Supplementary materials inventory

The supplementary materials included 3 supplementary Tables and 3 supplementary Figures.

Supplementary Table

Table S1: Summary of Clinicopathologic Variables of 72 HCC patients.

Table S2: The primer sequences for clone and qPCR.

Table S3: Summary of Clinicopathologic Variables of 199 HCC patients in the tissue array.

Supplementary Figure

Figure S1 Down-regulation of PANK1 in the HCC. (A) The screening strategy for PANK1. (B) The expression of PANK1 between normal and primary HCC tumor in TCGA database. (C) Survival analysis of PANK1 in KM Plotter database. (D) The expression of PANK1 in normal tissues in The Human Protein Atlas database.

Figure S2 The correlations between the expression of PANK1 and serum bio-marker of 199 HCC patients in the tissue array. The contents of Alpha fetal protein (AFP) (A), α-L-focusidase (AFU) (B), Alkaline phosphatase (ALP) (C), Alanine aminotransferase (ALT) (D), Aspartate aminotransferase (AST) (E), Carbohydrate antigen199 (CA199) (F), Carcino-embryonic antigen (CEA) (G), Gamma-glutamyl transpeptidase (GGT) (H), Hepatitis B virus (HBV) DNA (I), Albumin (J),

Prothrombin time (PT) (K), Direct Bilirubin (DBIL) (L), and Total bilirubin (TBIL) (M) were measured and the correlations were analyzed.

Figure S3 The interaction between exogenously expressed PANK1 (Flag-PANK1) and RNF43 (A), AXIN1 (B), LRP6 (C), β-catenin (D), DVL2 (E), GSK3β (F) was examined in 293T cells.

Supplementary Table S1 Summary of Clinicopathologic Variables of 72 HCC patients

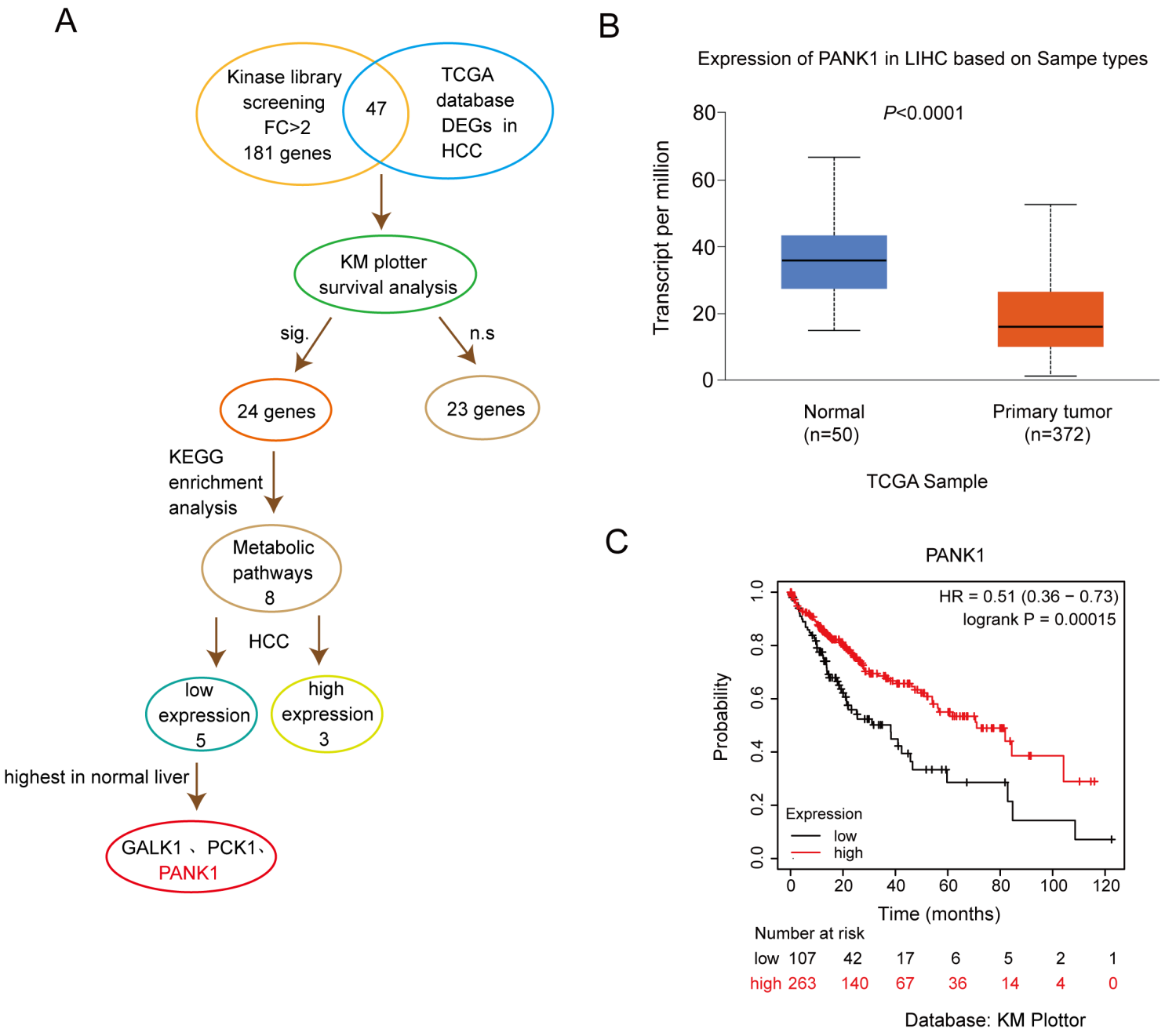
Characteristic	No. of Patients
Gender	
Male	60
Female	12
Age (years)	
<55	26
≥55	46
Tumor size (cm)	
<55	31
≥5	41
Tumor number	
≤1	60
≥2	12
HBV infection	
Yes	62
No	10
Organ metastasis	
Yes	7
No	65
Edmondson grading	
I/II	2
II/III	40
III/IV	30
Microvascular invasion (MVI)	
M0	19
M1	35
M2	18

