



Two Stable Gut Microbiome Guilds Predict Liver Tumor Class and Treatment Responses

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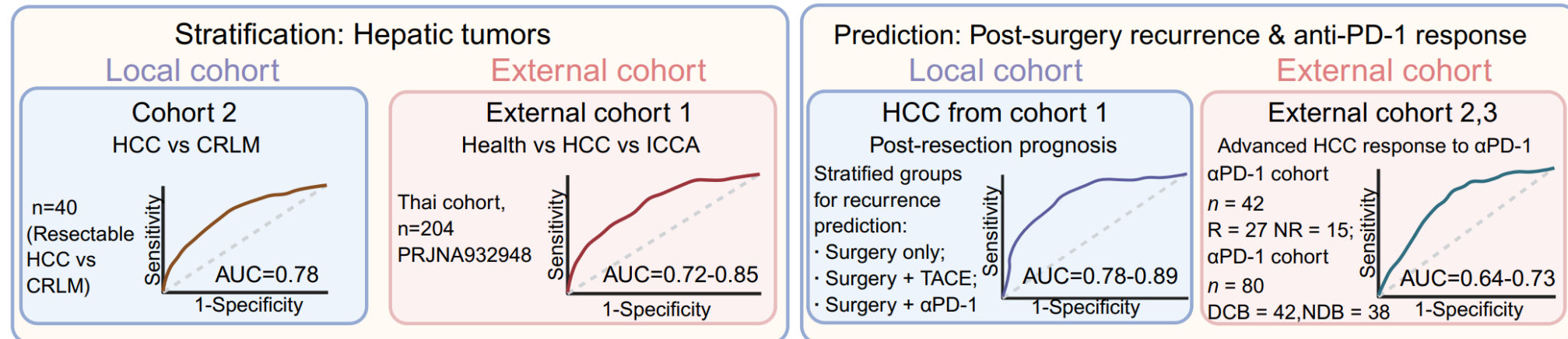
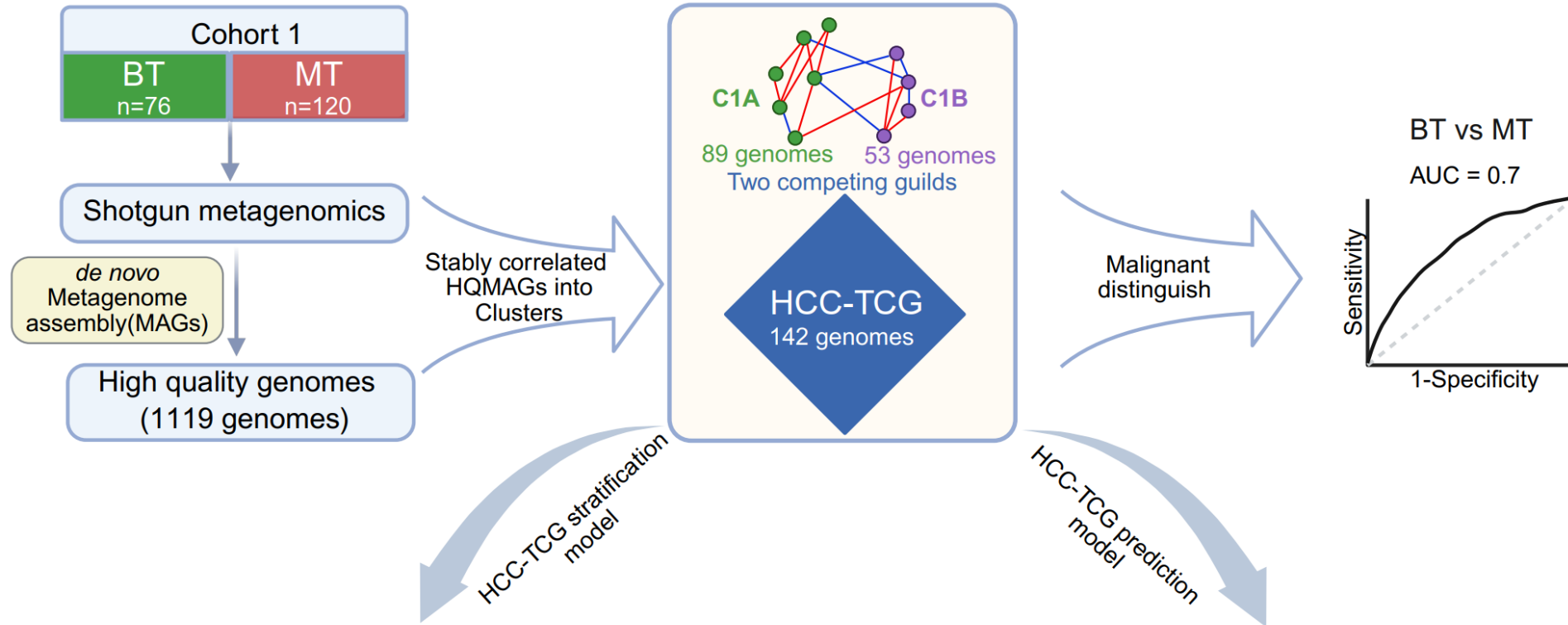
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Abstract Overview



