

Responses to reviewers:

1. **In this study, the SMARCA4-specific competing endogenous RNA network and its correlation with poor prognosis and immune cell infiltration in HCC were analyzed. Overall, the analysis was well performed, and data were presented well except for data in Figure S2A. Some suggestions, The manuscript type, this manuscript looks like a meta-analysis but is not evidence-based medicine. Abbreviations should be listed in full names for the first time shown in the manuscript and the abstract. Take care of the space between words, such as cancer(Figure1); in Figure2; What is the major limitation of this study? This should be listed in the discussion part. Figure 1, listing cancer abbreviations in the legend. Figure 2, what is the number of cases in Figures 2A and 2B? Are they the same patients? Figure 4 legend, capitalize C of Correlation. Figure 5, what is the target of SMARCA4? Change the color of the two boxes in the transcription part. And what is the role of CA9? Listing the full name of CA9 in the legend. Replace Figure 2A. Amplify Figure S4.**

Thank you very much for the suggestions.

- (1) Figure S2A has been updated.
- (2) Abbreviations should be listed in full names for the first time shown in the manuscript and the abstract. Abbreviations of the manuscript have been updated.
- (3) Limitations of the study have been added to the manuscript.
- (4) cancer abbreviations were listed in Figure legends.
- (5) Correlation has been polished.
- (6) CA9 is the target of SMARCA4

2. **The manuscript entitled “Delineation of a SMARCA4-specific competing endogenous RNA network and its correlation with poor prognosis and immune cell infiltration in hepatocellular carcinoma” focuses on the investigation of lncRNA-miRNA-SMARCA4 axis involved in post-transcriptional regulation of immune infiltration during hepatocarcinogenesis. Additionally, the authors assessed the prognostic value of this axis in HCC. Major concerns: 1. The work was carried out with the use of differential gene expression and non-coding RNA expression analysis based on bioinformatics approaches. Therefore, a major concern is the absence of experimental confirmation of the results obtained in this work.**

Thank you very much for the advice. This is the major limitation of our study. In the future, we aim to complete the experimental confirmation of the study.

On my opinion, major results obtained in this work is prediction of lncRNA-miRNA-SMARCA4 axis. However, this was not reflected in the title and Abstract. Other concerns: 1. Title is somewhat long and does not contain main results obtained in this work.

Thank you very much for the suggestions. The lncRNA-miRNA-SMARCA4 axis was included in the SMARCA4-related ceRNAs because we found two lncRNAs which can modulate SMARCA4.

Abstract: Methods subsection is vague; it should contain more detailed description of methods including prediction of lncRNAs and miRNAs.

Thank you very much for the advice. Methods subsection has been updated.

Results subsection should contain data on predicted interactions between miRNAs,

lncRNAs, and SMARCA4. The same for Conclusion section.

Thank you very much for the advice. We have added the detailed data to the results, ‘Approximately, 20 miRNAs that could potentially bind to SMARCA4 were detected (Table1)’. A total of 75 lncRNAs were identified and correlation analysis was performed to identify the upstream lncRNAs.

Methods: Since miRNAs interact with genes and lncRNAs compete with genes, it is recommended to use the word “interact” instead “upstream”. The same for Results section.

Thank you very much for the advice. ceRNA mechanism was proposed by Salmena and his colleagues¹. The core of this ceRNA theory was miRNA, we aimed to construct the ceRNAs based on miRNAs in this study, and this is why we used upstream instead of interact. We will explore the interact relationship between ncRNAs and other gene coding RNAs in the next study.

Results: Subsection 3.1, as shown on Fig. 1, the SMARCA4 expression is elevated in some cancer types (GBM, KICH, etc.). However, the authors stated that “to be substantially higher than in normal in all 18 types of cancer”.

Thank you for the important suggestions. We have corrected the expression on the basis of the results.

Subsection 3.2 stated that “higher expression levels of SMARCA4 were correlated with poor prognosis in patients with HCC”, however, Fig. 2 shows that higher 2-year, 5-year, and 10-year patients’ OS at higher SMARCA4 levels is not obvious. Abbreviations should be explained at their first usage.

Thank you for the advice. We have calculated the survival rate using R2 online tool.

1. Salmena L, Poliseno L, Tay Y, et al. A ceRNA hypothesis: the Rosetta Stone of a hidden RNA language? *Cell* 2011; 146: 353-358. 2011/08/02. DOI: 10.1016/j.cell.2011.07.014.