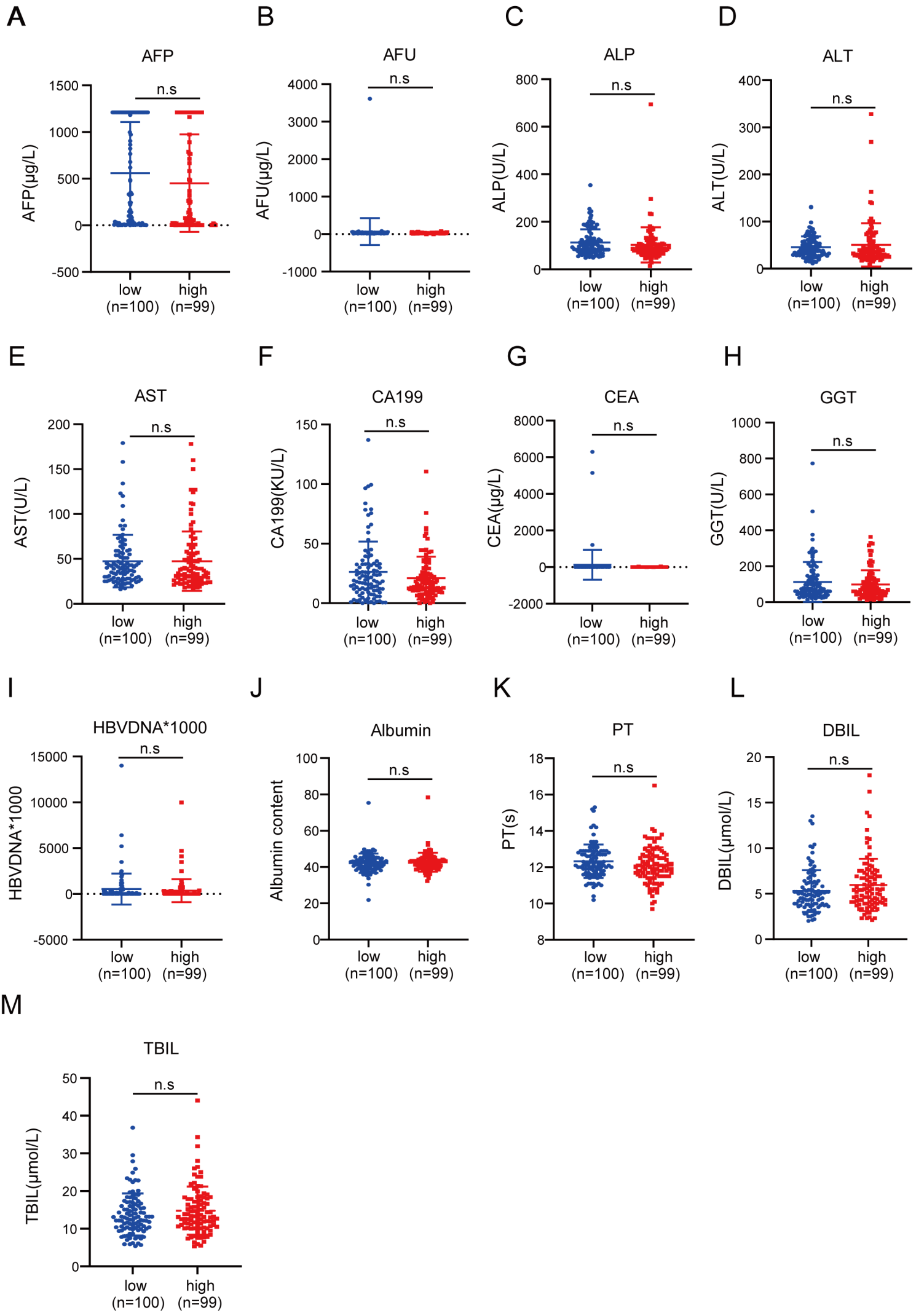
Supplementary Table S2 The primer sequences for clone and qPCR

