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Identification of transcriptomic and epigenomic markers associated with FDG PET/CT in hepatocellular carcinoma

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Background: Hepatocellular carcinoma (HCC) ranks among the top five malignancies with the highest incidence worldwide and is the third leading cause of cancer-related mortality. A hallmark of cancerous tissues is their elevated glucose uptake, often linked to enhanced glycolytic activity. DNA methylation, a critical mechanism of epigenetic regulation, plays a significant role in cancer development and progression. In this study, we conducted an integrated analysis of transcriptomic and epigenetic modifications in HCC patients to identify biomarkers associated with glycolysis.

Results: Based on the standardized uptake value (SUV) results of tomography/computed tomography (FDG PET/CT), sixty patients were stratified into two groups: one with higher SUV values (n=30) and the other with lower SUV values (n=30). FDG PET/CT scans were performed prior to any treatment. RNA sequencing was conducted using the TrueSeq Kit (Illumina), while DNA methylation data were obtained using the Infinium Methylation EPIC platform (Illumina). From the transcriptomic analysis, three key biological pathways (glycolysis, gluconeogenesis, and glycerolipid metabolism) were identified as significant. In the methylation data, two major pathways (glycosaminoglycan biosynthesis and Mucin type O-glycan biosynthesis) were found to be significant. Several other pathways identified were consistent with those commonly found across all solid tumors. Furthermore, we identified a coherent relationship between methylation events and gene expression profiles, linked to tumor-associated signatures, using Cytoscape.

Conclusion: The transcriptomic and epigenetic evidence from this study highlights the critical role of personalized precision diagnostics in understanding tumor progression and prognosis.