Thank you for your interesting work. I have the following comments:

1. There are a lot of errors in the English in the manuscript. This sometimes makes it difficult to understand.

Response: Thanks for your kindly reminding. The article have been revised by professional English language editing company. Please check the language certificate in the attachment.

2. There are a few errors in the conventions of taxonomic classifications. Ensure genus names have a capital letter at the start and species names have a lower case letter e.g. *Ligustrum robustum*

Response: We are sorry for the mistake. All the errors mentioned above have been corrected according to your comment.

3. Be consistent with either US English or UK English in your spelling

Response: Thanks for your suggestions. The article have been revised in American English style by Jing-Yun Ma Expert Group for SCI Biomedical Editing and Publishing.

4. I found the results (text) regarding the T-RFLP analysis difficult to understand

Response: Thank you for careful reading of our manuscript. This part has been deeply revised to make it more understandable.

5. The figure legends are lacking in detail. There is no information about group size/number of experiments performed etc.

Response: Thank you for your valuable suggestion. The figure legends and the details including the group size/number of experiments have been added.

6. Many tables lack units for the values shown

Response: We are sorry for not revealing the units. All the tables in this manuscript have been double checked, and the units for the values have been added.

7. Is it usual that results vary depending on the detection methods used, as you found with the *Bifidobacterium*? You discuss that different groups obtain different results but not if other groups have had similar discrepancies when they use more than one method of detection.

Response: Thanks for your valuable question. This is the first time that we applied culture methods and qPCR for quantification of gut bacteria. As far as we know, a few results from different detection method vary. These results could happen when the target bacteria requiring strict culture condition. While, the majority results, targeting bacteria which can easily grow in loose culture condition, could have consistent trends.

In our experiment, to guarantee the parallelism between different groups, every sample treatment step was conducted by the same people, and the colony counting of each gut bacteria from different

groups is consistently completed by the same sophisticated researcher of our study group. Meanwhile, *Bifidobacteria* need more strict culture condition than the other major gut bacteria (such as *Escherichia coli*, *Enterococci* and *Lactobacilli*). And BBL, the only media we used, cannot satisfy the requirement of all kinds of *Bifidobacteria*. On the other hand, the decreased amount of *Bifidobacteria* detected by qPCR might be vulnerable to LR treatment. And according to our other results, this kind of *Bifidobacteria* might contribute less to the control of host's body weight than those could grow up on BBL plate. Besides, there are only 2000 types of bacteria that can be used for 16S rRNA sequencing, and a large proportion of the 16S rRNA sequence is still unknown. Thus, we suppose this controversial result of *Bifidobacteria* might largely derive from the different principles of the detection methods. However, this speculation is expecting for further research and confirmation.

8. I think many of your results would be better presented as graphs rather than tables.

Response: We totally agree with you. Table 5 ~ table 10 in previous manuscript have been replaced by graphs.