Reviewer’s report

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

Version: 0 Date: 28 Feb 2019

Reviewer: David Tan

Reviewer's report:

Points that should be addressed for this study are as follows:

* The study from Liao et al identified a potential regulatory network of lncRNA and protein coding genes within PBNCs that correlate with CHD. The study has generated raw data from patients, unfortunately this data will not be available for the research community due to Chinese law. Given the large number of differentially expressed genes identified in this study it would be prudent to provide a supplementary table listing these genes, there fold change and associated statistical values.

* Abstract. Does not mention that the study focuses on identifying biomarkers for CHD from PBNCs. I would recommend mentioning PBNCs within the abstract.

* Methods: The authors did not provide information on sequencing depth per sample (pre and post QC filtering) for both RNA-Seq and microRNA-Seq. Please provide.

* When examining CTA-384D8.35 I can see that it is a short 602 bp transcript annotated in gencode (source UCSC browser). Interestingly there is a partially overlapping lincRNA that appears to be related to this ncRNA called TCONS_00029745 (via the Non-coding RNA track available in UCSC browser) which is expressed in white blood cells. It is therefore possible that CTA-384D8.35 and TCONS_00029745 are actually the same transcript. CTA-384D8.35 would extend the second exon of TCONS_00029745. If this is true then the authors have only incorporated a small portion of transcript in there studies. This has implications for the overexpression part of the study (see below). The authors could use stringtie (which is faster + superior to cufflinks), and check to see if full length transcript is reconstructed from the raw data.

* When examining CTB-114C7.4 I learnt that this is a two exon ncRNA transcript identified by gencode. Interestingly this ncRNA also has an identical refseq entry (NR_147701.1 or LOC100128059). Refseq is a conservative gene model and enhances the validity of this ncRNA candidate, therefore I would recommend that the authors reference this transcript with the refseq identifier.
* There are no figure legends in submitted manuscript. This made interpreting some figures difficult (for example no y-axis labels on figures 6 and 7).

* Over expression studies: The authors over-expressed candidate genes in human umbilical vein endothelial cells (UVECs). Presumably the expression of the gene candidates is low compared to the PBNCs. Can the authors please comment. More importantly was the over-expression levels in UVECs comparable to the difference seen between controls and disease patients (PBNCs)? Also given that CTA-384D8.35 may also represent a part of a longer lncRNA can the authors confirm exactly what sequence was over expressed. It is possible that the full length transcript may not act as the partial transcript.

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.

No

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.

I recommend additional statistical review

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