Research Abstract 02:

Plasma-Based Gene Signature for Early Detection of Hepatocellular Carcinoma via Bioinformatics Profiling

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Introduction
Hepatocellular carcinoma (HCC) is the third leading cause of cancer-related deaths worldwide, with late diagnosis contributing to poor prognosis [1]. Current biomarker lacks sensitivity and specificity, highlighting the need for more accurate alternatives. Recent studies have reported that ribosomal proteins can act as oncogenic drivers in several cancers [2,3], suggesting their potential role as diagnostic or prognostic biomarkers. This study uses a bioinformatics-driven approach to identify plasma-specific gene signatures as minimally invasive biomarkers for the early detection of HCC.

Materials & Methods
Plasma transcriptomic data (GSE142987) were analysed to identify differentially expressed genes (DEGs). Enrichment analysis, protein–protein interaction networks, and hub gene identification were performed. Diagnostic and prognostic potentials were evaluated using ROC and survival analyses.

Results & Discussion
A total of 661 DEGs were detected, with ten hub genes showing strong diagnostic accuracy (AUC > 0.9). Among these, RPS7 and RPS27A were significantly linked to poor survival outcomes, consistent with previous findings that ribosomal proteins such as eEF1A1 and RPL9 contribute to cancer progression and poor prognosis [2,3]. Functional analysis implicated ribosomal and viral-related pathways in HCC progression.

Conclusion
A ten-gene plasma signature was identified, showing high diagnostic accuracy (AUC > 0.9) in distinguishing early HCC from healthy plasma. Prognostic relevance was observed for RPS7 and RPS27A. This signature highlights the potential for a non-invasive, plasma-based diagnostic tool for early HCC detection, but further validation in larger independent cohorts is needed.

Keywords: *Hepatocellular carcinoma; plasma biomarker; gene expression; early detection; bioinformatics*

References:

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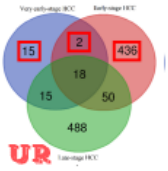
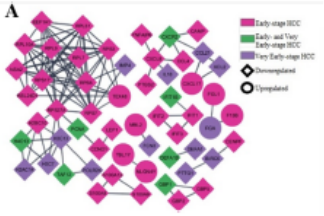
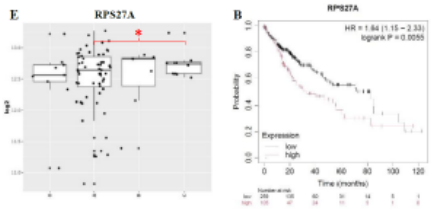
3. Li A, Chen Y, Liu Y, Zhang Y, Wang J, Zhou H, et al. RPL9 acts as an oncogene by shuttling miRNAs through exosomes in human hepatocellular carcinoma cells. Int J Oncol. 2024;64(6):1–16.



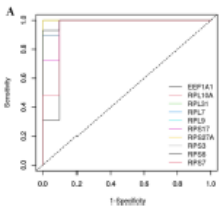
- 661 DEGs identified (453 up, 208 down)
- Pathways: GPCR signaling, Ribosome, Coronavirus disease, transcriptional misregulation in cancer



10 Hub Genes: RPS3, RPS6, RPS7, RPS17, RPS27A, RPL7, RPL9, RPL10A, RPL31, EEF1A1



High expression of RPS27A is significantly associated with poor overall survival in HCC patients ($p < 0.05$), suggesting their potential as biomarkers for early vs late disease.



All ten hub genes demonstrated excellent diagnostic accuracy (AUC > 0.9) in distinguishing early HCC plasma from healthy controls.