Supplementary Table 1. Sequence of primers for *q*RT-PCR

Gene	Forward primer (5’------3’)	Reverse primer (5’------3’)
SLC29A1	5’-GGGTGTAGCCTCGGCATTT-3’	3’-CTCCACTGGCCTGCACAAG-5’
Actin	5’-CTGGAACGGTGAAGGTGACA-3’	3’-CGGCCACATTGTGAACTTTG-5’
CTNNA3	5’-TGGGCAATACTCTGTCCTGC-3’	3’-TGGTAACCTGGATTATGAGAGGC-5’
CDH4	5’-TGGCCATCCTCATCTGCATC-3’	3’-GTCGTAGTCCTGGTCCTCCT-5’
CLDN1	5’-CTGTCATTGGGGGTGCGATA-3’	3’-CTGACCAAATTCGTACCTGGC-5’
TRIM9	5’-TTTGCAGATTTCTGACGCCC-3’	3’-GATAGGGGTTGCTGGGACTG-5’
ZEB2	5’-CCTCTGTAGATGGTCCAGTGAA-3’	3’-GTCACTGCGCTGAAGGTACT-5’
TGFBR1	5’-TTGGTACCCAAGGAAAGCCA3’	3’-GAGAACTTCAGGGGCCATGT-5’

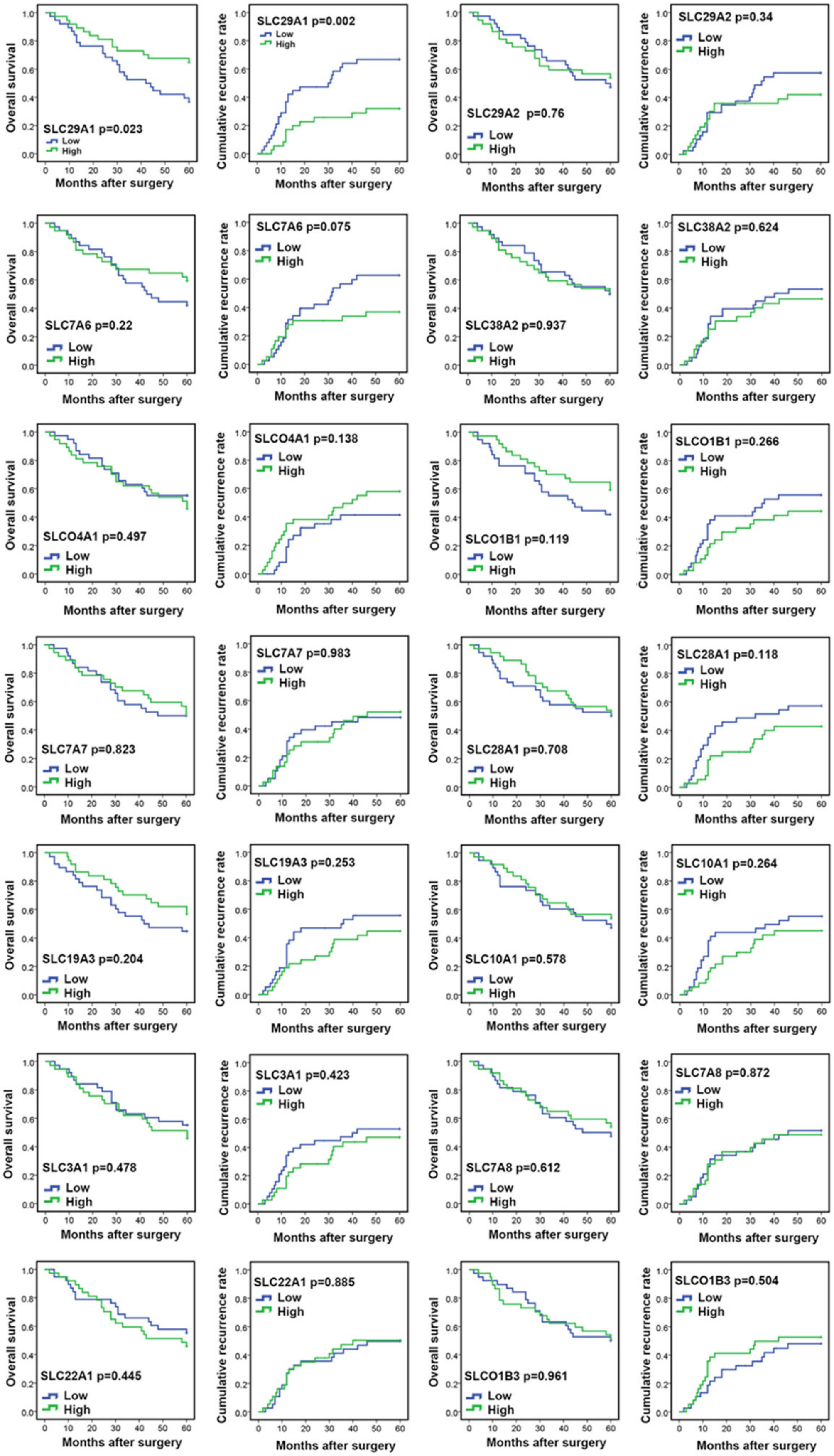
Abbreviations: *q*RT-PCR, quantitative real-time polymerase chain reaction.

