

LETTER TO ANSWER THE REVIEWERS

To the Reviewers,

We're appreciated your advice and patient. We correct and provide necessary tables, figures and explanation as followed.

Firstly, according to your suggestion, we provide the primers in to a table (RNA extraction, RT-PCR and quantitative real-time PCR), and correct the description.

Secondly, baseline characteristics of patients were provided in supplementary table. We also make analysis in the manuscript. The results showed that there are not significant differences between GSRCC group and adenocarcinoma group in most baseline characteristics of age, gender, TNM stages, lymphovascular invasion and nerve invasion. There are significant differences only between Lauren type ($p < 0.001$) and histology differentiation ($p = 0.038$). The results are consistent to the pathological characters of GSRCC with poorly differentiation and diffuse type. However, there is no multivariate analysis in our study caused by the samples we chose are recently within 1 year. The median survival is not reached, and survival analysis still needs more observation time to follow. In the future, we will explore further to find out significant risk factors based on the survival for GSRCC.

Thirdly, based on reviewer's advice, we demonstrated that 408 gastric cancer tissues and 211 normal tissues with the description. We acquired and analyzed the genes expression in 408 gastric cancer tissues and 211 normal tissues from the TCGA and GTEx data using GEPIA (<http://gepia.cancer-pku.cn/index.html>). The database does not provide the information of the pathological classification of these gastric cancer patients, so we cannot demonstrate GSRCC, non-GSRCC, and normal tissue with P-value in Figure 4A. Also, we provide confidence interval of HR in Fig 4B. The zero point of vertical line in Fig 4B should be explained. The reason is that the Fig 4B was generated from the website (GEPIA, <http://gepia.cancer-pku.cn/index.html>), and we could not adjust the figure. We provide the top 10 up-regulated genes and down-regulated genes among 1162 differential genes in table 2 as commanded.

Fourthly, we as suggested correct the language mistakes and add the related reference in article.

Finally, we again give our thanks to these three reviewers for proposing the great advice.