

**Expression of long non-coding RNA *MF12-AS1* is a strong predictor of recurrence in sporadic localized clear-cell renal cell carcinoma**

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**Supplementary Tables.**

**Supplementary Table 1.** Intratumor heterogeneity of *MF12-AS1* expression in the validation cohort.

<b>Sample name</b>	<b>Region of the primary tumor</b>	<b><i>MF12-AS1</i> expression</b>	<b>Normalized quantitation of <i>MF12-AS1</i> expression</b>
<b>HET11</b>	<b>1</b>	<b>Yes</b>	<b>0,51</b>
	<b>2</b>	<b>Yes</b>	<b>12,73</b>
	<b>3</b>	<b>Yes</b>	<b>10,56</b>
<b>HET1</b>	<b>1</b>	<b>Yes</b>	<b>3,58</b>
	<b>2</b>	<b>Yes</b>	<b>6,32</b>
<b>HET16</b>	<b>1</b>	<b>Yes</b>	<b>9,92</b>
	<b>2</b>	<b>Yes</b>	<b>6,15</b>
<b>HET2</b>	<b>1</b>	<b>Yes</b>	<b>8,22</b>
	<b>2</b>	<b>Yes</b>	<b>0,88</b>
	<b>3</b>	<b>Yes</b>	<b>80,45</b>
	<b>4</b>	<b>Yes</b>	<b>1,10</b>
<b>HET17</b>	<b>1</b>	<b>Yes</b>	<b>1,32</b>
	<b>2</b>	<b>Yes</b>	<b>7,94</b>
	<b>3</b>	<b>No</b>	<b>0,00</b>
<b>HET5T</b>	<b>1</b>	<b>Yes</b>	<b>0,13</b>
	<b>2</b>	<b>Yes</b>	<b>0,60</b>
	<b>3</b>	<b>Yes</b>	<b>0,93</b>

**Supplementary Table 2.** Hazard ratios for disease-free survival according to Leibovich (< 5 or ≥ 5) and *MF12-AS1* (expression or no expression) stratification. NS: not significant

<b>Group comparison</b>	<b>Hazard Ratio [95% confidence interval]</b>	<b>p-value</b>
L+M+ vs. L+M-	12,16 [3,76 - 39,34]	<0.0001
L+M+ vs. L-M+	10,82 [2,61 - 44,85]	<0.0001
L+M+ vs. L-M-	15,28 [2,61 - 89,57]	<0.0001
L+M- vs. L-M+	0,56 [0,15 - 2,15]	NS
L+M- vs. L-M-	0,99 [0,22 - 4,40]	NS
L-M+ vs. L-M-	1,70 [0,64 - 4,49]	NS

## Supplementary Figures

### Supplementary Figures Legends

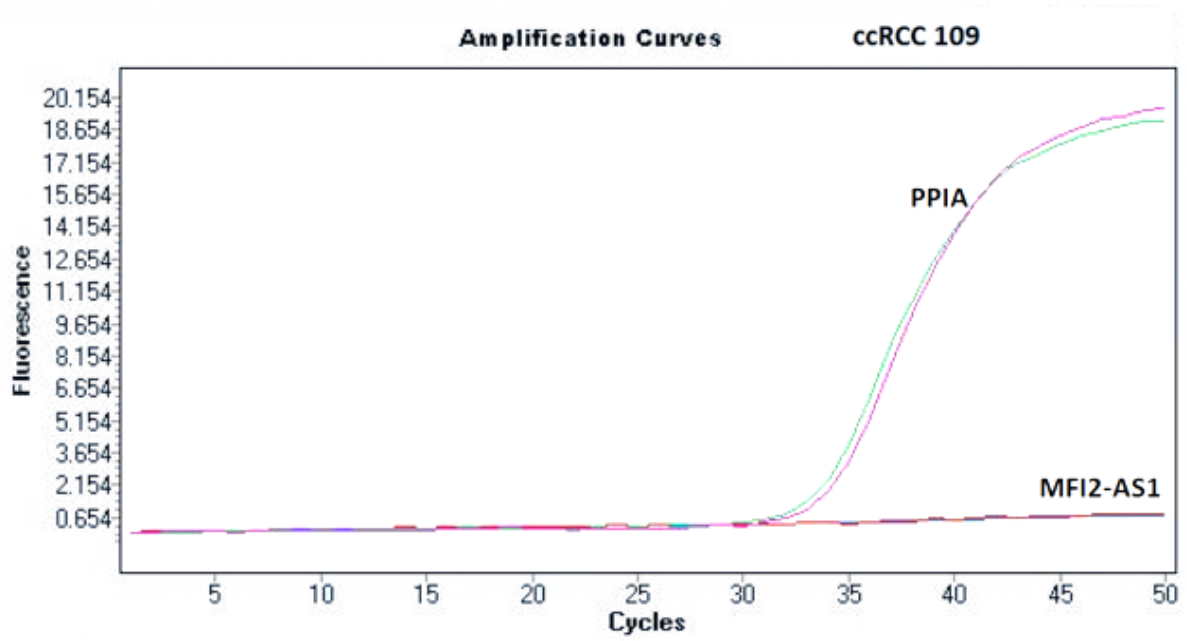
**Supplementary Figure 1.** Example of qPCR curves for *MF12-AS1* assessment in the validation cohort. A) No detectable *MF12-AS1* expression B) Detectable *MF12-AS1* expression

