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Abstract

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Early detection of cancer is crucial to better the chances of survival. For hepatocellular carcinoma people that suffer from fatty liver or cirrhosis increase their chances of developing HCC in the future. Studies have been able to improve early detection of HCC throughout the years, but one thing has had little progress. Differentiating tumor associated antigens (TAA's) specific to cancerous cells from those expressed in normal tissues remains a fundamental challenge. This is because TAA's are also present, at lower levels, in healthy or regenerating cells, and this creates an overlap that complicates their use for early detection in HCC. This study aims to identify HCC-specific TAA's by focusing on two crucial antigens that play a role in HCC, GNA11 and PAX5. Using the databases The Cancer Genome Atlas (TCGA), Human Protein Atlas (HPA), and Hepatocellular Carcinoma Database (HCCDB) we developed an experimental pipeline that isolates GNA11 and PAX5 to differentiate between their cancerous and healthy counterparts. Analyzing data gathered through serological proteome analysis (SERPA) we will be able to identify the impact of both antigens GNA11 and PAX5 on HCC.