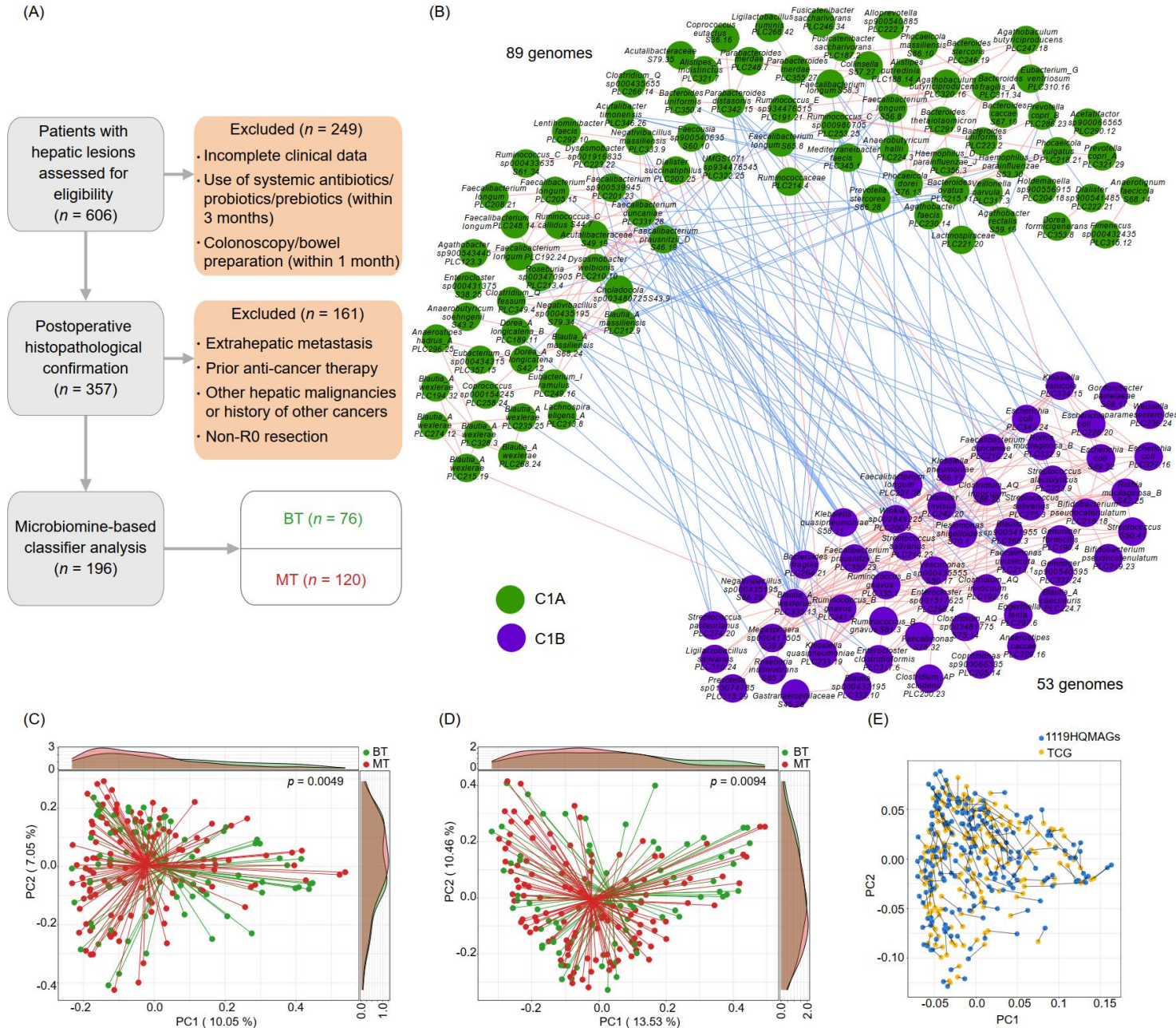


Highlights

- ❑ A genome-resolved, database-independent framework defines the core microbiome as two competing guilds with stable ecological connectivity in hepatocellular carcinoma (HCC) patients..
- ❑ The HCC-two competing guilds (HCC-TCG) signature enables robust liver tumor