

Peer Review File

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Reviewer A:

In this study, the authors aim to explore the prognostic role of SNAIL family members in breast cancer (BC) patients based on public databases.

Although the topic of the article is relevant for the translational research, the paper presents a series of flaws that limits the publication in its present form.

Major points:

- The authors concluded that ‘SNAI1 mRNA expression was a negative prognostic factor, and on the contrary, mRNA of SNAI3 was positive correlation with prognosis in BC.’ However, this conclusion seems too strong: the data hereby presented suggests this prognostic role but not proves this. Thus, the authors should mitigate the discussion section and the conclusions.

Reply: Thank you for your comment. Indeed, we should not make too strong conclusion, and we have mitigated the discussion section and the conclusions in the revised manuscript according to your advice.

Changes in the text: we have made modification about the conclusions in Abstract, Discussion and Conclusions sections, highlighted in red.

- The results are not clearly presented.

Reply: We have reorganized and rewritten the results, and we hope the revised part could be acceptable for you.

Changes in the text: we have made modification in Results section in red.

- The whole manuscript is not well written and includes several linguistic mistakes throughout the text; a native language revision is mandatory.

Reply: We feel sorry for our poor writings and we have tried our best to polish the language in the revised manuscript. In addition, we will invite AME Editing Service to help polish our article. And we hope the revised manuscript could be acceptable for you.

Changes in the text: we have revised this paper, highlighted in red.

Reviewer B:

In the manuscript, the authors identified the prognostic values of SNAI family members in breast cancer patients.

[Main Points:]

1. The data reported in this manuscript are too preliminary. Using bioinformatics analysis, the authors found different roles of SNAI1 and SNAI3 in breast cancer patients.

However, we did not find any experimental practice associated with their different biological functions. Specially, more laboratory experiments are mandatory to sustain the probable theoretical mechanisms for the SNAI1 upregulation and SNAI3 downregulation in this paper.

Reply: Thank you for your suggestion. In this work, we utilized public databases to probe the association of SNAIL family members with survival outcomes in patients with breast cancer (BC), and we confirmed the prognosis value of SNAI1 as reported in previous studies. The role of SNAI1 in BC have been explored by laboratory experiments, which was discussed in the Discussion section. As for SNAI3, this is the first paper that report the association between SNAI3 and survival of BC patients, and the result is indeed very preliminary, just like your comment. We have investigated the pathway and biological process related to SNAI3, which preliminarily indicated the function of SNAI3 in BC. So far, we have not yet study the exact function of SNAI3 in vivo and vitro experimentation, but we will focus the function of SNAI3 in BC in future.

Changes in the text: we have discussed the function of SNAI1 and SNAI3 in the Discussion section.

2. Why the authors showed the protein expression status of the SNAI family in other normal tissues, not the breast tissues in Supplementary Figure S1A?

Reply: Thank you for your reminder. We have showed the protein expression status of the SNAI family in normal tissues, including the breast tissues, and we described these result in the Results section.

Changes in the text: None.

3. The authors evaluated the genomic alternations in cancers. However, what're the biological significances of these alternations for cancer development and progression? The authors should discuss these issues in detail.

Reply: Thank you for your kind suggestion. We have rewritten the discussion section according to your advice, and discussed the biological significances in detail.

Changes in the text: we added more discussion about the biological significances of genomic alternations in the discussion section.

[Minor Points:]

4. The authors must consider having a native English speaker, or English Language Editing Service – preferably with the background in biology – to revise this work. Please uniform the format of the p-value.

Reply: We feel sorry for our poor writings and we have tried our best to polish the language in the revised manuscript. In addition, we will invite AME Editing Service to help polish our article. And we have uniformed the format of the p-value according your kindly reminder.

Changes in the text: we have revised this paper, highlighted in red.

5. The image resolution is very poor and should be improved using Adobe Illustrator or Photoshop.

Reply: We are sorry for the poor resolution. We have submitted figures with high resolution as per your suggestion.

Changes in the text: We have submitted figures with high resolution together with the revised manuscript.