Reviewer's report

Title: Screening differentially expressed genes of pancreatic cancer between Mongolian and Han people using bioinformatics technology

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Reviewer: Helmut Friess

Reviewer's report:

Major revision

In this manuscript, Xu and co-authors carried out a descriptive study comparing transcriptional profiles of PDAC between Mongolian and Han populations. In total, 40 samples (20 vs 20) were investigated using microarrays. The differentially expressed genes were further characterized by KEGG pathway and GO functional analysis. Certainly, it is a valid study to uncover the potential impact of different ethnic background on PDAC biology. However, this study cannot be published in the present form.

Major points

Figure 1 and Figure 2 are not really required, but they can be included as supplementary figures.

Figure 5 is not really understandable, as far as I understood, 40 samples (20 Mongolian vs 20 Han) were analyzed. Then, it is expected that 40 samples should be shown in this heatmap instead of 20 samples. In any event, the description of this figure need be optimized.

Figure 8 is very confusing; the authors claim that this figure is to confirm the array data using QRT-PCR assay. However, the figure itself is very misleading. No one can really understand this. The "Normal tissue" appeared in this figure which is not really described before. Certainly, it is highly relevant to know whether the differentially expressed genes such as CPB1 and
COL11A1 between Mongolian and Han pancreatic cancers were also differentially expressed in normal tissues.

Minor point

Figure legend is, in general not acceptable; more information is needed.

The font size of table 2 is different as others

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Yes

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
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Not relevant to this manuscript

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