RESPONSES TO REVIEWER 1
We would like to thank the reviewer for taking the time to review our manuscript and appreciate the helpful comments to improve the manuscript. The critical comments and suggestions have been carefully considered in the revision of this manuscript. In the following responses, the comments of the reviewer have been reproduced in Italics and our answer and the corresponding modifications in the manuscript have been listed. The modifications made in the manuscript have been highlighted in yellow and are indicated by page/line numbers to find these modifications more easily in the manuscript. Some formal changes by edition of the text, corrections of typos etc. have not been listed since the actual content of the manuscript was not changed.

Responses to reviewer #1

Item 1: Page 15. Line 343 "In Figure 4..." this should be "In Figure 7...?"
Response: This mistake has been corrected (page 15, line 362).

Item 2: “I recommend that the authors re-examine their genes by using TCGA dataset analysis. This can be done using a plethora of potential websites including: KM-Plot, ALCAN or ProgGeneV2. At least for me, ELGN3 panned out in KM-PLot (RNA-Seq analysis), so may add additional weight to your already impressive data.”
Response: We thank the reviewer for this good suggestion. We have analyzed the RNAseq TCGA data. This data collection does not contain circRNAs. Using R for all three linear transcripts, we observed a characteristic association of all transcripts with overall survival, which confirms the findings in our patient cohort. The text has been completed as follows:

Page 11, line 280-283: The results for the linear transcripts were validated using the The Cancer Genome Atlas Kidney Renal Clear Cell Carcinoma (TCGA-KIRC) dataset, as this data collection does not contain circRNAs. Low expression of linEGLN3 and linNOX4 as well as high expression of linRHOBTB3 were associated with shorter overall survival of TCGA ccRCC specimens (Supplemental Figure S4A-C).

Page 20, line 548-550: TCGA-KIRC RNAseq data were downloaded and analyzed with R (version 3.6) using the "TCGA2stat" library and the “survival” library for Kaplan-Meier analysis.

Page 21, line 592-593 (according to the TCGA citation rules): The results here are in part based upon data generated by the TCGA Research Network: https://www.cancer.gov/tcga.

Item 3: “Could the authors discuss (or even test), how the observations for ELGN3 and circELGN3 in ccRCC, might be with respect to EGLN3-AS1 in these tissues?”
Response: We agree that this would be very interesting to test. Unfortunately, EGLN3-AS1 as well as circEGLN3 are both not analyzed by RNAseq in the TCGA data, so we were not able to correlate their expression with each other. Testing it in our patient set was beyond the scope of this revision. We would like to ask the reviewer for his understanding of this decision.