Supporting legends

Figure S1. (A, B) Volcano and heatmap plots show DE-mRNAs between HCC and non-tumor samples. **(C)** 10-fold cross-validation for parameter λ selection. The solid vertical lines are partial likelihood deviance ± standard error (SE). The two dotted vertical lines are drawn at the optimal values by minimum criteria (left) and 1-SE criteria (right). Parameter λ = 0.04269 [log (λ) = -3.154] is chosen via minimum criteria. **(D)** Univariate Cox regression analysis of the 16 key mRNAs. **(E1, E2)** Expression difference of the16 key mRNAs between HCCs and non-tumor samples in the TCGA training set. **(F)** Distribution of the mRNA risk score, survival status of HCC patients, and the expression level of the 16 key mRNAs.

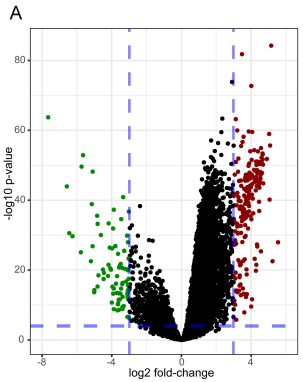
Figure S2. (A, B) Volcano and heatmap plots show DE-lncRNAs between HCC and non-tumor samples. **(C)** 10-fold cross-validation for parameter λ selection. Parameter λ = 0.05027 [log (λ) = -2.99] is chosen via minimum criteria. **(D)** Univariate Cox regression analysis of the 20 key lncRNAs. **(E1, E2)** Expression difference of the 20 key lncRNAs between HCCs and non-tumor samples in the TCGA training set. **(F)** Distribution of the lncRNA risk score, survival status of HCC patients, and the expression level of the 20 key lncRNAs.

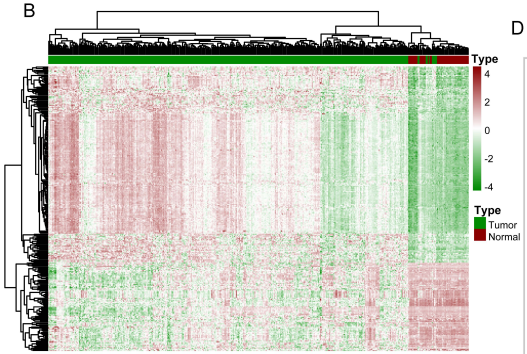
Figure S3. (A, B) Volcano and heatmap plots show DE-miRNAs between HCC and non-tumor samples. **(C)** Expression difference of the 5 key miRNAs between HCCs and non-tumor samples in the TCGA training set. **(D)** Distribution of the miRNA risk score, survival status of HCC patients, and the expression level of the 5 key miRNAs.

Figure S4. (A) 10-fold cross-validation for parameter λ selection. Parameter λ = 0.07177142 [log (λ) = -2.634269] is chosen via minimum criteria. **(B)** Copy number alteration of the 5 key CNV genes in HCCs and non-tumor samples in the TCGA training set. **(C)** Univariate Cox regression analysis of the 5 key CNV genes. **(D)** Distribution of the CNV risk score, survival status of HCC patients, and the copy number alteration of the 5 key miRNAs in the TCGA training set.

Figure S5. (A) Distributions of various mutation types of the 85 high-frequency SNPs. The histogram in the top indicates the sum of non-synonymous and synonymous mutations in every case, and the histogram on the right stands for the sample number suffering from gene mutation. In the heat map, the various colors stand for various mutation types, whereas the white color represents no mutation. **(B)** Univariate Cox regression analysis of the 10 high-frequency SNPs. **(C)** Distribution of the SNP risk score, survival status of HCC patients, and the mutation status of the 7 key SNPs in the TCGA training set.