**Supplementary Figure 2.** ROC curves for recurrence prediction according to Leibovich classification and *MF12-AS1* status in the validation cohort. A) Combined Leibovich (<5/≥ 5) and *MF12-AS1* (expression/no expression) classification. B) Leibovich classification (<5/≥5) alone. C) *MF12-AS1* (expression vs. no expression). D) *MF12-AS1* (continuous).

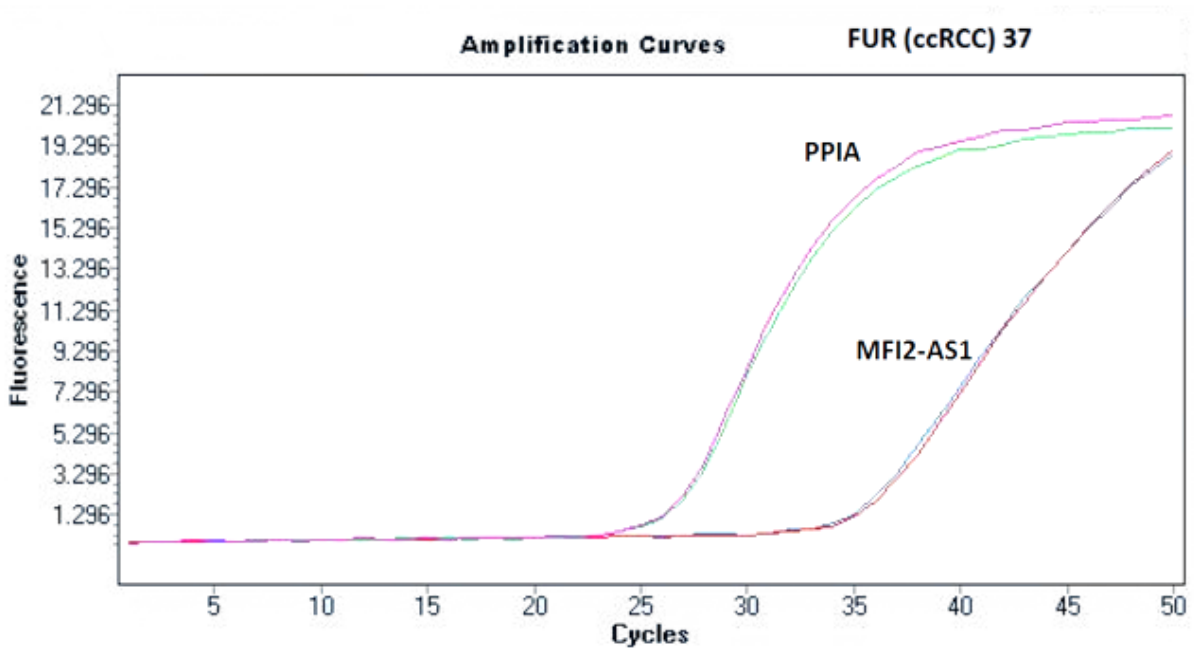
**Supplementary Figure 3.** Disease-free survival according to *MF12-AS1* and distinct Leibovich classification cutoffs in the validation cohort. A) *MF12-AS1* and Leibovich low, intermediate or high B) *MF12-AS1* and Leibovich low or intermediate + high

Supplementary Figure 1.

A.