Supplementary Table 2. The mRNA expressions of SLC-family genes in 75 patients with hepatocellular carcinoma

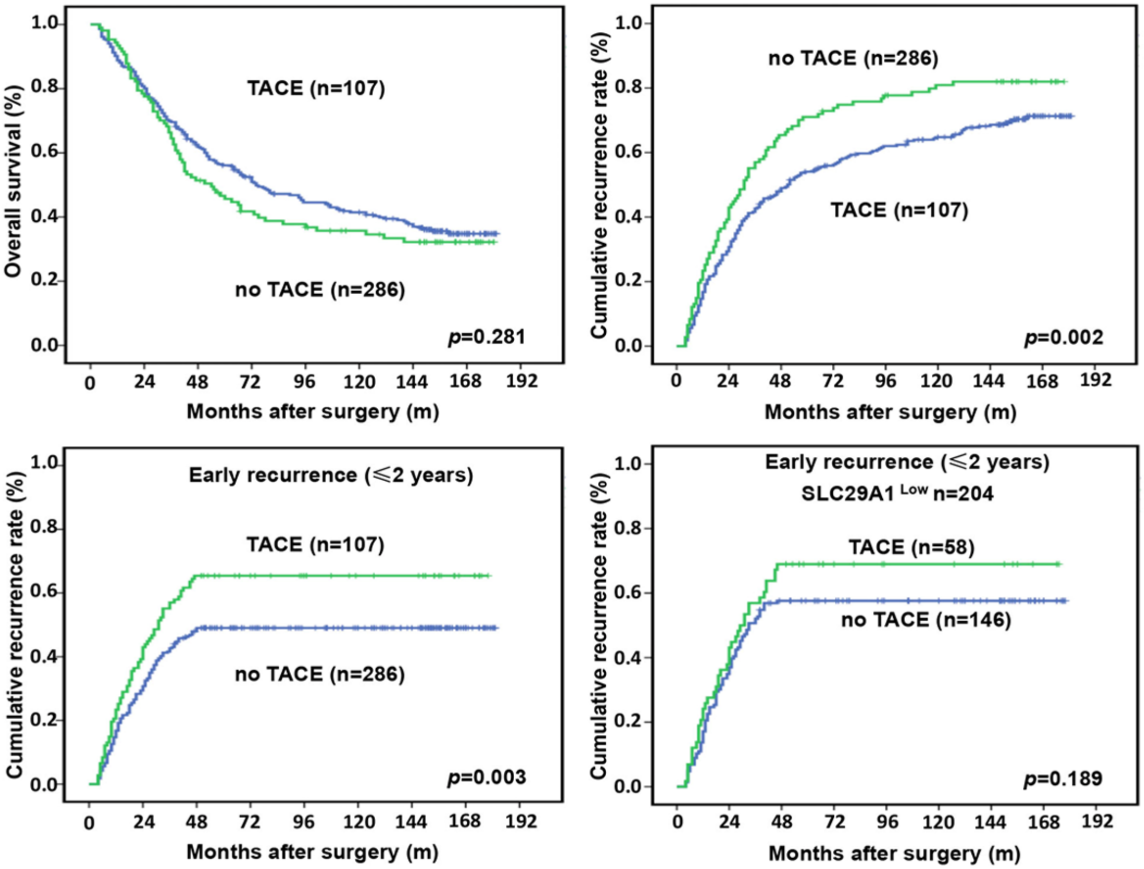
Symbol	Well	AVG ΔC_t (Ct(GOI) - Ave Ct (HKG))		2^-ΔC_t		Fold Change	T-TEST	Fold Up- or Down-Regulation	Comments
		HCC	Para-carcinoma	HCC	Para-carcinoma	HCC/para-carcinoma	*p* value	HCC/para-carcinoma	
SLC10A1	C11	3.79	2.20	7.2E-02	2.2E-01	0.33	N/A	-3.02	OKAY
SLC10A2	C12	15.80	16.55	1.7E-05	1.0E-05	1.67	N/A	1.67	B
SLC15A1	D01	6.11	6.30	1.4E-02	1.3E-02	1.14	N/A	1.14	OKAY
SLC15A2	D02	10.06	9.67	9.4E-04	1.2E-03	0.76	N/A	-1.31	OKAY
SLC16A1	D03	4.96	4.82	3.2E-02	3.5E-02	0.91	N/A	-1.10	OKAY
SLC16A2	D04	5.99	5.02	1.6E-02	3.1E-02	0.51	N/A	-1.96	OKAY
SLC16A3	D05	15.70	16.56	1.9E-05	1.0E-05	1.81	N/A	1.81	B
SLC19A1	D06	9.93	9.82	1.0E-03	1.1E-03	0.93	N/A	-1.08	OKAY
SLC19A2	D07	7.03	7.16	7.7E-03	7.0E-03	1.10	N/A	1.10	OKAY
SLC19A3	D08	9.55	8.09	1.3E-03	3.7E-03	0.36	N/A	-2.75	OKAY
SLC22A1	D09	4.98	2.17	3.2E-02	2.2E-01	0.14	N/A	-7.04	OKAY
SLC22A2	D10	16.49	16.18	1.1E-05	1.4E-05	0.81	N/A	-1.24	B
SLC22A3	D11	7.97	7.80	4.0E-03	4.5E-03	0.89	N/A	-1.12	OKAY
