Reviewer’s report

Title: Expression of circulating miR-486 and miR-150 in patients with acute myocardial infarction

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Reviewer: Emanuela Bostjancic

Reviewer’s report:

In an article of Zhang et al, entitled “Expression of circulating miR-486 and miR-150 in patients with acute myocardial infarction” the authors analysed potential of certain miRNAs as biomarkers for NSTEMI and STEMI in plasma of patients with MI. However, it is nice and straightforward study, but there are some questions that should be answered before publication.

Major Compulsory Revisions

Abstract

Results
- “…in discriminating AMI patients and NSTEMI…” NSTEMI are also AMI patients, please re-write the sentence.

Introduction

Last paragraph
- Please define, why miR-150 and miR-486.
- Please include as the aim also discrimination of NSTEMI and STEMI.

Methods

qRT-PCR
- TaqMan human microRNA assay kits are not from Qiagen.
- Please define the preparation of cDNA (detailed reaction with cycling/incubation conditions or according to manufacture)? What was the input of RNA (equal among 220 samples or different)?
- How the reaction of qPCR was performed (detailed reaction with cycling/incubation conditions)? Was the cDNA diluted or un-diluted? Was the one-step or two-step real time PCR performed? Based on what did you choose U6 as an internal control? Did you perform efficiency analysis? Further, according to Livak et al, Methods, 2001, 2-#Ct may be used to analyze relative gene expression data when only one gene is being studied. For an example, when you analyze differences before and after i.e. treatment for reference gene, to determine the effect of treatment on the expression of a candidate internal control gene, where the target gene and the endogenous reference gene are one in the same. It would be therefore useful to perform detailed description of
equation or define the reference, where the above equation is described as possible to use also in case of target gene and reference gene. Another consideration is using this equation, in different samples you have used different amounts of total RNA, which can be affected by efficiency (when is not the same for target and reference gene) that was not performed.

Statistical analysis
- “… to asses distinguishing AMI.” From what?

Results
Circulating miR-486 and miR-150 expression levels as predictors of AMI
- Last paragraph first sentence. It is not clear which value is for certain miRNA.
Pattern of expression pattern of miR-486 and miR-150 in STEMI and NSTEMI
- One word “pattern” should be removed from title. Last two sentences: again, it is not clear which value is for certain miRNA or condition.

Discussion
- Third paragraph, first sentence. You have obtained RNAs from plasma; however, they have obtained from serum. Please, include this. First and forth sentence should be part of introduction for better understanding of the aims of your study.
- Last paragraph. Including some other expression patterns/function of miR-150 in other cardiac disease (I believe there are approx. 10 publications) would improve the discussion.

Conclusion
- Why therapeutic target from your results?

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:
I declare that I have no competing interests.