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Creation of Gene Expression Signature for Renal Clear-Cell Carcinomas

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Renal cell carcinoma accounts for approximately 3% of adult cancers and has the highest lethality of urological malignancies. Clear-cell renal cancer (RCC) is the most frequent type of renal cancer, accounting for 80-85% of adult renal neoplasms. Renal-cell carcinoma is a highly vascularized tumour, and therapy targeted at the vascular endothelial growth factor (VEGF) and mammalian target of rapamycin (mTOR) pathways now represents the standard of care in metastatic RCC. Today, microarray technologies are some of the most efficient methods used in gene expression studies. The most frequently used of the microarray technologies are DNA microarrays enabling global analysis of the mRNA (messenger RNA) expression, while recently, microarray platforms modified to detect short non-coding RNAs (microRNAs) have been employed (microRNA microarrays).

At the moment, there is no reliable molecular-based classification of renal cell tumors. We investigated genome-wide expression profiles of RCCs in all human chromosomes using bioinformatics analysis of all accessible cDNA microarray experiments. R Project for Statistical Computing (www.r-project.org) was used for analysis. We compared 11 independent experiments and got 84 normal and 83 tumor samples for analysis differently expressed genes. We have obtained 100 differently expressed genes, which partly coincide in results of Microarray and previously organized in our laboratory SAGE analysis for our future discovering. According to their function and part in renal cancerogenesis we chose 20 genes for research their genetic and epigenetic changes in cRCC, as potential candidate for our future signature.