Gene (homo)	Forward (5'-3')	Reverse (5'-3')
PANK1 (clone)	GGATCCATGTTGAAACTCGTC	GAATTCCTACTTGTCATCAGT
shPANK1 1# (clone)	CCGGGCCTGCTTTATGTCGACTCTGCTCGAGCAGAGTCGACATAAAGCAGGCTTTTTG	AATTCAAAAAGCCTGCTTTATGTCGACTCTGCTCGAGCAGAGTCGACATAAAGCAGGC
shPANK1 2# (clone)	CCGGGCTATGCACAGGTCATTCAGCTCGAGCTGAATGAACCTGTGCATAGCTTTTTG	AATTCAAAAAGCTATGCACAGGTTCATTCAGCTCGAGCTGAATGAACCTGTGCATAGC
PANK1 (qPCR)	CTGCCTTGATAACCCATACCCT	CTTGGAGTACACGGCTAGAATG
GAPDH (qPCR)	TGTTGCCATCAATGACCCCTT	CTCCACGACGTACTCAGCG
Axin2 (qPCR)	TACACTCCTTATTGGGCGATCA	TTGGCTACTCGTAAAGTTTTGGT
18S (qPCR)	AGGCCCTGTAATTGGAATGAGTC	GCTCCCAAGATCCAACTACGAG

Supplementary Table S3 Summary of Clinicopathologic Variables of 199 HCC patients in the tissue array.

Characteristic	No. of Patients
Gender	
male	184
female	15
Age (years)	
≤50	114
>50	85
BMI (kg/m^2)	
≤18.5	9
18.5-25	127
≥25	63
Tumor size (cm)	
≤11	170
>11	29
Tumor number	
≤1	174
≥2	25
Paracancerous microtumor	
No	128
Yes	71
Intracancerous hemangioma	
No	116
Yes	83
Ascites	
No	181
Yes	18
Cirrhosis	
I-II	118
III-IV	81
PVTT	
No	174
Yes	25
Capsular invasion	
I-II	140
III	59
Tumor grade	
I-II	50
III	149
Recurrence	
No	57
Yes	142


