

**Manuscript NO.: 67878**

**Title: Bone marrow mesenchymal stem cells therapy regulates gut microbiota to improve the post-stroke neurological function recovery in rats**

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We have submitted a revised manuscript entitled "Bone marrow mesenchymal stem cells therapy regulates gut microbiota to improve the post-stroke neurological function recovery in rats" (manuscript NO.:67878). We immensely appreciate your suggestions and the reviewers' insightful comments. Those comments are all valuable and very helpful for revising and improving our paper. We have studied comments carefully and have made corrections, which we hope to meet with approval. Based on the instructions provided in your letter, we uploaded the file of the revised manuscript. The following part is the point-by-point responses to the reviewers' comments. The comments are reproduced and our responses are given directly afterward in a different color (black).

**Reviewer #1:**

1. There are still some grammatical mistakes in the article. Please correct them carefully, eg: “the third generation cells” should be “the third generation of cells”.

Thank you so much for your suggestion. We have checked our manuscript carefully and corrected some grammatical mistakes.

2. “OTUS”, “Shannon and Chao index”, “PICRUSt”. Please explain in the materials and methods section of the manuscript.

As for the reviewer's concern, the full descriptions of “OTUS”, “Shannon and Chao index”, and “PICRUSt” have been supplemented in the materials and methods section of the manuscript.

3. In Figure 4B, “others” accounted for a large proportion. Which microbes did others specifically represent and what roles did others play?

We apologize for presenting an incorrect figure, which confused the reviewer. A large proportion of "others" are "unclassified", but we did not describe this clearly previously, and we have corrected Figure 4B.

4. “Predictive analysis of gut microbiota function” This part of the content is lack of experimental data support, please add relevant experiments to verify the microbiota function.

For example, whether the function of lactic acid bacteria in the BMSC group was consistent with the function predicted by KEGG.

We are very fortunate to meet a responsible reviewer like you. Your comments and suggestions are very relevant to our further research. As we describe in the paper, we used PICRUSt software to predict the metabolic function of the gut microbiota. Subsequently, we reviewed the literature and found that changes in lactic acid bacteria and metabolites could affect the metabolic pathway involved in galactose metabolism, secondary bile acid biosynthesis, and Sphingolipid metabolism, which will be further validated in later metabolomics.

5. The figures quality is too poor, please improve the quality of the figures. I can't read the text clearly on some figures. There is a big difference between the horizontal and vertical fonts in Figure 4AB and CD. The authors need to modify it carefully.

Thanks for the professionalism of the reviewer. We have improved the quality of the figures and modified the fonts in the figures.