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# PEER-REVIEW REPORT

**Name of journal:** *World Journal of Clinical Oncology*

**Manuscript NO:** 80526

**Title:** A 5-mRNA-based prognostic signature of survival in lung adenocarcinoma

**Provenance and peer review**: Invited Manuscript; Externally peer reviewed

**Peer-review model:** Single blind

**Reviewer's code:** 06281593
**Position:** Peer Reviewer
**Academic degree:** MD

**Professional title:** Doctor

**Reviewer's Country/Territory:** Egypt

**Author's Country/Territory:** China

**Manuscript submission date:** 2022-10-05

**Reviewer chosen by:** AI Technique

**Reviewer accepted review:** 2022-10-08 13:00

**Reviewer performed review:** 2022-10-08 13:19

**Review time:** 1 Hour

| | |
|---|---|
| **Scientific quality** | [ ] Grade A: Excellent [ ] Grade B: Very good [ Y] Grade C: Good<br>[ ] Grade D: Fair [ ] Grade E: Do not publish |
| **Language quality** | [ ] Grade A: Priority publishing [ Y] Grade B: Minor language polishing<br>[ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection |
| **Conclusion** | [ ] Accept (High priority) [ Y] Accept (General priority)<br>[ ] Minor revision [ ] Major revision [ ] Rejection |
| **Re-review** | [ Y] Yes [ ] No |
| **Peer-reviewer** | Peer-Review: [ ] Anonymous [ Y] Onymous |

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| | |
|---|---|
| **statements** | Conflicts-of-Interest: [ ] Yes [ Y] No |

**SPECIFIC COMMENTS TO AUTHORS**

1.The article is innovative. 2.The statistical method of the article is reasonable. 3.The Conclusion exhibits some clinical applicability.

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**Title:** A 5-mRNA-based prognostic signature of survival in lung adenocarcinoma

**Provenance and peer review**: Invited Manuscript; Externally peer reviewed

**Peer-review model:** Single blind

**Reviewer's code:** 06336248
**Position:** Peer Reviewer
**Academic degree:** PhD

**Professional title:** Senior Lecturer

**Reviewer's Country/Territory:** China

**Author's Country/Territory:** China

**Manuscript submission date:** 2022-10-05

**Reviewer chosen by:** AI Technique

**Reviewer accepted review:** 2022-10-08 18:18

**Reviewer performed review:** 2022-10-15 22:10

**Review time:** 7 Days and 3 Hours

| | |
|---|---|
| **Scientific quality** | [ ] Grade A: Excellent [ Y] Grade B: Very good [ ] Grade C: Good<br>[ ] Grade D: Fair [ ] Grade E: Do not publish |
| **Language quality** | [ Y] Grade A: Priority publishing [ ] Grade B: Minor language polishing<br>[ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection |
| **Conclusion** | [ Y] Accept (High priority) [ ] Accept (General priority)<br>[ ] Minor revision [ ] Major revision [ ] Rejection |
| **Re-review** | [ ] Yes [ Y] No |
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| **statements** | Conflicts-of-Interest: [ ] Yes [ Y] No |
|---|---|

**SPECIFIC COMMENTS TO AUTHORS**

1. Title. Does the title reflect the main subject/hypothesis of the manuscript? yes 2 Abstract. Does the abstract summarize and reflect the work described in the manuscript? yes 3 Key words. Do the key words reflect the focus of the manuscript? yes 4 Background. Does the manuscript adequately describe the background, present status and significance of the study? yes 5 Methods. Does the manuscript describe methods (e.g., experiments, data analysis, surveys, and clinical trials, etc.) in adequate detail? Yes ,but according to arrive guidelines should mention the ethical approval (the authors attached it but just mention in methodology) 6 Results. Are the research objectives achieved by the experiments used in this study? What are the contributions that the study has made for research progress in this field? Yes, predict survival 5 year by genes 7 Discussion. Does the manuscript interpret the findings adequately and appropriately, highlighting the key points concisely, clearly and logically? Are the findings and their applicability/relevance to the literature stated in a clear and definite manner? Is the discussion accurate and does it discuss the paper's scientific significance and/or relevance to clinical practice sufficiently? Yes(make references superscript) 8 Illustrations and tables. Are the figures, diagrams and tables sufficient, good quality and appropriately illustrative of the paper contents? Do figures require labeling with arrows, asterisks etc., better legends? Yes but some figures need to be submitted seperately 9 Biostatistics. Does the manuscript meet the requirements of biostatistics? yes 10 Units. Does the manuscript meet the requirements of use of SI units? yes 11 References. Does the manuscript cite appropriately the latest, important and authoritative references in the introduction and discussion sections? Does the author self-cite, omit, incorrectly cite and/or over-cite references? Yes No,they did not omit or incorrectly cite 12 Quality of

