

CC patients

NO	Age (years)	Expression			Group	Cervical cancer	Stage	Survival state	Survival time
		BCYRN1	miR-330-5p	HMGB3					
1	56	1.48	0.67	1.65	High expression	squamous cell carcinoma	FIGO stage II	death	33
2	46	1.27	0.49	0.88	High expression	squamous cell carcinoma	FIGO stage II	alive	60
3	53	1.11	0.74	0.97	Low expression	squamous cell carcinoma	FIGO stage I	death	12
4	39	0.59	1.10	0.93	Low expression	adenocarcinoma	FIGO stage I	alive	60
5	50	1.27	0.59	1.58	High expression	squamous cell carcinoma	FIGO stage I	alive	60
6	44	1.11	1.16	1.65	Low expression	adenocarcinoma	FIGO stage I	alive	21
7	45	1.92	0.41	1.78	High expression	squamous cell carcinoma	FIGO stage II	death	6
8	46	1.01	1.08	1.34	Low expression	adenocarcinoma	FIGO stage II	death	42
9	58	0.62	1.27	1.56	Low expression	adenocarcinoma	FIGO stage I	alive	60
10	40	1.16	1.23	1.54	Low expression	adenocarcinoma	FIGO stage II	death	9
11	58	1.39	0.64	1.34	High expression	adenocarcinoma	FIGO stage I	alive	60
12	65	1.02	1.04	0.91	Low expression	squamous cell carcinoma	FIGO stage I	death	12
13	51	1.64	0.78	1.16	High expression	adenocarcinoma	FIGO stage I	death	48
14	46	1.23	1.30	0.82	High expression	squamous cell carcinoma	FIGO stage II	alive	60
15	50	1.71	0.64	1.38	High expression	adenocarcinoma	FIGO stage I	death	18
16	50	1.12	1.16	0.81	Low expression	squamous cell carcinoma	FIGO stage II	death	15
17	57	1.48	0.53	0.95	High expression	squamous cell carcinoma	FIGO stage I	death	21
18	53	1.27	1.05	0.78	High expression	adenocarcinoma	FIGO stage I	alive	60
19	51	0.74	0.49	1.20	Low expression	squamous cell carcinoma	FIGO stage I	death	60
20	43	1.22	1.24	0.65	Low expression	squamous cell carcinoma	FIGO stage II	death	3
21	41	1.14	1.25	0.76	Low expression	adenocarcinoma	FIGO stage I	death	6
22	59	1.26	1.14	0.96	High expression	adenocarcinoma	FIGO stage II	alive	60
23	55	0.53	1.36	0.63	Low expression	squamous cell carcinoma	FIGO stage II	alive	60
24	39	1.72	0.67	1.69	High expression	adenocarcinoma	FIGO stage I	death	15
25	37	0.83	0.65	0.80	Low expression	squamous cell carcinoma	FIGO stage I	death	6
26	55	1.00	0.99	0.68	Low expression	adenocarcinoma	FIGO stage II	death	45
27	50	0.97	1.21	0.84	Low expression	squamous cell carcinoma	FIGO stage I	death	57
28	52	0.92	1.08	0.70	Low expression	squamous cell carcinoma	FIGO stage II	death	27
29	61	1.24	0.76	1.59	High expression	adenocarcinoma	FIGO stage I	alive	60
30	47	0.80	0.99	1.01	Low expression	squamous cell carcinoma	FIGO stage I	death	48
31	59	1.21	1.07	1.05	Low expression	adenocarcinoma	FIGO stage II	death	6
32	39	1.01	0.96	0.88	Low expression	squamous cell carcinoma	FIGO stage I	death	12
33	45	1.43	0.97	0.71	High expression	adenocarcinoma	FIGO stage II	death	60
34	53	0.72	1.03	0.81	Low expression	adenocarcinoma	FIGO stage I	alive	60
35	67	1.38	0.61	0.88	High expression	squamous cell carcinoma	FIGO stage II	alive	60
36	53	0.69	0.86	0.76	Low expression	squamous cell carcinoma	FIGO stage II	alive	60
37	59	0.95	0.96	1.45	Low expression	adenocarcinoma	FIGO stage I	alive	21
38	64	0.90	1.29	1.67	Low expression	squamous cell carcinoma	FIGO stage I	death	9
39	37	1.09	1.02	1.26	Low expression	adenocarcinoma	FIGO stage II	death	24
40	51	1.55	0.62	0.90	High expression	adenocarcinoma	FIGO stage II	death	51
41	46	0.77	0.49	0.77	Low expression	squamous cell carcinoma	FIGO stage I	death	60
42	47	0.97	0.95	0.98	Low expression	adenocarcinoma	FIGO stage I	death	9
43	61	0.99	1.29	1.51	Low expression	squamous cell carcinoma	FIGO stage I	death	15
44	55	1.45	0.52	1.16	High expression	adenocarcinoma	FIGO stage II	alive	54
45	58	1.03	0.84	0.98	Low expression	adenocarcinoma	FIGO stage I	death	33
46	65	1.41	0.81	1.37	High expression	squamous cell carcinoma	FIGO stage I	alive	60
47	67	1.52	0.69	1.25	High expression	adenocarcinoma	FIGO stage II	death	21
48	43	1.26	0.97	1.48	High expression	squamous cell carcinoma	FIGO stage I	alive	60
49	36	0.59	1.35	0.65	Low expression	squamous cell carcinoma	FIGO stage I	alive	60
50	56	1.23	0.85	1.02	High expression	squamous cell carcinoma	FIGO stage I	alive	60
51	41	1.52	0.68	1.64	High expression	adenocarcinoma	FIGO stage II	death	33
52	55	1.80	0.44	1.71	High expression	squamous cell carcinoma	FIGO stage I	alive	12
53	44	1.00	0.80	1.18	Low expression	adenocarcinoma	FIGO stage II	alive	12
54	46	1.69	0.76	1.46	High expression	squamous cell carcinoma	FIGO stage I	death	27
55	42	1.67	0.52	1.45	High expression	squamous cell carcinoma	FIGO stage II	death	42
56	46	1.65	0.81	1.68	High expression	adenocarcinoma	FIGO stage I	death	45
57	48	1.23	0.59	1.37	High expression	adenocarcinoma	FIGO stage II	alive	60
58	52	1.27	0.73	1.27	High expression	squamous cell carcinoma	FIGO stage II	alive	60
59	44	1.30	1.31	1.55	High expression	squamous cell carcinoma	FIGO stage I	alive	60
60	49	1.68	0.68	1.66	High expression	adenocarcinoma	FIGO stage II	death	33
61	52	1.14	1.15	1.55	Low expression	squamous cell carcinoma	FIGO stage II	death	15
62	59	1.61	0.53	1.01	High expression	squamous cell carcinoma	FIGO stage I	death	57

Fig. 1

Fig. 1. BCYRN1 is overexpressed in CC, and it is responsible for poor prognosis and DDP-resistance of CC patients.

A, the relation between BCYRN1 and CC predicted by Incrnadisease database.