A
Kinase library screening FC>2 181 genes
47
TCGA database DEGs in HCC
KM plotter survival analysis
sig.
n.s
24 genes
23 genes
KEGG enrichment analysis
Metabolic pathways 8
HCC
low expression 5
high expression 3
highest in normal liver
GALK1、PCK1、PANK1
B
Expression of PANK1 in LIHC based on Sampe types
P<0.0001
Transcript per million
80
60
40
20
0
Normal (n=50)
Primary tumor (n=372)
TCGA Sample
C
PANK1
HR = 0.51 (0.36 − 0.73)
logrank P = 0.00015
Probability
1.0
0.8
0.6
0.4
0.2
0.0
Expression
low
high
0
20
40
60
80
100
120
Time (months)
Number at risk
low 107 42 17 6 5 2 1
high 263 140 67 36 14 4 0
Database: KM Plottor
D
HPA dataset
pTPM
70
60
50
40
30
20
10
0
Liver
Kidney
Duodenum
Rectum
Small intestine
Thyroid gland
Colon
Skin
Parathyroid gland
Cerebral cortex
Adrenal gland
Esophagus
Testis
Heart muscle
stomach
Fallopian tubes
Epididymis
Urinary bladder
Appendix
Lung
Smooth muscle
Skeletal muscle
Tonsil
Breast
Seminal vesicle
Prostate
Ovary
Gallbladder
Spleen
Lymph node
Asipose tissue
Salivary gland
Bone marrow
Pancreas
Database:THE HUMAN PROTEIN ATLAS


