Comments to the Editor,

The authors has solved majority of my comments. However, I still have several concerns on the clinical application for the present study. In general, I'd recommend publication after the authors can address the following concerns.

1, Table 3 is great to show the differential expression between cancer and normal samples. Can authors provided similar table for that of DNA methylation as the supplementary or in the main body of the manuscript.

2, The authors mentioned that the annealing temperatures were experimentally determined in a set of gradient PCRs, for each MSP primer. However, the criterion is not provided in the manuscript. It is important because the specificity of the MSP greatly depended on the annealing temperatures of the PCR.

3, The authors gives a great interpretation to my 13rd questions. In the background section, the authors has provide the latest progress of the role of DNA methylation, however, the reference is a paper a review. Here actually, a quantitative evaluation on how much DNA methylation can be used to be a diagnosis a prognosis biomarker can be showed. I think the following two lasted literatures can be cited in the background to give more numerically introduction.

Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). Clinical epigenetics 2015, 7:3.

Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. Clinical epigenetics 2014, 6:5.

Further