LncRNA name	Disease name	Dysfunction type	Description	Chr	Start	End	Strand	Species	Alias	Genbank	Sequence	Reference
BCYRN1	cervical cancer	Expression	BC200 RNA was expressed in carcinomas of the breast, cervix, oesophagus, lung, ovary, parotid and tongue, but not in corresponding normal tissues	chr2	47335315	47335314	+	Human	BC200; BC200a; LINC00004; NCRNA00004	NR_001568	GeneRNA	9422992

B, BCYRN1 expression in 62 pairs of CC and paracancerous tissues verified via RT-qPCR.

qRT-PCR data of BCYRN1 (GAPDH as internal reference)						
Sample	NO.	Ct values		ΔCt	ΔΔCt	relative expression
		GAPDH	BCYRN1	BCYRN1	BCYRN1	BCYRN1
para-carcinoma tissue	1	17.12	21.36	4.24	-0.03	1.02
	2	18.23	21.97	3.74	-0.53	1.45
	3	18.43	22.54	4.11	-0.16	1.12
	4	17.99	22.56	4.57	0.30	0.81
	5	17.99	22.15	4.16	-0.11	1.08
	6	18.10	22.02	3.92	-0.36	1.28
	7	18.66	22.57	3.91	-0.36	1.28
	8	18.42	22.13	3.71	-0.56	1.48
	9	17.87	22.78	4.91	0.64	0.64
	10	18.67	22.56	3.89	-0.38	1.30
	11	17.78	21.89	4.11	-0.16	1.12
	12	18.67	23.23	4.56	0.29	0.82
	13	17.66	21.78	4.12	-0.15	1.11
	14	18.66	22.86	4.20	-0.07	1.05
	15	18.43	23.32	4.89	0.62	0.65
	16	17.44	22.45	5.01	0.74	0.60
	17	18.44	22.42	3.98	-0.29	1.22
	18	18.40	22.84	4.44	0.17	0.89
	19	18.54	22.67	4.13	-0.14	1.10
	20	17.76	21.77	4.01	-0.26	1.20
	21	17.54	22.16	4.62	0.35	0.79
	22	18.56	23.13	4.57	0.30	0.81
	23	18.42	22.56	4.14	-0.13	1.10
	24	17.78	21.78	4.00	-0.27	1.21
	25	16.80	21.59	4.79	0.52	0.70
	26	16.90	20.76	3.86	-0.41	1.33
	27	18.67	22.76	4.09	-0.18	1.13
	28	18.66	23.16	4.50	0.23	0.85
	29	18.65	23.24	4.59	0.32	0.80
	30	17.55	22.36	4.81	0.54	0.69
	31	16.78	20.78	4.00	-0.27	1.21
	32	18.54	22.69	4.15	-0.12	1.09
	33	18.54	22.46	3.92	-0.35	1.28
	34	18.56	23.36	4.80	0.53	0.69
	35	17.56	21.67	4.11	-0.16	1.12
	36	18.65	22.91	4.26	-0.01	1.01
	37	17.78	21.78	4.00	-0.27	1.21
	38	18.65	22.67	4.02	-0.25	1.19
	39	18.65	23.36	4.71	0.44	0.74
	40	18.56	22.56	4.00	-0.27	1.21
	41	17.56	21.45	3.89	-0.38	1.30
	42	18.54	23.41	4.87	0.60	0.66
	43	18.43	22.36	3.93	-0.34	1.27
	44	18.56	22.65	4.09	-0.18	1.13
	45	18.57	23.66	5.09	0.82	0.57
	46	18.56	22.56	4.01	-0.27	1.20
	47	18.43	22.81	4.38	0.11	0.93
	48	17.11	21.11	4.00	-0.27	1.21
	49	18.21	22.58	4.37	0.10	0.93
	50	17.67	21.56	3.89	-0.38	1.30
	51	17.68	21.67	3.99	-0.28	1.22
	52	18.32	22.64	4.32	0.05	0.97
	53	17.54	22.56	5.02	0.75	0.60
	54	18.12	22.00	3.88	-0.39	1.31
	55	17.86	22.76	4.90	0.63	0.65
	56	18.65	22.54	3.89	-0.38	1.30
	57	17.56	22.36	4.80	0.53	0.69
	58	18.65	22.67	4.02	-0.25	1.19
	59	17.76	22.36	4.60	0.33	0.80
	60	17.88	21.92	4.04	-0.23	1.17
	61	18.21	22.32	4.11	-0.16	1.12
	62	18.24	22.43	4.19	-0.08	1.06
	AVERAGE	18.12	22.39	4.27	0.00	1.03
	STDEV	0.53	0.63	0.37	0.37	0.24
	1	17.64	21.32	3.68	-0.56	1.48
	2	18.34	21.74	3.40	-0.34	1.27
	3	18.27	22.23	3.96	-0.15	1.11
	4	17.08	22.41	5.33	0.76	0.59
	5	17.11	20.93	3.82	-0.34	1.27
	6	17.56	21.32	3.76	-0.16	1.11

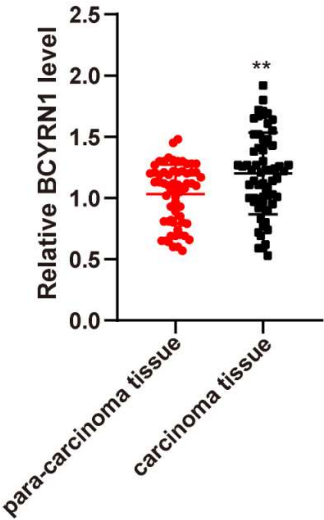
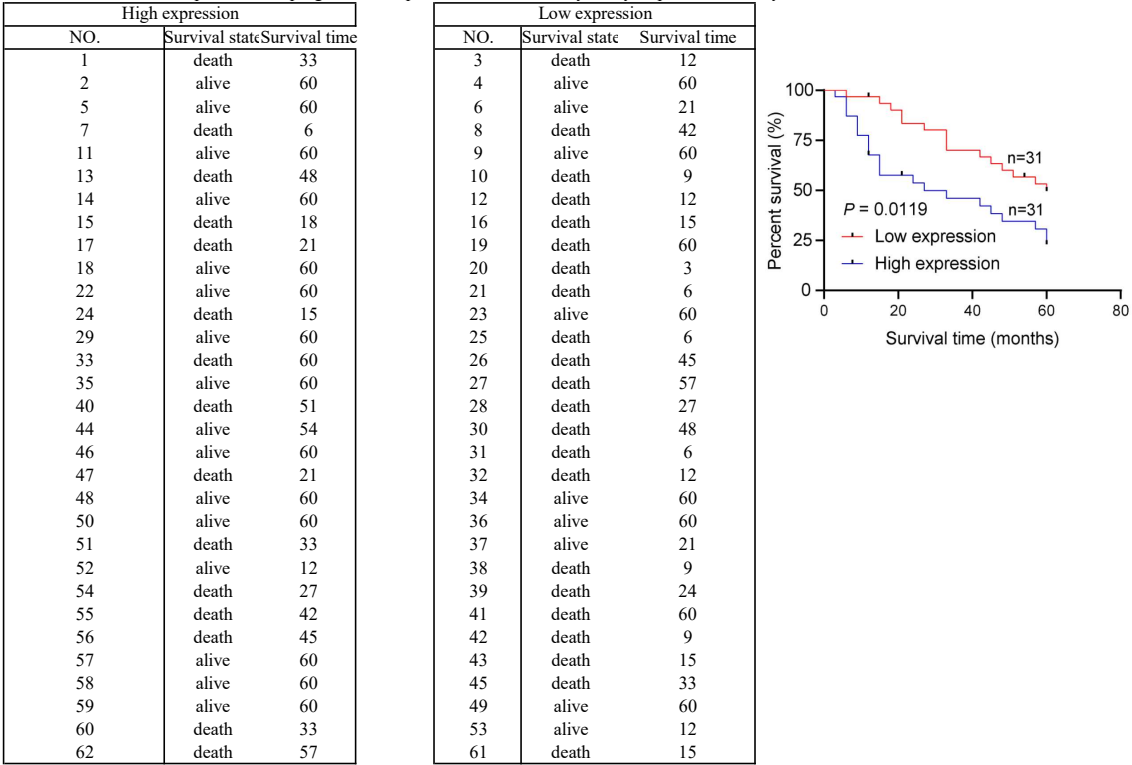


