
Peer Review File

Article information: https://dx.doi.org/10.21037/jgo-23-94

Review Comments-reviewer A

The paper titled "Screening of potential pain genes in pancreatic ductal adenocarcinoma (PDAC) based on bioinformatics methods" is interesting. By data mining the PDAC tumor expression, dozens of differentially expressed genes were identified in this study, several of which have been associated with the frequency and severity of cancer pain. This study provides an important foundation for the pain treatment of PDAC tumor patients. However, there are several minor issues that if addressed would significantly improve the manuscript.

1) The bioinformatics analysis in this study is too simple. It is recommended to conduct WGCNA analysis on the data to determine the key modules, which may be more meaningful.

Answer: The main purpose of our research is to quickly obtain some genes related to cancer pain of pancreatic ductal adenocarcinoma through bioinformatics analysis, so that we can carry out further cytological experiments and clinical verification in the future.
Change in the text: None.

2) All figures are not clear enough. It is recommended to provide clearer figures again.

Answer: We have replaced it with pictures with higher definition.
Change in the text: None.

3) This study is based on bioinformatics analysis. It is recommended to increase in vivo and in vitro experimental studies, which may be more meaningful.

Answer: In future research, I will add relevant in vitro and in vivo experiments and relevant clinical trials to further verify the scientific research value and clinical value of the key genes we screened.
Change in the text: None.

4) It may be more meaningful to add functional research on key genes.

Answer: At present, the main purpose of this study is to quickly obtain the genes related to the cancer pain of pancreatic ductal adenocarcinoma through bioinformatics. In future research, we will conduct further functional detection and screening of these key genes, so as to obtain more reliable research results.

Change in the text: None.

5) The description of some methods in this study is too simplistic, please describe in detail.

Answer: The purpose of this study is to preliminarily screen the genes related to the cancer pain of pancreatic ductal adenocarcinoma, and then apply the results to clinical application. In the future research, we will further analyze the functions of the key genes screened in the database and the possible signal pathways.
Change in the text: None.

6) The introduction part of this paper is not comprehensive enough, and the similar papers have not been cited, such as “Identification of solute carrier family genes related to the prognosis and tumor-infiltrating immune cells of pancreatic ductal adenocarcinoma, PMID: 35282128”, “Screening key genes related to neuropathic pain-induced depression through an integrative bioinformatics analysis, PMID: 36660683”. It is recommended to quote the articles.

Answer: We have added these two references in the preface.
Change in the text: Page 3，line78,85

7) How to use bioinformatics to mine the core genes of PDAC and analyze the survival prognosis of patients? It is recommended to add the content of the discussion.

Answer: Thank you very much for your valuable comments. At present, the main purpose of this study is to analyze and screen cancer pain genes of pancreatic ductal adenocarcinoma by bioinformatics analysis, so as to provide evidence for pain treatment of pancreatic ductal adenocarcinoma patients. The clinical data of patients were not involved in this study, including the study on the correlation between the key genes screened and the prognosis of patients. In the future research, we will further improve the collection and collation of some clinical data, and analyze the role of these key genes in the prognosis of these patients, from bioinformatics analysis to clinical analysis, to provide better help to improve the symptoms of these patients.
Change in the text: None.

8) It may be more meaningful if it is combined with proteomic analysis.

Answer: Thank you very much for your valuable comments. At present, the main purpose of this study is to analyze and screen cancer pain genes of pancreatic ductal adenocarcinoma by bioinformatics analysis, so as to provide evidence for pain treatment of pancreatic ductal

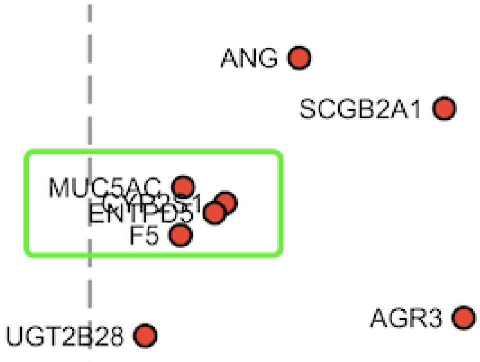
adenocarcinoma patients. In the next step of research, we will increase in vivo and in vitro experiments to further verify the accuracy of the research results. At the same time, we will combine proteomics, space transcriptomics, single cell sequencing and other methods to build a nomogram prediction model, so as to better provide better help for the clinical management of these patients.

Change in the text: None.

Review Comments-reviewer B

1. Figure 2:

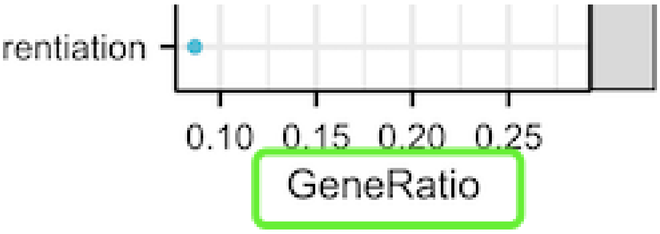
The gene names are not clear. Please revise.



Reply: Thank you for your comment. We have revised figure 2 and provided it to you.

2. Figure 3:

Please revise all “GeneRatio” to “Gene Ratio”.



Reply: Thank you for your comment. We have revised figure 3 and provided it to you.