Peer Review File

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Reply to Reviewer:

We thank the reviewer for the overall evaluation of this work and the comments. The point-by-point responses to each comment are as follows.

However, with regard to the reviewer's reply to comments 2-4, I would like to clarify that the content of comments 2-4 in the article has only modified the two parts of the mark, and no other relevant modifications have been made. The position indicated in the reply is the content of comments 2-4 in the article. Due to the lack of literature feedback and our incomplete research, there is less content about the review part. In the future, we will refer to the reviewer's comments for further research.

(1) There are many genes that regulate the proliferation of RCC. Why did the author choose CENPF for research? Please describe the reason.

Response:

We thank the reviewer for pointing out this problem. We found that CENPF was highly involved in RCC by combining cases with relevant literature and using microarray data set analysis. The expression level of CENPF was significantly correlated with OS and RFS in clear cell RCC.

Changes in the text: None

（2) What are the relevant characteristics of the tumor microenvironment of RCC? What is the correlation between CENPF and the tumor microenvironment? What are the possible goals of future drug development? It is recommended to add relevant content to the discussion.

Response:

We thank the reviewers for pointing out this problem. This article briefly explains the following positions in the text (see Pg7, Ln33-34; Pg8, Ln1-6, Ln15-18).

(3) In addition to CENPF, what other key driver gene play an important role in the progression of RCC? Please explain in conjunction with relevant references.

Response:

We thank the reviewer for pointing out this problem. It has been found from previous studies that vascular endothelial growth factor (VEGF) and mammalian target of rapamycin (mTOR) play an important role in the occurrence and development of RCC. At the same time, microarray dataset analysis has indicated that MT2A, MYC, CENPF, and NEK2 have a high degree of participation in

RCC. This article briefly explains the following positions in the text (see Pg3, Ln15-17; Pg8, Ln6-11, Ln15-17).

(4) There have been many studies on RCC. What is the difference between this study and previous studies? What is the innovation? These need to be described in the introduction.

Response:

We thank the reviewer for pointing out this problem. This article briefly explains the following positions in the text (see Pg3, Ln12-24).

(5) There are still some weak points in this paper. It is suggested that the author increase the research of signaling pathway. This is more conducive to support the conclusions of this study.

Response:

We thank the reviewer for pointing out this problem. We will strengthen the research of signal pathway in the follow-up experiment, further supplement the appeal results, and further explain the role of CENPF in RCC.

Changes in the text: None

(6) Can CENPF be used as a potential biomarker for patient risk stratification and local regional metastasis in RCC? It is recommended to add relevant content.

Response:

We thank the reviewer for pointing out this problem. We will strengthen this supplement in the follow-up experiment, improve the information of RCC patients, and further elaborate the role of CENPF in the risk stratification and local regional transfer of RCC patients.

Changes in the text: None