Dr. Chen and colleagues conducted a routine DNA methylation assay to laryngeal squamous cell carcinoma. All the analysis are very routine without any innovation. The only interesting part maybe the data could provide a methylation reference for LSCC, however, the authors didn’t upload the data to public database. The authors identified some interesting differential methylation regions (DMR) however the statistical analysis is not solid without multiple test correction. What’s worse, the authors didn’t make full preparation to the manuscript, I suggest the author to rewrite the manuscript to be clear and explicit style.

1. It will be better to show left and right sub-panel of Figure 1A in one panel so that the reader can easily compare the difference. I am quite interested in the methylation change in promoter region, why the methylation level is decreasing step by step in promoter region? What’s the difference between Figure 1A and 1B? if they are for same presentation, I suggest to remove Figure 1A. Same to Figure 1C, I suggest the authors to move Figure 1A and 1C to supplementary Figures.

2. Patient’s clinical characteristics in WGBS should be provided as a supplementary table.

3. I don’t know why multi-test correction was not conducted in Figure 2A? The whole analysis should be re-conducted with multi-test correction to avoid too much false positive.

3. TCGA have huge numbers of larynx squamous cell carcinoma DNA methylation and gene expression data, the authors should download them and compare the result they have in this study.

4. In the background section, the author could list the similar pipeline papers in multiple cancers so that later these result can be compared.

5. Figure 4 should move to supplementary Figure since it is very basic and simple data analysis to public data.