

Peer Review File

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Reviewer A

In their review, the authors describe the prognostic role of homologous recombinant deficiency in glioblastomas. The article provides interesting insights, but has some weaknesses:

Main points:

Comment 1: According to Table 1, WHO grade 2 and 3 (no longer Roman numerals since the latest classification!) are also included. It also includes patients with 1p19q deletion and IDH mutation. This means that a large proportion of them are certainly not to be categorised as glioblastoma according to the latest classification.

Reply 1: We collected data and started analysis from April 2021. At that time, the 2021 WHO classification hasn't been published. Thus, the analysis and classification of this study was based on the edition of 2016 WHO classification.

Comment 2: The HRP subgroup is discussed in the results without this being explained.

Reply 2: We have added the full explanation of HRP. (see Page 7, Line 184).

Changes in the text: The other mutation types (frameshift mutations, in-frame insertions and deletions, splice sites, and promoter alterations) occurred less often than 10% of the time. PTEN (chi-squared test, $p < 0.001$) and EGFR (chi-squared test, $p < 0.001$) showed considerably greater mutation frequency in the homologous recombination proficient (HRP) subgroup, but IDH1 ($p < 0.001$), ATRX (chi-squared test, $p < 0.001$) and TP53 (chi-squared test, $p < 0.05$) mutations were significantly more prevalent in the HRD subgroup (Figure 1C).

Comment 3: There is a lot of general description in the results - e.g. page 10, lines 246-253 - such sections belong in the introduction. Instead, the actual data are only paraphrased and not named precisely

Reply 3: We have added actual data of Cox regression analysis.

Changes in the text: The predictive performance of the 14-gene model was superior to those of prognostic parameters such as age (Univariable OR = 2.19 [1.51-3.19], $p < 0.001$) and IDH mutation (Univariable OR = 0.24 [0.17-0.34], $p < 0.001$).

Minor comments:

Comment 4: Introduce abbreviations (e.g. SNP)

Reply 4: We have added explanation for all of the abbreviation. (e.g. SNP, MSI, PARP, TCGA, CGGA, and FGA)

Changes in the text: single nucleotide polymorphism (SNP), Microsatellite instability (MSI), poly ADP-ribose polymerase (PARP), The Cancer Genome Atlas (TCGA), the Chinese Glioma Genome Atlas (CGGA), Fraction of genome altered (FGA)

Comment 5: Highlight box - last line is probably a template

Reply 5: We have deleted the last line.

Changes in the text:

Comment 6: Heading for methods - TME (instead of TIME)

Reply 6: It was “TME” in the heading for methods.

Comment 7: Results - IDH1 is missing a character in the p-value

Reply 7: We have added “<” to the IDH1 p-value

Changes in the text: PTEN (chi-squared test, $p < 0.001$) and EGFR (chi-squared test, $p < 0.001$) showed considerably greater mutation frequency in the homologous recombination proficient (HRP) subgroup, but IDH1 ($p < 0.001$), ATRX (chi-squared test, $p < 0.001$) and TP53 (chi-squared test, $p < 0.05$) mutations were significantly more prevalent in the HRD subgroup (Figure 1C).

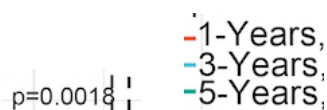
Reviewer B

1. Please provide the full name of “MGMT” in the Abstract and “SNP”, “ANNOVAR”, “LASSO”, “TME”, “SNVs”, “OR”, “WHO”, “IC50”, “SWI/SNF” “mRNA” in the main text. Please also check through your article to make sure **all** the abbreviated terms have been defined when they **FIRST** appear in the Abstract and the main text.

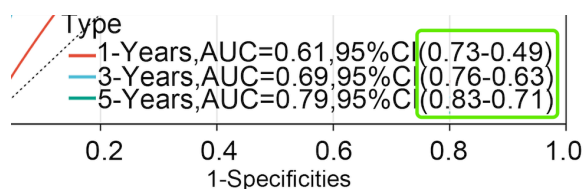
Reply: All abbreviated terms have been defined at the first appearance.

