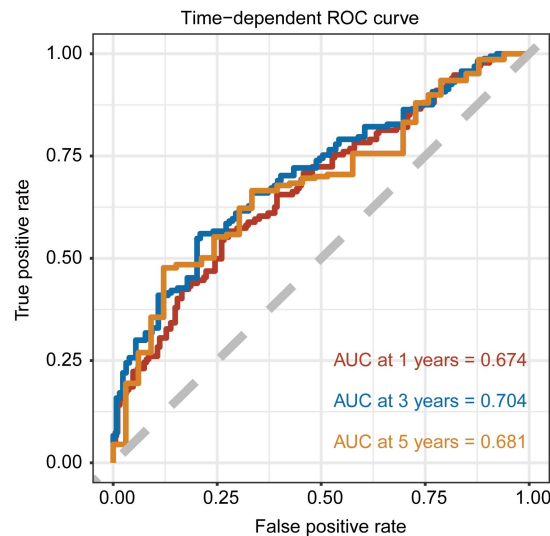


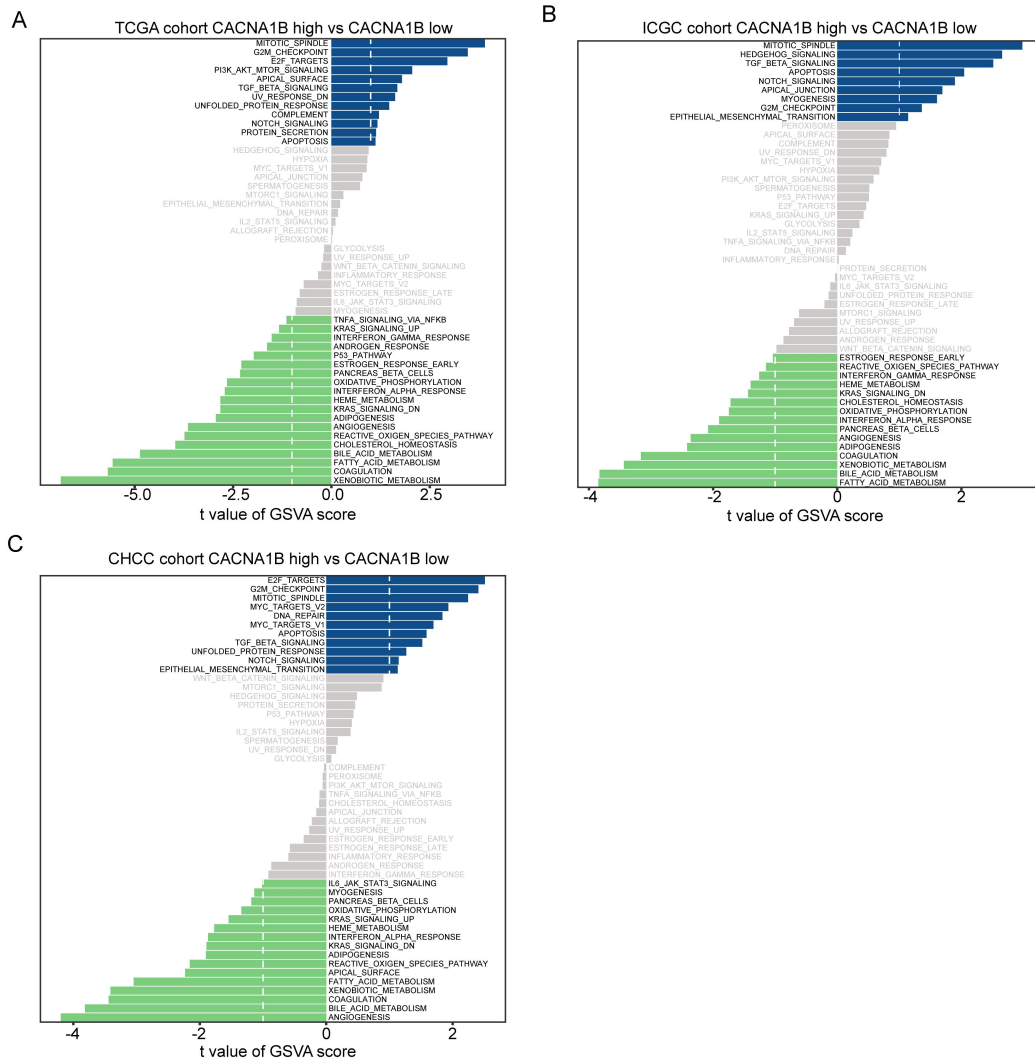
**Supplementary Figure1: Pathway Characteristics of CPRS.**

(A-C) Gene Set Variation Analysis (GSVA) comparing high- and low-CPRS patients.



