Comments to the Authors,

This manuscript studied the genome-wide mRNA and lncRNA alterations in three paired samples of uterine adenomyoma versus matched eutopic endometrial tissues from China population using the Agilent platform. Large number of abnormal expression of mRNA and lncRNA were identified and validated with QRT-PCR. The study was performed rigorously and the findings are interesting. However, the sample size in the present study was too small which might not guarantee the powerful and stable conclusion. I'd recommend publication if the authors can increase the sample size and address the following concerns and prepare a more elegant draft.

**Major Compulsory Revisions**

1, the sample size must be increase to 12 pairs which I think would provide more stable results and conclusions. In addition, all the data should be upload to public database so that the reader can validate the analysis and the corresponding result. When the sample size is small, the power estimation should be provided. Further, the differential expression criterion of fold-change with P<0.05 was not suitable for the genome-wide dataset analysis. Multiple test correction or feature deduction should be applied to decrease the false positive result.

2, in the method section, clustering analysis was mentioned: Hierarchical clustering was performed to show distinguishable expression patterns of lncRNAs and mRNAs, however, there is no any result to show the hierarchical clustering result.

3, PCA analysis based on the genome-wide mRNA and lncRNA should be provided to show source of the variance of the dataset. In addition, the hierarchical clustering result should be provided.

4, How many samples were applied in the Q-RT-PCR? How many samples were collected in the method section? The sample information should be provided while the HE staining should be provided for all the samples rather than an example.

5, Figure 3a-3d are not clear at all. It can be replaced with tables.