Dr. Shi and colleagues provided a meta-analysis to investigate the relationship between SG13S114 and SG13S32 polymorphism of ALOX5AP and ischemic stroke in Chinese population. The study was performed rigorously and the findings are interesting. However, I still have some concerns which should be addressed by the authors.

1, The author suppose the genetic association was different between Chinese population with other population, therefore, the author conducted the meta-analysis only within Chinese population, however, within Chinese population, there are still quite large number different races (South Chinese Han, North Chinese Han, Uighur, Tibetan). According to the author’s hypothesis, subgroup analysis in difference race within China should be conducted in the meta-analysis. However, in current study, majority of the study are miss the race information as shown in Table 1 and Table 2. In this situation, I suggest the author extent the study inclusion and collect all the population/race, including European, African population and conduct the meta-analysis again. In the Table 1, the regions information should be remove, they are not representative to race and didn’t provide any information to the conclusion, also include HWE, since the basic hypothesis of association study should be HWE. You can mention the HWE in the footnote of the table.

2, Since there have been already several meta-analyses to this problem, the current study is only the update and comprehensive analysis to the previous study, the present manuscript should be change to ‘brief report’ and the manuscript should be as short as possible. Keep the most important and unique Figure and Table in the main-manuscript and remove Figures and Tables which might not be so important to the supplementary to avoid to repeat or plagiarize with previous research.

3. In current study, the authors provided all the analysis based on different genetic models, such as dominate model, recessive model and so on. However, few of other model were omitted, why? Such as genotype-based analysis, additive model? Another question is, as the reality biology, maybe on only one kind of model are truth, how to deal with this problem?

4, Please provide exact STATA input as the supplementary so that the readers could check the result and make the manuscript more reproducible. The actual input can be attached as supplementary or can be upload to Github and provide the link in the manuscript.

5, the authors mentioned Quality assessment to each study, however, no any related information was shown in the paper.