40 Identification and characterization of a novel long non-coding RNA RCA-lncRNA1 in clear cell renal cell carcinoma

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Introduction & Objectives: Non-coding RNAs, notably long non-coding RNAs (lncRNA) have recently been under intensive investigation for their role in carcinogenesis. In renal cell carcinoma (RCC), angiogenesis and cancer stem cells are important hallmarks, and the involvement of lncRNAs are not fully understood yet.

Materials & Methods: Using a 3-dimensional model for enrichment of RCC stem-like cells, we measured more than 40.000 lncRNA transcripts using a non-coding RNA microarray platform. We further picked up promising lncRNA candidates and performed in vitro assays with the focus on stem cell and angiogenesis functionality. Clinical cohorts were used to test the clinical relevance of these lncRNAs.

Results: Based on our whole lncRNA transcriptome analysis in the stem cell enriched cell line model, we identified RCC-stem cell associated long non-coding RNA 1 (RCA-lncRNA1), which is significantly up-regulated in RCC tissue compared to normal kidney tissue (for $p < 0.0001$).
High expression levels of RCA-lncRNA1 were significantly associated with poor disease-free survival. In kidney cancer cell lines, changes in RCA-lncRNA1 expression levels did not impact cellular proliferation, migration or tube formation in HUVEC cells. Decrease of RCA-lncRNA1 expression resulted in down-regulation of pro-angiogenic and stem cell associated genes.

Conclusions: In this study we identified RCA-lncRNA1 as a potentially novel pathogenic factor in RCC carcinogenesis.