SLC22A6	D12	14.13	14.46	5.6E-05	4.4E-05	1.26	N/A	1.26	B
SLC22A7	E01	3.91	2.93	6.7E-02	1.3E-01	0.51	N/A	-1.96	OKAY
SLC22A8	E02	13.18	15.97	1.1E-04	1.6E-05	6.94	N/A	6.94	B
SLC22A9	E03	4.14	4.72	5.7E-02	3.8E-02	1.49	N/A	1.49	OKAY
SLC25A13	E04	4.47	4.22	4.5E-02	5.4E-02	0.84	N/A	-1.19	OKAY
SLC28A1	E05	9.38	7.96	1.5E-03	4.0E-03	0.37	N/A	-2.67	OKAY
SLC28A2	E06	10.98	10.30	5.0E-04	7.9E-04	0.63	N/A	-1.59	OKAY
SLC28A3	E07	13.04	10.34	1.2E-04	7.7E-04	0.15	N/A	-6.49	A
SLC29A1	E08	3.71	4.81	7.7E-02	3.6E-02	2.15	N/A	2.15	OKAY
SLC29A2	E09	8.34	9.51	3.1E-03	1.4E-03	2.24	N/A	2.24	OKAY
SLC2A1	E10	11.25	11.78	4.1E-04	2.8E-04	1.44	N/A	1.44	OKAY
SLC2A2	E11	3.35	2.76	9.8E-02	1.5E-01	0.67	N/A	-1.50	OKAY
SLC2A3	E12	9.45	8.68	1.4E-03	2.4E-03	0.59	N/A	-1.70	OKAY
SLC31A1	F01	3.37	2.79	9.6E-02	1.4E-01	0.67	N/A	-1.49	OKAY
SLC38A2	F02	4.94	3.84	3.3E-02	7.0E-02	0.47	N/A	-2.15	OKAY
SLC38A5	F03	11.93	11.52	2.6E-04	3.4E-04	0.75	N/A	-1.34	OKAY
SLC3A1	F04	8.23	6.47	3.3E-03	1.1E-02	0.29	N/A	-3.40	OKAY
SLC3A2	F05	3.52	3.71	8.7E-02	7.6E-02	1.14	N/A	1.14	OKAY
SLC5A1	F06	13.41	9.44	9.2E-05	1.4E-03	0.06	N/A	-15.67	A
SLC5A4	F07	11.47	11.79	3.5E-04	2.8E-04	1.25	N/A	1.25	OKAY

