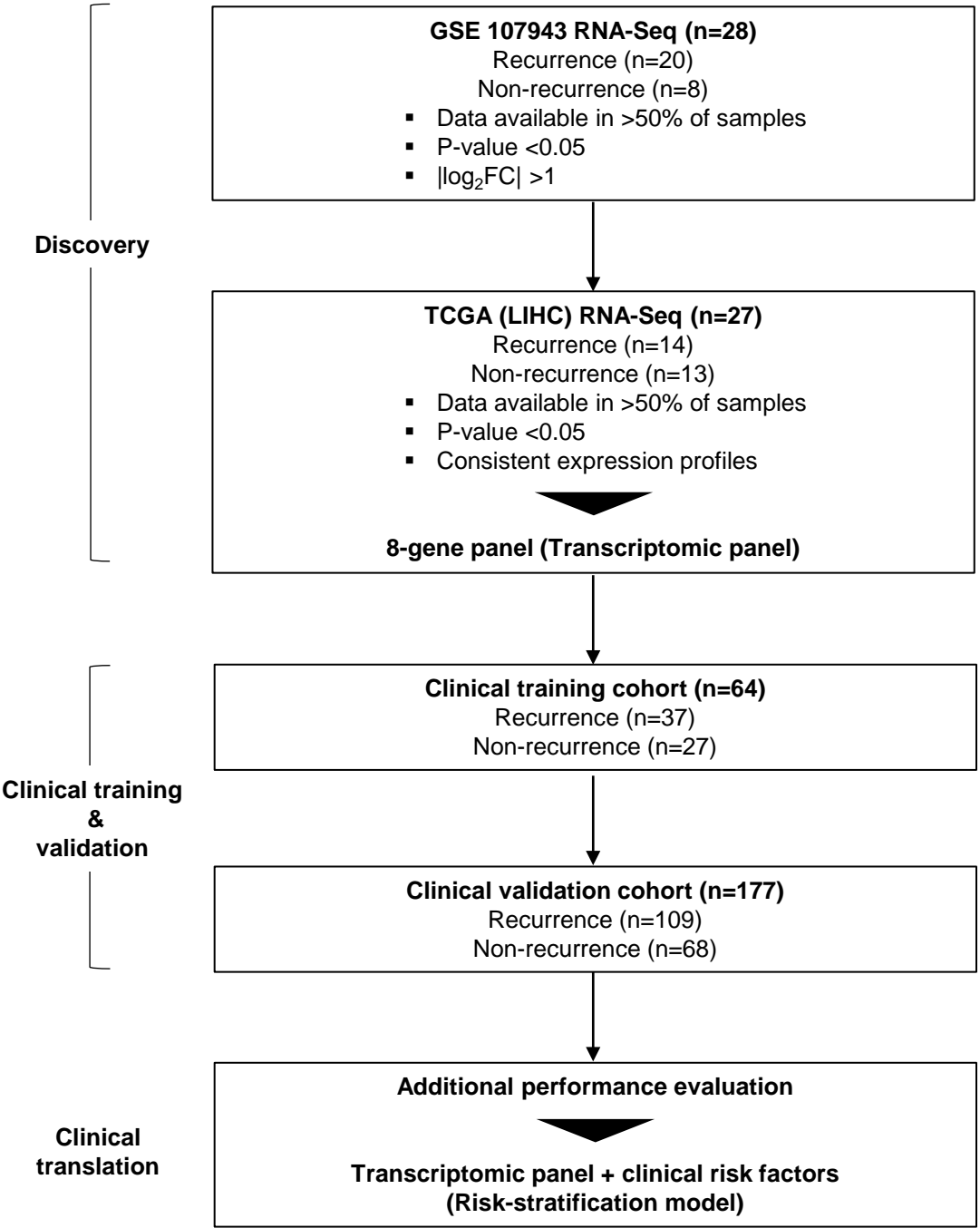


**Supplemental figure S1.** Overview of the study.

**Supplemental figure S2.** Genome-wide discovery and validation of a novel gene panel to detect recurrence in patients with ICC. **A–B)** A ROC curve demonstrates the diagnostic performance of the 8-gene panel for distinguish the patients with recurrence in **(A)** GSE107943 (AUC = 0.92), and **(B)** TCGA (AUC = 0.91). **C–D)** A comparison of RFS between high and low-risk group estimated by the panel in **(C)** GSE107943, and **(D)** TCGA.

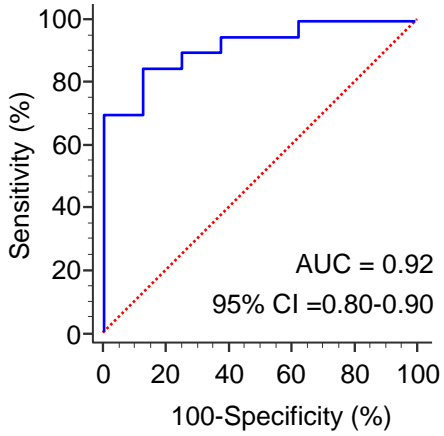
**Supplemental Figure S3.** ROC curves for the detection of recurrence in training and validation cohorts without transcriptomic panel. **A)** ROC curve for combined clinical risk factors (CA19-9, CE A, vascular invasion, and tumor size) for recurrence without the transcriptomic panel in the training cohort (AUC = 0.71). **B)** ROC curve for the clinical risk factors for recurrence without the panel in the validation cohort (AUC = 0.69).