Fig. 1

carcinoma tissue	7	18.22	21.19	2.97	-0.94	1.92
	8	17.56	21.26	3.70	-0.01	1.01
	9	16.78	22.38	5.60	0.69	0.62
	10	18.56	22.24	3.68	-0.21	1.16
	11	18.67	22.30	3.63	-0.48	1.39
	12	17.80	22.33	4.53	-0.03	1.02
	13	17.87	21.28	3.41	-0.71	1.64
	14	18.22	22.12	3.90	-0.30	1.23
	15	18.44	22.56	4.12	-0.77	1.71
	16	18.67	23.52	4.85	-0.16	1.12
	17	18.67	22.08	3.41	-0.57	1.48
	18	18.67	22.77	4.10	-0.34	1.27
	19	17.65	22.21	4.56	0.43	0.74
	20	17.67	21.39	3.72	-0.29	1.22
	21	18.11	22.54	4.43	-0.19	1.14
	22	17.86	22.10	4.24	-0.33	1.26
	23	18.20	23.26	5.06	0.92	0.53
	24	18.42	21.64	3.22	-0.78	1.72
	25	17.56	22.62	5.06	0.27	0.83
	26	18.24	22.10	3.86	0.00	1.00
	27	17.56	21.69	4.13	0.04	0.97
	28	18.45	23.07	4.62	0.12	0.92
	29	18.50	22.78	4.28	-0.31	1.24
	30	17.67	22.80	5.13	0.32	0.80
	31	18.56	22.28	3.72	-0.28	1.21
	32	17.77	21.91	4.14	-0.01	1.01
	33	17.88	21.28	3.40	-0.52	1.43
	34	18.23	23.50	5.27	0.47	0.72
	35	18.56	22.21	3.65	-0.46	1.38
	36	18.44	23.24	4.80	0.54	0.69
	37	18.56	22.63	4.07	0.07	0.95
	38	18.46	22.63	4.17	0.15	0.90
	39	17.56	22.15	4.59	-0.12	1.09
	40	18.56	21.93	3.37	-0.63	1.55
	41	18.21	22.48	4.27	0.38	0.77
	42	17.45	22.36	4.91	0.04	0.97
	43	17.56	21.50	3.94	0.01	0.99
	44	18.40	21.95	3.55	-0.54	1.45
	45	18.45	23.50	5.05	-0.04	1.03
	46	17.55	21.06	3.51	-0.50	1.41
	47	18.45	22.23	3.78	-0.60	1.52
	48	18.65	22.32	3.67	-0.33	1.26
	49	17.45	22.58	5.13	0.76	0.59
	50	17.56	21.15	3.59	-0.30	1.23
	51	18.40	21.79	3.39	-0.60	1.52
	52	18.45	21.92	3.47	-0.85	1.80
	53	17.55	22.57	5.02	0.00	1.00
	54	18.45	21.57	3.12	-0.76	1.69
	55	18.26	22.42	4.16	-0.74	1.67
	56	18.46	21.63	3.17	-0.72	1.65
	57	18.56	23.06	4.50	-0.30	1.23
	58	17.11	20.79	3.68	-0.34	1.27
	59	18.45	22.67	4.22	-0.38	1.30
	60	18.56	21.85	3.29	-0.75	1.68
	61	18.56	22.48	3.92	-0.19	1.14
	62	17.78	21.28	3.50	-0.69	1.61
	AVERAGE	18.08	22.15	4.07	-0.20	1.20
	STDEV	0.49	0.66	0.64	0.43	0.33

Fig. 1

C, the relation between BCYRN1 expression and prognosis in 62 pairs of CC tissues analyzed by Kaplan-Meier analysis.



D, DDP-resistance of CC cells in each group examined through MTT assay.

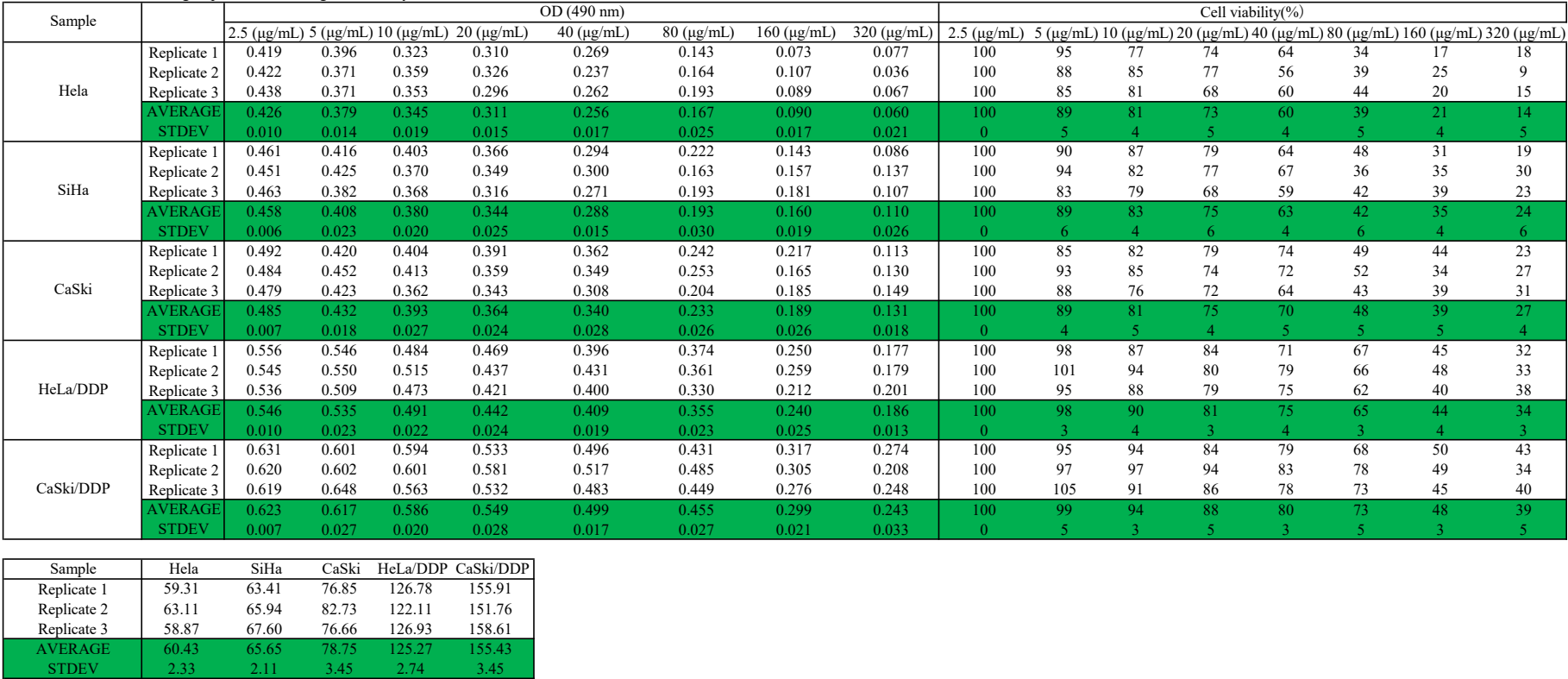


Fig. 1

E, BCYRN1 expression in CC cells verified via RT-qPCR.