stratification and predicts recurrence and immunotherapy response across independent cohorts.
- ❑ Guild-based modeling overcomes taxonomic ambiguity, delivering a reproducible and clinically actionable signature for precision oncology in HCC.

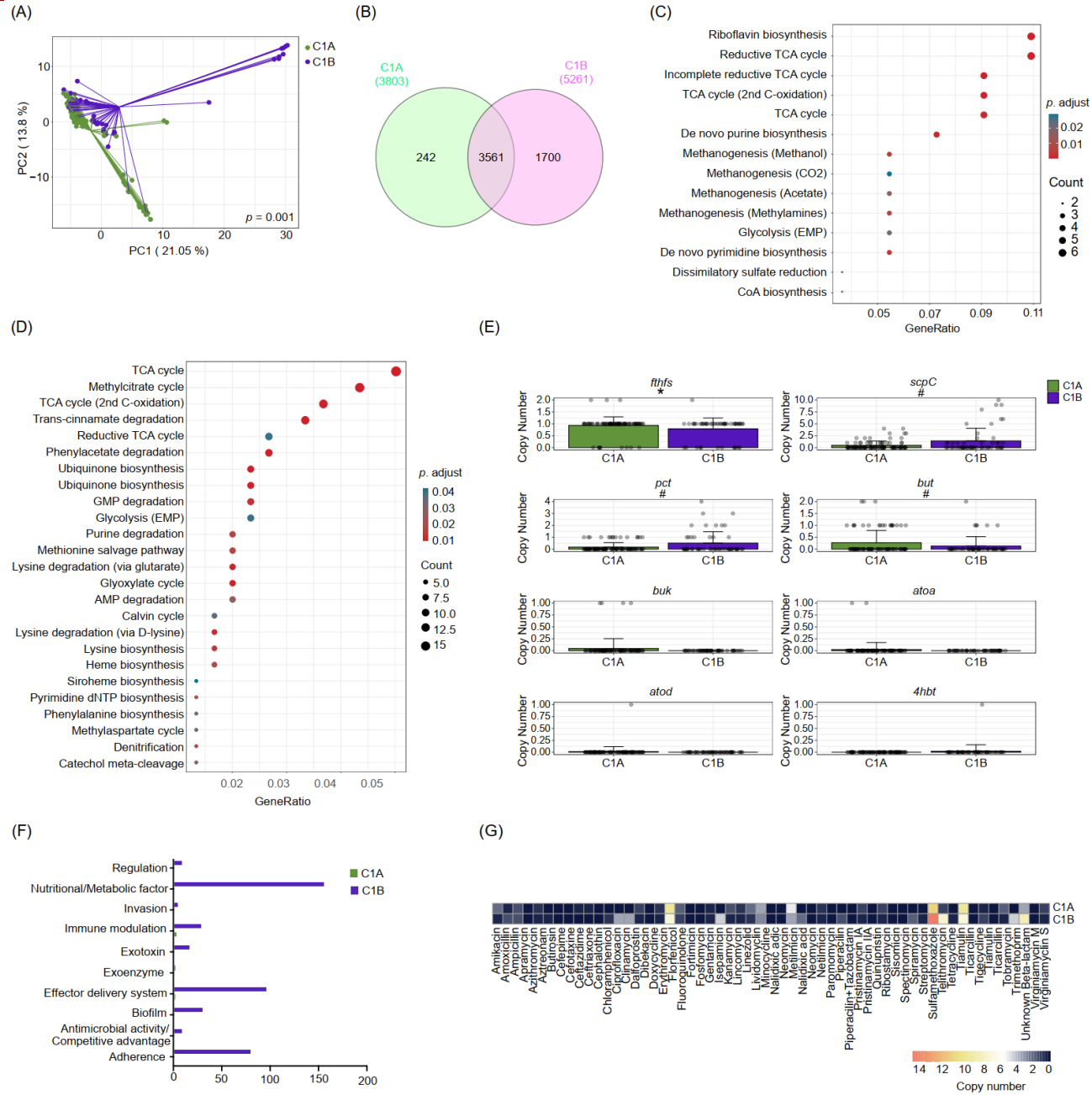
Result 1: Two stable gut microbiome guilds