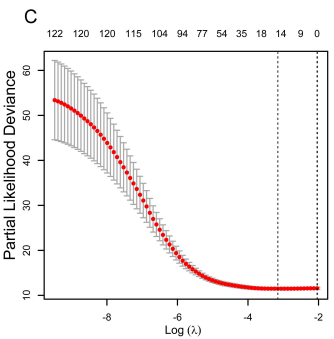
Figure S1

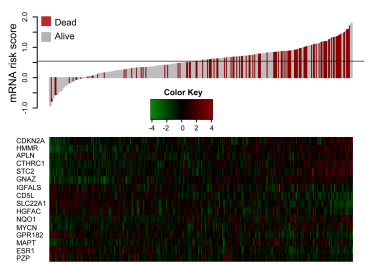


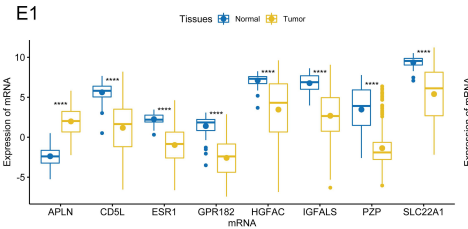


D

Variables	HR(95% CI)	P Value
APLN	1.127(1.006-1.263)	0.0384
CD5L	0.905(0.854-0.959)	0.0007
CDKN2A	1.167(1.051-1.296)	0.004
CTHRC1	1.168(1.073-1.272)	0.0003
ESR1	0.867(0.799-0.940)	0.0006
GNAZ	1.184(1.080-1.298)	0.0003
GPR182	0.862(0.795-0.933)	0.0003
HGFAC	0.941(0.899-0.985)	0.0086
HMMR	1.279(1.126-1.451)	0.0001
IGFALS	0.926(0.865-0.990)	0.0237
MAPT	1.176(1.045-1.322)	0.0069
MYCN	1.095(1.015-1.180)	0.0183
NQO1	1.083(1.02-1.150)	0.0088
PZP	0.905(0.831-0.986)	0.0226
SLC22A1	0.909(0.859-0.961)	0.0009
STC2	1.245(1.107-1.399)	0.0002







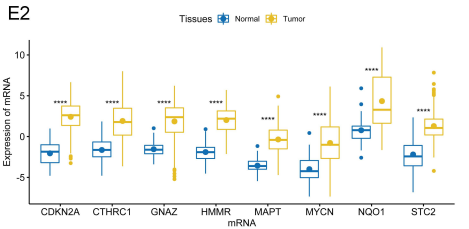
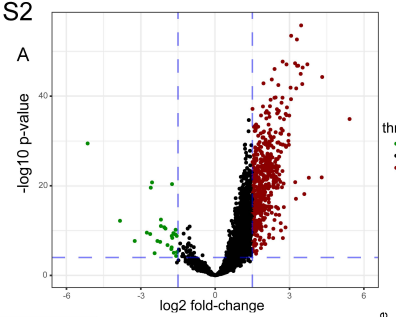
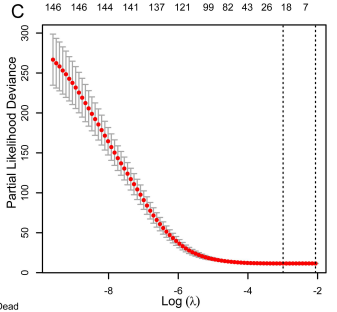


