Author's response to reviews

Title: Fibronectin 1 mRNA expression correlates with risk of progression in renal cell cancer

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Author's response to reviews: see over
Dear Editor,

thank you for your letter concerning our manuscript entitled “Fibronectin 1 mRNA expression correlates with risk of progression in renal cell cancer” (MS: 6679237203944838).

We have carefully studied all of the reviewers’ comments and revised the manuscript accordingly.

Attached please find the revised manuscript as well as a list providing a detailed explanation of all revisions.

We hope that the manuscript is now suitable for publication in BMC Cancer and look forward to hearing from you soon,

Yours sincerely,

Sandra Waalkes
Editor’s comments:
We recommend that you copyedit the paper to improve the style of written English.
The paper was copyedited to improve the style of written English with the help of a native speaker.

Please confirm that you had patient consent to obtain and study the samples used in this work.
We had patient consent to obtain and study the samples used in this work.

Please provide an email address for every author on the manuscript's title page.
We have added the email address of every author on the title page.
Reviewer #1:

Major compulsory revisions:

1. Title:
The manuscript title suggests that a follow-up study including assessment of fibronectin-1 mRNA expression on renal cancer was performed. It might be better to slightly change the title to something like “...expression correlates with advanced disease in renal cancer”

We have changed the title according to this suggestion.

2. Material and Methods:
Please specify how the three endogenous control assays were included in the calculation of the results. Which algorithm was used to relate the fibronectin-1 Ct values to all three endogenous controls?
Three endogenous controls were combined using the DataAssist software V1.0 (Applied Biosystems, Foster City, CA, USA) and “arithmetic mean” as normalization method. The method of Livak et al. and reference delta Ct values obtained from the biological control RPTEC were applied for calculation of delta-delta Ct and relative quantity values, respectively.

3. Figures:
Figure legends should also explain any abbreviations used in the figure, f. ex. FN1RQ, PRTEC.

We have added the explanation for the abbreviations in the figures in the legends.

Minor essential revisions:

4. Results, clinical observations:
In line two median age of patients was reported to be 63 ±11.9 years. In Table 1 the same values were reported to be the mean age. Both terms are not interchangeable, they are defined differently. This should be corrected. Also, minimum and maximum age should be reported instead of standard deviation if using median.

We calculated mean age and not median. We have changed it in the script.

5. Results, clinical observations, first paragraph:
The numbers of patients suffering from papillary and unclassified RCC differ from those mentioned in Table 1. (Results: papillary n = 23 and unclassified n = 6; Table1: papillary n = 22 and unclassified n = 7). This should be corrected.

Thank you for this remark. The correct numbers are the ones in table 1. papillary n = 22 and unclassified n = 7.
6. Figure 1:
The groups were named normal, oncocytooma, tumor. This is slightly misleading. Oncocytooma is also a tumor, but it is benign. Therefore the last group should be renamed, f. ex. “renal cell carcinoma”, “RCC” or “malignant tumors”.
We have renamed the group to RCC.

Minor comments, not for publication:
Some typing and formatting errors have occurred and are listed below.

We have corrected these points recommended under 7 to 11.
8. Introduction, first paragraph:
Omit line break in line 9 after “…demonstrating the limited…”
9. Introduction, third paragraph:
Insert “from” in line 1 after suffering (“…were detected in patients suffering from gastrointestinal….”)”
10. Material and Methods, quantitative real-time PCR analysis, first paragraph:
Delete second “n” of “…expressionn assays…” in line three. Insert “used” in: “For visual comparison of univariate data we [used] beanplots…” in the third line of the second paragraph.
11. Table 1:
The values of the “%” column are duplicated in brackets in the “number of patients” column. This should be corrected. Also, if using mean age, correct SD to 11.9 (now it reads 11,9).

12. Figure legends:
Bean plots are a useful tool to display the distribution of observations and every single observation within a single plot for different groups. Unfortunately, this kind of display has not widely spread yet and therefore, most readers are familiar with box plots only. The authors should provide a very short description of the most important features in the (first) figure legend. This would be quite helpful for many readers.
A description regarding the function of bean plots has been added to figure 1.

13. Figures:
Consistent axis labelling should be provided throughout all bean plots. Currently, Figures 1 to 4a use another annotation than 4b. Better picture quality should be provided for online publication, the submitted ones are somewhat blurred.
We have changed the figures, provided the same axis labelling, the same annotations and have submitted the figures in higher quality.
14. Figure 4a:
The bean plot in Figure 4a is called Figure 4. This should be corrected. We have corrected this mistake.

15. Figure 4b:
The bean plot in Figure 4b is called Figure 5. This should be corrected. The file is named 4b. However, as the system can only upload one file at the time and the boxes are already prenamed it is not possible to upload this file otherwise.

All changes in the text and tables are indicated in red ink.