**Supplementary Figure2:**The time-dependent ROC curve analysis for the CPRS in

predicting progression-free survival (PFS) among HCC patients in the TCGA-LIHC cohort.



**Supplementary Figure3:** Gene Set Variation Analysis (GSVA) comparing CACNA1B-high and CACNA1B-low groups across the TCGA(A), ICGC(B), and CHCC cohorts(C).

**Supplementary table1.The baseline clinical characteristics of CHCC cohort**

<b>Characteristic</b>	<b>N = 159<sup>a</sup></b>
Gender (male)	128 (81%)
PFStime(months)	23 (7, 37)
Ostime(months)	34 (22, 44)
PFS(yes)	80 (50%)
OS(dead)	56 (35%)
Liver.cirrhosis(yes)	112 (70%)
Tumor.size(cm)	5.5 (3.5, 9.0)
Lymph.node.metastasis(yes)	2 (1.3%)
Tumor.thrombus(yes)	37 (23%)
Tumour.enapsulation(yes)	111 (70%)
Preoperative.AFP(>500ng/ml)	115 (8, 2,524)
BCLC.stage	
A	68 (43%)
B	52 (33%)
C	39 (25%)
TNM.stage	
IA	5 (3.1%)
IB	86 (54%)
II	14 (8.8%)
IIIA	15 (9.4%)
IIIB	37 (23%)
IVA	2 (1.3%)

<sup>a</sup> n (%); Median (IQR)

**Supplementary table2.The baseline clinical characteristics of CHCC cohort**

<b>Characteristic</b>	<b>N = 203<sup>a</sup></b>
Gender(male)	153 (75%)
HBV(Positive)	57 (28%)
HCV(Positive)	121 (60%)
TNM4	
1	33 (16%)
2	96 (47%)
3	59 (29%)
4	15 (7.4%)
Vascular.invasion	
0	140 (69%)
1	37 (18%)
2	13 (6.4%)
3	5 (2.5%)
4	6 (3.0%)
5	2 (1.0%)

<sup>a</sup> n (%)

**Supplementary table3. Detailed information of included cohorts**

<b>Cohort Name</b>	<b>Tumor numb</b>	<b>Nomal numbe</b>	<b>Country</b>	<b>Year</b>	<b>Platform</b>
<b>Bulk RNA-seq cohort</b>					
CHCC	159	159	China	2019	Illumina HiSeq X Ten
ICGC-LIRI-JP	203	0	Japan	2016	Illumina HiSeq Illumina HiSeq
TCGA-LIHC	370	50	USA	2017	RNAseqV2
<b>ScRNA-seq cohort</b>					
GSE149614	13	8	China	2020	Illumina NovaSeq 6000

**Supplementary table4. siRNA sequences**

<b>siRNA-negative control strand</b>		<b>sequences</b>
siRNA-negative control	sense strand	UUCUCCGAACGUGUCACGUTT
siRNA-negative control	antisense strand	ACGUGACACGUUCGGAGAATT
CACNA1B-human-si2	sense strand	GGAUCUUCAAGUCACGAATT
CACNA1B-human-si2	antisense strand	UUCGUGACUUUGAAGAUCCTT
CACNA1B-human-si3	sense strand	GUUCAGAUGCAGAGCAUAATT
CACNA1B-human-si3	antisense strand	UUAUGCUCUGCAUCUGAACTT

**Supplementary table5. Primer sequences for qPCR**

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<b>Gene name</b>	<b>Sequence</b>
CACNA1B-Forward	GTGGGCTTTCCGAACACAAC
CACNA1B-Forward	GTTGTGTTCGGAAAGCCCAC
GAPDH-Forward	TGACATCAAGAAGGTGGTGAAGCAG
GAPDH-Rorward	GTGTCGCTGTTGAAGTCAGAGGAG

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**Supplementary table6. Antibody information**

<b>Antibodies</b>	<b>Cat No</b>	<b>Manufacturer</b>	<b>Country</b>
Anti-CACNA1B	19681-1-AP	Proteintech	China
Anti-GAPDH	60004-1-Ig	Proteintech	China
Anti-N-cadherin	22018-1-AP	Proteintech	China
Anti-Vimentin	10366-1-AP	Proteintech	China
Anti-CDK2	10122-1-AP	Proteintech	China

