Peer Review File

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Reviewer A

1. Many of the conclusions in the abstract need to be presented in the results section.
Reply 1: We have revised the abstract accordingly. See page 2, line 43-54.

2. How was the tissue collected, handled, stored, sectioned and processed? How many samples per patient were used?
Reply 2: We have added related contents. See page 5, line 131-138.

3. Where in the aorta was the sample taken? Did this include dissection flap? How was heme handled and processed?
Reply 3: We have added related contents. See page 5, line 131-138.

4. Were the p-values used adjusted for multiple tests (q-value, FDR)? An unadjusted p-value is not appropriate for the analysis.
Reply 4: Yes. See page 17 and page 18, figure 4 and figure 5. The q-values were showed in the figures.

Reviewer B

The paper titled "A bioinformatics analysis of the susceptibility genes in Stanford type A aortic dissection and the correlation with the risk of aortic dissection rupture" is interesting. Gene ontology analysis demonstrated that many genes in Stanford type A aortic dissection were involved in cell biological functions, cell components, and molecular functions through upregulating and downregulating the levels of expression. Subgroup analysis of lncRNAs suggested that many lncRNAs with different functions are involved in epigenetic modification, as well as transcription and posttranscriptional regulation of mRNAs, and play important roles in the regulation of gene expression. However, there are several minor issues that if addressed would significantly improve the manuscript.

1) This study is based on bioinformatics analysis. It is recommended to increase in vivo and in vitro experimental studies, which may be more meaningful.

Reply1: We have discussed it as a limitation in the discussion. See page 10, line 317-321.

2) It is suggested to determine the role of necrosis and immune infiltration in Stanford type A aortic dissection through bioinformatics analysis, which may make this study more complete.

Reply 2: We have discussed it as a limitation in the discussion. See page 10, line 317-321.

3) There have been many studies on Stanford type A aortic dissection. What is the difference between this study and previous studies? What is the innovation? These need to be described in the introduction.

Reply 3: We have added it in the introduction. See page 4, line 114-118.

4) Figures 4 and 6 are not clear enough. It is recommended to provide clearer figures again.

Reply 4: Attached files please find revised figure 4 and figure 6.

5) The bioinformatics analysis in this study is too simple. It is recommended to conduct WGCNA analysis on the data to determine the key modules, which may be more meaningful.

Reply 5: We have discussed it as a limitation in the discussion. See page 10, line 317-321.

6) It may be more meaningful to add functional research on key genes.

Reply 6: We have discussed the function in the figure 4 and figure 5.

7) How to assess the risk of aortic dissection rupture? What are the late events associated with aortic dissection? It is recommended to add relevant information.

Repley 7: We have revised the title accordingly. See page 1, line 3-4.