qRT-PCR data of BCYRN1 (GAPDH as internal reference)						
Sample		Ct values		ΔCt	ΔΔCt	relative expression
		GAPDH	BCYRN1	BCYRN1	BCYRN1	BCYRN1
HcerEpic	Replicate 1	17.84	22.03	4.19	-0.01	1.00
	Replicate 2	17.65	21.89	4.24	0.04	0.97
	Replicate 3	18.09	22.25	4.16	-0.04	1.03
	AVERAGE	17.86	22.06	4.20	0.00	1.00
	STDEV	0.22	0.18	0.04	0.04	0.03
Hela	Replicate 1	17.73	20.61	2.88	-1.31	2.48
	Replicate 2	18.56	21.64	3.08	-1.16	2.23
	Replicate 3	18.12	20.88	2.76	-1.40	2.64
	AVERAGE	18.14	21.04	2.91	-1.29	2.45
	STDEV	0.42	0.53	0.16	0.12	0.20
SiHa	Replicate 1	18.28	21.13	2.85	-1.34	2.53
	Replicate 2	17.02	19.85	2.83	-1.41	2.66
	Replicate 3	16.98	19.84	2.86	-1.30	2.46
	AVERAGE	17.43	20.27	2.85	-1.35	2.55
	STDEV	0.74	0.74	0.02	0.06	0.10
CaSki	Replicate 1	17.99	20.54	2.55	-1.64	3.12
	Replicate 2	18.31	20.93	2.62	-1.62	3.07
	Replicate 3	17.83	20.33	2.50	-1.66	3.16
	AVERAGE	18.04	20.60	2.56	-1.64	3.12
	STDEV	0.24	0.30	0.06	0.02	0.04
HeLa/DDP	Replicate 1	17.42	19.74	2.32	-1.87	3.66
	Replicate 2	17.10	19.60	2.50	-1.74	3.34
	Replicate 3	17.89	20.07	2.18	-1.98	3.94
	AVERAGE	17.47	19.80	2.33	-1.86	3.65
	STDEV	0.40	0.24	0.16	0.12	0.30
CaSki/DDP	Replicate 1	17.86	19.92	2.06	-2.13	4.38
	Replicate 2	17.29	19.47	2.18	-2.06	4.17
	Replicate 3	17.89	19.86	1.97	-2.19	4.56
	AVERAGE	17.68	19.75	2.07	-2.13	4.37
	STDEV	0.34	0.24	0.11	0.07	0.20

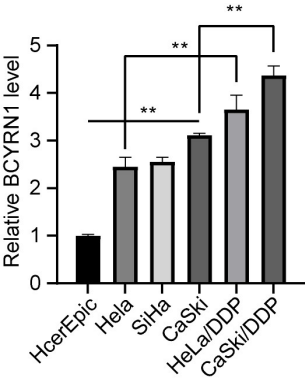
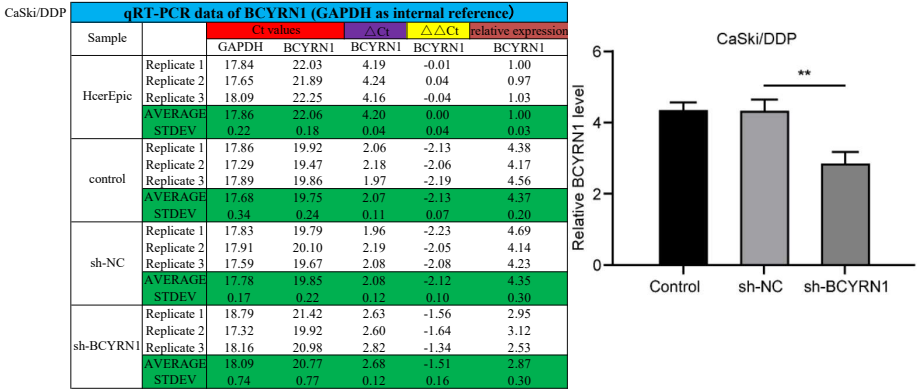
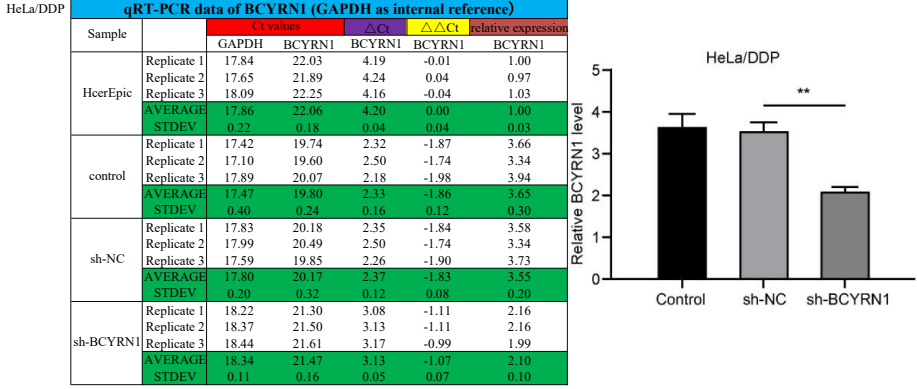
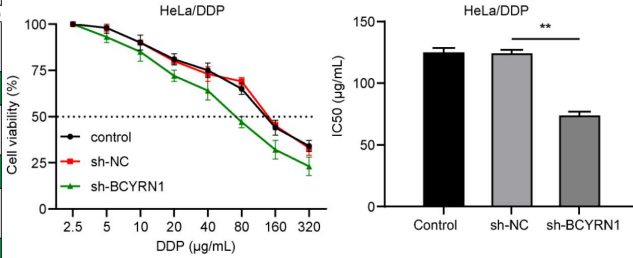
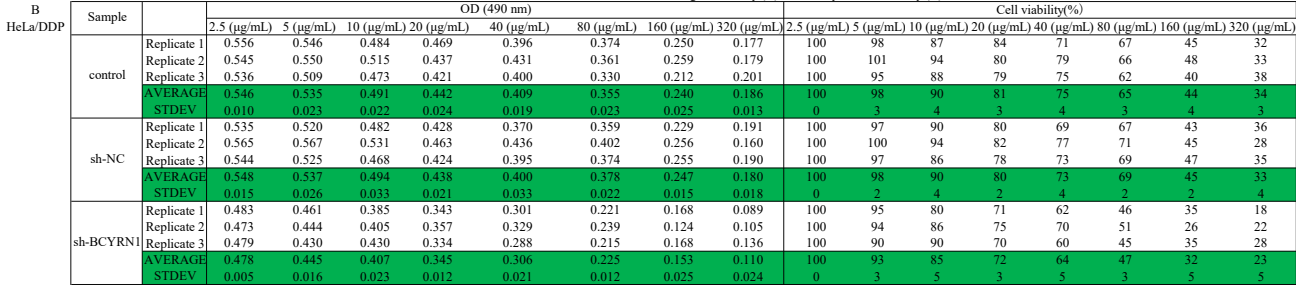


Fig. 2. BCYRN1 knockout reduces DDP-resistance of CC cells.

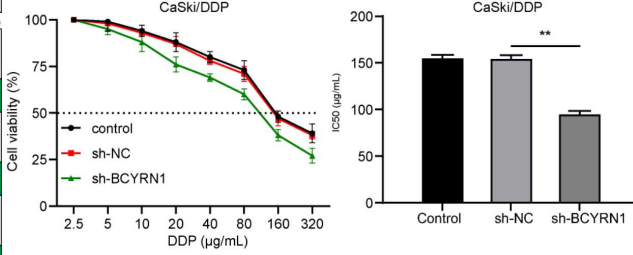
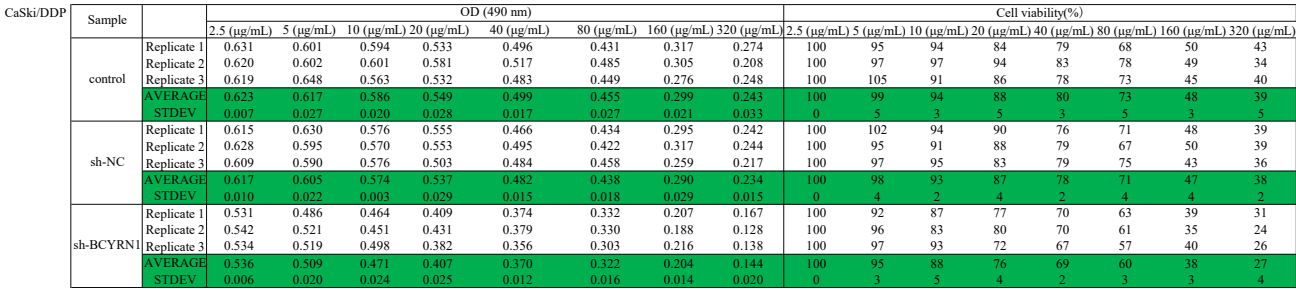
HeLa/DDP and CaSki/DDP cells were infected with sh-BCYRN1, with sh-NC as NC. A. interfere efficiency of sh-BCYRN1 tested via RT-qPCR.



