Peer Review File

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Reviewer A

The paper titled "Identification of prognostic and driver gene mutations in acute myeloid leukemia" is interesting. The results performed the systemic analysis of the gene mutation in patients with AML and identified representative and driver mutations between the prognostic group. However, there are several minor issues that if addressed would significantly improve the manuscript.

Comment 1:

1) The abstract is not adequate and needs further revisions. The research background does not indicate the clinical needs of this research focus. The study results need to show the clinical characteristics of the three groups of patients.

Reply 1: Yes, we modified the abstract.

Change in the text: Please see Page 2, lines 3-5 and 15-18.

Comment 2:

2) How does this genetic diversity define the pathophysiology of AML and provide information for clinical practice? It is recommended to add relevant content.

Reply2: The prognostic classification is a widely used system for predicting the prognosis of patients with acute myeloid leukemia (AML). The three groups are favorable, intermediate, and poor. The classification is based on cytogenetic and molecular abnormalities that are associated with different outcomes. The pathophysiology of AML is complex and involves the accumulation of genetic mutations that lead to the transformation of hematopoietic stem cells into leukemic cells. The characteristics of pathophysiology for each CALGB prognostic classification in AML are not well defined in the literature. We have discussed the association of those genetic mutaitons with the AML and the targeted therapy.

Comment 3:

3) All figures are not clear enough. It is recommended to provide clearer figures again.

Reply 3: Yes, we upload the PDF format of those figures.

Comment 4:

4) The introduction part of this paper is not comprehensive enough, and the similar papers have not been cited, such as "Screening diagnostic markers for acute myeloid leukemia based on bioinformatics analysis, PMID: 35836534". It is recommended to quote the articles.

Reply 4: Agree. We add this citation.

Change in the text: Please see Page 3, line 13.

Comment 5:

5) What new ideas can be provided for the diagnosis and treatment of AML? It is recommended to add relevant content.

Reply 5: Thank you for this suggestion. We discussed the diagnosis and treatment of AML using those genetic mutation.

Change in the text: Please see Page 11, line 6-22.

Comment 6:

6) It may be more meaningful to add functional research on key genes.

Reply 6: Yes, we add the function research on those genes.

Change in the text: Page 9, lines 18-20.

Comment 7:

7) What is the correlation between the immunophenotype and prognosis of patients with AML? It is recommended to add relevant content.

Reply 7: Thank you for the suggestion. Yes, there is an association between the immunophenotype and prognosis in AML. Several studies have identified the relationship. We discussed it in the discussion.

Change in the text: Page 11, lines 8-15.

Reviewer B

Comment 1:

1) First, the title needs to indicate the research design of this study, i.e., a bioinformatics analysis.

Reply 1: Yes, we add it.

Comment 2:

2) Second, the abstract needs some revisions. The background needs to indicate the potential clinical significance of this research focus and knowledge gaps on the prognostic biomarkers of AML. The methods need to briefly describe the clinical sample, clinical factors, and prognosis outcomes in the TCGA dataset. The results need to first describe the prognosis of the whole clinical sample in the dataset and quantify the findings by reporting statistics such as HR and accurate P values for the prognostic roles of the identified genes. The conclusion needs more detailed comments for the clinical implications of the findings.

Reply 2: Thank you for the suggestion. The background and results in abstract were revised (descripted as Comment 1 of Review 1). We also add the clinical implications in the conclusion.
Change in the text: Page 2, lines 30-31.

Comment 3:

3) Third, in the introduction of the main text, the authors need to review what has been known on the prognostic biomarkers of AML, including genetic biomarkers, have comments on the limitations and knowledge gaps of prior studies, and explain the clinical needs of the current research focus.

Reply 3: Yes, we add those related contents in the Introduction.
Change in the text: Page 3, lines 12-21.

