In this manuscript, Dr. Leask and colleagues conducted comprehensive fine-mapping study to investigate the regulatory function of Urate-associated genetic variants derived from previous GWAS study to MAF, MAFTRR and LINC01229 with multiple methods, including eQLT, Hi-C, ChIP-qPCR and zebrafish experiments. The study was performed rigorously and the findings are quite interesting. I am really enjoy the manuscript. Here, I only have several tiny comments:

Minor Essential Revisions

In the background section between line 54-61, the authors mentioned that the causal variants might be linked with the GWAS-hits. Therefore, we cannot directly assign the intergenic GWAS-hits as non-coding variants (ncRNA). The authors should make a little bit modification for these statements.

The authors should be explicitly state the reason that SUA3-4 were filter out in the further analysis between line 106-108.

In the Figure 1, It will be helpful to label WWOX, MAFTRR and LINC01229 in the bottom of the Figure.

I suggest the author to short the section of result 2.1, since it is hard to evaluate the false negative with the re-analysis to public database. It is not easy to make conclusion that the variants in SUA1 and SUA2 do not directly influence 146 the expression of MAF without cell biology experiments, even though the authors have tried several different database.

In the Figure 3F, LINC01229, LINC01228 and MAFTRR should be labelled even though they have been shown in previous Figures.

How about HNF4a binding ability in HEK293 cell except HEPG2 (Line 293)?

Discretionary Revisions

I suggest the author to change an explicit manuscript title. It is clear these genetic variants are not Urate-associated genetic variants. Obviously, they are important causal variants which have been shown in your evidences. Meanwhile, multiple genes are also not explicitly.