



Figure S1 Correlation between the HTCIRS and sensitivity to targeted drugs in HCC. (A-F) Box plots and corresponding scatter plots indicating a significant positive correlation between HTCIRS scores and IC₅₀ values for gefitinib, axitinib, erlotinib, gemcitabine, doxorubicin, and docetaxel. Data are presented as the mean ± SD. *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.

Table S1 Primers for RT-PCR assays

Gene	Forward primer (5'-3')	Reverse primer 5'-3'
KLF2	AAACGCACCGCCACTCA	GGTAGGGCTTCTCACCTGTGT
GAPDH	GGAAGCTTGTCATCAATGGAATC	TGATGACCCTTTTGGCTCCC

RT-PCR, reverse transcription polymerase chain reaction.

Table S2 36 TCI related genes associated with prognosis

Gene	P value	HR	HR.95L	HR.95H	Weight	Weight_HR
<i>ANXA2</i>	0.004013	1.298548	1.086846	1.551486	2.396529	29.85481
<i>S100A9</i>	1.44E-05	1.23791	1.124123	1.363215	4.842857	23.79101
<i>DYNLT1</i>	0.013348	1.475327	1.084199	2.007555	1.874572	47.53267
<i>OPTN</i>	0.006869	1.537262	1.125489	2.099686	2.163082	53.72616
<i>CTSL</i>	0.005541	1.525618	1.131936	2.056219	2.256411	52.56176
<i>LGALS3</i>	0.009486	1.172623	1.039692	1.32255	2.022939	17.2623
<i>KLRB1</i>	0.020109	0.743742	0.579429	0.954652	1.696607	-25.6258
<i>CTSC</i>	0.002905	1.331731	1.102862	1.608095	2.536844	33.17308
<i>FCER1G</i>	0.039248	1.184559	1.008383	1.391514	1.406185	18.45586
<i>ARPC2</i>	0.004519	1.626927	1.162702	2.276501	2.344936	62.69273
<i>RGS2</i>	0.008442	1.172888	1.041646	1.320666	2.073561	17.28877
<i>ADGRE5</i>	0.013053	1.249424	1.047974	1.489599	1.884286	24.94244
<i>PRNP</i>	0.023321	1.220705	1.027467	1.450285	1.632257	22.07048
<i>CYBB</i>	0.048679	1.185612	1.000987	1.404289	1.312654	18.56116
<i>PMAIP1</i>	0.033045	1.398766	1.027381	1.904403	1.480899	39.87665
<i>TGFB1</i>	0.047346	1.160398	1.001744	1.34418	1.324712	16.03982
<i>RHOG</i>	0.019287	1.403788	1.056622	1.865021	1.714732	40.37883
<i>SP110</i>	0.037615	1.50134	1.023545	2.202173	1.424643	50.13403
<i>CXCL8</i>	0.00735	1.148372	1.037891	1.270615	2.133715	14.83723
<i>NPC2</i>	0.019708	1.324722	1.045868	1.677926	1.705354	32.47225
<i>PPT1</i>	0.003045	1.442879	1.132162	1.838871	2.516425	44.2879
<i>ARRB2</i>	0.048554	1.288375	1.001609	1.657242	1.313771	28.83746
<i>IER3</i>	0.01486	1.179019	1.032693	1.34608	1.827982	17.90193
<i>KLF2</i>	0.00467	0.700822	0.547824	0.89655	2.330672	-29.9178
<i>PSAP</i>	0.012707	1.503213	1.090904	2.071354	1.895957	50.32125
<i>SFT2D1</i>	0.014073	1.480284	1.082358	2.024508	1.851611	48.02842
<i>TAGLN2</i>	0.00128	1.456097	1.158444	1.830231	2.892931	45.60973
<i>PKM</i>	0.005313	1.173537	1.048649	1.3133	2.274628	17.35374
<i>LGMN</i>	0.044898	1.350789	1.006867	1.812187	1.347773	35.07891
<i>AP1S2</i>	0.016019	1.459596	1.072963	1.98555	1.795378	45.95964
<i>S100A11</i>	0.010476	1.170914	1.037662	1.321277	1.979823	17.09135
<i>CTSB</i>	0.043281	1.279567	1.007471	1.62515	1.3637	27.9567
<i>CALM1</i>	0.026977	1.546742	1.050922	2.276486	1.569001	54.67418
<i>RBM3</i>	0.034243	1.335821	1.021736	1.746458	1.465423	33.58213
<i>GRN</i>	0.021624	1.357468	1.045853	1.76193	1.66506	35.74681
<i>SRI</i>	0.009013	1.369318	1.081578	1.733607	2.045108	36.93178