**Supplementary table7. 132 differentially expressed calcium-related genes**

<b>gene</b>	<b>logFC</b>	<b>logCPM</b>	<b>F</b>	<b>PValue</b>	<b>FDR</b>
CACNA1C	1.2414	1.3256	32.2874	2.47E-08	9.02E-08
RYR2	2.2159	0.7487	21.8006	4.06E-06	1.06E-05
CACNA1S	2.6717	-2.5402	37.9805	1.66E-09	7.26E-09
CACNA1E	3.1310	-0.2464	27.7053	2.25E-07	7.08E-07
CACNA1G	2.0619	-2.6673	22.6346	2.69E-06	7.20E-06
CACNB1	1.0755	0.1622	35.7363	4.79E-09	1.94E-08
CACNA1I	3.3520	0.4948	30.5923	5.57E-08	1.93E-07
CACNB3	1.1253	1.5128	36.7906	2.91E-09	1.22E-08
CACNB4	3.1785	-0.0114	54.8884	6.93E-13	5.14E-12
CAMK2A	1.9453	-0.2821	15.8999	7.86E-05	1.70E-04
S100A6	1.1605	6.3632	16.3176	6.36E-05	1.40E-04
CACNG1	4.8995	-1.8557	43.9599	1.02E-10	5.34E-10
CACNA2D3	2.1092	-0.0282	26.2853	4.48E-07	1.35E-06
KCNN3	1.5319	1.6951	72.8276	2.52E-16	3.05E-15
CABP1	1.7306	-1.5853	38.6781	1.20E-09	5.34E-09
S100A8	-1.0607	2.5888	11.5286	7.50E-04	1.40E-03
FGF23	-3.5798	-2.1164	103.9953	5.42E-22	1.38E-20
S100A1	1.6924	-1.0509	43.0106	1.58E-10	8.09E-10
KCNN1	2.5997	-1.3079	45.2938	5.50E-11	2.99E-10
SLC8A1	-1.3005	1.6522	79.3218	1.55E-17	2.19E-16
CAMK4	-1.7133	0.5906	114.1830	9.06E-24	2.83E-22
CAMK1G	1.8546	-0.1311	15.7543	8.46E-05	1.83E-04
CACNG4	4.0499	2.0824	35.7451	4.77E-09	1.94E-08
CAMK2B	-1.5828	2.3330	24.2734	1.20E-06	3.39E-06
AGXT	-1.1709	10.4737	28.9252	1.24E-07	4.09E-07
KCNN2	-3.4081	1.6849	166.4287	2.29E-32	2.38E-30
S100A12	-2.9384	-1.8007	168.7319	9.96E-33	1.11E-30
S100P	5.9448	5.9536	57.3961	2.24E-13	1.80E-12
KCNMB3	1.3058	0.2171	35.9654	4.29E-09	1.76E-08
CACNG8	1.3975	-1.9834	25.1402	7.84E-07	2.28E-06
CABYR	4.3188	2.1175	66.3006	4.33E-15	4.54E-14
S100A10	1.2903	7.0782	53.5589	1.26E-12	8.99E-12
CIB2	1.6369	1.0578	35.6431	5.00E-09	2.03E-08
HRCT1	2.8889	3.1290	58.6341	1.29E-13	1.08E-12
BGLAP	1.9392	-1.9682	55.3130	5.72E-13	4.30E-12
GRHPR	-1.1564	8.5174	68.7350	1.49E-15	1.65E-14
EGF	4.7337	0.3929	44.9874	6.33E-11	3.42E-10
S100A3	1.9856	-0.8849	30.9948	4.59E-08	1.61E-07
ATP2A1	1.5957	-0.2891	53.8721	1.10E-12	7.87E-12
CASKIN1	3.5292	-1.7644	51.3253	3.47E-12	2.28E-11
ALB	-1.8026	16.0359	99.4080	3.51E-21	7.95E-20
PLA2G6	1.3830	3.7509	76.1905	5.91E-17	7.72E-16
CALCA	4.0411	2.6278	29.3719	1.00E-07	3.34E-07
NECAB1	1.0821	0.0253	11.9950	5.88E-04	1.11E-03
CALB1	1.1777	-0.9449	6.6227	1.04E-02	1.61E-02
SPP1	4.3312	9.1533	52.6072	1.94E-12	1.34E-11
S100A14	1.4115	4.7501	12.3257	4.94E-04	9.46E-04
CAMK1G.1	1.8546	-0.1311	15.7543	8.46E-05	1.83E-04
SLC34A3	3.0498	-2.4518	52.1401	2.40E-12	1.63E-11
TACSTD2	-1.5079	2.6257	20.1806	9.09E-06	2.25E-05
CASQ1	1.6260	-2.0644	23.4355	1.81E-06	4.98E-06
PDGFRB	1.1782	5.9977	45.8663	4.22E-11	2.34E-10
SCGN	2.1865	3.7242	25.8088	5.65E-07	1.68E-06

