Reviewer's report

Title: Promoter hypermethylation-induced transcriptional down-regulation of the gene MYCT1 in Laryngeal Squamous Cell Carcinoma

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Reviewer: Pierre-François Cartron

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Major points (by order of appearance into the article):

Firstly, the authors need to perform qPCR analysis to quantify the MYCT1mRNA expression since the main topic of their article is to correlate the epigenetic regulation of MYCT1 gene and the MYCT1mRNA expression.

Secondly, the fact that the MYCT1mRNA expression increased when the Hep2 cells were treated with 5aza is not an evidence that “DNA methylation modification down-regulated MYCT1 gene expression” (as written in section 3.2). To claim this point/conclusion, the authors need to show that the 5aza treatment promoted the demethylation of the MYCT1 gene.

Thirdly, in section 3.4, the authors claim that “methylation interferes with the binding between the MYCT1 promoter and c-Myc”, but the EMSA experiments is not adequate to support this conclusion since no antibody directed against c-Myc was used to abrogate the band gel shift. In addition to EMSA experiments, the authors need to perform ChIP experiments to evaluate the quantity of c-Myc on methylated and unmethylated MYCT1 gene i.e. in Hep2 cells and hep2 cells treated with 5aza, for example.

Finally, the authors need to clearly identify and discuss the role that the Dnmt3a/c-Myc complex can play into the epigenetic regulation of the MYCT1 gene. For this purpose, reChIP using antibodies directed against Dnmt3a and c-Myc need to be realize.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.