

Singapore develops new tool to accurately predict liver cancer recurrence

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Liver cancer often returns after surgery, but doctors currently lack reliable tools to identify which patients face the greatest risk



A Singapore team of clinician-scientists and researchers has developed a new tool that accurately predicts which liver cancer patients are likely to experience a recurrence after surgery. The machine-learning tool combines genetic and clinical information and was found to outperform the commonly used TNM staging system, which is based on tumour burden, across independent patient groups.

Researchers from the National Cancer Centre Singapore (NCCS), Duke-NUS Medical School (Duke-NUS) and the A*STAR Genome Institute of Singapore (A*STAR GIS) also uncovered two biologically distinct ways in which hepatocellular carcinoma (HCC), the most common form of primary liver cancer, can recur. The findings could help doctors tailor follow-up care, identify patients most likely to benefit from additional treatment after surgery and design more targeted clinical trials.

The study was conducted through the National Medical Research Council-funded **PLANet** (Precision Medicine in Liver Cancer across an Asia-Pacific Network) research programme and published in *Gut* in July 2026.

Liver cancer is the third leading cause of cancer-related death globally and disproportionately affects Asian populations. In Singapore, it is the third most common cause of cancer death in men and the fifth in women, with approximately 72% of global cases occurring in Asia, largely driven by the high prevalence of hepatitis B virus (HBV) infection in the region.

Yet, clinicians currently lack reliable biomarkers to identify which patients are most at risk of recurrence. This makes it difficult to tailor follow-up care, as well as select patients for additional treatment and design clinical trials efficiently.

The research team is currently using spatial sequencing technologies to identify tumour microenvironment biomarkers that could serve as drug targets to treat HCC. They are also working to further improve the accuracy of the multi-omics tool by incorporating additional data sources such as CT imaging and machine learning. This could further enhance recurrence prediction and improve targeted surveillance for high-risk patients.