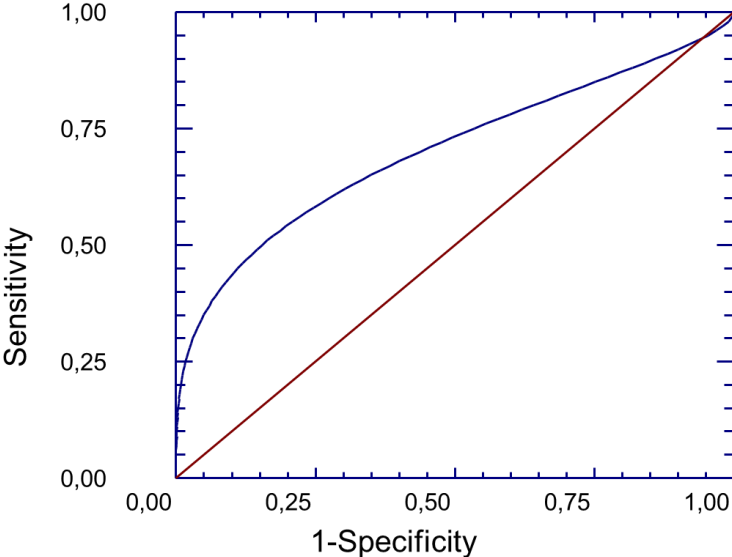


B.