2. Figures and Table

- **All abbreviations** in figures/table and legends should be explained. “HRD” “TCGA-GBM” “OS” “HRP” “GBMs” “MSI” “HR” “CI” “AUC” “FGA” in Figure 1, and “WHO” “MGMT” “OR” in Table 1 for example. Please check all abbreviations and provide the full names in the corresponding figure legend/table footnote.
- Please revise “p” to “P”, “Years” to “Year” in Figure 1A.



- Figure 1A: please revise the data of 95% CI.

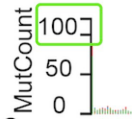


- Please double check the data in the following sentence, since it is inconsistent with Figure 1A.

“In this discovery cohort, there was a statistically significant difference in survival probability between groups when utilizing an HRD score of 17 (log-rank test, $p =$

0.00018).”

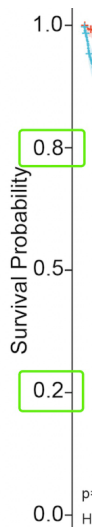
- Please check the scale bar in Figure 1B.



- Please indicate the meaning of “*” “***” in Figure 1C legend.
- There is a spelling mistake in Figure 1C.



- Please revise “p value” to “P value” in Figure 2A, “p” to “P” in Figure 2D and Figure 4A.
- Please double check the scale bars in Figure 2D and Figure 4A.



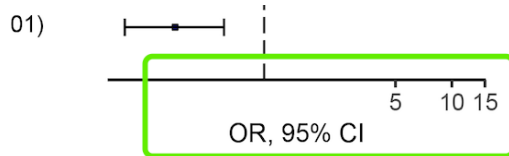
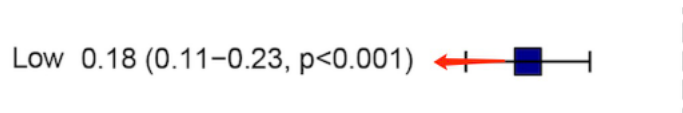
- Please add unit for **Time** in the y-axis of Figure 2E.
- Please add description for the x-axes in Figure 2E.
- Please double check the highlighted content in the following sentence, “*CH3L1*” or “*CHI3L1*”, “*C2orf62*” or “*C21orf62*”. Please also check through the manuscript.

“Finally, a prognostic model was developed when $\lambda = 0.03$ and 14 genes (*CHL1*, *CCL2*, *PDPN*, *POSTN*, *CH3L1*, *IL8*, *FABP5*, *IGFBP3*, *LGALS3*, *EMP3*, *TAGLN*, *DCX*, *GPR37*, *C2orf62*) were selected”

- The number seems incomplete in Figure 3B.

12,500

- Please indicate the meaning of “*” “**” “***” “****” “-” “.” in Figure 3C legend.
- Please indicate the meaning of “-” “.” in Figure 4C legend.
- **A summarized legend** for a figure with different parts should be provided, followed by legends for each part. Please provide the summarized legend for Figure 5.
- Please revise “p-value” to “P value”, “p” to “P” in Figure 5A.
- It is suggested to specify the scale bars in Figure 5A. And to standardize the results, the part that exceeds the horizontal coordinates should be indicated by **arrow**.



- It is suggested to modify the header to make it and the data be in one column in Figure 5A.

survival: OR (95% CI, p-value)	
age.factor <40 years	-
40-59 years	2.08 (1.23-3.55, p=0.006)

- It is suggested to report the exact P value.

“First, knocking out the PARP1 gene resulted in a considerably greater loss of fitness score in the low-risk group than in the high-risk group (Wilcoxon signed-rank test, **P < 0.05**).”

- Please indicate how data are presented in Table 1.

OR (univariable)↵	OR (multivariable)↵
↵	↵
2.19(1.51-3.19, p < 0.001)↵	2.23(1.31-3.82, p = 0.003)↵

- Please add a table **header** for the first and second column of Table 1.

Reply: We've made revision as indicated.