Peer Review File

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Reviewer A

I have reviewed the manuscript titled "[Identification of a signature for the CD8T cell-related tumor microenvironment for predicting the prognosis of gastric cancer from single-cell and bulk sequencing data]" and found it to be well-written and thorough. However, I would like to bring to your attention that a similar article on the same topic was recently published.The published article, "[Identification of the CD8+ T-cell Related Signature for Predicting the Prognosis of Gastric Cancer Based on Integrated Analysis of Bulk and Single-cell RNA Sequencing Data]," addresses similar research questions and methodologies even the title is almost identical. Given the close similarity, it might be beneficial to evaluate whether the current manuscript offers new insights or significant advancements beyond the existing literature.

Response: Thanks a lot for your good question. Indeed, you pointed out that there was a previous article similar to our research. We summarized the differences between the previous article and our manuscript. However, the most significant difference lies in the methods used for selecting genes. In the research conducted by Zhu et al., 174 immune-related genes were identified, and a novel risk model was subsequently developed. However, they did not perform any further screening of these genes. In our study, combined with univariate Cox analysis, we ultimately identified 23 CD8T cell-related prognostic genes: TCIM, AADAC, SLC2A3, ZNF331, TSC22D3, CMTM3, ZFP36, VIM, CLDND1, GABARAPL1, SOCS3, RGS1, TCEAL9, RGS2, CD59, SPRY1, EMP3, ZEB2, PDE4B, GLIPR1, ERRFI1, and LBH. Moreover, using the Cox regression model to prioritize the 23 CD8T cell-related genes, we finally selected 7 genes: CXCR4, AADAC, SLC2A3, CMTM3, RGS2, CD59, and ZEB2. Our findings have the potential to provide novel insights into the diagnosis and treatment of GC. We have added the differences in the discussion of the manuscript (line 294-304).

References

[1] Zhu ZG, Wang Z, Wu Q, et al. Identification of the $CD8^{+}$T-cell Related Signature for Predicting the Prognosis of Gastric Cancer Based on Integrated Analysis of Bulk and Single-cell RNA Sequencing Data. Journal of Immunotherapy, 2024, 47(7):239-248.

Reviewer B

The article is very interesting, and the topic it examines is highly important. Currently, the progression of oncology is increasingly focusing on the role of the tumor microenvironment (TME) and the interactions between the cells within the TME and cancer cells. Therefore, it is crucial to identify which cells can assist in therapy and to understand the role of these cells as predictors. The article is well-written, comprehensive, and includes all necessary details. I believe its publication will be highly beneficial.

However, there is one area that could be improved: the discussion section. The discussion is too extensive compared to the other sections, and many of the details included there would be more appropriate in the results section. The discussion should focus on explaining the results and their implications for the prognosis of gastric cancer.

Response: Thanks very much for the reviewer's suggestion. We have revised the problem in the discussion section (line 277-304).