Dr. Jiang and colleagues conducted an association and function validation study for the SNPs located in the 3’UTR region of lncRNA HOTAIR in a large pancreatic cancer cohort from Chinese population.

Major:

1. In the background section, the authors mentioned overexpression of HOTAIR is associated with the metastasis and poor prognosis, Is there any previous evidence to show the roles of HOTAIR in the diagnosis of pancreatic cancer. If not, how to understand the hypothesis of that high expression of HOTAIR caused by the inhabited binding of miRNA-29a increase the risk to pancreatic cancer. If over-expression HOTAIR could be a diagnostic biomarker for pancreatic cancer, any quantitative evaluation for the diagnosis performance. These information should be mentioned in the background section.
2. In the method section, the author should give explicit description rather than ‘Data was analyzed by MassARRAY Typer software 4.0.3’. What kind of analysis did MassARRAY Typer conduct?
3. Is there any previous evidence to show any of the SNPs in present study were significantly associated with diabetes (type I or II)
4. It would be helpful if the authors should provide the diagram to show the relative location about the four SNPs and HOTAIR in the Figure 1.
5. In the section of “Association of SNP rs200349340 Genotypes with miR-29a binding”, how the author could make the conclusion without confirming the binding alleles (in HOTAIR) for the sw1990 cell line? What would happen if sw1990 have C allele in HOTAIR?
6. In the figure 1 and 2, the significance star should be labelled and with P-value.
7. The authors mentioned Li et .,2018 investigated common variants in HOTAIR,
8. The authors should show the coefficient and P-values for confounders (can be as the supplementary materials)
9. Please add the line number in the manuscript in the further manuscript.
10. I want to know whether this region was nearby any pancreatic cancer GWAS significant regions.
11. Linkage disequilibrium among these four SNPs should be mentioned in the manuscript in Chinese population.
12. In the background section, the authors should provide more details how to select the candidate SNPs. Only 4 miRNA-SNP were found or the authors add more filters to excluded certain miRNA-SNP
13. The authors mentioned batch effect of the samples collected from different hospital, why not take it as one of the confounders in the regression models.
14. How many sample size should be mentioned for Figure 2 and boxplot with scatters, which represents each sample, should be provided. Meanwhile, is there any possibility to show the OR based on gene expression for PC?
15. It would be better to remove 3 non-significant SNPs (from Table 2) to the supplementary and merge Table 2 and Table 3 together to show the conclusion clearly.

N