Author’s response to reviews

Title: Promoter methylation of CDKN2A and the lack of p16 expression characterize patients with hepatocellular carcinoma

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Author’s response to reviews: see over
To
Rachel Neilan, MSc
Assistant Scientific Editor
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Title: Promoter Methylation of CDKN2A and Lack of p16 Expression Characterize Patients With Hepatocellular Carcinoma.

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Dear Mrs Neilan,

we reconsider to publish our experiences on changes of promoter methylation of CDKN2A gene and expression of p16 in patients with different liver tumors after further editing the manuscript.

The content of the manuscript is original and it has not been published or accepted for publication, either in whole or in part, in any form. No part of the manuscript is currently under consideration for publication elsewhere.

With kind regards,

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Referee 3

1. Yes. It should be table 3.

2. Yes, it should be table 2.

3. Yes, it could be hypermetylation.

4. We did not find correlation between methylation und grade of differentiation of tumors. Therefore, we do not want to discuss. It is because of the relative small number of tumor probes in each differentiation group investigated in this study.

5. Patient No 12. There was the only one non-tumor tissue probe proved to be hypermethylated in our study.

6. You have right. CCC5`s PMR was 25,86%.

All your comments have been edited in the manuscript.

Thank you.

Referee 2

In some tumor probes from patients with liver metastases who expressed p16 methylated CpG islands were found. The explanation for this finding is not clear. It can be speculated that these CpG islands investigated in our study do not represent the sites responsible for complete silencing the gene or further factors and mechanisms lead to gene silencing. Further discussion of this finding do not see necessary.