Comments to the Authors,

In the present study, the meta-analysis of the association between the polymorphisms of GSTM1, GSTT1, GSTP1 and esophageal cancer was conducted. Actually, the meta-analysis to each of three genes was completed few year ago separately. The authors combined the three genes together and with updated data come out in the past few years. The authors found null genotype of GSTM1 and GSTT1 were significantly associated with the risk of esophageal cancer while GSTP1 were non-significantly associated with esophageal cancer. In addition, subgroup analysis showed GSTM1 and GSTT1 were strongly associated with esophageal squamous cell carcinoma. The study was performed rigorously and the findings are very interesting. However, I'd recommend publication if the authors can address the following concerns.

**Maor Essential Revisions**

1, Please introduce the GWAS results for these three genes in the background section.

2, Why the P-value for some rows of the HWE test were missed in the Table 1?

3, Meta-regress analysis should be conducted to analyze all the heterogeneity of race, cancer type and so on simultaneously.

4, How to explain GSTM1 was only associated with esophageal cancer in Asian population rather than Caucasian population? It is a false heterogeneity or it is a truth. Is there any other evidence to support this result?

5, Why not extract the gender, age information from the literature and analyze the influence to the conclusion?

6, Data on risk factors for individuals such as smoking and eating habits should be included to increase the credit of the meta-analysis.

7, In the last sentence of the Discussion section, the author mentioned “For *GSTM1* null genotype, there were only 9 studies on EAC and 6 studies on Caucasians. Therefore, the power in subgroup analyses was not sufficient.”. What’s the criterion of the sufficient or no sufficient?

8, As the conclusion said, “This result suggests the polymorphisms in GSTs can be used as clinical references and biomarkers for esophageal cancer diagnosis and treatment.” As the OR of the three genes are only between 1.12 and 1.27, I do not know how can we conclude that they could be considered as biomarker for diagnosis or treatment? Please calculate the sensitivity, specificity and accuracy for the diagnosis of ES in the method section.