In this manuscript, Dr. Yang and colleagues conducted a genome-wide methylation analysis to sinonasal inverted papilloma(SNIP) and squamous cell carcinomas (SCC). The authors identified several interesting different methylation loci/regions between two situation. The study was performed rigorously and the findings are quite interesting. However, the manuscript was not well prepared. The following comments hope to be helpful to improve the study.

**Major Compulsory Revisions**

1. The authors should explain why 27 samples is enough for the study. Whether power estimation has been conducted before the study design.
2. The author should give more details about the methylation microarray. What it is exactly? What targets are included? How to normalize microarray data after you get the raw data? Is there any SNPs located in microarray probes? What’s the missing ratio for each samples and is there any significant difference between SNIP and SCC.
3. Whether the data can be used to estimate and compare the genome-wide DNA methylation level difference between SNIP and SCC?
4. Since it is microarray, when conducting the statistical analysis, multiple test correction should be conducted, therefore, P-value significance threshold should be set at 4.46x10-6
5. The authors must upload the microarray data to GEO to guarantee the reproducible of the manuscript.
6. For table 1, P-value should be provided. And What’s Diff Score should be explained.
7. Figure 1 can be removed and only showed as supplementary Tables. And be careful the P-values should be provided for each gene ontology.
8. Figure 2 can be removed to Supplementary Figure since it is easy to get from String 9.0 and no need to show here as a main figure.
9. Figure 3B why only shown 9 Pap and 5 Car samples? I thought they should be paired, right? Why not repeat it within 27 samples?
10. The methylation status for these significant loci should be validated with BSP since you didn’t receive lots of significant loci. It will be very easy to validate them so that the paper will be more solid.