

**Supplementary**

**Table S1** Primer sequences used in qRT-PCR

Primer	sequence
SLC26A6-F	CGGAGGGGAGACTACCACA
SLC26A6-R	ACCAAACCGGGAGGTGTTG
GAPDH-F	GGAGCGAGATCCCTCCAAAAT
GAPDH-R	GGCTGTTGTCATACTTCTCATGG

**Table S2** The genetic alterations in HCC patients from TCGA cohort (n=366)

Gene symbol	Number of samples altered	Percent samples altered
SLC45A4	64	17%
SLC39A4	60	16%
SLC52A2	60	16%
RHBG	45	12%
SLC41A1	37	10%
SLC26A9	36	10%
XPR1	36	10%
FLVCR1	35	10%
SLC35F3	35	10%
SLC16A3	29	8%
SLC26A11	26	7%
SLC6A19	25	7%
SLC22A23	24	7%
SLC9A3	23	6%
SLC25A19	23	6%
SLC16A6	20	5%
SLC45A1	18	5%
LETM2	18	5%
SLC2A5	16	4%
SLC30A3	14	4%
SLC35E2A	12	3%
SLC25A12	12	3%
SLC35E2B	12	3%
SLC7A10	11	3%
SLC47A2	11	3%
SLCO3A1	11	3%
SLC8A1	11	3%
SLC5A10	10	2.70%
SLC1A3	10	2.70%
SLC38A11	10	2.70%
SLC43A2	10	2.70%
SLC4A3	9	2.50%
SLC39A10	9	2.50%
SLC25A35	9	2.50%
SLC35E3	9	2.50%
SLC22A1	9	2.50%
SLC5A1	9	2.50%
SLC12A1	8	2.20%
SLC12A5	8	2.20%
SLC6A8	8	2.20%
SLC26A3	8	2.20%
SLC7A1	8	2.20%
SLC12A9	8	2.20%
SLC44A5	7	1.90%
SLC5A4	7	1.90%
SLC13A4	7	1.90%
RHCG	7	1.90%
SLC22A5	7	1.90%
SLCO2A1	7	1.90%
SLC37A1	7	1.90%
SLC9A6	7	1.90%
SLC4A4	7	1.90%
SLC3A1	7	1.90%
SLC6A11	6	1.60%
SLC1A7	6	1.60%
SLC2A6	6	1.60%
SLC29A2	6	1.60%
SLC44A3	6	1.60%
SLCO1B3	6	1.60%
SLC6A14	5	1.40%
SLC4A11	5	1.40%
SLC5A11	5	1.40%
SLC30A2	5	1.40%
SLC45A2	5	1.40%
SLC16A8	5	1.40%
SLC52A3	5	1.40%
SLC22A4	5	1.40%
SLC51B	5	1.40%
SLC14A2	5	1.40%
SLC36A1	5	1.40%
SLC35F2	5	1.40%
SLC16A9	5	1.40%
SLC29A4	5	1.40%
SLC25A14	5	1.40%
NPC1	5	1.40%
SLC2A11	5	1.40%
SLC15A2	5	1.40%
SLC46A1	5	1.40%
SLC7A8	5	1.40%
SLC7A4	5	1.40%
SLCO4C1	5	1.40%
SLC26A6	4	1.10%
SLC6A2	4	1.10%
SLC35G2	4	1.10%
SLC25A53	4	1.10%
SLC6A6	4	1.10%
SLC16A14	4	1.10%
SLC12A8	4	1.10%
SLC10A1	4	1.10%
SLC16A4	4	1.10%
SLC22A10	4	1.10%
SLC7A11	3	0.80%
SLC22A12	3	0.80%
SLC22A31	3	0.80%
SLC6A9	3	0.80%
SLC22A15	3	0.80%
SLC5A2	3	0.80%
SLC26A2	3	0.80%
SLC38A5	3	0.80%
SLC38A6	3	0.80%
SLC1A4	3	0.80%
NIPA1	3	0.80%
SLC19A3	3	0.80%
SLC22A11	2	0.50%
SLC7A6	2	0.50%
SLC35E4	2	0.50%
UCP3	2	0.50%
SLC25A29	2	0.50%
SLC2A1	2	0.50%
SLC38A1	2	0.50%
SLC41A3	2	0.50%
SLC39A13	2	0.50%
SLC39A3	2	0.50%
SLC25A47	2	0.50%
SLC38A8	1	0.30%
SLC2A14	1	0.30%
SLC10A6	1	0.30%
SLC25A51	1	0.30%