SLC7A11	F08	12.89	15.31	1.3E-04	2.5E-05	5.36	N/A	5.36	B
SLC7A5	F09	9.10	8.36	1.8E-03	3.1E-03	0.60	N/A	-1.67	OKAY
SLC7A6	F10	8.85	9.90	2.2E-03	1.0E-03	2.07	N/A	2.07	OKAY
SLC7A7	F11	6.69	5.29	9.7E-03	2.6E-02	0.38	N/A	-2.65	OKAY
SLC7A8	F12	9.58	7.54	1.3E-03	5.4E-03	0.24	N/A	-4.12	OKAY
SLC7A9	G01	5.78	5.92	1.8E-02	1.6E-02	1.11	N/A	1.11	OKAY
SLCO1A2	G02	7.99	7.82	3.9E-03	4.4E-03	0.89	N/A	-1.13	OKAY
SLCO1B1	G03	5.00	3.63	3.1E-02	8.1E-02	0.39	N/A	-2.57	OKAY
SLCO1B3	G04	7.62	4.50	5.1E-03	4.4E-02	0.12	N/A	-8.69	OKAY
SLCO2A1	G05	9.44	9.82	1.4E-03	1.1E-03	1.30	N/A	1.30	OKAY
SLCO2B1	G06	4.99	4.00	3.1E-02	6.2E-02	0.50	N/A	-1.99	OKAY
SLCO3A1	G07	8.13	8.05	3.6E-03	3.8E-03	0.95	N/A	-1.06	OKAY
SLCO4A1	G08	10.50	9.22	6.9E-04	1.7E-03	0.41	N/A	-2.42	OKAY
TAP1	G09	4.34	4.75	4.9E-02	3.7E-02	1.33	N/A	1.33	OKAY
TAP2	G10	6.79	7.29	9.0E-03	6.4E-03	1.41	N/A	1.41	OKAY
VDAC1	G11	1.74	2.09	3.0E-01	2.4E-01	1.27	N/A	1.27	OKAY
VDAC2	G12	2.48	2.53	1.8E-01	1.7E-01	1.04	N/A	1.04	OKAY
ACTB	H01	-1.30	-0.92	2.5E+00	1.9E+00	1.30	N/A	1.30	OKAY
B2M	H02	-0.15	-1.08	1.1E+00	2.1E+00	0.53	N/A	-1.90	OKAY
GAPDH	H03	0.00	0.00	1.0E+00	1.0E+00	1.00	N/A	-1.00	OKAY
HPRT1	H04	6.73	6.65	9.4E-03	9.9E-03	0.95	N/A	-1.05	OKAY
RPLP0	H05	-1.60	-1.07	3.0E+00	2.1E+00	1.44	N/A	1.44	OKAY