CCBE1	-3.5336	1.0460	178.1089	3.49E-34	4.55E-32
CYP27B1	1.7385	0.1461	40.5288	5.02E-10	2.36E-09
ALPL	-1.5627	5.8482	44.7829	6.96E-11	3.73E-10
CADPS	2.5107	0.3960	16.5420	5.67E-05	1.26E-04
KCNH2	3.6458	1.5689	32.4563	2.28E-08	8.37E-08
NECAB3	1.5105	5.4024	105.9498	2.46E-22	6.54E-21
SLC8A2	1.9635	-2.4236	22.1025	3.50E-06	9.21E-06
CRACR2B	1.3521	2.6340	23.7060	1.58E-06	4.40E-06
CALB2	1.6807	-1.9320	12.5656	4.37E-04	8.42E-04
TRPC6	2.1482	-0.2081	117.2261	2.71E-24	9.27E-23
TRPC4	1.3401	-0.3590	21.0378	5.93E-06	1.51E-05
CAMK2N2	2.4366	2.2749	48.6614	1.17E-11	7.05E-11
KCNU1	7.3907	1.7079	54.3780	8.72E-13	6.37E-12
STX1A	1.6181	0.9477	87.5421	4.79E-19	8.31E-18
SLC34A2	1.8879	4.0574	7.7165	5.71E-03	9.27E-03
CLDN19	2.9287	0.2230	28.8135	1.31E-07	4.30E-07
CABP7	2.2501	-2.3112	41.4740	3.23E-10	1.58E-09
UMODL1	1.3073	-1.5079	6.9642	8.62E-03	1.35E-02
TRPC3	1.8847	-1.0371	13.7183	2.40E-04	4.83E-04
CASQ2	1.4255	0.2828	25.6975	5.97E-07	1.76E-06
ACE	1.0660	2.4285	40.0060	6.42E-10	2.97E-09
PTH1R	-3.2364	2.6055	292.1277	3.08E-50	4.52E-47
TRPC5	-1.0391	-0.7927	9.4895	2.20E-03	3.82E-03
PTHLH	2.2563	1.1777	18.6482	1.96E-05	4.62E-05
ANO1	-1.0751	5.9316	17.9049	2.85E-05	6.58E-05
SYT1	1.0275	2.0529	6.8267	9.30E-03	1.45E-02
REN	1.9930	1.2436	21.4745	4.77E-06	1.23E-05
PVALB	-3.6445	-1.4901	205.1819	2.94E-38	7.91E-36
PHEX	3.1753	-0.2413	47.7417	1.78E-11	1.04E-10
EFCAB12	1.1812	2.2273	15.5447	9.42E-05	2.01E-04
HOGA1	-1.7050	4.3517	70.8612	5.91E-16	6.86E-15
C2CD4B	-1.5001	0.1099	35.5196	5.30E-09	2.14E-08
ITPR3	1.3204	3.3761	15.2537	1.09E-04	2.31E-04
SCN5A	2.1393	-2.1934	22.3400	3.11E-06	8.25E-06
PLN	1.2797	0.8064	10.9935	9.93E-04	1.81E-03
CYP3A4	-1.6156	10.5962	13.1658	3.20E-04	6.29E-04
TRPM6	1.0241	-1.4110	7.7359	5.65E-03	9.18E-03
ANXA2	1.2028	8.2658	59.2011	1.00E-13	8.53E-13
FXYD2	2.1601	0.8776	16.5250	5.72E-05	1.27E-04
EFCAB8	1.0921	-2.9162	13.6297	2.52E-04	5.04E-04
PLCG1	1.0215	5.0805	72.3183	3.14E-16	3.75E-15
FOS	-3.1051	6.9994	228.7876	1.14E-41	4.61E-39
C2CD4D	1.4087	-1.7020	33.3045	1.52E-08	5.72E-08
NOX5	1.4407	-2.5097	18.0401	2.66E-05	6.17E-05
CRP	-1.1402	11.2358	7.9112	5.14E-03	8.39E-03
RET	-2.1966	1.3684	46.8168	2.73E-11	1.55E-10
C2CD6	1.4049	-2.1325	20.2343	8.85E-06	2.20E-05
KCNJ5	2.1683	2.4368	46.4641	3.21E-11	1.80E-10
BSND	3.2351	-2.5195	36.5867	3.20E-09	1.33E-08
SYT2	2.1004	-0.7793	25.7203	5.90E-07	1.75E-06
ASPH	1.0037	7.4503	26.2677	4.52E-07	1.36E-06
SPARCL1	2.8054	7.2006	54.1462	9.68E-13	7.01E-12
TRPV4	-1.2588	2.9998	24.0519	1.34E-06	3.76E-06
IL6	-1.9006	-0.4772	41.1128	3.83E-10	1.85E-09
KCNIP3	1.5791	1.8225	19.9780	1.01E-05	2.48E-05
TNNC1	3.0928	1.4746	42.3708	2.13E-10	1.07E-09

