



**PEER-REVIEW REPORT**

**Name of journal:** World Journal of Gastroenterology

**Manuscript NO:** 38835

**Title:** Evaluation of the prognostic power of liver cancer by molecular marker

**Reviewer's code:** 00503516

**Reviewer's country:** Italy

**Science editor:** Xue-Jiao Wang

**Date sent for review:** 2018-03-22

**Date reviewed:** 2018-03-26

**Review time:** 4 Days

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input checked="" type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input checked="" type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input checked="" type="checkbox"/> Minor revision
<input checked="" type="checkbox"/> Grade E: Poor		BPG Search:	<input type="checkbox"/> Major revision
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input checked="" type="checkbox"/> No	

**COMMENTS TO AUTHORS**

Yanzhou Song et. al systemically evaluated the prognostic power of different omics data for liver cancer using as source data the Cancer Genome Atlas. The work is well written and informative and can contribute to expand our knowledge with regard to the identification of HCC prognostic/diagnostic markers. I suggest the author to better specify which are, among the individuated pathways, (WNT/beta-catenin, E2F targets, mitotic spindle and G2M checkpoint) the specify variations in gene expression levels. For example, which are the E2F targets differently regulated? Do they include E2F family members? This piece of information would be very interesting as not all E2F family members are thought to play the same role in HCC.



## PEER-REVIEW REPORT

**Name of journal:** World Journal of Gastroenterology

**Manuscript NO:** 38835

**Title:** Evaluation of the prognostic power of liver cancer by molecular marker

**Reviewer's code:** 01558002

**Reviewer's country:** Greece

**Science editor:** Xue-Jiao Wang

**Date sent for review:** 2018-03-28

**Date reviewed:** 2018-03-31

**Review time:** 3 Days

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		<input type="checkbox"/> No	<input type="checkbox"/> Major revision
		BPG Search:	
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input type="checkbox"/> No	

### COMMENTS TO AUTHORS

For clinical researchers lacking bioinformatics expertise, extrapolating desired information from the copious amounts of data supplied by The Cancer Genome Atlas (TCGA) proves to be a difficult task. The authors are congratulated on accomplishing the task using molecular and clinical data on the TCGA, in which specific genes were shown to correlate with survival for patients with liver cancer. However, English writing, including the title, abstract and text, is suboptimal. The title may be changed to "Integrated genomic analysis for prediction of survival for patients with liver cancer using the Cancer Genome Atlas". Also, the abstract appears not to summarize the study results. The abbreviations, such as LASSO and CNP, should be defined on their first use. An additional figure, which explains the statistical process (algorithm), would improve the readability.



**PEER-REVIEW REPORT**

**Name of journal:** World Journal of Gastroenterology

**Manuscript NO:** 38835

**Title:** Evaluation of the prognostic power of liver cancer by molecular marker

**Reviewer's code:** 00053419

**Reviewer's country:** Spain

**Science editor:** Xue-Jiao Wang

**Date sent for review:** 2018-03-22

**Date reviewed:** 2018-04-03

**Review time:** 12 Days

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input checked="" type="checkbox"/> Grade B: Very good	<input checked="" type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good		<input type="checkbox"/> Duplicate publication	
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade E: Poor	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input checked="" type="checkbox"/> Minor revision
		BPG Search:	<input type="checkbox"/> Major revision
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input checked="" type="checkbox"/> No	

**COMMENTS TO AUTHORS**

The authors report a meta analysis of high density molecular data from TCGA experiments on HCC. Genetic, epigenetic and expression data (miRNA and mRNA) have been considered in the analysis. Regrettably protein data did not reach statistical significance to support prognostic power. Perhaps the reasons explaining why protein profiling has no prognostic value in this case should be further discussed. Is it a consequence of the analytical methodology used or, alternatively is it associated to the complexity of the proteome? Minor points are as follows: Figure 1 legend should be extended to make the figure self-explanatory. Heatmaps in figures 2, 3, 4 and 5 are too small. Figure legend extension is also recommended in these cases.