The authors conducted a genetic-association study between the polymorphisms/SNPs from MMP-2 genes and susceptibility to Alcohol-induced Osteonecrosis of the Femoral Head in a Han Chinese male population (299 case vs 396 normal). Within a loose significant threshold, the authors identified 3 risk alleles within MMP-2. The study was completed with comprehensive statistical analysis and with interesting result. However, I have several concerns,

1, The authors didn’t give comprehensive description to the genetic-association research in ONFH. How many genes/variation have been identified in ONFH before? Whether GWAS has been conducted? Any significant association between MMP-2 and ONFH was identified? The introduction section should provide more logic process for the study and should be more concise while too much non-related contents were attached in the introduction section.

2, In the current study, there is only one discovery dataset, no further independent validate dataset. It is difficult to eliminate the probability of false-positive finding. Even the author didn’t set any positive and negative control, therefore, it is hard to judge whether the result is solid or not. In addition, when there are several SNPs were investigated in same study, multiple test correction should be conducted to control the false positive.

3, In the LD analysis, which samples were used should be provided? Case, control or total samples? Meanwhile, for the LD block analysis, the detail method should be provided rather than only the ‘software’.