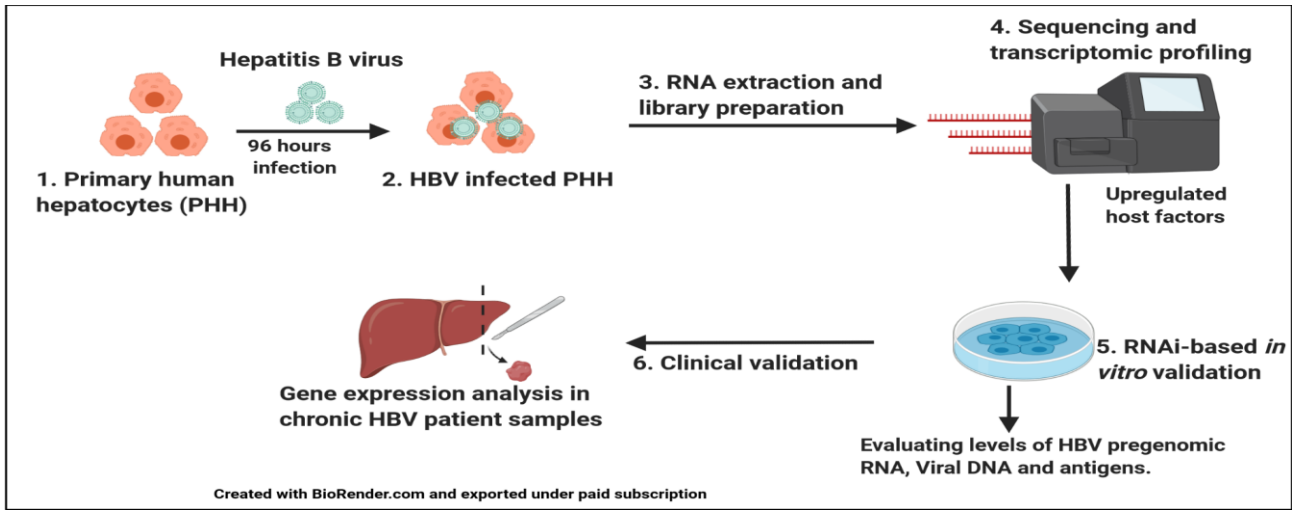
IDENTIFICATION OF NOVEL HOST FACTORS IN PATHOBIOLOGY OF HEPATITIS B VIRUS (HBV) INFECTION



Whole transcriptomic profiling of HBV infected primary human hepatocytes and RNAi-based functional validation studies identify novel HBV host factors.

Chronic Hepatitis B (CHB) virus infection remains a threat to global health, with over 800,000 deaths reported yearly worldwide. The pathogenesis of HBV infection and mechanisms by which the virus hijacks the host cellular machinery remains to be fully elucidated.

In this study, we carried out whole transcriptomic profiling of HBV-infected primary human hepatocytes and identified novel pathways and genes enriched during HBV replication. Some of the new pathways identified from the screen include epithelial-mesenchymal transition (EMT), Aurora Kinase pathway, and matrisome interactions. In addition, employing RNA interference technique *in vitro*, we identified specific HBV host factors, among them *MCM5, AKR1B1,* and *HSPA2*.

Finally, transcriptomic data analysis of microarray datasets of different patient cohorts collectively revealed that the expression of these host factors is significantly associated with CHB, liver disease, and HBV-related HCC. This enhanced expression in chronic HBV patients highlights their putative role in HBV replication and virus-induced liver disease. Altogether this study offers novel insights into the mechanisms of HBV infection and a new perspective in developing host-directed therapies.

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