PKD1L1	1.1822	-0.8114	22.3227	3.14E-06	8.32E-06
PLA2G4C	1.2818	4.1545	45.3309	5.41E-11	2.94E-10
DMD	-1.2553	5.2298	72.5954	2.79E-16	3.35E-15
MGP	1.0971	4.6741	16.8351	4.89E-05	1.09E-04
DNAH8	2.1448	-1.8255	30.7138	5.25E-08	1.83E-07
TNFSF11	-1.1086	0.5561	14.3722	1.72E-04	3.53E-04
ADCY8	3.1052	0.6152	17.6563	3.23E-05	7.40E-05
PRKCB	-1.1425	2.0672	36.3215	3.63E-09	1.50E-08
CDKN3	3.9474	3.0061	219.5868	2.36E-40	8.10E-38
GRIN2A	2.8021	0.2867	25.0766	8.09E-07	2.34E-06
OXT	-1.5853	0.6318	14.5039	1.60E-04	3.31E-04
RGN	-1.0479	7.3649	38.0151	1.63E-09	7.15E-09
F9	-1.8506	8.0868	47.5632	1.94E-11	1.13E-10
F2RL3	2.3268	1.9808	54.5802	7.96E-13	5.84E-12
CCL2	-1.3585	4.0531	39.5044	8.11E-10	3.71E-09
GRIN1	2.9596	-2.1596	37.6234	1.96E-09	8.50E-09
TP53I3	1.9099	4.5694	76.4036	5.40E-17	7.08E-16
MYLK2	1.5730	-2.2643	25.8318	5.59E-07	1.66E-06
HDAC4	1.0125	3.1753	70.5985	6.63E-16	7.63E-15
AIF1L	1.4203	3.3271	29.6046	8.96E-08	3.01E-07
PPEF1	2.2649	-2.2815	42.6813	1.84E-10	9.34E-10
IGF1	-1.1837	3.0308	21.7854	4.09E-06	1.07E-05
GATA3	-1.2959	0.6950	38.0656	1.59E-09	6.99E-09

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**Supplementary table8. The relationship between the CPRS and clinical characteristics in HCC patients**

Characteristic	Overall, N = 368 <sup>a</sup>	High-risk, N = 184 <sup>a</sup>	Low-risk, N = 184 <sup>a</sup>	p-value <sup>b</sup>
age (>median)	191 (52%)	97 (53%)	94 (51%)	0.8
gender(male)	248 (67%)	121 (66%)	127 (69%)	0.5
Alcohol.consumption(Yes)	117 (32%)	66 (36%)	51 (28%)	0.093
Family.history (Yes)	111 (30%)	55 (30%)	56 (30%)	0.7
HBV (Positive)	104 (28%)	36 (20%)	68 (37%)	<0.001
HCV (Positive)	56 (15%)	30 (16%)	26 (14%)	0.6
AFP(>500ng/ml)	65 (24%)	30 (24%)	35 (24%)	>0.9
Vascular.invasion (Yes)	108 (35%)	64 (43%)	44 (27%)	0.002
Histologic.grade (G3-G4)	134 (37%)	77 (42%)	57 (32%)	0.04
TNM (III-IV)	92 (27%)	58 (34%)	34 (20%)	0.002
OS(dead)	130 (35%)	86 (47%)	44 (24%)	<0.001
PFS (Yes)	210 (57%)	120 (66%)	90 (49%)	0.002
CSN1S1	0.02 (1.07)	0.20 (1.47)	-0.15 (0.26)	0.066
S100A9	-0.03 (1.04)	0.59 (1.03)	-0.65 (0.58)	<0.001
CACNA1B	0.03 (1.07)	0.17 (1.49)	-0.12 (0.18)	<0.001
FKBP1A	0.19 (0.90)	0.68 (0.80)	-0.30 (0.70)	<0.001
SLC25A24	0.03 (1.05)	0.50 (1.17)	-0.43 (0.65)	<0.001
SPP1	0.09 (1.03)	0.82 (0.72)	-0.65 (0.72)	<0.001