**Table S3** The associations of the 31 DESLCs with the clinical features

Gene symbol	P value (TNM stage)	P value (Grade)	P value (AFP level)	P value (vascular invasion)
<i>SLC1A5</i>	0.001031041	2.67E-05	1.61E-05	0.04370871
<i>SLC39A1</i>	0.002481512	6.99E-06	0.000190563	0.029499451
<i>SLCO4A1</i>	0.000372292	0.040850387	0.026442158	0.027618599
<i>SLC41A2</i>	0.023785383	0.032130973	0.00021766	0.027254897
<i>SLC50A1</i>	0.034895852	7.61E-05	0.00025576	0.023024909
<i>SLC9B2</i>	0.032850072	0.008783796	0.034917913	0.022302926
<i>SLC22A25</i>	0.000227375	0.000197008	0.029605659	0.0207215
<i>PQLC2</i>	0.023129834	0.000492411	4.56E-05	0.020417266
<i>SLC4A11</i>	0.000472158	0.002939092	0.000547743	0.018221205
<i>SLC39A10</i>	0.001889347	0.003342986	0.003439371	0.0167365
<i>SLC26A6</i>	0.024984841	9.66E-07	0.00030123	0.015889946
<i>SLC25A6</i>	0.000421119	0.001381644	0.000240923	0.015027551
<i>SLC7A1</i>	7.29E-05	0.000171785	0.025185645	0.014348794
<i>SLCO1B1</i>	1.47E-06	0.00520757	0.042674226	0.012495662
<i>SLC25A19</i>	3.61E-05	6.24E-06	0.000146627	0.00614604
<i>SLC27A5</i>	2.61E-06	4.80E-07	5.50E-10	0.005643085
<i>SLC2A2</i>	1.62E-06	0.002187411	0.002080227	0.005365904
<i>SLC35E3</i>	0.006975046	0.001610488	0.036071997	0.005181756
<i>SLC6A8</i>	2.03E-06	0.043624064	0.00034759	0.003968756
<i>SLC16A3</i>	4.45E-05	0.00128943	0.001355686	0.003133764
<i>SLC39A4</i>	0.014872664	0.000807146	4.58E-07	0.003093701
<i>SLC10A1</i>	3.86E-06	4.03E-08	1.21E-09	0.002023281
<i>LETMD1</i>	0.030626109	0.042870881	0.011641613	0.001909833
<i>SLC27A2</i>	2.31E-06	8.18E-07	4.53E-05	0.001681575
<i>SLC52A2</i>	0.000403736	4.42E-05	0.000904722	0.001500199
<i>SLC25A25</i>	0.000271766	0.009798229	2.48E-05	0.00136914
<i>FLVCR1</i>	0.000733314	4.64E-09	1.44E-08	0.001218744
<i>SLCO2A1</i>	0.000590375	0.001094139	0.003140637	0.000313974
<i>SLC22A1</i>	2.03E-06	8.35E-07	2.33E-06	0.000172057
<i>SLC25A47</i>	0.00028925	0.000725968	0.029350583	2.17E-05
<i>SLC16A2</i>	2.79E-05	4.47E-06	1.70E-08	2.66E-06

**Table S4** The associations between the clusters and the clinical or genetic features

	Cluster1	Cluster2	P value (Chi-square)
TP53-wildtype	153	20	0.027
TP53-mutation	59	17	
CTNNB1-wildtype	150	34	0.012
CTNNB1-mutation	62	3	
ALB-wildtype	188	35	0.427
ALB-mutation	24	2	
APOB-wildtype	187	33	1
APOB-mutation	25	4	
ARID1A-wildtype	193	36	0.335
ARID1A-mutation	19	1	
MYC-wildtype	175	28	0.32
MYC-amplification	37	9	
AFP-low	155	15	0.0001
AFP-high	57	22	
Grade 1-2	129	11	0.0004
Grade 3-4	83	26	
TNM stage I	130	12	0.001
TNM stage II-IV	82	25	
No-vascular invasion	147	16	0.002
Vascular invasion	65	21	