Comments to the Authors,

This manuscript conducted a case-control study to evaluate the association of three SNPs, rs416748, rs13306541 as well as rs3747531, located in MSR1 and essential hypertension (EH) in a Chinese Han population. The authors found rs13306541 and rs3747531 were significantly associated with an increased risk of EH with OR=1.63 and 1.29, respectively. The findings are interesting, However, I have several major concerns.

1, The most important Tables, such as Table 2 and Table 3, cannot be seen in the present manuscript.

2, The association between rs13306541, rs374753 and EH is very weak, the power estimation or another independent validation was essential to guarantee the conclusion is solid.

3, The confounding should be adjusted in logistic regression model.

4, The comprehensive situation of risk alleles from 0 to 4 should be provided one by one to show the cumulative effect of risk alleles, even parts of recombination were not significant.

5, Is there any GWAS in EH should be mentioned in the introduction. If yes, the strength of the association etween MSR1 and EH should be provided.

5, From HGP project to the completion of hundreds GWAS, large number of disease associated SNPs have been identified to be associated with kinds of complex disease, However, Dr. Guo and his colleagues found the prediction ability to the disease was very limited even with the most significant SNPs discovered in different populations. (Guo, S., et al., *Significant SNPs have limited prediction ability for thyroid cancer.* Cancer Med, 2014. **3**(3): p. 731-5). Please provide corresponding discuss to this question. What’s the significance to the present stduy even if the association is solid and truth. And please discuss the stregy and apprach how to push the population based assocition study to the next stage to solve the problems of the disease susceptibility and risk prediction.