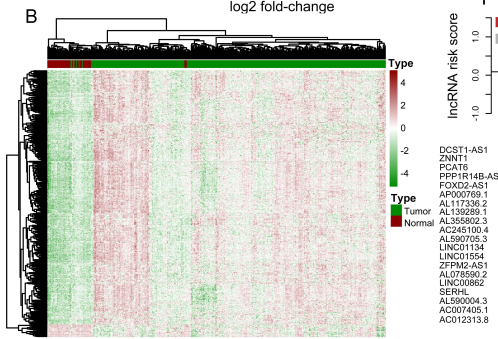
Figure S2

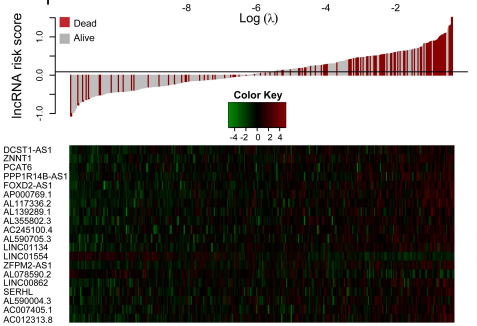


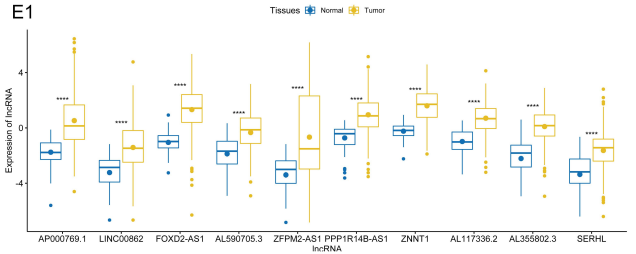


D

Variables	HR(95% CI)	P Value
AP000769.1	1.186(1.083-1.299)	0.0002
LINC00862	1.207(1.079-1.351)	0.0010
PCAT6	1.192(1.044-1.361)	0.0093
AC245100.4	1.232(1.070-1.417)	0.0036
DCST1-AS1	1.238(1.065-1.438)	0.0053
AL078590.2	0.858(0.772-0.953)	0.0044
AC007405.1	1.218(1.062-1.398)	0.0048
AL139289.1	1.221(1.062-1.403)	0.0049
LINC01134	1.324(1.135-1.545)	0.0004
FOXD2-AS1	1.257(1.104-1.431)	0.0005
AL590705.3	1.239(1.079-1.424)	0.0024
ZFPM2-AS1	1.109(1.041-1.181)	0.0013
PPP1R14B-AS1	1.231(1.084-1.397)	0.0013
AL590004.3	1.093(1.011-1.181)	0.0254
ZNNT1	1.272(1.090-1.484)	0.0023
AC012313.8	1.221(1.060-1.408)	0.0058
AL117336.2	1.424(1.181-1.717)	0.0002
AL355802.3	1.254(1.076-1.461)	0.0037
LINC01554	0.907(0.859-0.957)	0.0003
SERHL	1.266(1.097-1.459)	0.0012







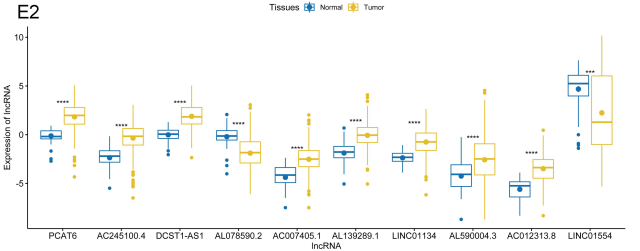


Figure S3

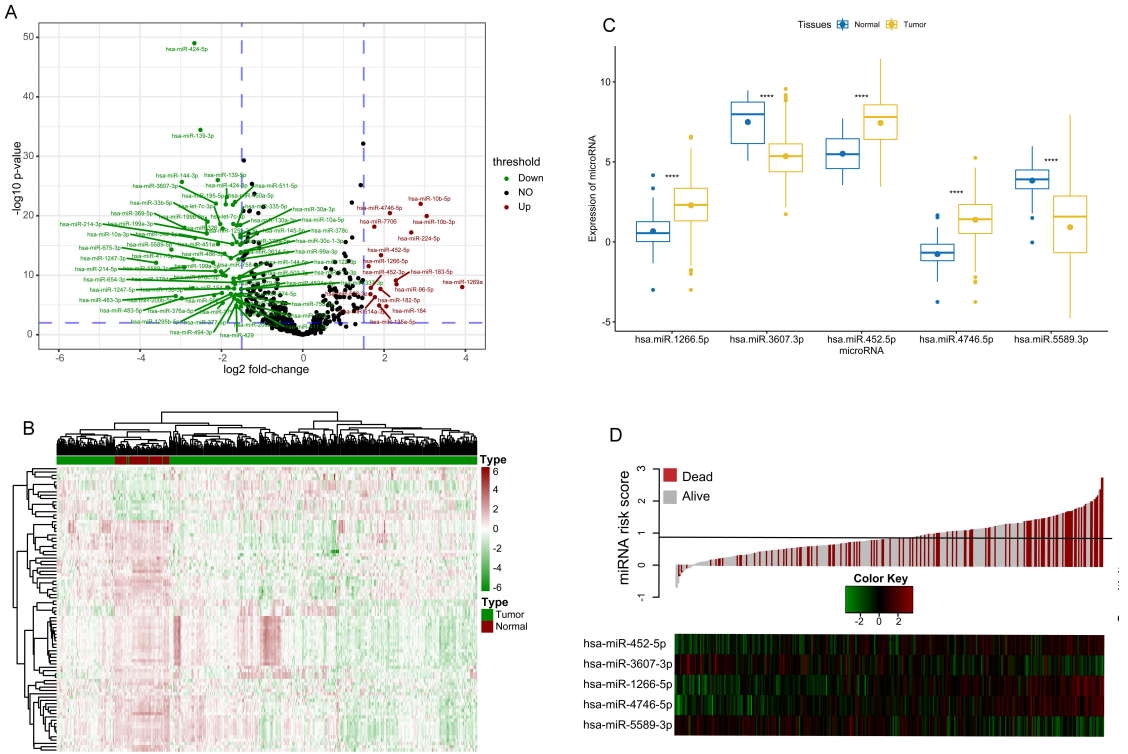
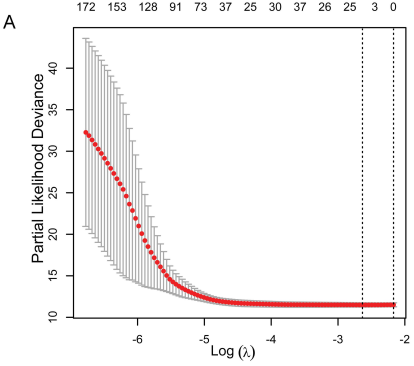
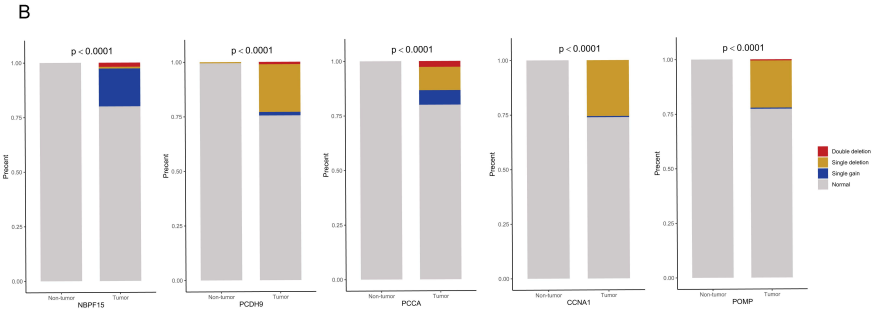

