Peer Review File

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Review Comments

Comment 1: This study partially revealed the role of SNHG9 in PCa. If SNHG9 is used in the diagnosis and prognosis of PCa, what optimization and research are needed?

Reply 1: We thank the reviewer for pointing out this question. As we have summarized in the introduction section, although prostate specific antigen (PSA) has been put into clinical use as a biomarker for the diagnosis and prognosis of PCa, it still has some limitations, such as differences in various races or ethnic groups and low sensitivity. Therefore, research could be conducted to explore the expression of this specific LncRNA in different ethnic groups. In addition, we may take efforts to improve the sensitivity to detect SNHG9. We believe that SNHG9 could be served as an effective biomarker by combination with the traditional PSA-measuring method if all these optimizations are completed.

Comment 2: It can increase the biological function and regulation mechanism of microRNA and key genes in prostate cancer.

Reply 2: We thank the reviewer's insightful suggestion. Previous studies have investigated the regulatory role of SNHG9 in both microRNA (PMID: 32943928) and key genes (PMID: 32007500). To improve the innovation of this study, we mainly focus on the role of SNHG9 in immune infiltration of PCa cells, which has not been reported before.

Comment 3: A lot of external experimental verification and clinical research are also needed.

Reply 3: We thank the reviewer's kind suggestion. We agree that the current study was performed primarily by bioinformatic analyses, which could be further strengthened by experimental research. This potential limitation of our study has been discussed in the discussion section. We will perform a follow-up project to investigate the underlying mechanism by which SNHG9 regulates PCa progression in the near future.

Comment 4: What is the prognostic value of SNHG9 in other cancers?

Reply 4: We thank the reviewer's valuable suggestion. The prognostic value of SNHG9 in other cancers was analyzed. As shown in Fig. 3B-3G, significant association between SNHG9 expression and poor PFS was also observed in patients diagnosis of bladder carcinoma (BLCA), Cervical Squamous Cell Carcinoma (CESC), Kidney Renal Clear Cell Carcinoma (KIRC), Low Grade Glioma (LGG), Pancreatic adenocarcinoma

(PAAD) and Uveal Melanoma (UVM). Please see Page 7, lines 18-23, Page 8, line 1 and Supplementary Figure 2 (Page 14, Lines 7-10).

Changes in the text:

Page 7, Lines 18-23; Page 8, Line 1;

Page 14, Lines 7-10

Comment 5: The identifications in the figure are inconsistent with those in the manuscript, for example, A and B are used in Figures, but a and b are used in the manuscript. Uniform identification is recommended.

Reply 5: We would like to thank the reviewer for this suggestion and we have revised the manuscript as suggested.

Comment 6: There have been many studies on prostate cancer. What is the difference between this study and previous studies? What is the innovation? These need to be described in the introduction.

Reply 6: We thank the reviewer's insightful suggestion. We have revised the introduction to emphasize on the innovation of our current study. All the changes are marked in red in the introduction on revised manuscript.

Comment 7: The statistical and analytical methods used in this study may have potential deviations. How to avoid and solve this problem?

Reply 7: We thank the reviewer's insightful suggestion. We use a variety of methods to analyze the same problem. For example, the relationship between clinical pathologic features and SNHG9 was analyzed using the Wilcoxon rank sum test, Chi-square test, Fisher exact test, and logistic regression, and TCGA patient survival rates were calculated using the Kaplan-Meier method, log-rank test and Cox proportional hazard models. In this way, using multiple methods to describe the same problem can well avoid and solve the potential deviations between various statistical methods. All the related description are marked in red in the Materials and Methods on revised manuscript.

Comment 8: This study is entirely data analysis, and verification of the expression of SNHG9 should be added, which should be more convincing.

Reply 8: We thank the reviewer's kind suggestion. We agree that the current study was performed primarily by bioinformatic analyses, which could be further strengthened by experimental research. This potential limitation of our study has been discussed in the discussion section. Please see Page 10, lines 12-15.

Changes in the text: **Page 10, Lines 12- 15**

Comment 9: The discussion part is only a re-description of the results and a listing of the literature. It is recommended to add relevant possible mechanism to further enrich the content of the discussion.

Reply 9: We thank the reviewer's critical suggestion. We have revised the discussion part totally to enhance the depth and quality. All the changes are marked in red in the discussion on revised manuscript.