1. For the multivariate analysis, please clarify the methods for variables selection in model. The association or casual inference is their aim the confounding factors according to previous knowledge should be included to the model for appropriate effect estimation. A stepwise selection might not appropriate for the variable selection. The collinearity and goodness-of-fit analysis should be performed and show in the results. For variable and model selection, please refer to these articles: I. Heinze G, Wallisch C, Dunkler D. Variable selection - A review and recommendations for the practicing statistician. Biometrical J [Internet]. 2018 May 1 [cited 2020 Oct 22];60(3):431–49. Available from:/pmc/articles/PMC5969114/?report=abstract II. VanderWeele TJ. Principles of confounder selection. Eur J Epidemiol [Internet]. 2019 Mar 15 [cited 2020 Oct 22];34(3):211–9. Available from: https://doi.org/10.1007/s10654-019-00494-6.

Reply:

After reading the papers recommended by the reviewer, we learned several 'new' criteria for variable selection such as the Akaike information criterion, the Bayesian information criterion and the LASSO penalties in additional to the commonly used significance criterion (which we used in our research). However, we were regretted to find out that some of the criteria above are either only suitable for studies with large sample size, or cannot be carried out with the SPSS software, or mainly used to select an optimal model from multiple statistical models. As a small-sized clinical research analyzed with the SPSS software, the purpose of our study was to explore the risk factors for a specific pathological condition from a series of general statistics and routine metabolic parameters. Meanwhile, the range of variables, and the size of subjects were not enough for the construction of an optimal statistical model. Therefore, we still used the classic significance criterion. In the linear regression analysis, the univariate regression analysis was first carried out to rule out the variables with P-value $\geqslant$ 0.1, then the multivariate regression analysis was carried out among the remaining variables with a stepwise algorithm processed automatically by the SPSS software. We repeated this procedure and chose a forward selection algorithm (based on the comparison of likelihood ratios) for the multivariate binary logistic regression analysis. Additionally, after reading the recommended papers, we tried to combine the change-to-estimate criterion with the significance criterion in selecting variables. The final results were almost consistent with our previous results, so we did not intend to describe the details in this paper.

We did not show the result of collinearity and goodness-of-fit analysis because after checking several papers published by this journal, we found that it was not necessary for showing these results in the article. In fact, we had calculated the variance inflation coefficient (VIF) of variables before multivariate regression analysis. A VIF > 10 was considered as an evidence of strong collinearity, under which circumstance only one of the collinear variables would be selected for multivariate regression analysis (the selection mainly conducted with clinical experience). After the collinearity analysis, the VIF of remaining variables varied from 1 to 4.5 before multivariate regression analysis. In the multivariate binary logistic regression analysis, we used the Hosmer-Lemeshow test for goodness-of-fit

analysis. The result of Hosmer-Lemeshow test was 0.353 (the final model), which meant the model fitted well.

2. Please provide flowchart of participants. Additionally, include full details of how the authors handled missing data and outliers in the 'Methods' section.

Reply：

The flowchart of participants has been added to the end of article. Meanwhile, we had collected complete data from each enrolled subject, so there was no need for handling missing data in statistical analysis. Outliers occurred in rare cases, under which circumstances they would be excluded from statistical analysis.

3. In "Methods" part, how the authors selected baseline characteristics and laboratory values for included in analysis?

Reply：

In this research, the subjects were enrolled from the T2DM patients hospitalized in the Endocrinology Department of the First Affiliated Hospital of Soochow University, Suzhou, China between January 2017 and March 2018. Each subject underwent the basic information and medical history collection, anthropometric measurement and physical examination after admission. And blood samples were collected for the routine evaluation of metabolic parameters and islet function. In this paper, the general data, metabolic characteristics and parameters of fasting islet function were included in statistical analysis as we aimed at exploring the risk factors for liver fat accumulation in T2DM patients from the commonly used clinical parameters, which is helpful to find out the patients with a higher risk of moderate to severe fatty liver in daily clinical work as soon as possible, then to start early intervention.

Additionally, we also read a quantity of clinical papers focused on NAFLD as references for variable selection. While most previous researchers used B-ultrasound and Computed Tomography to diagnose hepatic steatosis, we used the MR mDIXON-Quant imaging to quantify the hepatic fat content and to diagnose the severity of hepatic fat accumulation. In the end, our results were in good agreement with some of previous studies, which proved the credibility of our research.

4. There are a lot of typos and grammatical errors that should be checked carefully and corrected throughout the manuscript.

Reply：

Thank very much for pointing out the spelling and grammatical errors in this article. After the last revision, we had invited a professional English language editing company for language polish, and the language quality of this paper had reached an A level. The editorial certificate is shown as follows.

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EDITORIAL CERTIFICATE

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Manuscript title

Influencing factors for hepatic fat accumulation in patients with type 2 diabetes mellitus

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