Figure 1. Overall variations in the gut microbial composition and the two competing guilds (TCG) associated with hepatocarcinogenesis.



Result 2: Functional genetic profiles

Figure 2. Distinct functional genetic profiles between C1A and C1B..



Result 3: Predicting tumor class

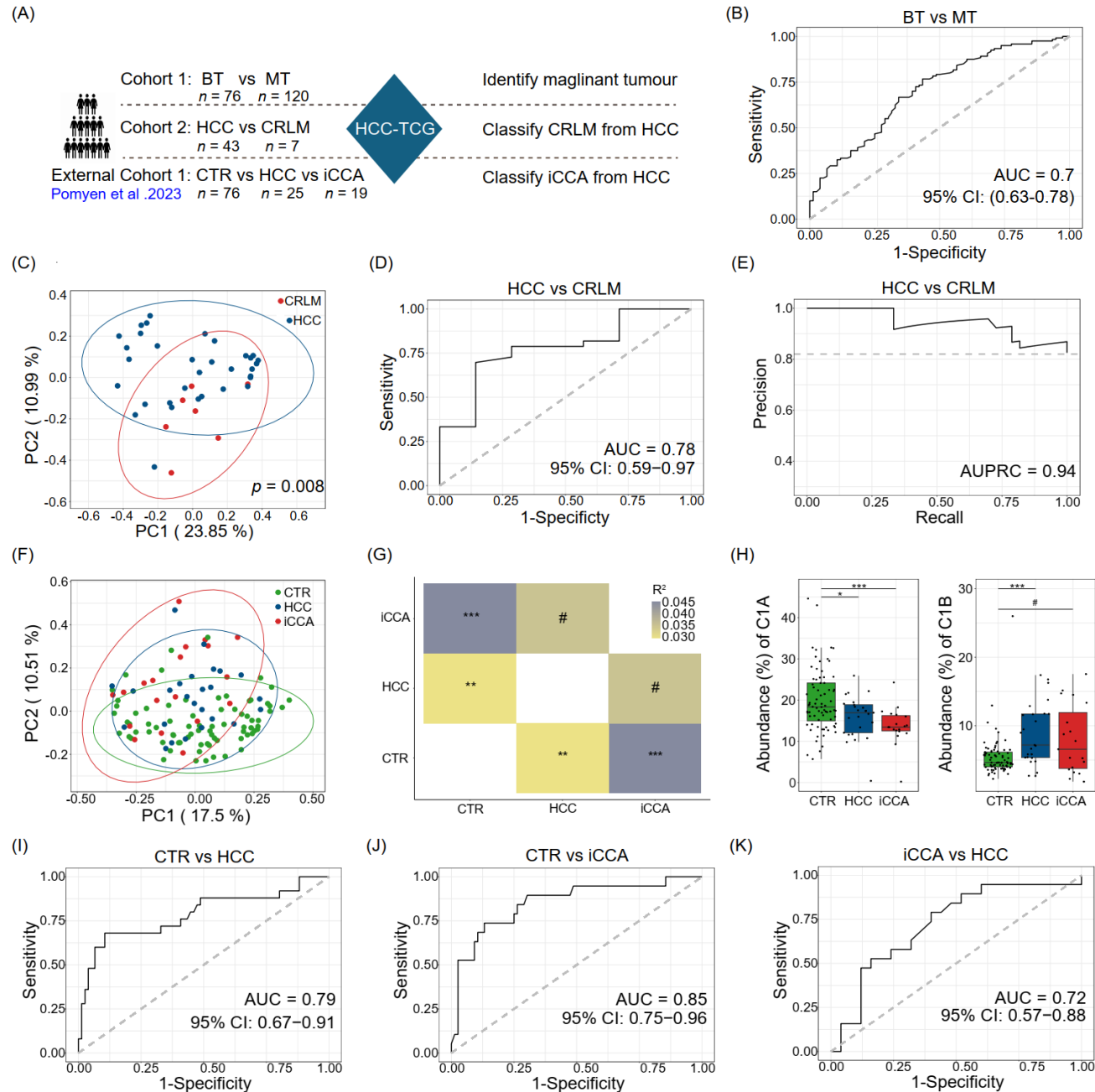


Figure 3. HCC-TCG as a signature to classify patients with different hepatic tumors.