HeLa/DDP and CaSki/DDP cells were infected with sh-BCYRN1, with sh-NC as NC. B and C, cell DDP-resistance determined using MTT assay (B) and colony formation assay (C).



Sample	control	sh-NC	sh-BCYRN1
Replicate 1	126.78	122.24	72.41
Replicate 2	122.11	124.11	77.13
Replicate 3	126.93	127.30	73.15
AVERAGE	125.27	124.55	74.23
STDEV	2.74	2.56	2.54



Sample	control	sh-NC	sh-BCYRN1
Replicate 1	155.91	158.23	99.01
Replicate 2	151.76	150.95	92.75
Replicate 3	158.61	155.09	94.53
AVERAGE	155.43	154.76	95.43
STDEV	3.45	3.65	3.23

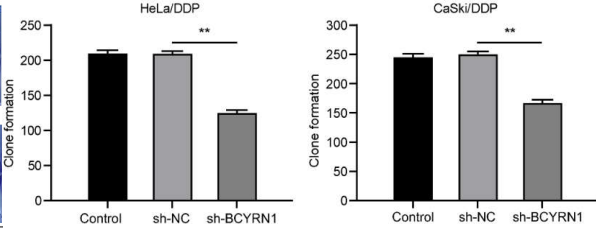
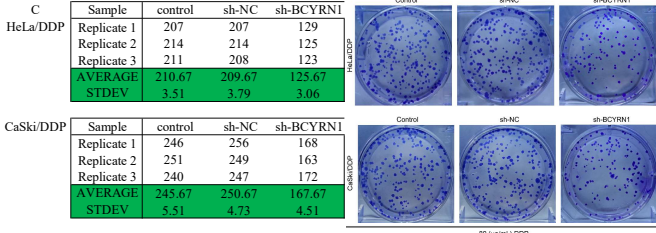


Fig. 3. BCYRN1 competitively binds to miR-330-5p to improve HMGB3 mRNA level.

A. BCYRN1 localization in CC cells predicted via online database (www.esbio.sjtu.edu.cn).

Subcellular locations	
Cytoplasm	0.544372743239
Nucleus	0.090174096514
Ribosome	0.047786196333
Cytosol	0.261352948281
Exosome	0.291529245439
Predicted location	
Cytoplasm	

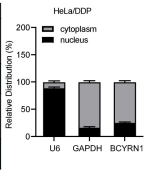
B. BCYRN1 expression in DDP-resistant CC cells measured by RT-qPCR following the fractionation of nuclear and cytoplasmic RNA assay.

qRT-PCR data of U6 (GAPDH as internal reference)							
Sample		Ct values		Δ Ct	$\Delta\Delta$ Ct	relative expression	
		GAPDH	U6	U6	U6		
HeLa/DDP	cytoplasm	Replicate 1	18.71	17.98	-0.73	-0.08	1.06
		Replicate 2	17.99	17.37	-0.62	0.03	0.98
		Replicate 3	17.83	17.23	-0.60	0.05	0.97
		AVERAGE	18.18	17.53	-0.65	0.00	1.00
		STDEV	0.47	0.40	0.07	0.07	0.05
	nucleus	Replicate 1	17.42	13.65	-3.77	-3.04	8.22
		Replicate 2	18.08	14.97	-3.11	-2.49	5.62
		Replicate 3	17.67	13.93	-3.74	-3.14	8.82
		AVERAGE	17.72	14.18	-3.54	-2.89	7.55
		STDEV	0.33	0.70	0.37	0.35	1.70
CaSki/DDP	cytoplasm	Replicate 1	18.39	18.35	-0.04	0.04	0.97
		Replicate 2	17.69	17.57	-0.12	-0.04	1.03
		Replicate 3	17.24	17.17	-0.07	0.01	1.00
		AVERAGE	17.77	17.70	-0.08	0.00	1.00
		STDEV	0.56	0.60	0.04	0.04	0.03
	nucleus	Replicate 1	17.38	15.57	-1.81	-1.77	3.41
		Replicate 2	17.75	15.54	-2.21	-2.09	4.26
		Replicate 3	17.66	15.41	-2.25	-2.18	4.53
		AVERAGE	17.60	15.51	-2.09	-2.01	4.07
		STDEV	0.19	0.09	0.24	0.22	0.58

qRT-PCR data of GAPDH (GAPDH as internal reference)							
Sample		Ct values			Δ Ct		relative expression
		GAPDH	GAPDH	GAPDH	GAPDH	GAPDH	
HeLa/DDP	cytoplasm	Replicate 1	18.26	14.34	-3.92	0.15	0.90
		Replicate 2	17.76	13.52	-4.24	-0.17	1.13
		Replicate 3	17.52	13.48	-4.04	0.03	0.98
		AVERAGE	17.85	13.78	-4.07	0.00	1.00
		STDEV	0.38	0.49	0.16	0.16	0.11
	nucleus	Replicate 1	17.71	16.74	-0.97	2.95	0.13
		Replicate 2	18.34	16.25	-2.09	2.15	0.23
		Replicate 3	17.99	16.25	-1.74	2.30	0.20
		AVERAGE	18.01	16.41	-1.60	2.47	0.19
		STDEV	0.32	0.28	0.57	0.43	0.05
	cytoplasm	Replicate 1	17.65	17.95	0.30	0.06	0.96
		Replicate 2	17.96	18.23	0.27	0.03	0.98
Replicate 3		18.11	18.27	0.16	-0.08	1.06	
AVERAGE		17.91	18.15	0.24	0.00	1.00	
STDEV		0.23	0.17	0.07	0.07	0.05	
CaSki/DDP	nucleus	Replicate 1	18.58	21.15	2.57	2.27	0.21
		Replicate 2	17.81	20.15	2.34	2.07	0.24
		Replicate 3	17.63	19.47	1.84	1.68	0.31
		AVERAGE	18.01	20.26	2.25	2.01	0.25
		STDEV	0.50	0.85	0.37	0.30	0.05

qRT-PCR data of BCYRN1 (GAPDH as internal reference)							
Sample			Ct values		Δ Ct	$\Delta\Delta$ Ct	relative expression
			GAPDH	BCYRN1	BCYRN1	BCYRN1	
HeLa/DDP	cytoplasm	Replicate 1	17.91	20.54	2.63	0.15	0.90
		Replicate 2	17.85	20.28	2.43	-0.05	1.04
		Replicate 3	18.05	20.43	2.38	-0.10	1.07
		AVERAGE	17.94	20.42	2.48	0.00	1.00
		STDEV	0.10	0.13	0.13	0.13	0.09
	nucleus	Replicate 1	17.76	22.29	4.53	1.90	0.27
		Replicate 2	17.50	21.58	4.08	1.65	0.32
		Replicate 3	17.55	21.28	3.73	1.35	0.39
		AVERAGE	17.60	21.72	4.11	1.63	0.33
		STDEV	0.14	0.52	0.40	0.28	0.06
	cytoplasm	Replicate 1	17.57	19.96	2.39	0.06	0.96
		Replicate 2	17.55	19.76	2.21	-0.12	1.09
Replicate 3		17.89	20.28	2.39	0.06	0.96	
AVERAGE		17.67	20.00	2.33	0.00	1.00	
STDEV		0.19	0.26	0.10	0.10	0.07	
CaSki/DDP	nucleus	Replicate 1	18.23	22.48	4.25	1.86	0.28
		Replicate 2	18.01	22.20	4.19	1.98	0.25
		Replicate 3	18.24	22.60	4.36	1.97	0.26
		AVERAGE	18.16	22.43	4.27	1.94	0.26
		STDEV	0.13	0.21	0.09	0.07	0.01

