

PEER-REVIEW REPORT

Name of journal: World Journal of Gastrointestinal Oncology

Manuscript NO: 47823

Title: Eight key long non-coding RNAs predict hepatitis virus positive hepatocellular carcinoma as the prognostic targets

Reviewer's code: 02860835

Reviewer's country: France

Science editor: Jin-Lei Wang

Reviewer accepted review: 2019-03-29 15:11

Reviewer performed review: 2019-04-04 09:34

Review time: 5 Days and 18 Hours

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

SPECIFIC COMMENTS TO AUTHORS

This manuscript of Huang ZL and coworkers aims at identifying a signature of long non-coding RNAs (LncRNAs) in hepatocellular carcinoma (HCC) associated with viral infections. Using the Cancer Genome Atlas (TCGA) datasets, they identified a signature

of 8 LncRNAs as prognosis factors for HCC associated with hepatitis B infection in particular. Some complementary information is needed to clarify this study. Major points: 1. Some figure legends are lacking (Figures 3-5-6), which rendered the paper difficult to read. In particular for figure 3, a detailed legend for the LASSO analysis is required: what is the optimal lambda value selected? In figure 3A, which curves correspond to the eight LncRNAs? 2. Nothing is said about the 149 selected samples (number of accession...). A table will be informative. Did the authors verify that all the samples were comparable if they were extracted from different datasets? 3. In figure 6, the authors compiled the three risk factors (TNM stage, RACE, LncRNA risk score) for the risk of recurrence. Have they obtained better results for the three than the risk of recurrence obtained for one risk factor independently analyzed? 4. It will be interesting to precise which LncRNAs among the 8 are involved in the Top 10 deregulated pathways in figure 8. Minor points: 1. The cut-off value used to discriminate high risk and low risk will be informative in figure 4 A and B. 2. The figure 2A is unreadable.

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

- ☐ The same title
- ☐ Duplicate publication
- ☐ Plagiarism
- ☒ No

BPG Search:

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[Y] No

PEER-REVIEW REPORT

Name of journal: World Journal of Gastrointestinal Oncology

Manuscript NO: 47823

Title: Eight key long non-coding RNAs predict hepatitis virus positive hepatocellular carcinoma as the prognostic targets

Reviewer's code: 02942798

Reviewer's country: Slovakia

Science editor: Jin-Lei Wang

Reviewer accepted review: 2019-03-28 10:24

Reviewer performed review: 2019-04-06 21:06

Review time: 9 Days and 10 Hours

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

SPECIFIC COMMENTS TO AUTHORS

Dear sir, thank you to select me to review manuscript Zi-Lin Huang et al. Eight key lncRNAs predict hepatitis virus positive hepatocellular carcinoma as the prognostic targets. The aim of this interesting study was to construct long non-coding RNAs

(lncRNAs) signature to predict overall survival (OS) in viral hepatitis hepatocellular cancer (VHCC). Authors analyzed data of 149 VHCC patients from The Cancer Genome Atlas (TCGA) database. A total of 1420 differentially expressed lncRNA (DElncRNAs) were identified, among which, 406 were significant in univariate Cox regression analysis. LASSO regression confirmed had 8 out of the 406 lncRNAs. the area under curve (AUC) of the prognostic model constructed based on the eight-lncRNA biomarkers were 0.73, 0.758, and 0.788 at 1-, 3-, and 5-year OS, respectively. Authors also constructed nomogram at the base the eight-lncRNA risk_score, TNM stage and race, nomogram predicted OS in VHCC patients. Paper is well made, but some changes are needed. 1) Better clinical characteristics of patients are needed - duration of viral hepatitis, HBeAg/anti HBe status, HBV DNA at the time of HCC diagnosis, Milano or metro ticket travel criteria for HCC, treatment of HCC, antiviral treatment for HBV or HCV, etc. If data are unavailable, please add this information to the limitation of the study. 2) Is the nomogram better for prediction of OS than prognostic model constructed from 8 lncRNAs? 3) Figures 2A and 6 are unreadable. 4) Figure 8 - please explain the role of 8 lncRNAs in HCC pathogenesis, add the information in the figure. My decision is minor revision.

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

- ☐ The same title
- ☐ Duplicate publication
- ☐ Plagiarism
- ☐ No

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[Y] No