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315-321 Lockhart Road,
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ESPS Peer-review Report

Name of Journal: World Journal of Gastroenterology

ESPS Manuscript NO: 4538

Title: To verify gene expression profiles for colorectal cancer using 12 internet public microarray data sets-

Reviewer code: 02451547

Science editor: Zhai, Huan-Huan

Date sent for review: 2013-07-06 17:33

Date reviewed: 2013-09-03 20:53

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	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 checked="" type="checkbox"/> Grade B: minor language polishing	<input type="checkbox"/> Existed	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C (Good)	<input type="checkbox"/> Grade C: a great deal of language polishing	<input type="checkbox"/> No records	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	<input type="checkbox"/> Existed	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> No records	<input checked="" type="checkbox"/> Major revision

COMMENTS TO AUTHORS

The authors mainly focus on verifying gene expression profiles for colorectal cancer using 12 internet public microarray data sets. The results suggest a novel gene expression profile was associated with CRC and can potentially be applied to blood-based detection assays. However, there are some concerns raised from this paper. 1. Table 1 should be one to list the characteristics of the included papers. 2. Why do the authors select the CRC-associated genes from 3 studies (Ref. 7-9) to verify external validation rather than from other studies. 3. Although this study included 12 public pooling microarray datasets, the sample size is relatively small, only including 519 cases of adenocarcinoma and 88 controls of normal mucosa. Do the authors think whether the statistical power is enough. 4. Have the authors considered to collect new sample by your lab to verify external validation of the selected gene.



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ESPS Manuscript NO: 4538

Title: To verify gene expression profiles for colorectal cancer using 12 internet public microarray data sets-

Reviewer code: 00555672

Science editor: Zhai, Huan-Huan

Date sent for review: 2013-07-06 17:33

Date reviewed: 2013-09-09 20:39

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	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 checked="" type="checkbox"/> Grade B: minor language polishing	<input type="checkbox"/> Existed	<input type="checkbox"/> High priority for publication
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<input checked="" type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> No records	<input checked="" type="checkbox"/> Major revision

COMMENTS TO AUTHORS

The manuscript by Huang and colleagues is a dataset analysis of three reported signature of colorectal cancer in a pooled dataset comprising 12 microarray studies. The study identifies a common signature which should be related to colorectal cancer. The premise of the study makes no sense. Authors want to develop a signature to detect CRC cells in peripheral blood, but they use microarray studies obtained from normal and cancer colonic tissue. In peripheral blood it would be expected a different background of gene expression ascribed to blood components which makes the study not useful for the purpose. Last and not least without qPCR validation it is not given that the differences noticed at the probe level can be reproduced with qPCR. Indeed, a microarray will never be used as a tool to detect CRC cells in blood. So definitely a qPCR validation step would be required.