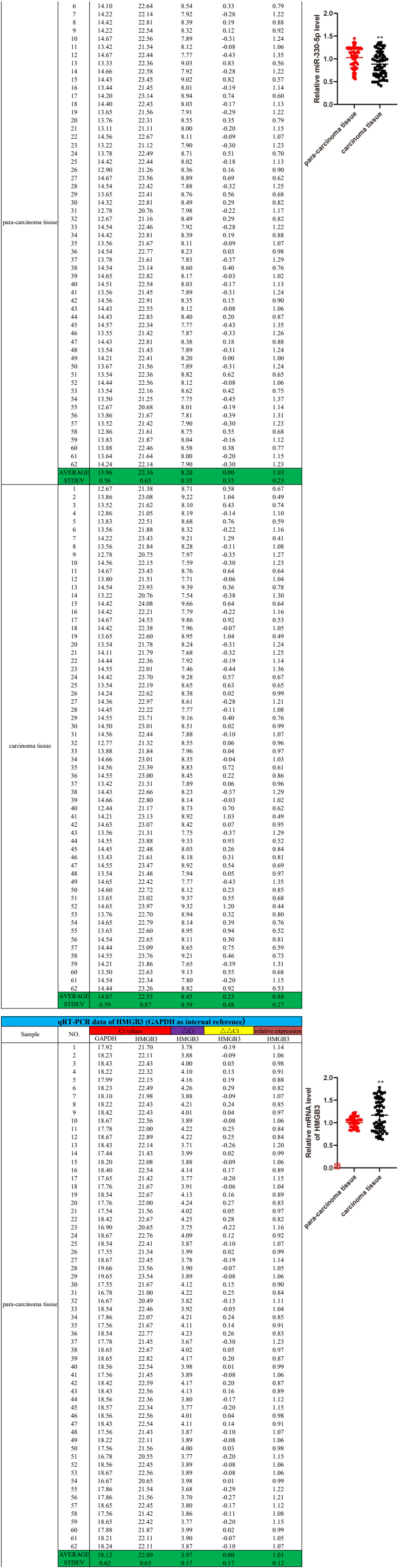
HeLa/DDP	Sample	U6	GAPDH	BCYRN1	U6	GAPDH	BCYRN1
cytoplasm	Replicate 1	1.06	0.90	0.90	11.39	87.47	77.08
	Replicate 2	0.98	1.13	1.04	14.85	83.35	76.47
	Replicate 3	0.97	0.98	1.07	9.88	82.86	73.21
	AVERAGE	1.00	1.00	1.00	12.04	84.56	75.58
	STDEV	0.05	0.11	0.09	2.55	2.53	2.08
		8.22	0.13	0.27	88.61	12.53	22.92
nucleus	Replicate 2	5.62	0.23	0.32	85.15	16.65	23.53
	Replicate 3	8.82	0.20	0.39	90.12	17.14	26.79
	AVERAGE	7.55	0.19	0.33	87.96	15.44	24.42
	STDEV	1.70	0.05	0.06	2.55	2.53	2.08



C. the binding sites of BCYRN1 and miR-330-5p and of miR-330-5p and HMGB3 predicted via RNA22 and Starbase databases.

miR Name	transcript name	leftmost position of predicted target site	folding energy (in -Kcal/mol)	heteroduplex	p value
hsa-miR-301b-3p MIMAT0004893	NC_000002.12_47335315_47335514 Human sapiens chromosome 2,GRCh38.p13 Primary Assembly	21	-18.50	GCGCTATATCCAGCTCTCAGGGA CGGATCTCTGTGTC-CGGGTCCTC	3.74E-3

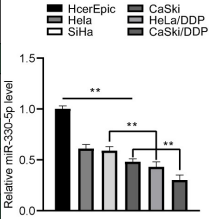
Fig. 3



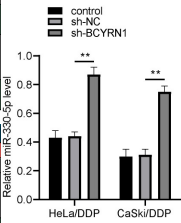
carcinoma tissue	1	17.83	20.89	3.06	-0.72	1.64
	2	17.56	21.63	4.07	0.19	0.88
	3	18.22	22.27	4.05	0.05	0.97
	4	17.56	21.76	4.20	0.10	0.93
	5	16.78	20.28	3.50	-0.66	1.58
	6	17.56	21.10	3.54	-0.72	1.65
	7	18.22	21.27	3.05	-0.83	1.77
	8	17.56	21.35	3.79	-0.42	1.34
	9	16.78	20.15	3.37	-0.64	1.56
	10	18.56	21.83	3.27	-0.62	1.54
	11	17.80	21.60	3.80	-0.42	1.34
	12	18.54	22.90	4.36	0.14	0.91
	13	18.22	21.71	3.49	-0.22	1.16
	14	18.42	22.69	4.27	0.28	0.82
	15	17.43	20.85	3.42	-0.46	1.38
	16	17.86	22.30	4.44	0.30	0.81
	17	17.20	21.05	3.85	0.08	0.95
	18	18.42	22.68	4.26	0.35	0.78
	19	17.56	21.43	3.87	-0.26	1.20
	20	18.24	23.10	4.86	0.62	0.65
	21	18.11	22.52	4.41	0.39	0.76
	22	18.44	22.75	4.31	0.06	0.96
	23	18.55	22.97	4.42	0.67	0.63
	24	18.42	21.75	3.33	-0.76	1.69
	25	17.56	21.76	4.20	0.33	0.80
	26	18.24	22.78	4.54	0.55	0.68
	27	18.66	22.70	4.04	0.26	0.84
	28	17.44	21.86	4.42	0.52	0.70
	29	18.21	21.43	3.22	-0.67	1.59
	30	18.65	22.75	4.10	-0.02	1.01
	31	18.56	22.71	4.15	-0.07	1.05
	32	17.77	21.78	4.01	0.19	0.88
	33	17.88	22.30	4.42	0.50	0.71
	34	18.11	22.63	4.52	0.31	0.81
	35	17.44	21.74	4.30	0.19	0.88
	36	18.56	23.18	4.62	0.39	0.76
	37	18.43	21.56	3.13	-0.54	1.45
	38	17.56	20.84	3.28	-0.74	1.67
	39	18.56	22.40	3.84	-0.33	1.26
	40	18.45	22.58	4.13	0.15	0.90
	41	17.55	21.81	4.26	0.37	0.77
	42	18.45	22.65	4.20	0.03	0.98
	43	18.32	21.85	3.53	-0.60	1.52
	44	17.45	21.03	3.58	-0.22	1.16
	45	18.45	22.25	3.80	0.03	0.98
	46	17.43	20.98	3.55	-0.45	1.37
	47	18.55	22.34	3.79	-0.32	1.25
	48	17.54	20.84	3.30	-0.57	1.48
	49	18.65	23.16	4.51	0.62	0.65
	50	18.60	22.57	3.97	-0.03	1.02
	51	17.65	20.71	3.06	-0.71	1.64
	52	18.54	21.66	3.12	-0.77	1.71
	53	16.89	20.54	3.65	-0.24	1.18
	54	18.56	21.99	3.43	-0.55	1.46
	55	18.33	21.47	3.14	-0.54	1.45
	56	18.45	21.40	2.95	-0.75	1.68
	57	18.56	21.91	3.35	-0.45	1.37
	58	17.44	20.96	3.52	-0.34	1.27
	59	18.55	21.69	3.14	-0.63	1.55
	60	18.21	21.47	3.26	-0.73	1.66
	61	17.50	20.77	3.27	-0.63	1.55
	62	17.78	21.63	3.85	-0.02	1.01
	AVERAGE	18.02	21.83	3.81	-0.16	1.17
	STDEV	0.52	0.76	0.50	0.45	0.35