TCI, T-cell inflammation; HR, hazard ratio.

Table S3 32 shared genes

Genes
<i>ANXA2</i>
<i>S100A9</i>
<i>DYNLT1</i>
<i>OPTN</i>
<i>LGALS3</i>
<i>KLRB1</i>
<i>CTSC</i>
<i>FCER1G</i>
<i>ARPC2</i>
<i>RGS2</i>
<i>PRNP</i>
<i>CYBB</i>
<i>PMAIP1</i>
<i>TGFB1</i>
<i>RHOG</i>
<i>SP110</i>
<i>NPC2</i>
<i>PPT1</i>
<i>ARRB2</i>
<i>IER3</i>
<i>KLF2</i>
<i>PSAP</i>
<i>SFT2D1</i>
<i>TAGLN2</i>
<i>LGMN</i>
<i>AP1S2</i>
<i>S100A11</i>
<i>CTSB</i>
<i>CALM1</i>
<i>RBM3</i>
<i>GRN</i>
<i>SRI</i>

Table S4 Correlation between KLF2 expression and clinicopathological characteristics of HCC patients

Variables	Number of patients			P value
	KLF2 high (N=67)	KLF2 low (N=23)	Total (N=90)	
Age, years				0.553
<60	27 (40.3%)	7 (30.4%)	34 (37.78%)	
≥60	40 (59.7%)	16 (69.6%)	56 (62.22%)	
Gender				0.010
Male	55 (82.1%)	12 (52.2%)	67 (74.00%)	
Female	12 (17.9%)	11 (47.8%)	23 (26.00%)	
Liver cirrhosis				0.079
No	20 (29.9%)	2 (8.7%)	22 (13.44%)	
Yes	47 (70.1%)	21 (91.3%)	68 (76.56%)	
Serum AFP, ng/mL				0.326
<20	39 (58.2%)	10 (43.5%)	49 (54.44%)	
≥20	28 (41.8%)	13 (56.5%)	41 (45.56%)	
Serum CA19-9, kU/L				0.225
<37	53 (93.3%)	21 (91.3%)	64 (82.22%)	
≥37	14 (6.67%)	2 (8.7%)	16 (17.78%)	
Serum CEA, ng/mL				0.184
<5	60 (89.6%)	23 (100%)	83 (92.22%)	
≥5	7 (10.4%)	0 (0%)	7 (7.78%)	
Tumor number				<0.001
Single	56 (83.6%)	6 (26.1%)	62 (68.89%)	
Multiple	11 (16.4%)	17 (73.9%)	28 (31.11%)	
MVI				0.197
No	58 (86.6%)	17 (73.9%)	75 (83.33%)	
Yes	9 (13.4%)	6 (26.1%)	15 (16.67%)	
TNM stage				<0.001
I	56 (83.6%)	4 (17.4%)	60 (66.67%)	
II-III	11 (16.4%)	19 (82.6%)	30 (33.33%)	

HCC, hepatocellular carcinoma; AFP, alpha-fetoprotein; CEA, carcinoembryonic antigen; MVI, microvascular invasion; TNM, Tumor-Node-Metastasis (Staging System).