Reviewer’s report

Title: Transcriptome sequencing of lncRNA, miRNA, mRNA and interaction network constructing in Coronary Heart disease

Version: 0 Date: 11 Mar 2019

Reviewer: John Beilby

Reviewer's report:

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This is a very interesting and complex manuscript that provides information that will be of interest to the readers of this journal and more widely in the area of coronary heart disease research. It provides a comprehensive analysis of lncRNA and miRNA in CHD, that to my knowledge has not been reported before. The authors investigated the expression profiles of lncRNA, miRNA, and mRNA in CHD patients with UA to explore the interactions of lncRNA, miRNA, and mRNA.

Points that require clarification:

Methods; Page 2; lines 9-12.

The authors need to include the sex of the patients and controls used in this study.
The authors need to state how the controls were selected.

Page 2; lines 33-38.

The authors need to state if they have done a time course study to determine if any of the RNA fractions deteriorated during the 48 hours from the onset of chest pain in the UA patients and up until the RNA was processed.

Page 3; lines 3-4.

The authors need to write in full what Ns stands for.
Page 3; line 57.
The authors need to write in full what DE stands for.

Results; Page 2; lines 3-4.
The authors state 'Applying the screening criterion established before and Cufflinks...'. The authors need to make clear what criteria they used before.
The authors do not mention Figure 1C in the text. This figure needs to be described in the results section.

Page 2; lines 46-60.
The results for GO enrichment and KEGG pathway enrichment are not expressed in the same order of significance as shown in figures 2 and 3. The authors need to indicate why they have only discussed certain of these parameters in the order used and not as listed in the figures by their level of significance. The authors need to also indicate why they selectively use the Biological Processes, Cellular and Molecular Functions in the upregulated data and different pathways in the down regulated data.

Discussion; Page 1; line 48.
The authors need to list what they are saying rather than using etc.

Page 2; line 38. The authors mention ceRNA network. The meaning of ce needs to be explained once in the text.

Page 3; line 13. The authors need to list what they are saying rather than using etc.

Page 3; line 25. The authors should write in full the meaning of EF, TC, and Hys.

Figures;
There were no legends for the figures. The authors need to include explanatory legends for all figures.
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?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

Not relevant to this manuscript

Quality of written English
Please indicate the quality of language in the manuscript:

Acceptable

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