<sup>a</sup> n (%); Mean (SD)

<sup>b</sup> Pearson's Chi-squared test; Wilcoxon rank sum test

**Supplementary table9. The result of Gene Set Variation Analysis**

<b>TCGA</b>	<b>logFC</b>	<b>AveExpr</b>	<b>t</b>	<b>P.Value</b>	<b>adj.P.Val</b>	<b>B</b>
HALLMARK_ALLOGRAFT_REJECTION	0.2357	-0.0103	6.5642	1.75E-10	1.10E-09	12.8947
HALLMARK_COMPLEMENT	0.1398	-0.0066	6.2390	1.20E-09	4.83E-09	11.0205
HALLMARK_P53_PATHWAY	0.0990	-0.0225	6.2304	1.26E-09	4.83E-09	10.9717
HALLMARK_MYC_TARGETS_V1	0.2246	-0.0304	6.1241	2.31E-09	7.71E-09	10.3767
HALLMARK_APOPTOSIS	0.1089	-0.0167	5.6735	2.81E-08	8.78E-08	7.9475
HALLMARK_KRAS_SIGNALING_DN	-0.1309	0.0381	-7.2583	2.29E-12	2.87E-11	17.1432
HALLMARK_BILE_ACID_METABOLISM	-0.4188	0.0220	-12.1042	1.12E-28	5.62E-27	54.2505

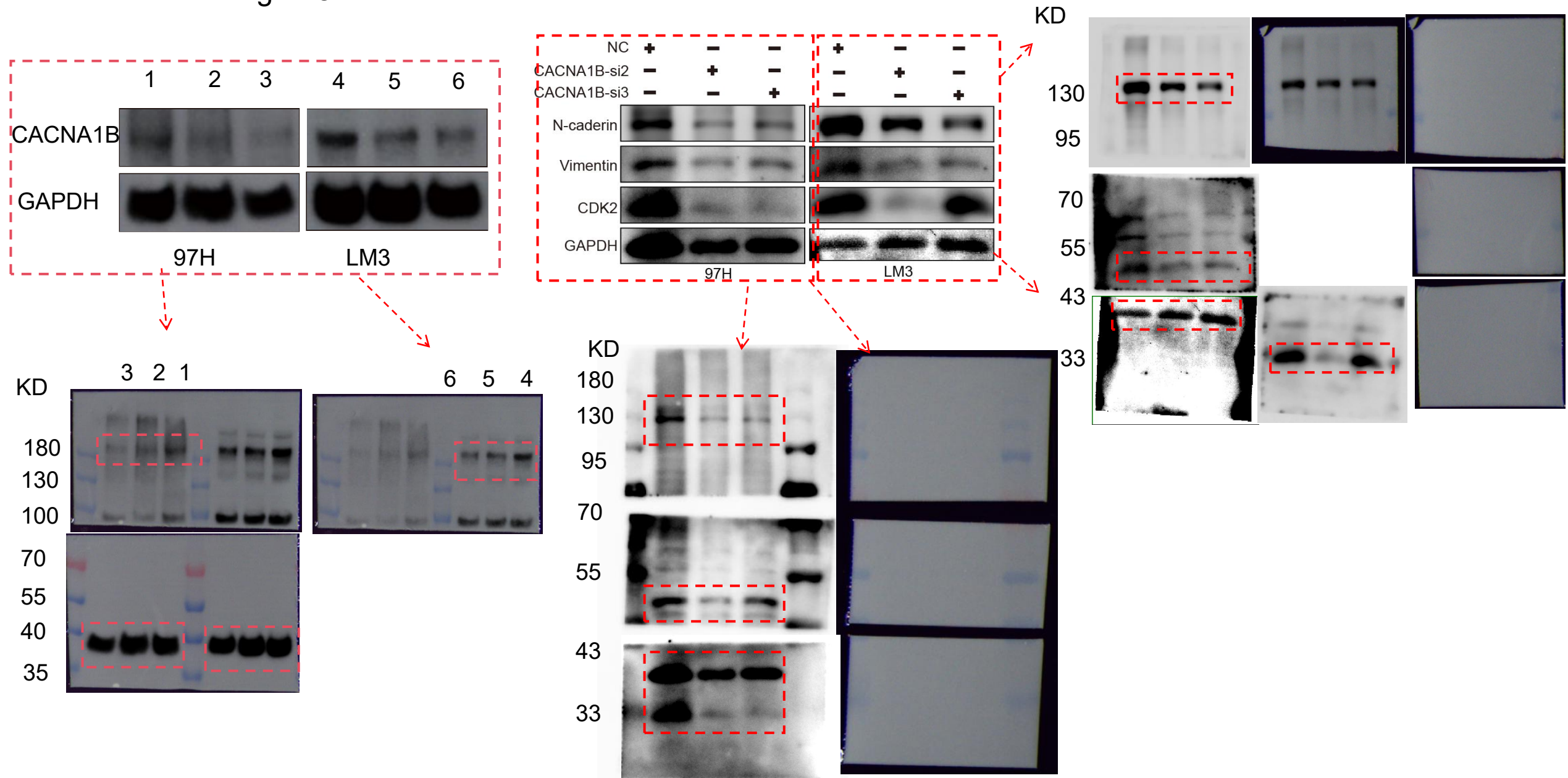
<b>ICGC</b>	<b>logFC</b>	<b>AveExpr</b>	<b>t</b>	<b>P.Value</b>	<b>adj.P.Val</b>	<b>B</b>
HALLMARK_APOPTOSIS	0.1470	-0.0164	5.3723	2.08E-07	2.60E-06	6.4787
HALLMARK_COMPLEMENT	0.1551	-0.0074	4.7484	3.82E-06	2.12E-05	3.6833
HALLMARK_ALLOGRAFT_REJECTION	0.2017	-0.0053	4.1526	4.80E-05	0.00016199	1.2749
HALLMARK_MYC_TARGETS_V1	0.2256	-0.0349	4.1496	4.86E-05	0.00016199	1.2636
HALLMARK_P53_PATHWAY	0.0911	-0.0285	4.1134	5.62E-05	0.00017568	1.1259
HALLMARK_KRAS_SIGNALING_DN	-0.1379	0.0260	-7.2203	9.67E-12	2.42E-10	16.1668
HALLMARK_BILE_ACID_METABOLISM	-0.3441	0.0013	-7.2822	6.71E-12	2.42E-10	16.5224