# Supplementary Figure 1

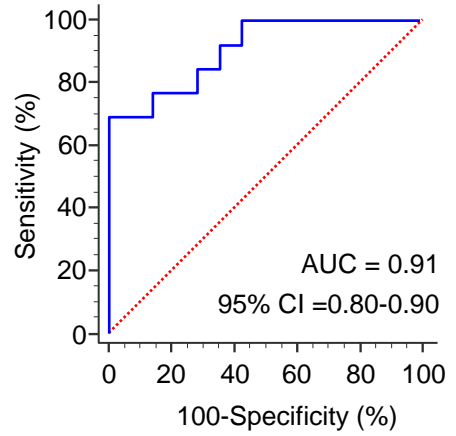


# Supplementary Figure 2

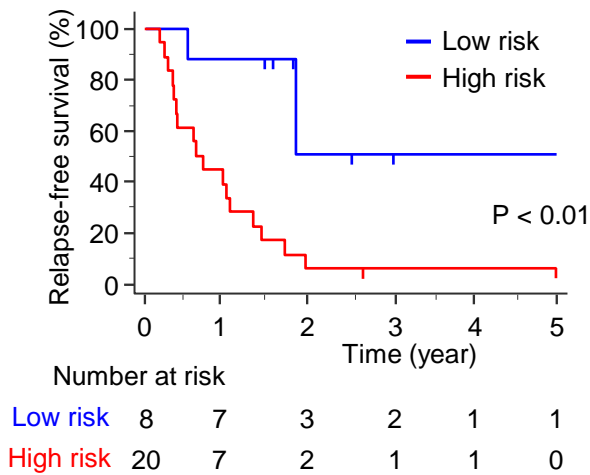
**A**



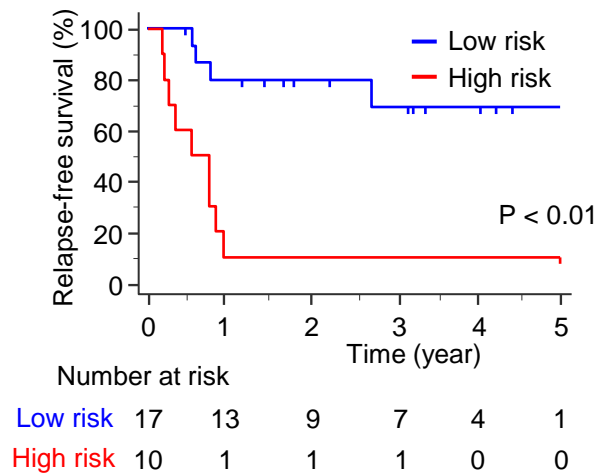
**B**



**C**

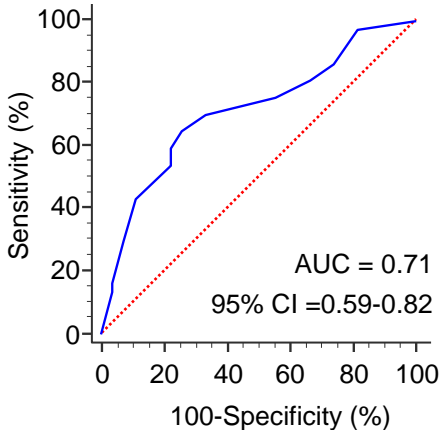


**D**

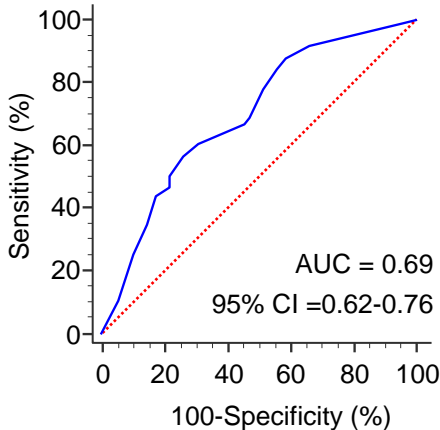


# Supplementary Figure 3

**A**



**B**



## Supplementary Table 1. Primer Sequences

Name	Sequence
BIRC5_F	TTCAAGGAGCTGGAAGGCTG
BIRC5_R	GCAACCGGACGAATGCTTTT
CDC20_F	GCAAGGAGAACCAGCCTGAA
CDC20_R	CGTTCAGGTTCAAAGCCCAG
CDH2_F	ATTGCCATCCTGCTCTGCAT
CDH2_R	TCCCGGCGTTTCATCCATAC
CENPW_F	GCCTCAACTTCGTCTGGAGA
CENPW_R	ACAAGCGTTTGTCTGGACT
JPH1_F	TGCCTTACTATTTTACCATCTGACG
JPH1_R	ATTCCTCGGGCAGTCGTT
MAD2L1_F	TCTGCCACTGTTGGAAGTTTCT
MAD2L1_R	TGGTCCCGACTCTTCCCATT
NEIL3_F	GCCCTCTTCTAAGGCATGTGA
NEIL3_R	TTCTTCACTCTTGAGCACTGAA
POC1A_F	GCATATCAACTGGGTCCGCT
POC1A_R	GTCATCACTGGCAGACACGA
Actin Beta_F	CCTTTGCCGATCCGCCG
Actin Beta_R	GATATCATCCATGGTGAGCTGG

*F, forward; R, reverse*