Comment 4:

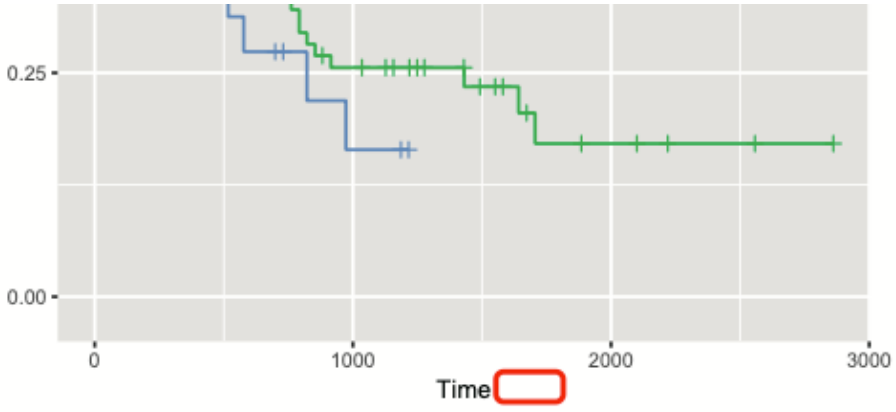
4) Fourth, in the methodology of the main text, please describe the clinical sample, clinical variables, and prognosis outcomes in the dataset used. Please also have an overview of the research procedures of this study including the questions to be answered by these procedures.

Reply 4: Yes, we add those related contents in the Methods.
Change in the text: Page 4, lines 12-17.

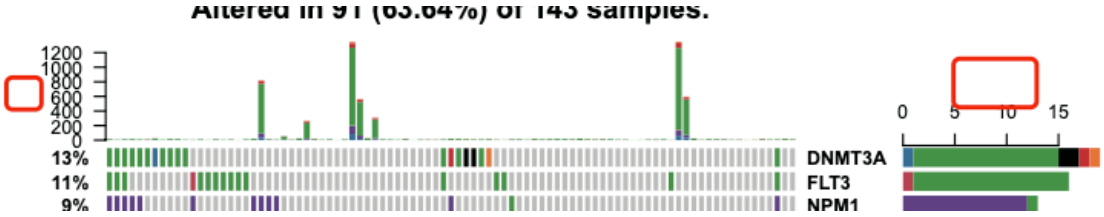
Reviewer C

1. Figure 1

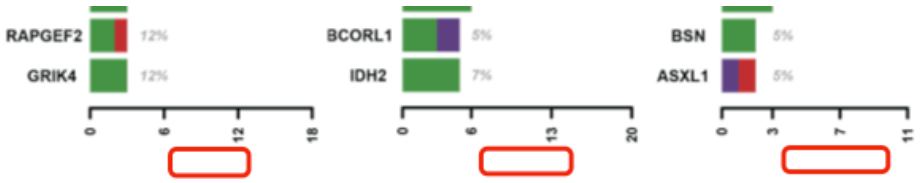
a. Figure 1A: Unit of X-axis is missing, please supplement it.



b. Figure 1B: Descriptions of X- and Y-axis are missing, please supplement them and resend us updated figure.

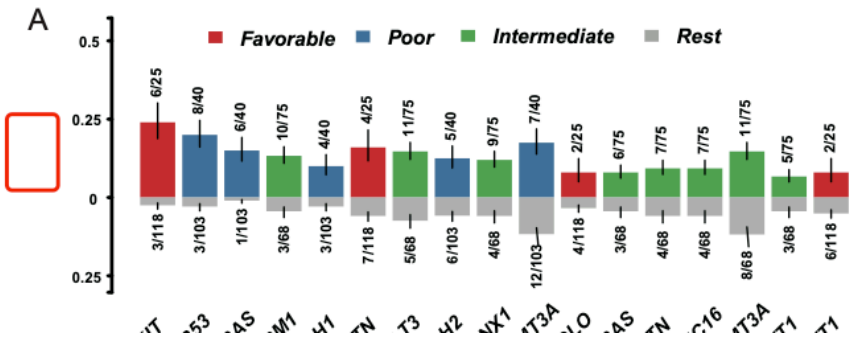


c. Figure 1C: Descriptions of X-axis are missing, please supplement them.



Reply: All above were corrected.

2. Figure 2: Description of Y-axis is missing, please revise.



Reply: We add the name of Y-axis.

3. Please define all abbreviations in Figure 2 legends. Like GO, KEGG, MAP…

Reply: Thank you for your comment. We have defined all the abbreviations in Figure 2 legends as follows:

GO: Gene Ontology KEGG: Kyoto Encyclopedia of Genes and Genomes MAPK: Mitogen-Activated Protein Kinase

4. Figure 5A: Please extend the X-axis, the value has extended the number (150).

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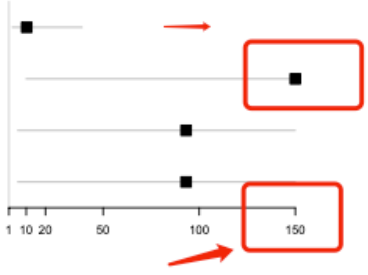
	10.2243	2.67267−39.1127	
	264.337	9.90768−7052.54	
	93.1682	5.53108−1569.37	
	93.1682	5.53108−1569.37	



Reply: we corrected it.