Result 4: Recurrence and treatment response prediction

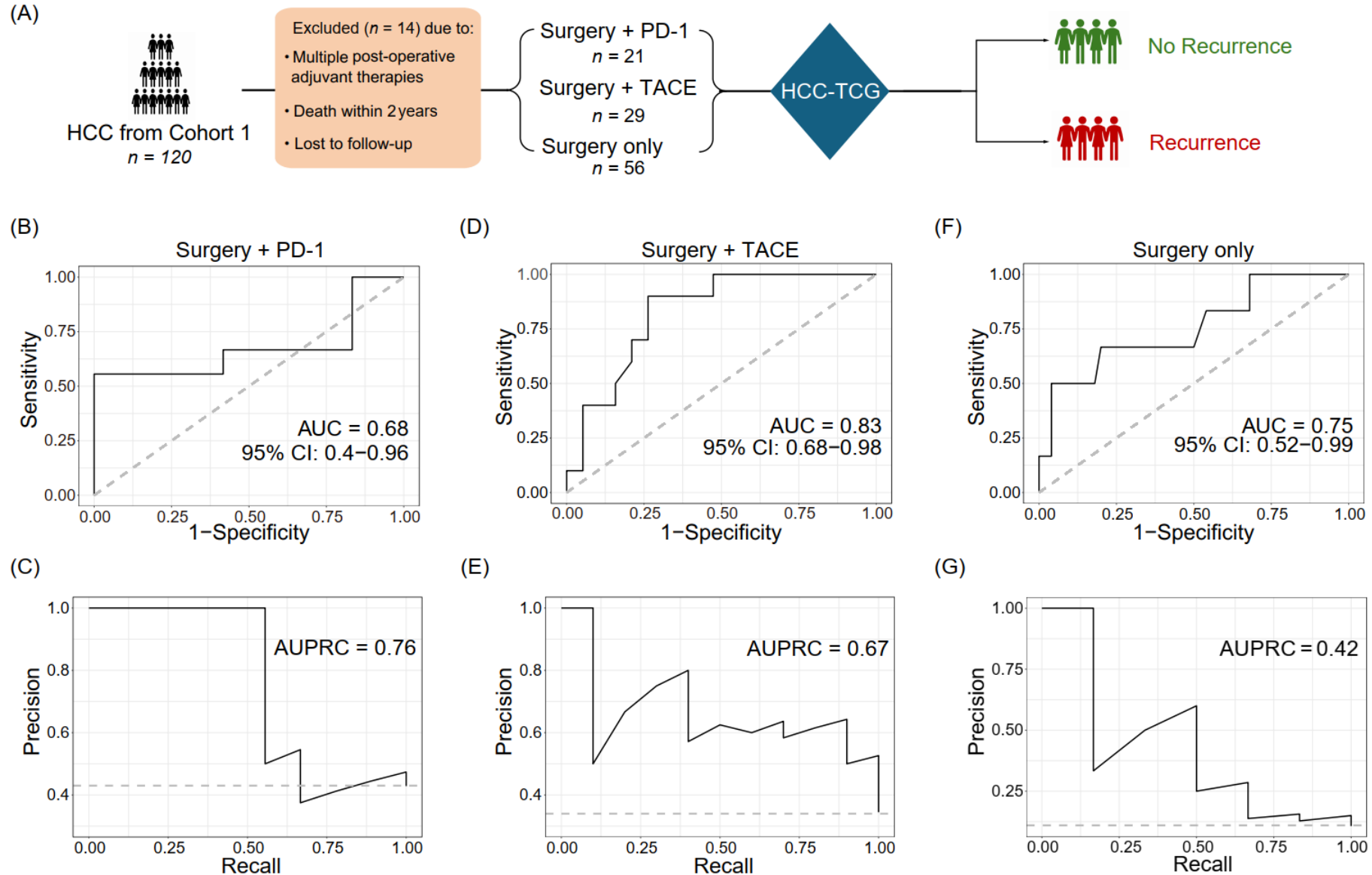


Figure 4. HCC-TCG as a biomarker to predict recurrence risk in resectable HCC patients.



