# FPN #700P: Real-World Performance of Dual Tissue and Liquid Biopsy Profiling for Managing Gastrointestinal and Hepatobiliary Cancers in Southeast Asia.

Van-Anh Nguyen Hoang[1], Le-Tho T Vo [1], Tu Nguyen[1], Lan N Tu[1,2]

[1]Medical Genetics Institute, Ho Chi Minh city, Vietnam; [2]Gene Solutions, Ho Chi Minh city, Vietnam Email: lantu@genesolutions.vn

## Background

Comparing **tumor mutation landscapes** and **ctDNA detection** across 9 types of **gastrointestinal (GI)** and **hepatobiliary (HPB)** cancers.

## Study Design and Workflow

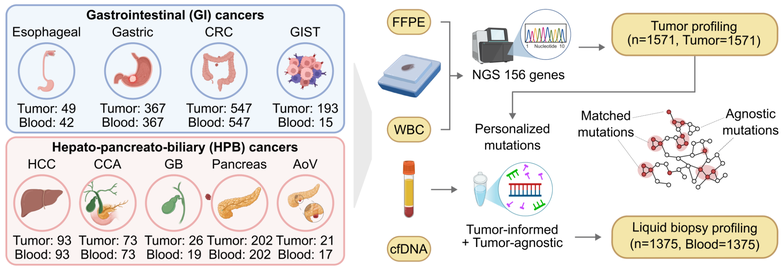



**Figure 1. Study design and ctDNA analysis workflow.** Diagram showing the number of cancer patients that were included in the study. gDNA of paired FFPE and WBC samples were sequenced to identify tumor-specific mutations in 155 cancer-associated genes. Top personalized mutations with the highest scores were used to detect ctDNA in plasma samples.

## Mutational Landscape

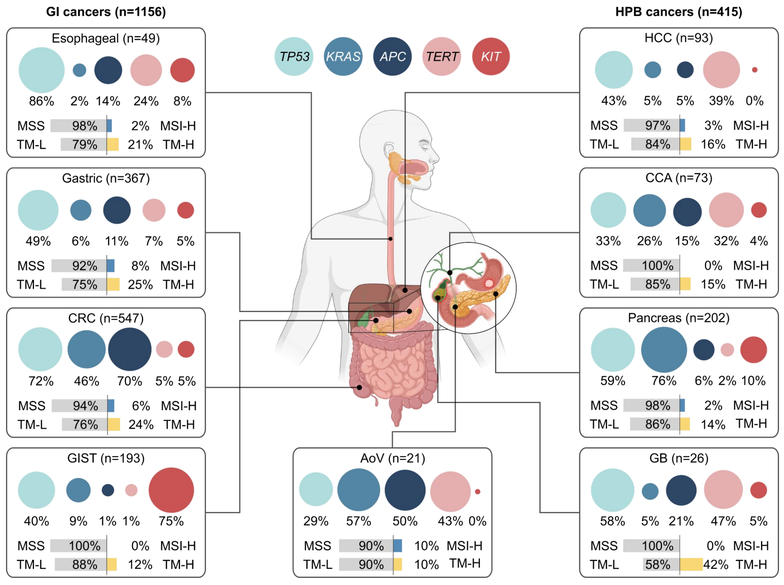



**Figure 2. Tumor mutation landscapes in GI and HPB cancers.** The diagrams show the top 5 significantly mutated genes across both cancer types: *TP53, APC, KRAS, TERT* promoter, and *KIT*. *TP53* and *APC* mutations are predominant in GI cancers, while *KRAS* and *TERT* promoter mutations are more prevalent in HPB cancers.

## ctDNA Pre-treatment Detection Rate

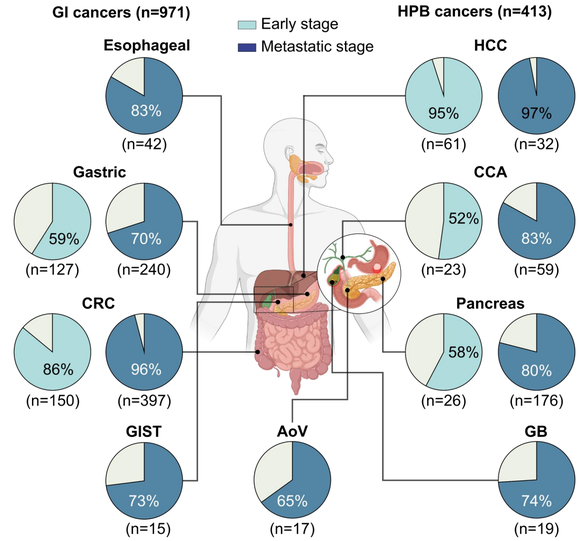



**Figure 3. Detection rate of ctDNA in early stage and metastatic cancer.** ctDNA shedding rates varied significantly by cancer types. At early stage, pre-treatment ctDNA detection rates were the highest in HCC and CRC. At metastatic stage, for GI, detection rate was higher in esophageal and CRC but lower in gastric and GIST. For most HPB cancers, the rate was high, except in gallbladder and AoV.

