

## Gene Expression Profiling of Human Hepatocytes Grown on Differing Substrate Stiffness

Fan Feng<sup>1</sup>, Tingting Xia<sup>1</sup>, Runze Zhao<sup>1</sup>, Mengyue Wang<sup>1</sup> and Li Yang<sup>1,\*</sup>

<sup>1</sup>Key Laboratory of Biorheological Science and Technology, Ministry of Education, Bioengineering College, Chongqing University, Chongqing 400044, China.

\*Corresponding Author: Li Yang. Email: yanglibme@cqu.edu.cn.

**Abstract:** Objective: To study the effects of different substrate stiffness on human hepatocytes using RNA sequencing (RNA-Seq) technology. The stiffness was corresponding to physiology and pathology stiffness of liver tissues.

Results: With the aid of RNA-Seq technology, our study characterizes the transcriptome of hepatocytes cultured on soft, moderate, stiff and plastic substrates. Compared to soft substrate, our RNA-Seq results revealed 1131 genes that were up-regulated and 2534 that were down-regulated on moderate substrate, 1370 genes that were up-regulated and 2677 down-regulated genes on stiff substrate. Functional enrichment analysis indicated that differentially expressed genes were associated with the regulation of actin cytoskeleton, focal adhesion, tight junction, adherens junction as well as antigen processing and presentation. RNA-Seq results were further verified by a quantitative real-time reverse transcriptase polymerase chain reaction.

Conclusion: Our study provides a comprehensive picture of the gene expression landscape in hepatocytes grown on different substrate stiffness, offering insights into the role of substrate stiffness in hepatic pathology.

**Keywords:** Differentially expressed gene; hepatocyte; RNA-sequencing; substrate stiffness

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