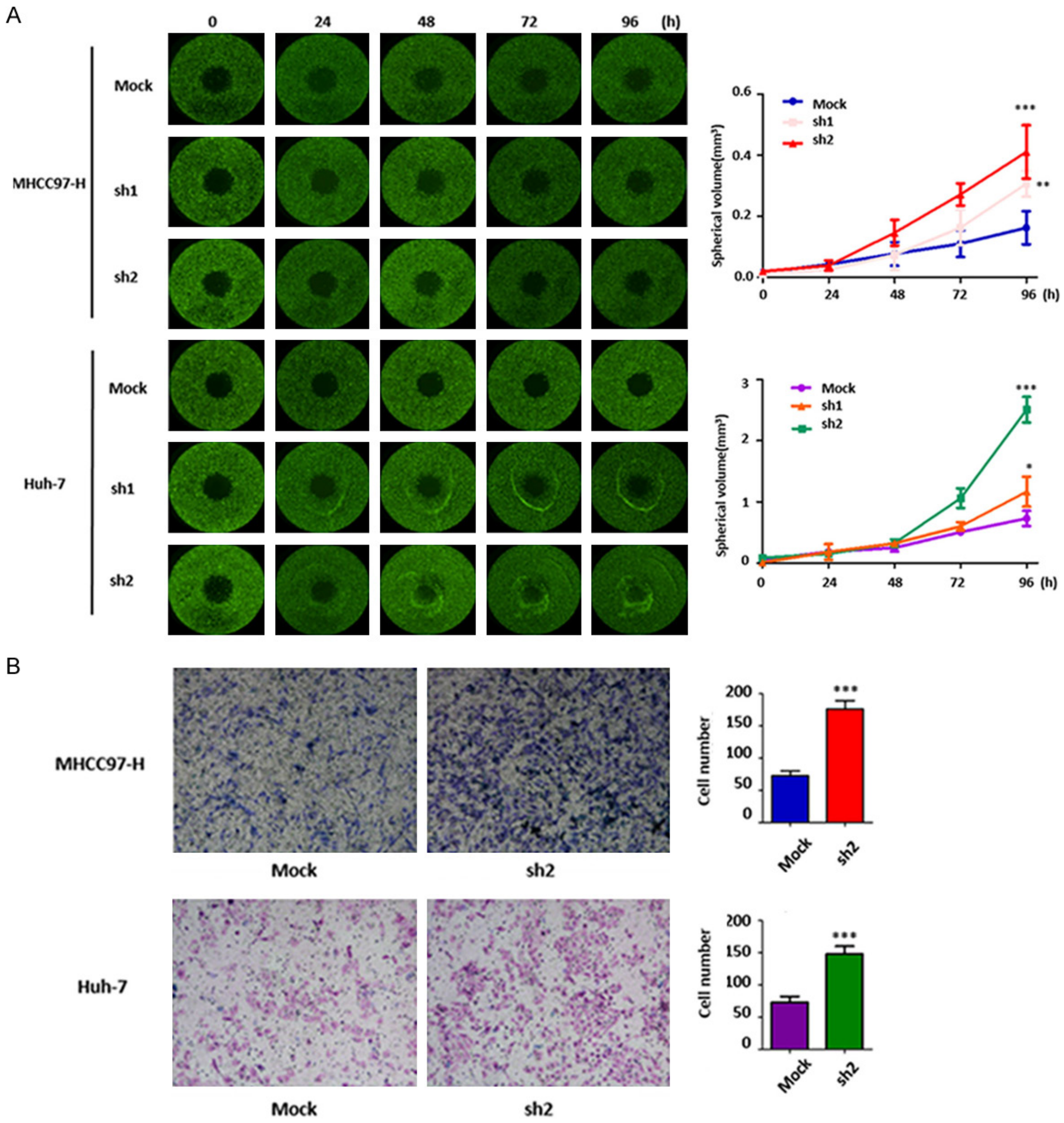
Legend: Fold-Change (2^(- Delta Delta Ct)) is the normalized gene expression (2^(-Delta Ct)) in the Test Sample divided the normalized gene expression (2^(-Delta Ct)) in the Control Sample. Fold-Regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicate a positive- or an up-regulation, and the fold-regulation is equal to the fold-change. Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change. Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than -2 are indicated in blue. *p*-values: The *p* values are calculated based on a Student's t-test of the replicate 2^(-Delta Ct) values for each gene in the control group and treatment groups, and *p* values less than 0.05 are indicated in red. Comments: A: This gene's average threshold cycle is relatively high (> 30) in either the control or the test sample, and is reasonably low in the other sample (< 30). These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result. This fold-change result may also have greater variations if *p* value > 0.05; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene. B: This gene's average threshold cycle is relatively high (> 30), meaning that its relative expression level is low, in both control and test samples, and the *p*-value for the fold-change is either unavailable or relatively high (P > 0.05). This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene. C: This gene's average threshold cycle is either not determined or greater than the defined cut-off (deault 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.


Overall survival
Cumulative recurrence rate
Months after surgery
0
10
20
30
40
50
60
0.0
0.2
0.4
0.6
0.8
1.0
Low
High
SLC29A1 p=0.023
SLC29A1 p=0.002
SLC29A2 p=0.76
SLC29A2 p=0.34
SLC7A6 p=0.22
SLC7A6 p=0.075
SLC38A2 p=0.937
SLC38A2 p=0.624
SLCO4A1 p=0.497
SLCO4A1 p=0.138
SLCO1B1 p=0.119
SLCO1B1 p=0.266
SLC7A7 p=0.823
SLC7A7 p=0.983
SLC28A1 p=0.708
SLC28A1 p=0.118
SLC19A3 p=0.204
SLC19A3 p=0.253
SLC10A1 p=0.578
SLC10A1 p=0.264
SLC3A1 p=0.478
SLC3A1 p=0.423
SLC7A8 p=0.612
SLC7A8 p=0.872
SLC22A1 p=0.445
SLC22A1 p=0.885
SLCO1B3 p=0.961
SLCO1B3 p=0.504

Supplementary Figure 1. Survival and recurrence analyses of 75 patients with hepatocellular carcinoma according to *SLCO1B3*, *SLC22A1*, *SLC7A8*, *SLC3A1*, *SLC10A1*, *SLC19A3*, *SLC28A1*, *SLC7A7*, *SLCO1B1*, *SLCO4A1*, and *SLC38A2*, *SLC7A6*, *SLC29A1*, and *SLC29A2* expression levels.



Supplementary Figure 2. Adjuvant transcatheter arterial chemoembolization (TACE) after surgery did not reduce the early recurrence (≤ 2 year) rate, compared with no adjuvant TACE treatment.



Supplementary Figure 3. A. Cancer cell migration was measured using an Aurora nucleic acid extraction system. B. The invasion of cancer cells was measured using transwell migration assay.