Result 5: Clinical parameters and HCC-TCG integration

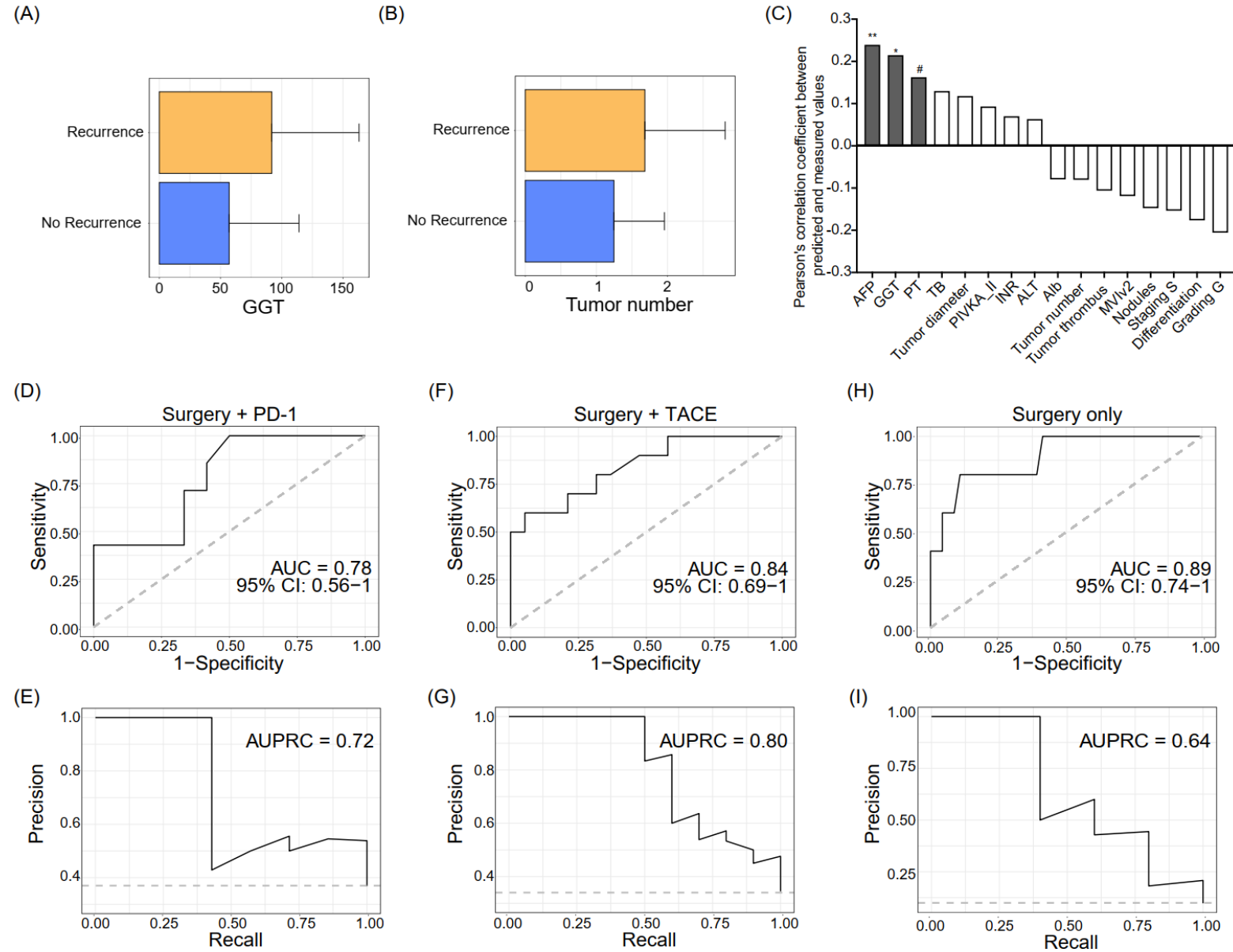


Figure 5. HCC associated clinical parameters enhance treatment prediction.

