Peer Review File

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Reviewer A

Comment 1: The authors should include some clinicopathological details (number of IDHwt and IDHmut cases, MGMT promoter methylation status, subtype, age, and if available, treatment).

Reply 1: Thank you for this excellent suggestion. We added the statistical table of clinical information (table 1) in section 2.3. Please check it in the manuscript.

Changes in the text: we added some data.(see Page 6 line 8-10 and page 7)

Comment 2: In the discussion, they should clarify the association of risk categories with subtype but not with standard biomarkers (for example, as the authors explain, there is an association between subtype and IDH status). I think there is too much emphasis on angiogenesis throughout the manuscript; while the prognostic significance of AR-DElncRNAs is a very interesting finding, mechanistically there is no indication that it is linked to neoangiogenesis and this should be included in the discussion.

Reply 2: As we showed in the results, the correlations between the risk categories and sex, age, MGMT status and IDH1 status were not significant ($P > 0.05$). Among the subtypes, only the proneural subtypes had a significantly lower risk score than the mesenchymal subtypes ($P < 0.05$). Therefore, in the discussion, we focused on the relationship between risk categories and this clinicopathological characteristic. According to the suggestion of the reviewer, we added the discussion on the relationship between these lncRNAs and angiogenesis.

Changes in the text: we have modified our text as advised .(see Page 20, line 4-8)

Reviewer B

Comment 1: Please, provide detailed information about the data sets, including IDs / specific URLs.

Reply 1: We are sorry for our negligence. We supplement the detailed information of TCGA (supplementary Table 1) and CGGA (supplementary Table 2) datasets in section 2.1.

Changes in the text: we added some data.(see Page 5, line 11-14)

Comment 2: The criteria to identify thousands of lncRNAs potentially related to angiogenesis is a correlation $|cor| > 0.3$ and $P < 0.01$. How many lncRNAs are present using a more stringent cutoff? What are the correlation coefficients for DGCR5, PRKAG2-AS1, and ACAP2-IT1?

Reply 2: Thank you for your comments. 5681 DElncRNAs were selected by Spearman correlation analysis. The correlation coefficients of DGCR5, PRKAG2-AS1 and ACAP2-IT1 are shown in the following table

lncRNA	lncRNA	cor	p.value
DGCR5	PRKAG2-AS1	0.46575744	9.41E-11

DGCR5	DGCR5	1	0
DGCR5	ACAP2-IT1	0.815011112	1.29E-42
PRKAG2-AS1	PRKAG2-AS1	1	0
PRKAG2-AS1	DGCR5	0.46575744	9.41E-11
PRKAG2-AS1	ACAP2-IT1	0.515692675	3.29E-13
ACAP2-IT1	PRKAG2-AS1	0.515692675	3.29E-13
ACAP2-IT1	DGCR5	0.815011112	1.29E-42
ACAP2-IT1	ACAP2-IT1	1	0

Comment 3: In vitro or In vivo angiogenesis assays would be an important method to validate the lncRNAs functions.

Reply 3: Angiogenesis assay is indeed an important method to validate the lncRNAs functions. However, verifying the function of lncRNAs is not the main purpose of this article. As we mentioned at the end of manuscript, this was a preliminary study, further experiments in vivo and in vitro on the function of lncRNAs will be described in detail in further research.

Comment 4: Fig. 2.B, and F. It would be interesting to see an unsupervised heatmap with the expression values of the three lncRNAs.

Reply 4: Thank you for your comments. We supplemented the unsupervised heatmap with 3 lncRNAs expression values (Fig.2 I)

Changes in the text: we added some data.(see Fig.2 I. Page 26, line 13-14)

Comment 5: How do the authors justify the different results in the types of immune cells?

Reply 5: Thank you for your comments. We used CGGA (n = 133) cohort to verify the immune cell infiltration in the high-risk and low-risk groups. We found that the CIBERSORT, ssGSEA, MCP counter, quantiseq and epic algorithms did not get consistent results. While the TCGA cohort had no leukocyte fraction data. The validation with CGGA cohort did not get satisfactory results, which may be related to the sample size and sample source. In future studies, we will further explore the impact of risk model genes on immune cell infiltration through cell and animal experiments.

Comment 6: Reference (13) was retracted.

Reply 6: According to the suggestion of the reviewer, the new reference has been cited.

Changes in the text: we have modified our text as advised .(see Page 18 line 2; Page 24 line 14-16)