



PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

Manuscript NO: 42268

Title: Identification and Prediction of Novel Non-Coding and Coding RNA-Associated Competing Endogenous RNA Networks in Colorectal Cancer

Reviewer's code: 03001816

Reviewer's country: United States

Science editor: Xue-Jiao Wang

Date sent for review: 2018-09-17

Date reviewed: 2018-09-17

Review time: 7 Hours

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 Grade E: Do not publish	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

SPECIFIC COMMENTS TO AUTHORS

This is a fine and interesting paper, and I have no problems with the bioinformatics or the general conclusions. One minor issue with the RT-qPCR. Is there any data that demonstrate whether the RNA used is DNA free? Trizol isolation is not necessarily



**Baishideng
Publishing
Group**

7901 Stoneridge Drive, Suite 501,
Pleasanton, CA 94588, USA
Telephone: +1-925-223-8242
Fax: +1-925-223-8243
E-mail: bpgoffice@wjgnet.com
https://www.wjgnet.com

going to get rid of all the DNA, and I do not see any indication that any subsequent DNase step was performed. Therefore, is there any negative control, such as doing the RT-PCR but skipping the RT step? If the RNA is really DNA free, then performing PCR directly on the RNA should not yield a band. Can the authors comment on this, at least? If they have any of these RNA samples left over, showing that no product is formed without the RT step would be helpful. Or do you use primers that span exon/intron junctions and thus can distinguish DNA from fully processed RNA?

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

- The same title
- Duplicate publication
- Plagiarism
- No

BPG Search:

- The same title
- Duplicate publication
- Plagiarism
- No



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Name of journal: World Journal of Gastroenterology

Manuscript NO: 42268

Title: Identification and Prediction of Novel Non-Coding and Coding RNA-Associated Competing Endogenous RNA Networks in Colorectal Cancer

Reviewer’s code: 00181023

Reviewer’s country: Austria

Science editor: Xue-Jiao Wang

Date sent for review: 2018-09-17

Date reviewed: 2018-09-25

Review time: 8 Days

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 checked="" type="checkbox"/> Grade B: Very good	<input checked="" type="checkbox"/> Grade B: Minor language polishing	(High priority)	<input checked="" type="checkbox"/> Anonymous
<input type="checkbox"/> Grade C: Good		<input type="checkbox"/> Accept	<input type="checkbox"/> Onymous
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		<input type="checkbox"/> Major revision	<input checked="" type="checkbox"/> General
		<input type="checkbox"/> Rejection	<input type="checkbox"/> No expertise
			Conflicts-of-Interest:
			<input type="checkbox"/> Yes
			<input checked="" type="checkbox"/> No

SPECIFIC COMMENTS TO AUTHORS

The manuscript entitled “Identification and Prediction of Novel Non-Coding and Coding RNA-Associated Competing Endogenous RNA Networks in Colorectal Cancer” reports an analysis of public TCGA data using a bioinformatics approach as research



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7901 Stoneridge Drive, Suite 501,
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tool. The only own data that the authors provide are data from three cell lines in which they show that the respective markers are “upregulated” without any functional evidence, that is functional assays. These data are incomplete and of no help and should be omitted. The alternative would be an own experimental approach including true functional studies – only these could support the database results.

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- No