## Multivariable Analysis of Gene Mutations Associated with ctDNA Detection

| Gene | Positive | Negative | OR (95%CI) | p-value |
|---|---|---|---|---|
| KRAS | 357 | 1 | 286.1 (15.5-791.6) | **<0.001** |
| TP53 | 616 | 2 | 165.3 (36.3-592.7) | **<0.001** |
| APC | 289 | 1 | 89.7 (11.4-587.0) | **<0.001** |
| PIK3CA | 102 | 2 | 11.7 (2.9-47.7) | **0.001** |
| SMAD4 | 90 | 0 | NA | 0.969 |
| BRAF | 37 | 0 | NA | 0.970 |

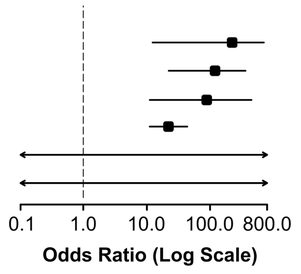



**Figure 4. Multivariable Analysis of gene associated with ctDNA detection.** The overall ctDNA shedding rates significantly increased (p<0.001) when tumors had either *KRAS* (OR=286.1), *TP53* (OR=165.3) or *APC* (OR=89.7) mutations

**Ethical approval by** the institutional ethics review board of the MGI for the analysis of de-identified genomic and clinical data (approval #: 03/2023/CT-VDTYH; 03/2024/CT-VDTYH).
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## ctDNA Predicted Early Recurrence

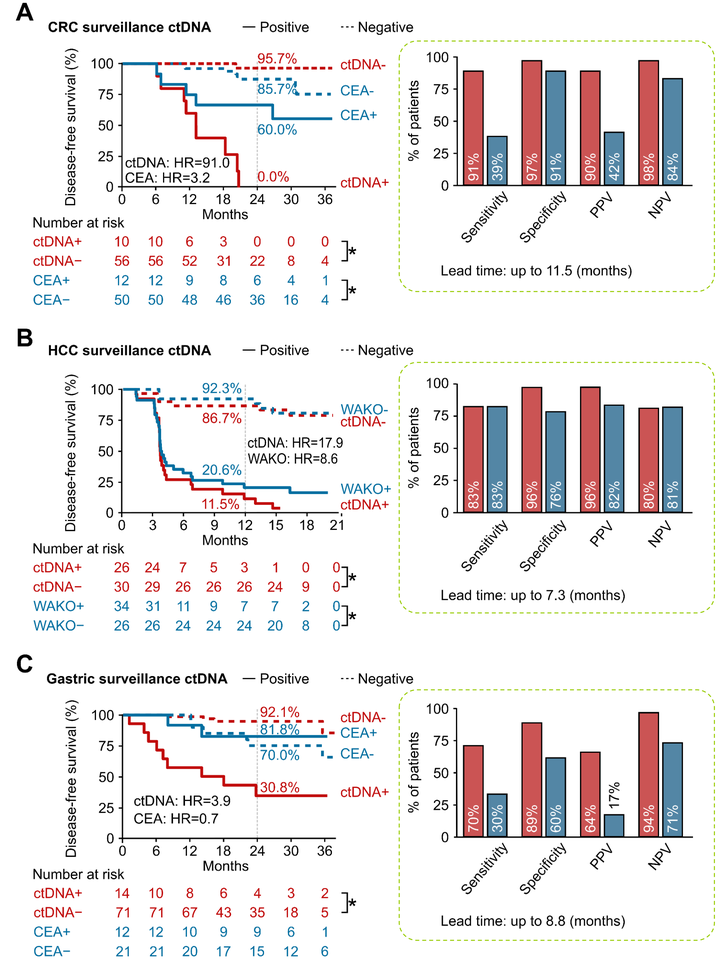



**Figure 5. Surveillance ctDNA outperformed SOC biomarkers to predict recurrence.** ctDNA positivity was an independent prognostic factor (p<0.001) that increased recurrence risk in CRC (HR=91.0, 11.3-736.9), HCC (HR=17.9, 5.9-54.1), and gastric cancer (HR=3.9, 2.0-7.7).

## Conclusion

- **Tumor mutation profiles were compared** across GI and HPB cancers, showing dominant *TP53* and APC in GI cancers, *KRAS* and *TERT* in HPB cancers.
- **Longitudinal ctDNA monitoring** outperformed SOC biomarkers in predicting cancer recurrence.