

Downregulation of ENSG00000241684 is associated with poor prognosis in advanced clear cell renal cell carcinoma

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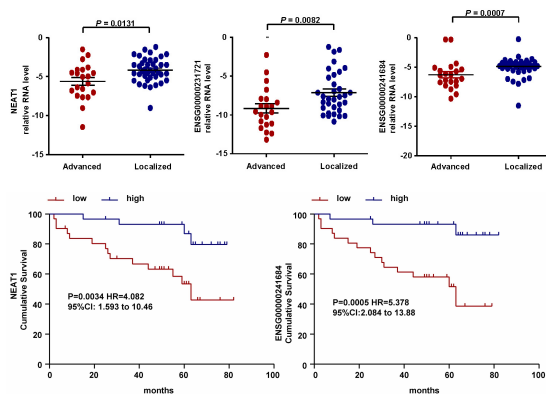
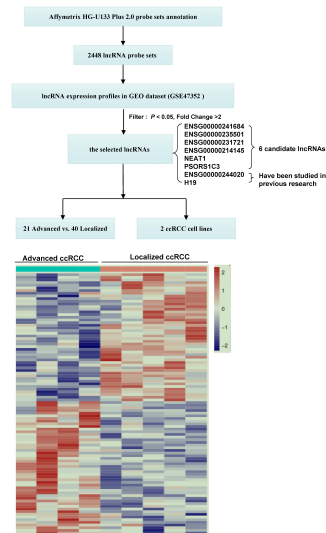
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I Objective

In order to identify potential novel biomarkers of advanced clear cell renal carcinoma (ccRCC), we re-evaluated published long non-coding RNA (lncRNA) expression profiling data.

II Method

The lncRNA expression profiles in ccRCC microarray dataset GSE47352 were analyzed and an independent cohort of 61 clinical samples including 21 advanced and 40 localized ccRCC patients was used to confirm the most statistically significant lncRNAs by real time PCR. Next, the relationships between the selected lncRNAs and ccRCC patients' clinicopathological features were investigated. The effects of lncRNAs on the invasion and proliferation of renal carcinoma cells were also investigated.



III Results

Three lncRNA were significantly downregulated in advanced ccRCC and 2 lncRNA were significantly associated with poor overall survival. lncRNA ENSG241684 had significant hazard ratios for predicting clinical outcome and was negatively correlated with pTNM stage. Overexpression of ENSG241684 significantly impaired cell proliferation and invasion ability in RCC cells.

Tab 1. Correlations between ENSG00000241684 expression and clinicopathological features

Clinicopathological feature	ENSG00000241684		P value
	Low (n=31)	High (n=30)	
Age (years)			
<55	15	14	0.893
≥55	16	16	
Gender			
Male	25	21	0.334
Female	6	9	
Location			
Left	14	12	0.694
Right	17	18	
TNM stage			
Stage I-II	15	25	0.004
Stage III-IV	16	5	
T classification			
T1-2	18	25	0.031
T3-4	13	5	
Lymph node metastasis			
N0	28	30	0.238
N1	3	0	
Distant metastasis			
M0	27	30	0.113
M1	4	0	
Fuhrman Grade			
Stage I-II	10	14	0.249
Stage III-IV	21	16	

IV Conclusion

lncRNAs are involved in renal carcinogenesis and decreased lncRNA ENSG00000241684 expression may be an independent adverse prognostic factor in advanced ccRCC patients.