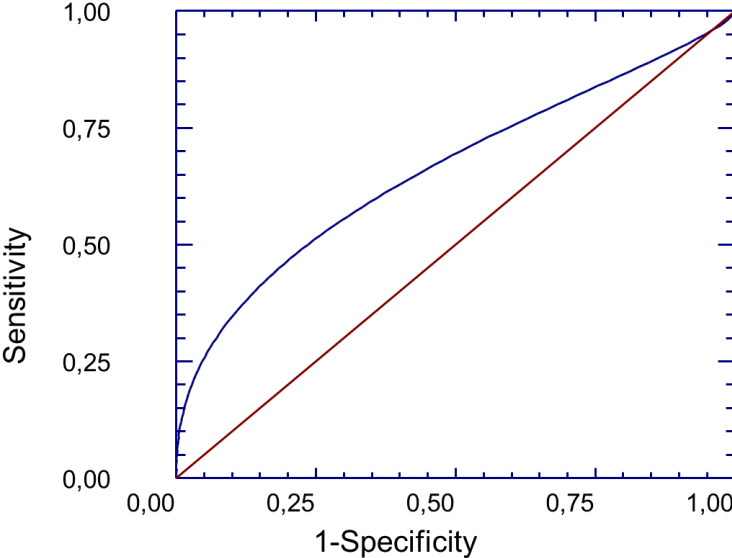
**Supplementary Figure 2.**

**A.**



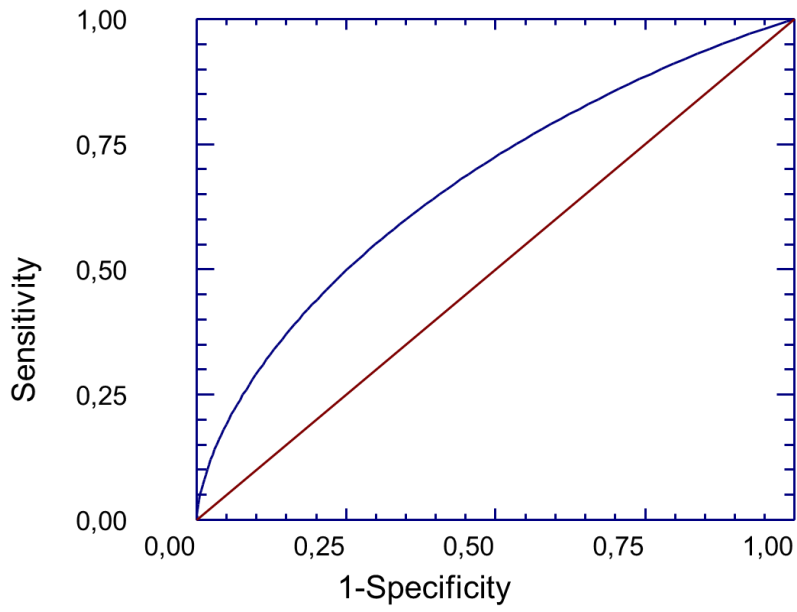
Binormal estimate of AUC 0,701960

**B.**



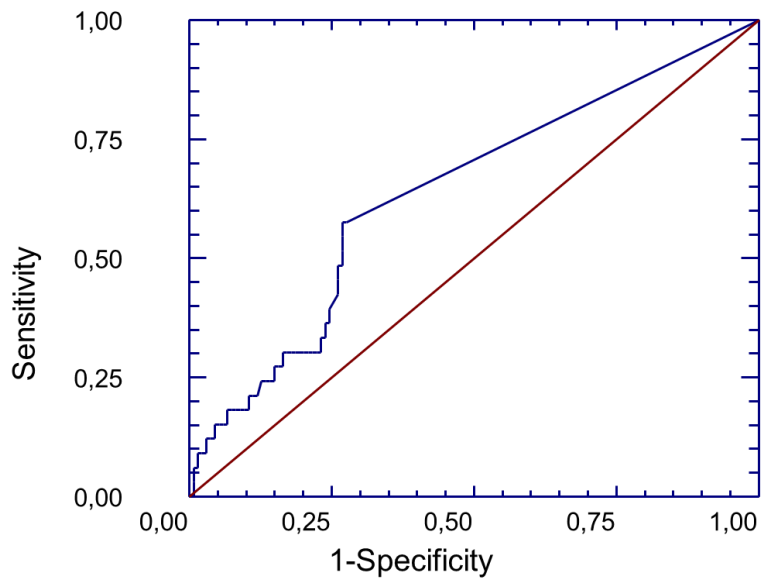
Binormal estimate of AUC 0,66100

**C.**



Binormal estimate of AUC 0,67186

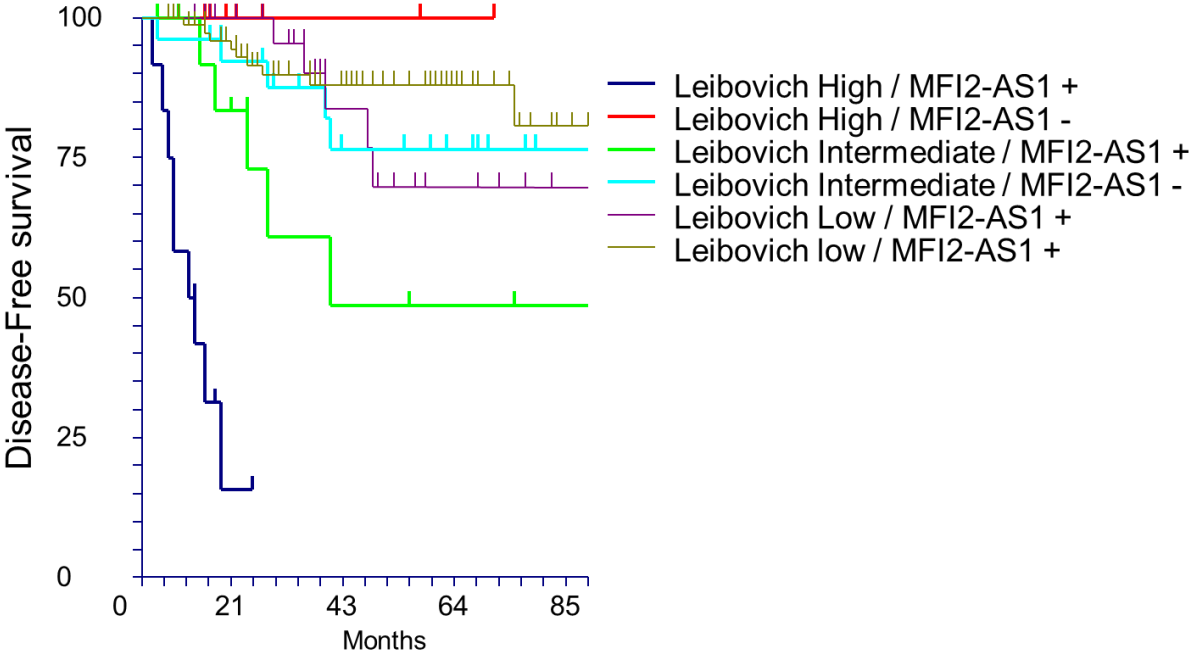
**D.**



Empirical estimate of AUC 0,63806

Supplementary Figure 3.

A.



B.

