PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

Manuscript NO: 51726

Title: The promising key genes associated with tumor microenvironment and prognosis of hepatocellular carcinoma

Reviewer's code: 00053659

Position: Editorial Board

Academic degree: MD, PhD

Professional title: Professor, Surgeon

Reviewer's country: Japan

Author's country: China

Reviewer chosen by: Jin-Zhou Tang

Reviewer accepted review: 2019-10-11 13:52

Reviewer performed review: 2019-10-11 15:52

Review time: 2 Hours

SCIENTIFIC QUALITY	LANGUAGE QUALITY	CONCLUSION	PEER-REVIEWER STATEMENTS
[ ] Grade A: Excellent	[ ] Grade A: Priority publishing	[ ] Accept (High priority)	Peer-Review:
[ ] Grade B: Very good	[ ] Grade B: Minor language polishing	[ ] Accept (General priority)	[Y] Anonymous
[Y] Grade C: Good	[Y] Grade C: A great deal of language polishing	[ ] Minor revision	[ ] Onymous
[ ] Grade D: Fair	[ ] Grade D: Rejection	[Y] Major revision	Peer-reviewer's expertise on the topic of the manuscript:
[ ] Grade E: Do not publish		[ ] Rejection	[ ] Advanced
			[Y] General
			[ ] No expertise
			Conflicts-of-Interest:
			[ ] Yes
			[Y] No

SPECIFIC COMMENTS TO AUTHORS

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Pan L et al. investigated to analyze several databases to identify a prognostic profile of the gene expressions using the ESTIMATE algorithm. They identified that ten key genes (STSL2, TMC5, DOK5, RASGRP2, NLRC3, KLRB1, CD5L, CFHR3, ADH1C, and UGT2B15) constructed a prognostic gene signature. They claimed that one of the ten key genes might be a candidate for targeted molecular therapy in the future. The analysis is quite unique and seems to be interesting. The only concern is that the clinical information of the data set was unclear. The etiology of the HCC is very unique, depending on viral status. I have no idea how the data provided in detail. However, the essential clinical background should be presented, such as viral status, liver functional status, and tumor status. The AUC of the model seems to be similar even though the value was higher than the conventional TNM stage. It is very hard to evaluate any clinical benefit of this study without clinical characters. Therefore, I am quite skeptical about their conclusion was that the results presented the future molecular target under the current results. A comparison of the AUC among their model and TNM stage should analyze multiple comparisons of the ROC analysis.

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

[   ] The same title

[   ] Duplicate publication

[   ] Plagiarism

[Y] No

BPG Search:

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SPECIFIC COMMENTS TO AUTHORS

In this study, Long Pan and colleagues analyzed The Cancer Genome Atlas (TCGA) in the aspect of genes associated with tumor microenvironment and prognosis of hepatocellular carcinoma. With the usage of ESTIMATE algorithm method, it would be possible to deeply investigate the gene expression according to t he cell types in target tissue. Generally, the results are interesting and the methods are reasonable. The manuscript is well prepared and the figures are well illustrated. The major question, which might also be the limitation, is the method in identifying the genes for predicting prognosis. It seems that the clinical stage and other well known risk factors are not adjusted in this model. Would is possible to do the multivariate analysis?

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SPECIFIC COMMENTS TO AUTHORS

This is pure bioinformatics/biostatistics work using data opened publically. To pick out significant genes from the database, authors should verify each genes in vitro/in vivo using theier own samples The phrase of introduction in the abstract is to be revised, language matter. significant, urgent demanded is not appropriate

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[Y] No