Author's response to reviews

Title: Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded tissue (FFPE) for PCR-based methylation analysis using SMART-MSP and MS-HRM

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Author's response to reviews: see over
Reviewer’s report
Title: Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded tissue (FFPE) for PCR-based methylation analysis using SMART-MSP and MS-HRM
Version: 2 Date: 29 October 2009
Reviewer: Hongdo Do
Reviewer’s report:
Minor Revision
1. It was previously asked why in Table 2, the estimates of methylation for RARB are up to 186%. The authors responded by adding the following sentence in the revised manuscript. "One sample was estimated to be methylated above 100% at the RARB promoter by SMART-MSP. Methylation estimates relative to in vitro methylated DNA may occasionally be obtained for heavily methylated genes because the control may be 100% methylated in spite of extensive SssI treatment [31]."
Presumably the word "not" is missing so that "the control may NOT be 100% methylated”?

It is correct that the word "not" is missing. This has now been corrected.

A number of grammatical errors remain to be remedied.

We have carefully read the manuscript and a number of grammatical errors have now been corrected.

Level of interest: An article of limited interest

It is noticeable that the reviewer’s comment was “An article whose findings are important to those with closely related research interests” after his first review.

Quality of written English: Needs some language corrections before being published
Statistical review: No, the manuscript does not need to be seen by a statistician.
Declaration of competing interests: I declare that I have no competing interests.
Reviewer’s report

Title: Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded tissue (FFPE) for PCR-based methylation analysis using SMART-MSP and MS-HRM

Version: 2 Date: 30 October 2009
Reviewer: Catherine Gratas

Reviewer's report:
The authors answered to most of my comments and improved their paper.

Discretionary revisions:
1- The number of unmethylated tumors and negative by IHC for p16 is high (12/30): some comments or references could be added on this point in the discussion.

The following has been added to explain this point in the discussion:

“Furthermore, we have evaluated whether immunohistochemical staining of the p16 protein correlated with methylation status of the CDKN2A (p16) gene. A highly significant correlation was found (p-value =0.001192), and all methylated samples except two, which were methylated at very low levels, were found to be negative. Twelve of 30 unmethylated samples were also negative by immunohistochemistry. This may be due to homozygous deletion of the CDKN2A (p16) gene, which often is found in NSCLC [32].”

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

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

Declaration of competing interests: I declare that I have no competing interests.