G, expression of miR-330-5p and HMGB3 mRNA in CC cells examined by RT-qPCR.

qRT-PCR data of miR-330-5p (U6 as internal reference)					
Sample	Ct values		$\Delta\Delta Ct$		relative expression
	U6	miR-330-5p	miR-330-5p	miR-330-5p	
HecrEpic	Replicate 1	13.89	22.09	8.20	-0.04
	Replicate 2	13.98	22.21	8.23	-0.01
	Replicate 3	14.33	22.62	8.29	0.05
	AVERAGE	14.07	22.31	8.24	0.00
	STDEV	0.23	0.28	0.05	0.03
Hela	Replicate 1	13.72	22.63	8.91	0.71
	Replicate 2	13.62	22.66	9.04	0.81
	Replicate 3	13.50	22.41	8.91	0.62
	AVERAGE	13.61	22.57	8.95	0.71
	STDEV	0.11	0.14	0.08	0.10
SiHa	Replicate 1	13.69	22.59	8.90	0.70
	Replicate 2	13.50	22.61	9.11	0.88
	Replicate 3	14.13	23.13	9.00	0.71
	AVERAGE	13.77	22.78	9.00	0.76
	STDEV	0.32	0.31	0.11	0.10
CaSki	Replicate 1	13.64	22.98	9.34	1.14
	Replicate 2	13.22	22.53	9.31	1.08
	Replicate 3	14.16	23.41	9.25	0.96
	AVERAGE	13.67	22.97	9.30	1.06
	STDEV	0.47	0.44	0.05	0.09
HeLa/DDP	Replicate 1	14.53	24.06	9.53	1.33
	Replicate 2	14.74	24.01	9.27	1.04
	Replicate 3	13.63	23.22	9.59	1.30
	AVERAGE	14.30	23.76	9.46	1.22
	STDEV	0.59	0.47	0.17	0.16
CaSki/DDP	Replicate 1	13.73	23.63	9.90	1.70
	Replicate 2	13.41	23.17	9.76	1.53
	Replicate 3	13.77	24.08	10.31	2.02
	AVERAGE	13.64	23.63	9.99	1.75
	STDEV	0.20	0.46	0.29	0.25

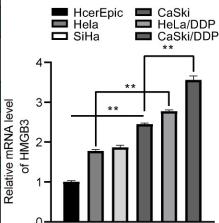


qRT-PCR data of miR-330-5p (U6 as internal reference)					
Sample	Ct values		$\Delta\Delta Ct$		relative expression
	U6	miR-330-5p	miR-330-5p	miR-330-5p	
HecrEpic	Replicate 1	13.89	22.09	8.20	-0.04
	Replicate 2	13.98	22.21	8.23	-0.01
	Replicate 3	14.33	22.62	8.29	0.05
	AVERAGE	14.07	22.31	8.24	0.00
	STDEV	0.23	0.28	0.05	0.03
control	Replicate 1	14.53	24.06	9.53	1.33
	Replicate 2	14.74	24.01	9.27	1.04
	Replicate 3	13.63	23.22	9.59	1.30
	AVERAGE	14.30	23.76	9.46	1.22
	STDEV	0.59	0.47	0.17	0.16
sh-NC	Replicate 1	13.86	23.35	9.49	1.29
	Replicate 2	13.56	22.88	9.32	1.09
	Replicate 3	14.38	23.85	9.47	1.18
	AVERAGE	13.93	23.36	9.43	1.19
	STDEV	0.41	0.49	0.09	0.10
sh-BCYRN1	Replicate 1	13.31	21.76	8.45	0.25
	Replicate 2	13.47	21.95	8.48	0.25
	Replicate 3	14.43	22.83	8.40	0.11
	AVERAGE	13.74	22.18	8.44	0.20
	STDEV	0.61	0.57	0.04	0.08



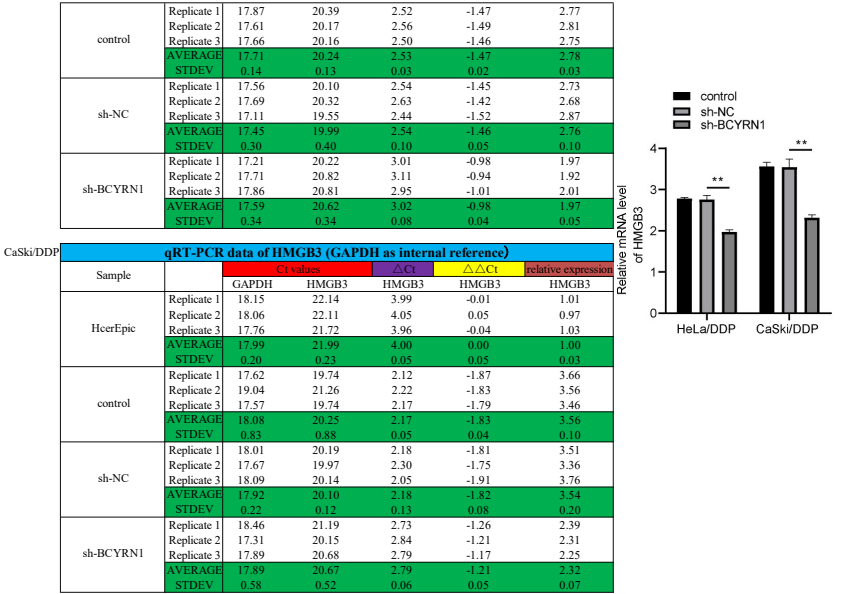
qRT-PCR data of miR-330-5p (U6 as internal reference)					
Sample	Ct values		$\Delta\Delta Ct$		relative expression
	U6	miR-330-5p	miR-330-5p	miR-330-5p	
HecrEpic	Replicate 1	13.89	22.09	8.20	-0.04
	Replicate 2	13.98	22.21	8.23	-0.01
	Replicate 3	14.33	22.62	8.29	0.05
	AVERAGE	14.07	22.31	8.24	0.00
	STDEV	0.23	0.28	0.05	0.03
control	Replicate 1	13.73	23.63	9.90	1.70
	Replicate 2	13.41	23.17	9.76	1.53
	Replicate 3	13.77	24.08	10.31	2.02
	AVERAGE	13.64	23.63	9.99	1.75
	STDEV	0.20	0.46	0.29	0.25
sh-NC	Replicate 1	14.10	23.88	9.78	1.58
	Replicate 2	14.04	23.86	9.82	1.59
	Replicate 3	14.32	24.53	10.21	1.92
	AVERAGE	14.15	24.09	9.94	1.70
	STDEV	0.15	0.38	0.24	0.19
sh-BCYRN1	Replicate 1	13.97	22.53	8.56	0.36
	Replicate 2	13.98	22.71	8.73	0.50
	Replicate 3	13.57	22.25	8.68	0.39
	AVERAGE	13.84	22.50	8.66	0.42
	STDEV	0.23	0.23	0.09	0.07

