Dear Editorial Department editors and reviewers:

Hello!

First of all, thank you very much for taking time out of your busy schedule to read and revise ***Elucidating the Molecular Basis of ATP-Induced Cell Death in Breast Cancer: Construction and Validation of a Robust Prognostic Model***, thank you for your valuable suggestions. Your suggestions can make up for my shortcomings, which will play a very important role in improving the quality of my paper. At the same time, it has very important guiding significance for my thesis writing and scientific research work.

I have carefully studied the suggestions of the reviewer, and carefully revised the paper one by one according to the suggestions, and the modified part is marked in red. The review experts' suggestions are hereby replied as follows:

The text has spelling and editorial errors that are noted in the manuscript. You are requested to review and address the observations

Thanks to the suggestions of the reviewers, we have revised the relevant questions and marked them in red.

The authors have aimed to explicate" the Molecular Basis of ATP-Induced Cell Death in Breast Cancer: Construction and Validation of a Robust Prognostic Model" through literature review. -By constructing "a miRNA prognostic model and mirroring the gene-based prognostic model, as autonomous prognostic factors "& - Aiming grouping analysis. -"MATERIALS AND METHODS: Literature search of AICD core genes" -Analysis of data is, absolutely, performed based on grouping. In fact personalized insight is required to be considered, i.e., at single cell level. - "Exploring the entire dataset's risk score distribution and expression heat map." also reflect the global insight. It is stated that: - :"The findings of this study show that AICD could be a potential target for breast cancer detection and therapeutic intervention, opening up a new research channel and perspective for breast cancer diagnostic and treatment. This discovery holds promise in providing valuable insights for precision treatment and accurate prognosis assessment of breast cancer." - The required analytical insight includes single cell assay of the end point of the road , i.e., Protein expression at single cell level by very high enumeration. - In brief: Single insight of cancer cells in each patient is required to be,

separately, assayed , analyzed and discussed. - There is no destination for group-analysis. Cancer is the single cell based territory. - The key aims include: Considering the functional insight, and at single cell level. Otherwise, the road map will not provide the translatable, personalized insight.

Thanks to the suggestions of the reviewers.Thank you for your insightful comments regarding our manuscript, “The Molecular Basis of ATP-Induced Cell Death in Breast Cancer: Construction and Validation of a Robust Prognostic Model.” We appreciate your suggestions and are pleased to provide a detailed response to address the points you have raised. We agree with your suggestion to incorporate a more personalized perspective into our study by analyzing data at the single-cell level. We acknowledge that while our current analysis is based on grouping, it is essential to consider the individuality of cancer cells within each patient. To address this issue, additional experiments are needed in the future to evaluate the expression of AICD core genes at the single-cell level. These data will provide valuable insights into the heterogeneity of AICD and its potential as a prognostic factor for breast cancer. However, due to funding problems related to this study, it is deeply regrettable that we could not supplement the experiment. In addition, we put forward the following outlook at the end of the article, hoping to get further confirmation.

Future investigations need to allocate greater focus on the examination, analysis, and discourse of discrete cancer cells, in order to reach more exacting insights. Recognizing the fact that the domain of cancer research is inherently rooted in single-cell substrates, it is imperative to note that a dearth of single-cell analyses for individual patients could potentially undermine the comprehensive nature of these studies. Subsequent to this, the primary objectives include giving precedence to functional insights at the single-cell level, thereby ensuring that later research provides actionable and targetted insights.

We appreciate your suggestion to focus on functional insights at the single-cell level. Emphasis is placed on the importance of considering functional aspects of cancer cells, which will help develop translatable, personalized insights into breast cancer diagnosis and treatment.

The above is my reply to the suggestions made by the reviewers, please review by the editors and the reviewers. If there is any improper place, please call or write to inform, in order to correct. Finally, I would like to thank the editors and review experts again for their valuable suggestions on the article, and thank you

for reviewing and revising my revised paper again. I hope that I can complete an excellent paper with your guidance and help, and sincerely hope that my paper can be published in your journal.

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