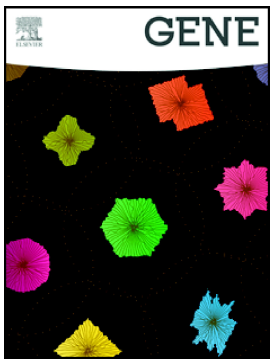


# The expression profiling and ontology analysis of non-coding RNAs in dexamethasone induced steatosis in hepatoma cell

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**Title**

# The expression profiling and ontology analysis of non-coding RNAs in dexamethasone induced steatosis in hepatoma cell

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## Abstract

Increasing amounts of evidence have indicated that non-coding RNAs (ncRNAs) have important regulatory potential in various biological processes. However, the contribution of ncRNAs, especially long non-coding RNAs (lncRNAs) to drug induced steatosis remain largely unknown. The aim of this study is to investigate miRNA, lncRNA and mRNA expression profiles and their potential roles in the process of drug induced steatosis. Microarray expression profiles of miRNAs, lncRNAs and mRNAs were determined in dexamethasone treated HepG2 cell as well as control cell. Differential expression, pathway and gene network analyses were developed to identify possible functional RNA molecules in dexamethasone induced steatosis. Compared with control HepG2 cell, 652 lncRNAs (528 up-regulated and 124 down-regulated), 655 mRNAs (527 upregulated and 128 down-regulated) and 114 miRNAs (55 miRNAs up-regulated and 59 down-regulated) were differentially expressed in dexamethasone treated HepG2 cell . Pathway analysis showed that the fatty acid biosynthesis, insulin resistance, PPAR signaling pathway, regulation of lipolysis in adipocytes, carbohydrate digestion and absorption, steroid hormone biosynthesis signaling pathways had a close relationship with dexamethasone induced steatosis. 10 highly dysregulated mRNAs and 20 miRNAs, which are closely related