<b>CHCC</b>	<b>logFC</b>	<b>AveExpr</b>	<b>t</b>	<b>P.Value</b>	<b>adj.P.Val</b>	<b>B</b>
HALLMARK_BILE_ACID_METABOLISM	-0.2535	-0.0089	-4.5713	9.48E-06	7.90E-05	2.9604
HALLMARK_KRAS_SIGNALING_DN	-0.0953	0.0082	-4.0443	8.05E-05	0.00044723	0.9355
HALLMARK_APOPTOSIS	0.1260	-0.0360	4.0106	9.17E-05	0.00045848	0.8129
HALLMARK_ALLOGRAFT_REJECTION	0.2718	-0.0289	5.2556	4.52E-07	5.65E-06	5.8684
HALLMARK_MYC_TARGETS_V1	0.3157	-0.0278	5.4115	2.17E-07	3.62E-06	6.5719
HALLMARK_COMPLEMENT	0.1827	-0.0350	5.7474	4.29E-08	1.07E-06	8.1350
HALLMARK_P53_PATHWAY	0.1500	-0.0327	6.1970	4.46E-09	2.23E-07	10.3227

## Supplementary Box1.392 calcium-related genes

Gene symbol								
CACNA1C	CALHM1	CALHM2	GRM1	KCNMB1	SLC24A1	PDGFB	CABYRP1	UMOD
ORAI1	EGF	RCVRN	TRPM2	CACNG2	GALNT3	PHEX	DNAH8	FOS
CACNA1A	MEN1	RRAD	PSEN1	LOC10013	CABP4	EFCAB12	TNFSF11	CAMKK1
CACNA1B	S100A3	TRPC3	GUCA1A	SLC8A1	MCUB	CAPN1	CPNE6	NOX5
RYR2	ATP2A1	PTK2B	LOC106736	GNA11	CYP27B1	HOGA1	S100A7P1	RCN2
CACNA1D	CASK	CACFD1	SDF4	CAMKK2	CABP2	EFCAB3	ALPP	PKD2L1
TRPV6	ATP2A3	CASQ2	CRP	PRKAR1A	CLCN5	SLC25A13	SLC25A23	C2CD4D
CACNB2	SLC8B1	SARAF	CALHM4	CALM1	MCUR1	C2CD4B	CETN2	CAPN3
CACNA1S	SLC34A1	C2CD5	CALHM5	MICU2	ALPL	ITPR3	CDH23	
CAMK2G	ALB	ATP2B3	ELN	CAMK4	CALM3	CLCA2	ADCY8	
CACNA1E	PLA2G6	ACE	KCNQ1-AS	CAMK1	SRI	TRPM4	MAPK3	
ANKH	SLC24A3	DSP	RET	CAMK2D	CALM2	TRPM7	MAPK10	
CACNA1H	ENPP1	PTH1R	C2CD6	ORAI2	CHERP	NR1I3	ANXA11	
CACNA1G	CAMK1D	CLCA1	MYORG	KCNMB4	HSPG2	C2CD4A	PLA2G2A	
KCNMA1	CALCA	CDH1	TANGO2	CACNG4	CADPS	KNG1	PRKCB	
CACNA1F	RYR3	TRPC5	KCNJ5	ADCY10	SLC24A2	SCN5A	CDKN3	
CACNA2D1	CRACR2A	PTHLH	TPCN2	ORAI3	HPCA	PLN	GRIN2A	
RYR1	NECAB1	ANO1	BSND	CAMK2B	KCNH2	CAB39L	FKBP1A	