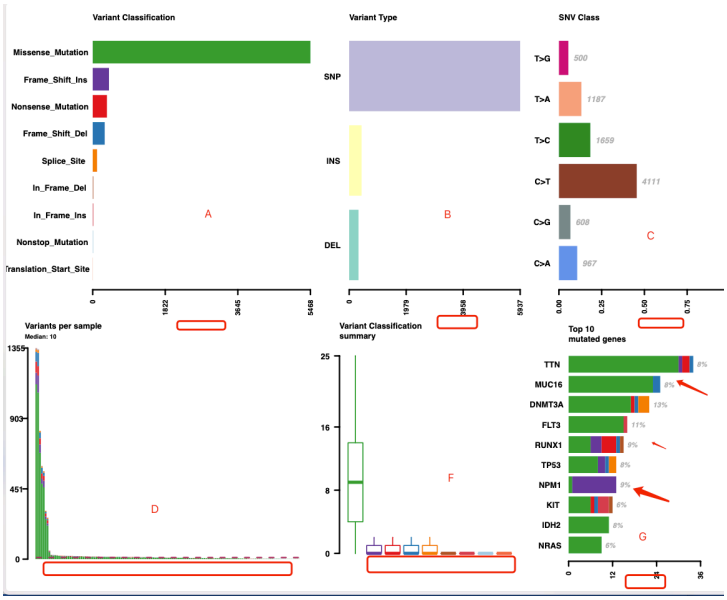
5. Figure S1:

a. A-C: Please add the descriptions for X-axis.

b. D: Please add the scale and the description for X-axis.

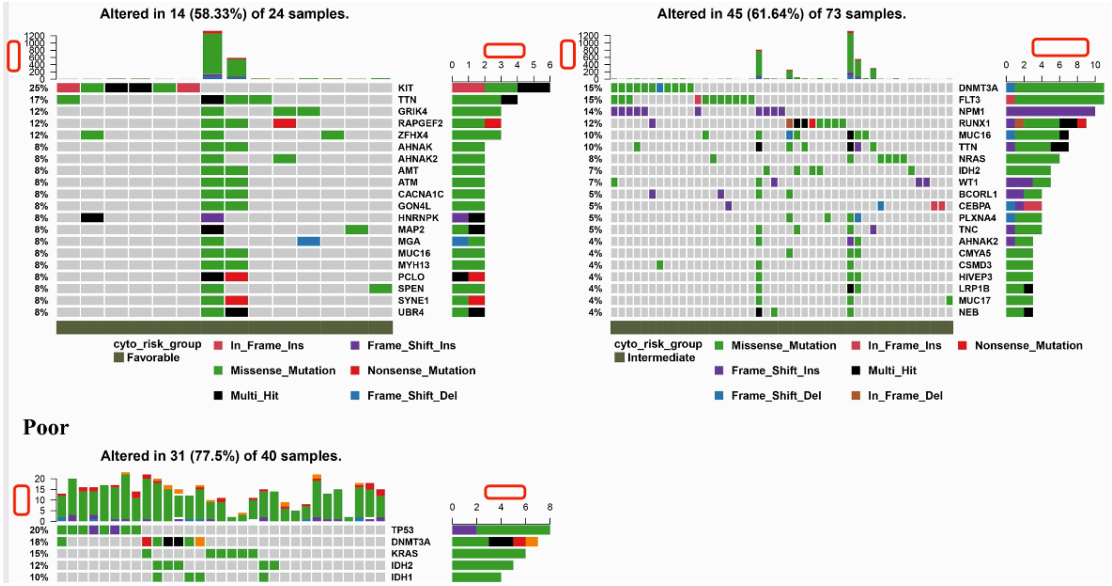
c. E: Please differentiate those box plot in different color and provide the description.

d. F: Please provide the description for X-axis and define those different colors in the figure.



Reply: All above were corrected.

6. Figure S2: Please provide the descriptions for X- and Y-axis and resend us updated figure.



Reply: All above were corrected.