

## Gene expression profiles in liver cancer and normal liver tissues

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### Abstract

**AIM:** To describe a liver cancer = specific gene expression profile and to identify genes that showed altered expression between liver cancer tissues and their adjacent nearly normal tissues.

**METHODS:** The cDNA probes which were labeled with  $\alpha$ -<sup>32</sup>P dATP were synthesized from total RNA of liver cancer and adjacent normal tissues and hybridized separately to two identical Atlas human cancer cDNA expression array membranes containing 588 known genes.

**RESULTS:** Autoradiographic results were analyzed by specific Atlas Image TM (version 1.0) software. Among the 588 genes analyzed, 18 genes were found up-regulated in cancer, including *TFDP2*, *Akt1*, *E2F-3* etc, and 25 genes were down-regulated in cancer, including *TDGF1*, *BAK*, *LAR*, etc. Expression levels of genes that associated with the regulation of cell proliferation, apoptosis, differentiation, cell-cell interaction, invasion regulators and cytokines altered mostly.

**CONCLUSION:** The result obtained from Atlas microarray provides a comprehensive liver cancer specific expression profile. The results can lead to the identification of liver cancer-specific biomarkers and may be helpful in early diagnosis and identification of target genes for designing rational therapeutic strategies.

**Key words:** Liver neoplasms/diagnosis; Gene expression; Differential hybridization; Microarray

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