Result 6: External validation

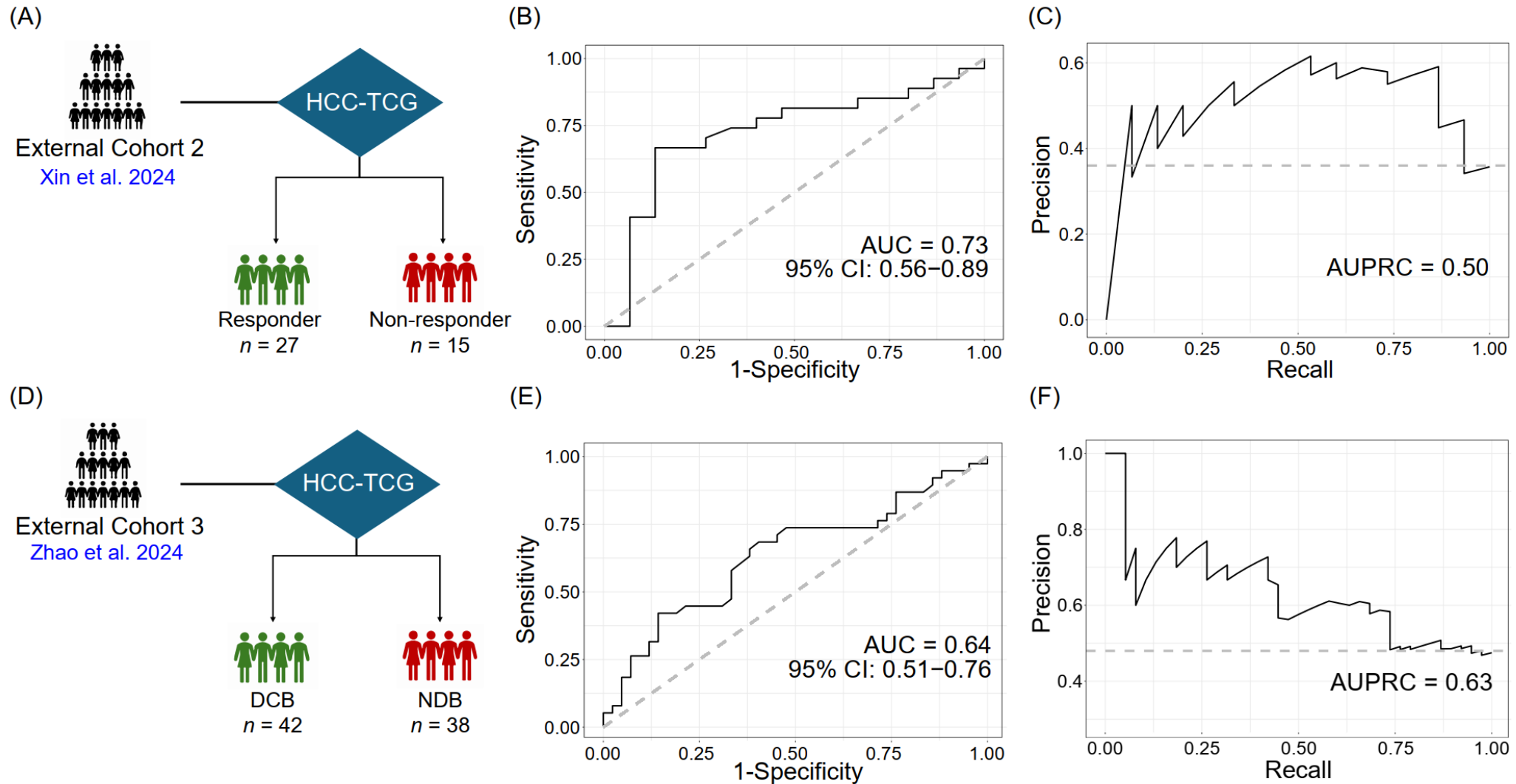


Figure 6. External validation of the HCC-TCG-based response prediction model in two independent anti-PD-1-treated HCC cohorts.

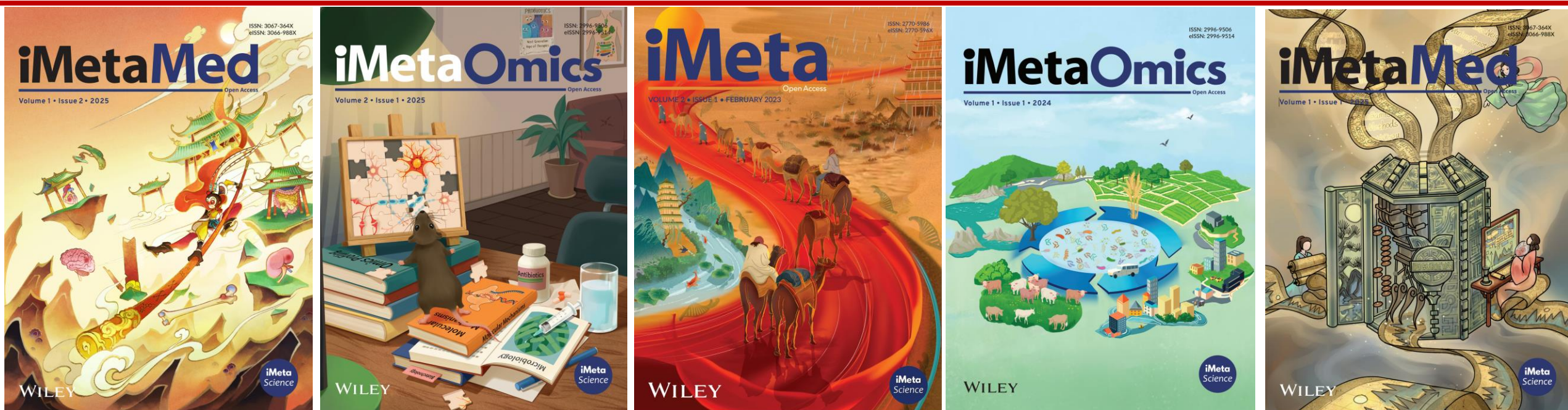


Summary

- ❑ In this study, the HCC-TCG framework shows that a stable, antagonistic Guild structure of the gut microbiome underlies malignant transformation, recurrence risk, and immunotherapy response along the gut–liver axis.
- ❑ This study extends the TCG paradigm into hepatic oncology and provides a structurally grounded, functionally interpretable, and clinically actionable ecological signature for hepatocellular carcinoma.
- ❑ By revealing a stable microbial architecture that spans benign and malignant states, primary and metastatic tumors, and surgical and immunotherapy settings, this work lays the foundation for a new class of Guild-based diagnostics and interventions in liver cancer.

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