Reviewer’s report

Title: Use of magnetic resonance imaging combined with gene analysis for the diagnosis of fetal congenital heart disease

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Reviewer: Lin Li

Reviewer's report:

Wang et al. presented a study with the combination of MRI and gene methods in the diagnosis of fetal congenital heart disease. This study aims to propose an improved diagnostic solution that has a higher diagnostic specificity and sensitivity, comparing to the MRI or gene method alone. I like this idea very much. The research of multi-modality prognosis approach is on the top flow of clinical-relevant study and have been shown to have significant improvement of the accuracy. The current study also provided a reasonable sample size (n=78) with a well-matched control subject (n=78), making this study with a reliable statistical power. However, I saw several critical issues in the presented manuscript, which need to be fixed before this manuscript to be published.

1. The first issue is the lack of information about the MRI. Neither the scanning parameters nor the data analysis has presented. The authors should provide very detailed information about the MRI scan hardware and software setup. The authors also should give detailed imaging processing steps, as well as the imaging screening process. I am also wondering which parameters were used to generate the diagnostic rate in Figure 1 and Table 2, for the MRI session?

I assume Figure 1 is to demonstrate the suspected case of fetal congenital heart disease. However, a more detailed description in the figure legend and the context should be included. Please also present an example image with health control.

In both MRI and gene analysis, the measurement values (for MRI, such as the size and location of malformation areas; for the gene, such as the 17q12 signaling) should be presented quantitatively, with descriptive statistics.

2. The second issue is that it lacks the information of how to distinguish Pulmonary stenosis and Arterial stenosis (which has been shown in table 2). Both MRI and gene analysis did not provide enough information about this part.

3. In table1, by reading the description, it seems like the HR is observed from the mother, which is abnormally high than usual. Please double check this data.
4. There is a typo in line 40, please correct.

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

No

**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 am able to assess the statistics

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

Needs some language corrections before being published

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