Dear editor,

Thank you for your information and reviewer's critical review of our manuscript. The reviewers made careful and professional suggestions to enhance the quality of our manuscript. The suggestions were all incorporated into the revised manuscript. We feel that these salient points that have been incorporated into the revised manuscript will now warrant acceptance of our work.

We also have corrected this paper according to the requirements suggested from the reviewers and highlighted the changes in red color. Please see the revision list for details. If you have question about our manuscript, please let us know.

Sincerely,

Xiangsheng Cai, Ph.D.

Reviewer #1:

Scientific Quality: Grade C (Good)

Language Quality: Grade B (Minor language polishing)

Conclusion: Major revision

Specific Comments to Authors: In this study, the authors have investigated the changes in the gut microbiota of pregnant women with GDM and compared the changes in the gut microbiota to the GLP-1 level. The outcomes of this study could point to implications of gut dysbiosis in the pathogenesis of GDM and provide further probiotic-based approaches for the treatment of this disease. However, The major concern is that there are not enough findings and the related interpretation about the correlation between the gut microbiota and GLP-1 levels. Hence, this study should be revised before publication, particularly in the interpretation of results and claims in the relation to the gut microbiota composition and GLP-1 level. Moreover, other minor concerns have been listed below. MATERIALS AND METHODS The history of recent antibiotic therapy is an influential factor in microbiome analysis. It should be stated in the exclusion criteria by the authors. RESULTS In the section "Alpha and Beta diversities" the authors mentioned some differences in alpha and beta diversity between GDM patients and NGT subjects, however, they have not stated what are? The authors should remark on any increase or decrease in microbiome diversity in the GDM cohort. There is no need to bring the related Phylum of the families in Paragraph 2 under the heading "Taxonomy". Please omit them. Under the subheading "Functional profiling of the gut microbiome," the authors should provide only microbial-related pathways and there is no need to provide human-related pathways. The entire manuscript has some grammatical and lexical errors.

Re：Thank you for your suggestion. In this study，we have implemented the correlation between the gut microbiota and GLP-1 levels. And we found that *Sutterella*, *Oscillibacter* and *Bifidobacterium* were significantly positively correlated with GLP-1. To the best of our knowledge, this is the first report on the associations between GLP-1 and genus including *Sutterella*, *Oscillibacter*, *Bifidobacterium* in GDM, these findings may help people improve GLP-1 levels by using these specific bacteria, so this finding is very meaningful. We have tried our best to explain the relationship between gut microbiota and GLP-1. Maybe our description is not clear enough. Therefore, we made some adjustments in the discussion section to make our description more

clear.

In the “MATERIALS AND METHODS” section, we have added the statement in the in the exclusion criteria: “(11) consumption of probiotics or antibiotics within 1 month before admission.”

We analyzed the differences of flora between GDM patients and normal pregnant women from the levels of phylum, family and genus. We think this statement can be retained.

Microbial-related pathways and human-related pathways are crucial for gut microbiome, they influenced each other, only providing the microbial-related pathways may not reflect the comprehensive pathways in this study, thus, human-related pathways are also necessary.

According to your advice, this manuscript was edited for proper English language, grammar, punctuation, spelling, and overall style by one or more of the highly qualified native English speaking editors at NativeEE. NativeEE specializes in editing and proofreading scientific manuscripts for submission to peer-reviewed journals.

Reviewer #2:
Scientific Quality: Grade B (Very good)
Language Quality: Grade B (Minor language polishing)
Conclusion: Minor revision
Specific Comments to Authors: The manuscript describes differential microbiota between women with normal pregnancy and gestational diabetes mellitus (GDM). The study included the recruitment of patients and bacterial 16S rRNA gene sequencing. Although the topic is interesting, there are concerns that the authors should take into account. 1. The authors stated that markers of glucose and insulin homeostasis were higher in the GDM group compared with the NGT group (Table 1). The data only showed that HbA1c (%) was significantly different between two groups. For OGTT, it appeared to be different at time = 0. Would it mean that the background of two groups was already different? It'd also be nice if the authors included the dot plots for the significant parameters so the readers can see their distribution. 2. Most of the data were from gene sequencing and the authors analyzed and showed us different aspects of the outputs. The concerns on the accuracy and validity of the data should be pointed out. The authors are advised to elaborate more on this and perhaps include a few validating results to support their findings.

RE: Thank you for your suggestion. Our data showed that OGTT at time 0, 1, 2h are also significantly different between two groups. The trend of these three indicators is the same, so there is no different background between two groups. We have built ensemble classifiers based on random forest (RF) algorithm and pointed out the accuracy and validity of the data by using ROC curve approach. Twenty genera plus Glu provided the best discriminatory power, as indicated by the area under the receiver operating characteristic (AUROCC) value of 0.94.