470 cellular microRNAs among 99 HCV positive liver samples before the IFN treatment. Then, they grouped these 99 patients based on the changes of HCV viral RNA abundances after the Peg-IFN and Ribavirin treatment. By selecting the differentially expressed microRNAs between groups, they claimed that they identified the cellular microRNAs associated with the different response to the IFN treatment.

In this manuscript, these authors addressed an important question that whether hepatic miRNAs can be used as the biomarkers for predicting the effectiveness of the IFN treatment to the HCV 1b infection as the HCV 1b genotype responds poorly to the IFN treatment. This is also the first report to address this question in a relative large sample set. The experiment design is appropriate and the statistical analysis is sound. The data are quite interesting.

To improve the quality of the manuscript, the authors may consider using a Venn diagram to demonstrate the relationships among microRNAs associated with rapid, early and final responses. It would help to identify the microRNAs predictive to all 3 stages and the microRNAs predictive to a particular stage only.

The authors may consider verifying the expression difference of some putative targets of identified microRNA biomarkers by qRT-PCR on the same sample set. It would be more convincing evidence suggesting that the differential expression of these biomarkers indeed has biological impact.