A
AFP
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AFP(μg/L)
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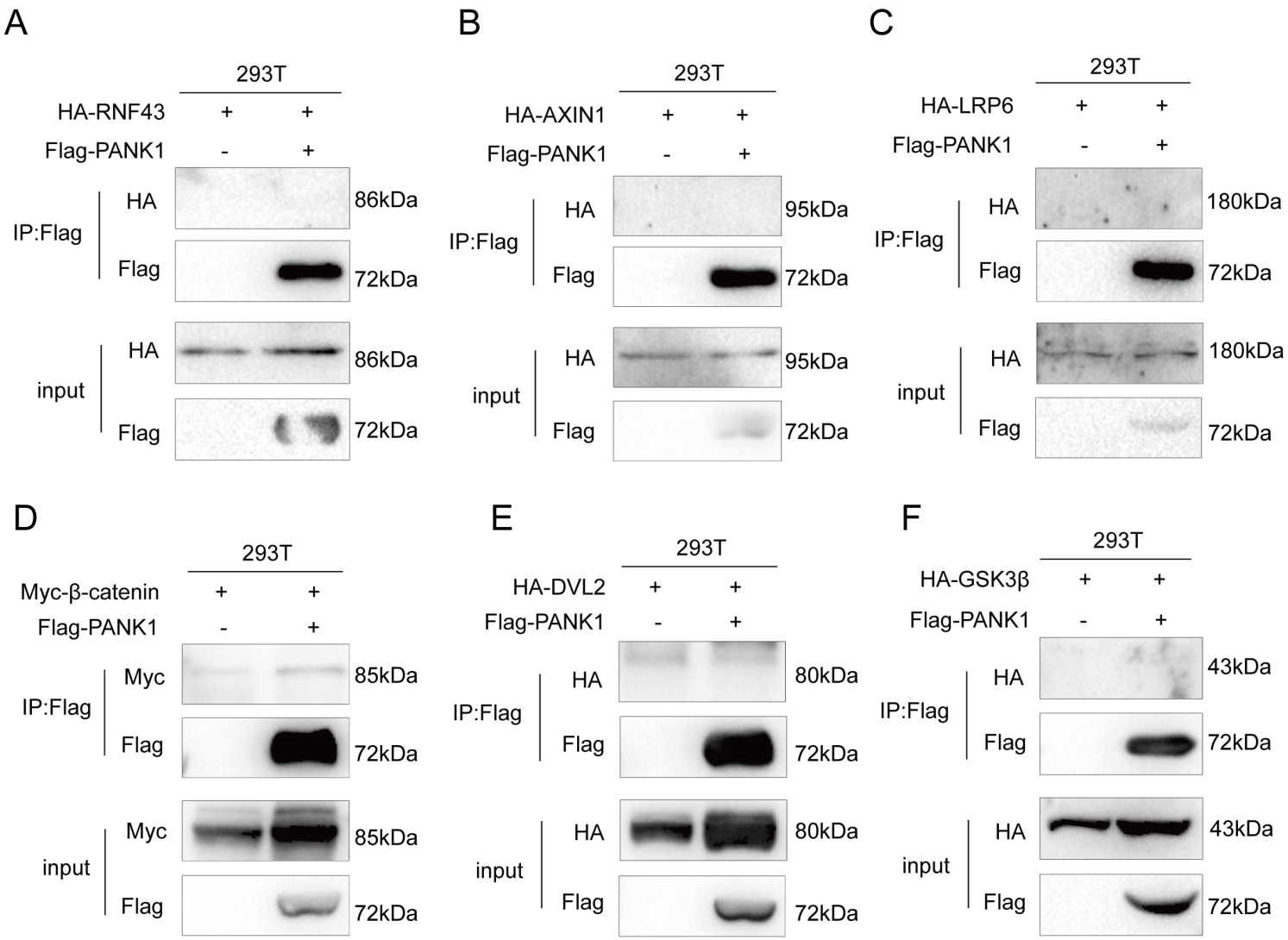
1000
500
0
-500
low (n=100)
high (n=99)
B
AFU
n.s
AFU(μg/L)
4000
3000
2000
1000
0
-1000
low (n=100)
high (n=99)
C
ALP
n.s
ALP(U/L)
800
600
400
200
0
low (n=100)
high (n=99)
D
ALT
n.s
ALT(U/L)
400
300
200
100
0
low (n=100)
high (n=99)
E
AST
n.s
AST(U/L)
200
150
100
50
0
low (n=100)
high (n=99)
F
CA199
n.s
CA199(KU/L)
150
100
50
0
low (n=100)
high (n=99)
G
CEA
n.s
CEA(μg/L)
8000
6000
4000
2000
0
-2000
low (n=100)
high (n=99)
H
GGT
n.s
GGT(U/L)
1000
800
600
400
200
0
low (n=100)
high (n=99)
I
HBVDNA*1000
n.s
HBVDNA*1000
15000
10000
5000
0
-5000
low (n=100)
high (n=99)
J
Albumin
n.s
Albumin content
100
80
60
40
20
0
low (n=100)
high (n=99)
K
PT
n.s
PT(s)
18
16
14
12
10
8
low (n=100)
high (n=99)
L
DBIL
n.s
DBIL(μmol/L)
20
15
10
5
0
low (n=100)
high (n=99)
M
TBIL
n.s
TBIL(μmol/L)
50
40
30
20
10
0
low (n=100)
high (n=99)


A
293T
HA-RNF43 + +
Flag-PANK1 - +
IP:Flag
HA
86kDa
Flag
72kDa
input
HA
86kDa
Flag
72kDa
B
293T
HA-AXIN1 + +
Flag-PANK1 - +
IP:Flag
HA
95kDa
Flag
72kDa
input
HA
95kDa
Flag
72kDa
C
293T
HA-LRP6 + +
Flag-PANK1 - +
IP:Flag
HA
180kDa
Flag
72kDa
input
HA
180kDa
Flag
72kDa
D
293T
Myc-β-catenin + +
Flag-PANK1 - +
IP:Flag
Myc
85kDa
Flag
72kDa
input
Myc
85kDa
Flag
72kDa
E
293T
HA-DVL2 + +
Flag-PANK1 - +
IP:Flag
HA
80kDa
Flag
72kDa
input
HA
80kDa
Flag
72kDa
F
293T
HA-GSK3β + +
Flag-PANK1 - +
IP:Flag
HA
43kDa
Flag
72kDa
input
HA
43kDa
Flag
72kDa