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manuscript organization and presentation. Is the manuscript well, concisely and coherently organized and presented? Is the style, language and grammar accurate and appropriate? yes 13 Research methods and reporting. Authors should have prepared their manuscripts according to manuscript type and the appropriate categories, as follows: (1) CARE Checklist (2013) - Case report; (2) CONSORT 2010 Statement - Clinical Trials study, Prospective study, Randomized Controlled trial, Randomized Clinical trial; (3) PRISMA 2009 Checklist - Evidence-Based Medicine, Systematic review, Meta-Analysis; (4) STROBE Statement - Case Control study, Observational study, Retrospective Cohort study; and (5) The ARRIVE Guidelines - Basic study. Did the author prepare the manuscript according to the appropriate research methods and reporting? yes 14 Ethics statements. For all manuscripts involving human studies and/or animal experiments, author(s) must submit the related formal ethics documents that were reviewed and approved by their local ethical review committee. Did the manuscript meet the requirements of ethics? yes Manuscript Peer-Review Specific Comments To Authors:* Please make your specific comments/suggestions to authors based on the above-listed criteria checklist for new manuscript peer-review and the below-listed criteria for comments on writing. The criteria for writing comments include the following three features:  First, what are the original findings of this manuscript? What are the new hypotheses that this study proposed? What are the new phenomena that were found through experiments in this study? What are the hypotheses that were confirmed through experiments in this study? Lung adenocarcinoma (LUAD) is the most common non-small cell lung cancer, with an increasing incidence and poor prognosis. To evaluate the prognosis of LUAD patients and optimize treatment, effective clinical research prediction models are urgently needed. In this study, we thoroughly mined LUAD genomic data from GEO (GSE43458, GSE32863, and GSE27262) and TCGA datasets, including 698 LUAD and 172 healthy (or adjacent normal) lung tissue samples.

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Single-factor Cox and LASSO regression analyses were used to screen DEGs related to patient prognosis, and multivariate Cox regression analysis was applied to establish the risk score equation and construct the survival prognosis model. Receiver operating characteristic (ROC) curve and Kaplan-Meier (KM) survival analyses with clinically independent prognostic parameters were performed to verify the predictive power of the model and further establish a prognostic nomogram. Second, what are the quality and importance of this manuscript? What are the new findings of this study? What are the new concepts that this study proposes? What are the new methods that this study proposed? Do the conclusions appropriately summarize the data that this study provided? What are the unique insights that this study presented? What are the key problems in this field that this study has solved? A 5-mRNA-based model was constructed to predict the prognosis of lung adenocarcinoma, which may provide clinicians with reliable prognostic assessment tools and help clinical treatment decisions. Third, what are the limitations of the study and its findings? What are the future directions of the topic described in this manuscript? What are the questions/issues that remain to be solved? What are the questions that this study prompts for the authors to do next? How might this publication impact basic science and/or clinical practice? First, our study only focuses on transcriptome sequencing data. If other omics techniques, such as DNA methylation and single nucleotide polymorphisms (SNPs), can be analyzed together, more favorable results may be obtained. Second, our research is limited to the bioinformatics analysis of the TCGA and GEO databases. Although we have verified the accuracy of the models internally and externally, the verification of large samples in the clinical diagnosis and treatment process will further enhance their diagnostic accuracy and clinical value. In summary, our study identified a 5-gene model and prognostic nomogram that combined gene models and clinical prognostic factors to predict the overall survival rate of lung adenocarcinoma patients, and this nomogram may be of

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great significance for the selection of personalized treatment options and clinical medical decisions in patients with lung adenocarcinoma.