A
-log10 p-value
log2 fold-change
threshold
Down
NO
Up
hsa-miR-424-5p
hsa-miR-139-3p
hsa-miR-144-3p
hsa-miR-3607-3p
hsa-miR-424-3p
hsa-miR-511-5p
hsa-miR-10b-5p
hsa-miR-4746-5p
hsa-miR-10b-3p
hsa-miR-224-5p
hsa-miR-452-5p
hsa-miR-1266-5p
hsa-miR-183-5p
hsa-miR-1269a
hsa-miR-96-5p
hsa-miR-182-5p
hsa-miR-184
hsa-miR-135b-5p
B
Type
6
4
2
0
-2
-4
-6
Type
Tumor
Normal
C
Tissues
Normal
Tumor
Expression of microRNA
hsa.miR.1266.5p
hsa.miR.3607.3p
hsa.miR.452.5p
hsa.miR.4746.5p
hsa.miR.5589.3p
microRNA
****
D
miRNA risk score
Dead
Alive
Color Key
hsa-miR-452-5p
hsa-miR-3607-3p
hsa-miR-1266-5p
hsa-miR-4746-5p
hsa-miR-5589-3p

Figure S4





C

Variables	Number	HR(95% CI)	P Value
CCNA1			0.0003
Normal	239	ref	
CNV	85	2.042(1.386-3.007)	
NBPF15			0.0058
Normal	258	ref	
CNV	66	1.798(1.185-2.729)	
PCCA			0.001
Normal	259	ref	
CNV	65	1.987(1.319-2.992)	
PCDH9			0.0008
Normal	245	ref	
CNV	79	1.945(1.317-2.872)	
POMP			0.0002
Normal	251	ref	
CNV	73	2.161(1.442-3.241)	

