Peer Review File

Reviewer Comments

Comment 1: First, in the title please clearly describe the clinical research design such as the development and validation of a prognosis prediction model with and without HALP. I also suggest the authors make the term "value" clear in the title such as prognostic role.
Reply 1: I revised the title according to reviewer's suggestion. (Title)

Comment 2: Second, the abstract needs some revisions. The background needs to explain why immune-nutritional indexes could aid in the prediction of prognosis in GBM and describe what the current knowledge gap is on this research focus.
Reply 2: I revised the manuscript according to reviewer's suggestion. (Line 10-11)

Comment 3: The methods need to describe the baseline clinical factors, follow-up procedures, and measure of prognosis outcome, as well as how to examine the predictive accuracy of the nomogram.
Reply 3: I revised the manuscript according to the reviewer's suggestions. However, I am concerned that the number of words in the abstract is limited. I described the baseline clinical factors and follow-up procedures in full text.   (line 21-23)

Comment 4: In the results, please briefly describe the baseline characteristics and prognosis of the study sample.
Reply 4: I revised the manuscript according to the reviewer's suggestions. (line 24)
Moreover, I further described baseline characteristics in results. (line 157-160)

Comment 5: The authors need to provide the comparative results of the models with and without HALP.
Reply 5: I reported the AUC of the nomogram without and with HALP in the abstract. (line 28-29)

Comment 6: The conclusion needs comments on the limitations of this study.
Reply 6: I revised the manuscript according to the reviewer's suggestions. (line 33-34)

Comment 7: Third, in the introduction, please further analyze the potential reasons for the inconsistent findings on the prognostic factors of GBM and explain why the current data or clinical study could address the limitations of prior studies.
The authors also need to explain why the current data could generate a prediction model with higher predictive accuracy.
Reply 7: I revised the manuscript according to the reviewer's suggestions. (line 66-71)

Comment 8: Fourth, in the methodology of the main text, the primary clinical research

design of this study should be the development and validation of a prognosis prediction model by using retrospective cohort data.

Please also describe the details of follow-up and details of the baseline clinical factors including pathological factors.

Reply 8: I revised the manuscript according to the reviewer's suggestions. (line 112-118, line 168-169)

Comment 9: In statistics, please report the threshold values for sensitivity and specificity for a good prognosis prediction model.

Reply 9: The threshold values for specificity and sensitivity of the prediction tool are not universally agreed upon. However, I added a discussion regarding the high specificity, which can be used as a confirmatory tool for the incidence of 2-year mortality due to its low false positive rate. (line 209-212)

Comment 10: Finally, please consider citing several related papers:

1. Chen K, Shi Y, Luo W, Zhang T, Bao K, Huang C. SMIM20: a new biological signal associated with the prognosis of glioblastoma. Transl Cancer Res 2023;12(10):2754-2763. doi: 10.21037/tcr-23-796.

2. Zhong H, Wang Y, Jia J, Yang H, Zhang H, Li T, Liu H, Wang Y. Ferroptosis-related genes are regulated by methylation and predict the prognosis of glioblastoma patients. Transl Cancer Res 2022;11(4):603-614. doi: 10.21037/tcr-21-2470.

3. Zhang B, Cheng Y, Li R, Lian M, Guo S, Liang C. Development of a novel angiogenesis-related lncRNA signature to predict the prognosis and immunotherapy of glioblastoma multiforme. Transl Cancer Res 2023;12(1):13-30. doi: 10.21037/tcr-22-1592.

Reply 10: I revised citations according to the reviewer's suggestions. (reference 10, 12,18)