CACNB1	S100A16	ANXA6	CFTR	AGXT	CCAL1	EFCAB13	OXT	
S100B	CALB1	SYT1	C2CD2	TNFRSF1	CADPS2	CYP3A4	RGN	
CACNA1I	SPP1	RASGRP1	CPNE1	ATP2A2	ATP2B2	TRPM6	F9	
CACNB3	ATP2B4	SLC12A3	SYT2	KCNN2	CABS1	CD36	CAV1	
PTH	S100A14	EFCAB11	GSN	S100A12	NECAB3	ITPR2	SLC25A25	
CACNB4	NECAB2	EDN1	ASPH	S100P	SMOC2	ANXA2	CASKP1	
CACNA2D2	PLA2G4A	CAB39	TRPC7	CACNG6	SLC8A2	JAM2	PPP3CA	
KCNN4	KCNQ1	NOS3	STIM2	CACNG7	CRACR2B	SLC25A12	CATSPER1	
CAMK2A	TRPV5	CAMK2N1	SPARC	GNAS	CIB4	CALCOCO1	EEF2K	
CIB1	S100A5	LRP2	TRPV4	KCNMB3	SLC20A2	FBN1	F2	
NCS1	CAMK1G	GCA	RCN1	CACNG8	CALCOCO1	FXRD	ATP2C2	
MICU1	MICU3	EFCAB7	CAST	CACNG3	CALB2	XPR1	TPCN1	
S100A6	S100Z	PRKCA	IL6	S100A7	TRPC6	CXADR	F10	
STIM1	CYP24A1	CALHM3	KCNIP3	CACNG5	CIB3	CREB1	CCL2	
CACNG1	PDCD6	SLC24A5	CDH2	GCM2	TRPC4	EFCAB8	GNAQ	
CACNA2D3	CABP5	CAPN2	S100A7P2	CAMLG	FAM20A	C2CD4C	GRIN1	
S100A4	SLC8A3	LOC108663	TNNC1	S100A11	RASGRP2	AMBP	TP53	
S100A9	SLC34A3	CABCOCOP	PKD1	CABYR	CARHSP1	PKP2	TGM2	
KCNN3	SMOC1	EFCAB6	CSN1S1	CANT1	CAPNS1	SLC25A24	MYLK	
SLC26A1	CARF	REN	CLCA4	KCNMB2	CAMK2N2	INS	HDAC4	
CABP1	TACSTD2	DSPP	VSNL1	S100A10	KCNU1	PNPLA8	AIF1	
VDR	S100A7A	EFCAB14	TMEM37	ATP2B1	STX1A	PKD2	BEST1	
S100A8	CASQ1	ANXA5	LBR	S100A2	SLC34A2	HPCAL1	GRIN2B	
FGF23	PDGFRB	EFCAB2	PLA2G4C	CIB2	SLC24A4	PLCG1	PPEF1	
S100A1	SCGN	KRIT1	DMD	KL	CLDN19	CALHM6	DOC2B	
MCU	AP2S1	S100A7L2	NOS1	HRC	CALR	TRPV1	NAGLU	
KCNN1	TRPC1	CHP1	MGP	BGLAP	MAPK1	CLCNKB	IGF1	
S100G	CCBE1	EFCAB5	CCND1	ITPR1	CABP7	TNF	PIK3C2A	
OTULIN	CDC73	PVALB	AIRE	S100A13	EFCAB9	CYP2R1	GATA3	
CACNA2D4	CLDN16	EFCAB10	PRKCE	GRHPR	ATP2C1	ANXA1	ABCC6	

# Source data of Figure8



Source data : Source gel images for Figure8C and 8K. The red rectangles show the cropping location.