Reviewer’s report

Title: Identifying differential miR and gene consensus patterns in peripheral blood of patients with cardiovascular diseases from literature data

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Reviewer: Thomas Dandekar

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Satrauskiene et al identify differential miR and gene consensus patterns by a step-wise evaluation procedure consisting of an excel sheet for first round of evaluation, followed by a miRTarBase screen and finally, consensus patterns were obtained and compared for CAD, ACS and HF.

Comments:

This is basically a helpful overview approach and screening the over 1000 articles is considerable work.

1) What should be done more (particular in the discussion) is pointing out the limitations of the approach, a proper meta-analysis, including only the top studies and then evaluating the results may be much better, furthermore, a clear model, considering miRNAs and pathologies, could be more penetrating then just a consensus vote where maybe the real signal is clouded by the many less well done studies.

--so please discuss this point a bit more, I completely agree that the study, after all, yields a plausible and useful result, so then it should also not harm to point these inherent limitations.

2) Regarding the target prediction results: Why was exactly this miRNA target strategy (miRTarBase screen) chosen? Would it not have been better to compare several predictors and take only consensus predictions?

3) Regarding the evaluation: Why did you chose just 4 and 1 / -4 and -1 as step values and criteria? Were there really never intermediate cases justifying a 2 or 3?

4) Regarding the evaluation: Why did you not consider the power of the study or the quality of the measurements with a higher weight

5) maybe exclude all studies which do not achieve a high quality and then take the 50 best quality studies would that have been a better alternative (stronger signal)?

In summary, this is a promising approach, but one has to consider some inherent limitations. My five remarks should help to better identify these.
Nevertheless, I think the finally obtained target genes are a helpful pointer for further studies and understanding key implied miRNAs for CAD, ACS and HF

**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.

Unable to assess

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

Unable to assess

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I am able to assess the statistics

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