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Genes directly regulated by human hepatocellularcarcinoma HepG2

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Abstract

It has been well-known that over activation of NF-ĐºB has close relationship with hepatitis and hepatocellular carcinoma (HCC). However, the complete and exact underlying molecular pathways and mechanisms still remain not fully understood. By manipulating activity with its recognized activator and using ChIP-seq and RNA-seq techniques, this study identified 699 direct target genes (DTGs) in a widely used HCC cell line, HepG2, including 399 activated and 300 repressed genes. In these DTGs, 216 genes (126 activated and 90 repressed genes) are among the current HCC gene signature. In comparison with target genes identified in LPS-induced THP-1 and induced HeLa cells, only limited numbers (24~46) of genes were shared by the two cell lines, indicating the HCC specificity of identified genes Functional annotation revealed that DTGs in HepG2 cell are mainly related with many typical related biological processes including immune system process, response to stress, response to stimulus, defense response and cell death and signaling pathways of MAPK, TNF, TGF, chemokine, and toll- like receptor. Some DTGs are also involved in hepatitis C and B pathways. It was found that 82 DTGs code secretory proteins, which include CCL2 and DKK1 that have already been used as HCC markers. Finally, the DTGs were further confirmed by detecting the binding and expression of 14 genes with ChIP-PCR and RT- PCR. This study thus provides a useful DTG list for future studies of NF-ĐºB-related molecular mechanisms and theranostic biomarkers of HCC.

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Biography

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