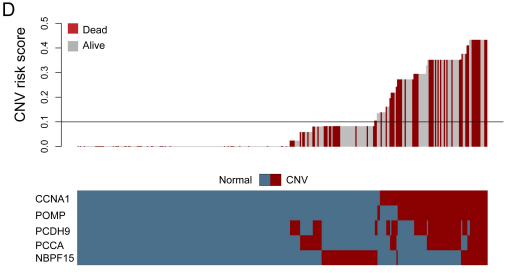
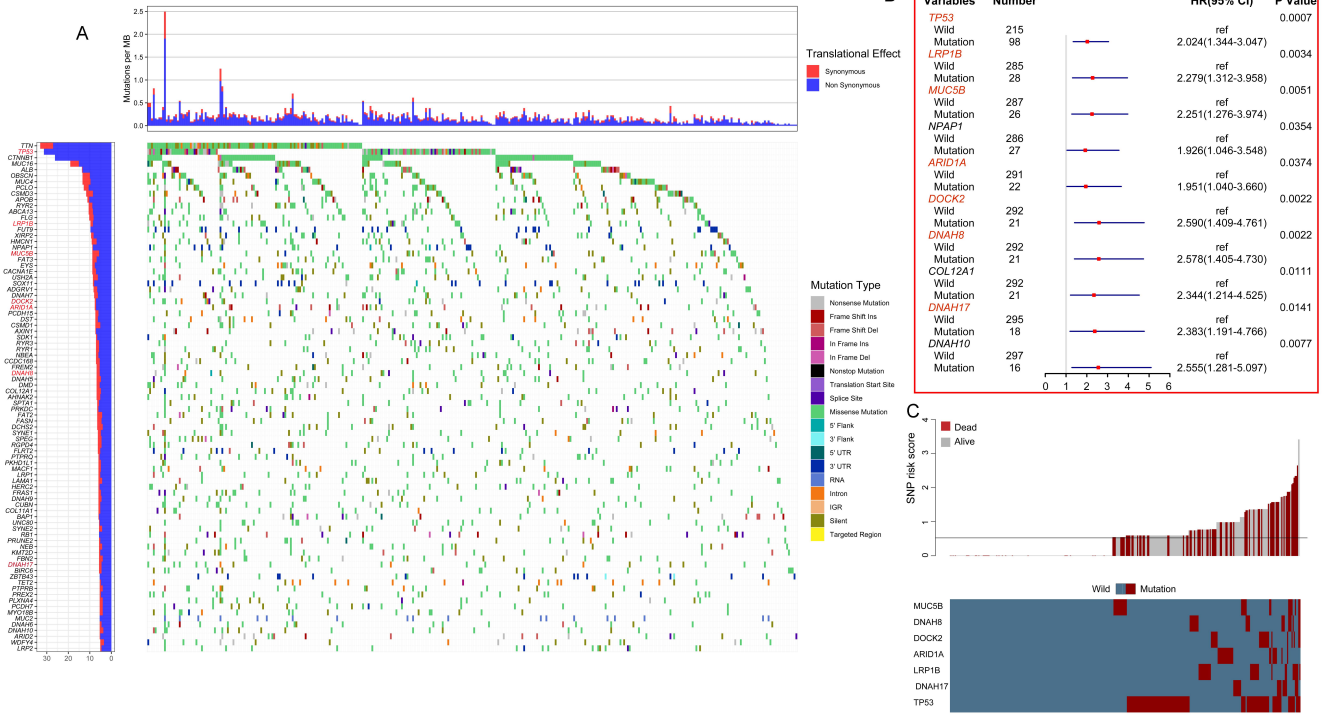


Figure S5


A
Mutations per MB
Translational Effect
Synonymous
Non Synonymous
Mutation Type
Nonsense Mutation
Frame Shift Ins
Frame Shift Del
In Frame Ins
In Frame Del
Nonstop Mutation
Translation Start Site
Splice Site
Missense Mutation
5' Flank
3' Flank
5' UTR
3' UTR
RNA
Intron
IGR
Silent
Targeted Region
B
Variables
Number
HR(95% CI)
P Value
TP53 0.0007
Wild 215 ref
Mutation 98 2.024(1.344-3.047)
LRP1B 0.0034
Wild 285 ref
Mutation 28 2.279(1.312-3.958)
MUC5B 0.0051
Wild 287 ref
Mutation 26 2.251(1.276-3.974)
NPAP1 0.0354
Wild 286 ref
Mutation 27 1.926(1.046-3.548)
ARID1A 0.0374
Wild 291 ref
Mutation 22 1.951(1.040-3.660)
DOCK2 0.0022
Wild 292 ref
Mutation 21 2.590(1.409-4.761)
DNAH8 0.0022
Wild 292 ref
Mutation 21 2.578(1.405-4.730)
COL12A1 0.0111
Wild 292 ref
Mutation 21 2.344(1.214-4.525)
DNAH17 0.0141
Wild 295 ref
Mutation 18 2.383(1.191-4.766)
DNAH10 0.0077
Wild 297 ref
Mutation 16 2.555(1.281-5.097)
C
SNP risk score
Dead
Alive
Wild
Mutation
MUC5B
DNAH8
DOCK2
ARID1A
LRP1B
DNAH17
TP53