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EXPRESSION ANALYSIS OF OESTROGEN RECEPTOR TARGET GENES IN RENAL CELL CARCINOMA

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Background: The aim of this study was to explore differentially expressed genes (DEGs) and target genes of oestrogen receptors in renal cell carcinoma.

Methods: Data (GSE12090) were downloaded from the gene expression omnibus database. After data preprocessing using the affy package, DEGs were selected with the significance analysis of microarray algorithm within the siggenes package. DEGs were then subjected to function and pathway enrichment analysis by using DAVID (Database for Annotation Visualization and Integrated Discovery) software. Furthermore, the transcriptional regulatory networks between the DEGs and transcription factors were constructed. Finally, the oestrogen receptor target genes were subjected to Gene Ontology enrichment analysis.

Findings: A total of 215 DEGs were identified between the chromophobe renal cell carcinoma samples and the oncocytoma samples, including 126 up-regulated and 89 down-regulated genes. Function enrichment showed that 25% of the DEGs were significantly enriched into plasma membrane. Among those DEGs, 105 were regulated by oestrogen receptors. Further regulatory network analysis indicated that oestrogen receptors were mainly involved in the expression regulation of oncogenes and tumour suppressor genes, such as PRSS8 (protease serine 8), CLDN7 (claudin 7), and RAB25 (Ras-related protein Rab-25).

Interpretation: In this study, the identified oestrogen receptor target genes were closely related to tumour development, which was helpful for understanding the regulation mechanism of oestrogen receptors during tumour development and for promoting the discovery of predictive markers in renal cell carcinoma.