qRT-PCR data of HMGB3 (GAPDH as internal reference)					
Sample	Ct values		$\Delta\Delta Ct$		relative expression
	GAPDH	HMGB3	HMGB3	HMGB3	
HecrEpic	Replicate 1	18.15	22.14	3.99	-0.01
	Replicate 2	18.06	22.11	4.05	0.05
	Replicate 3	17.76	21.72	3.96	-0.04
	AVERAGE	17.99	21.99	4.00	0.00
	STDEV	0.20	0.23	0.05	0.03
Hela	Replicate 1	17.25	20.42	3.17	-0.82
	Replicate 2	17.80	21.03	3.23	-0.82
	Replicate 3	18.37	21.47	3.10	-0.86
	AVERAGE	17.81	20.97	3.17	-0.83
	STDEV	0.56	0.53	0.07	0.02
SiHa	Replicate 1	17.18	20.26	3.08	-0.91
	Replicate 2	18.00	21.19	3.19	-0.86
	Replicate 3	18.31	21.34	3.03	-0.93
	AVERAGE	17.83	20.93	3.10	-0.90
	STDEV	0.58	0.59	0.08	0.04
CaSki	Replicate 1	18.28	20.96	2.68	-1.31
	Replicate 2	17.70	20.47	2.77	-1.28
	Replicate 3	18.22	20.90	2.68	-1.28
	AVERAGE	18.07	20.78	2.71	-1.29
	STDEV	0.32	0.27	0.05	0.02
HeLa/DDP	Replicate 1	17.87	20.39	2.52	-1.47
	Replicate 2	17.61	20.17	2.56	-1.49
	Replicate 3	17.66	20.16	2.50	-1.46
	AVERAGE	17.71	20.24	2.53	-1.47
	STDEV	0.14	0.13	0.03	0.02
CaSki/DDP	Replicate 1	17.62	19.74	2.12	-1.87
	Replicate 2	19.04	21.26	2.22	-1.83
	Replicate 3	17.57	19.74	2.17	-1.79
	AVERAGE	18.08	20.25	2.17	-1.83
	STDEV	0.83	0.88	0.05	0.04



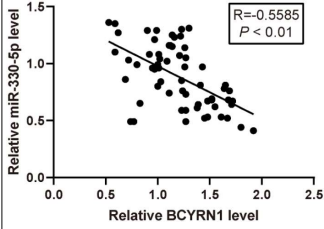
HeLa/DDP		qRT-PCR data of HMGB3 (GAPDH as internal reference)				
Sample		Ct values		$\Delta\Delta Ct$		Relative expression
		GAPDH	HMGB3	HMGB3	HMGB3	
HecrEpic	Replicate 1	18.15	22.14	3.99	-0.01	1.01
	Replicate 2	18.06	22.11	4.05	0.05	0.97
	Replicate 3	17.76	21.72	3.96	-0.04	1.03
	AVERAGE	17.99	21.99	4.00	0.00	1.00
	STDEV	0.20	0.23	0.05	0.05	0.03

Fig. 3



H, correlation between BCYRN1 and HMGB3 and between miR-330-5p and HMGB3 analyzed by pearson's correction analysis.

NO.	BCYRN1	miR-330-5p	NO.	BCYRN1	miR-330-5p
1	1.48	0.67	32	1.01	0.96
2	1.27	0.49	33	1.43	0.97
3	1.11	0.74	34	0.72	1.03
4	0.59	1.10	35	1.38	0.61
5	1.27	0.59	36	0.69	0.86
6	1.11	1.16	37	0.95	0.96
7	1.92	0.41	38	0.90	1.29
8	1.01	1.08	39	1.09	1.02
9	0.62	1.27	40	1.55	0.62
10	1.16	1.23	41	0.77	0.49
11	1.39	0.64	42	0.97	0.95
12	1.02	1.04	43	0.99	1.29
13	1.64	0.78	44	1.45	0.52
14	1.23	1.30	45	1.03	0.84
15	1.71	0.64	46	1.41	0.81
16	1.12	1.16	47	1.52	0.69
17	1.48	0.53	48	1.26	0.97
18	1.27	1.05	49	0.59	1.35
19	0.74	0.49	50	1.23	0.85
20	1.22	1.24	51	1.52	0.68
21	1.14	1.25	52	1.80	0.44
22	1.26	1.14	53	1.00	0.80
23	0.53	1.36	54	1.69	0.76
24	1.72	0.67	55	1.67	0.52
25	0.83	0.65	56	1.65	0.81
26	1.00	0.99	57	1.23	0.59
27	0.97	1.21	58	1.27	0.73
28	0.92	1.08	59	1.30	1.31
29	1.24	0.76	60	1.68	0.68
30	0.80	0.99	61	1.14	1.15
31	1.21	1.07	62	1.61	0.53



NO.	BCYRN1	HMGB3	NO.	BCYRN1	HMGB3
1	1.48	1.65	32	1.01	0.88
2	1.27	0.88	33	1.43	0.71
3	1.11	0.97	34	0.72	0.81
4	0.59	0.93	35	1.38	0.88
5	1.27	1.58	36	0.69	0.76
6	1.11	1.65	37	0.95	1.45
7	1.92	1.78	38	0.90	1.67
8	1.01	1.34	39	1.09	1.26
9	0.62	1.56	40	1.55	0.90
10	1.16	1.54	41	0.77	0.77
11	1.39	1.34	42	0.97	0.98
12	1.02	0.91	43	0.99	1.51
13	1.64	1.16	44	1.45	1.16
14	1.23	0.82	45	1.03	0.98
15	1.71	1.38	46	1.41	1.37
16	1.12	0.81	47	1.52	1.25
17	1.48	0.95	48	1.26	1.48
18	1.27	0.78	49	0.59	0.65
19	0.74	1.20	50	1.23	1.02
20	1.22	0.65	51	1.52	1.64
21	1.14	0.76	52	1.80	1.71
22	1.26	0.96	53	1.00	1.18
23	0.53	0.63	54	1.69	1.46
24	1.72	1.69	55	1.67	1.45
25	0.83	0.80	56	1.65	1.68
26	1.00	0.68	57	1.23	1.37
27	0.97	0.84	58	1.27	1.27
28	0.92	0.70	59	1.30	1.55
29	1.24	1.59	60	1.68	1.66
30	0.80	1.01	61	1.14	1.55
31	1.21	1.05	62	1.61	1.01

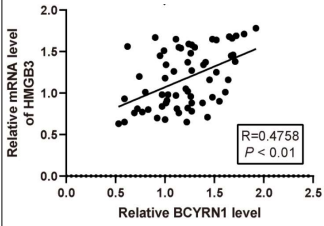
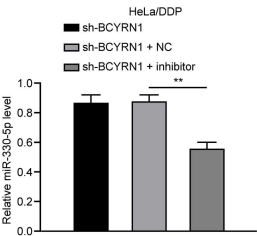


Fig. 4

Fig. 4. miR-330-5p depletion neutralizes the suppressive function of BCYRN1 knockdown to DDP-resistance of CC cells.

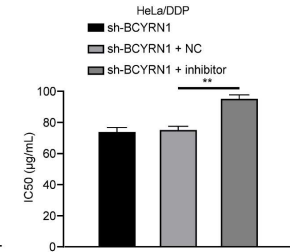
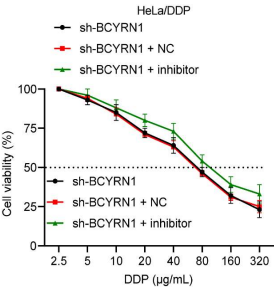
miR-330-5p inhibitor was transfected into HeLa/DDP cells with silenced BCYRN1, with inhibitor NC as NC. A, miR-330-5p inhibitor transfection efficiency in CC cells determined by RT-qPCR.

qRT-PCR data of miR-330-5p (U6 as internal reference)					
Sample		Ct values		relative expression	
		U6	miR-330-5p	miR-330-5p	miR-330-5p
HeerEpic	Replicate 1	13.89	22.09	8.20	-0.04
	Replicate 2	13.98	22.21	8.23	-0.01
	Replicate 3	14.33	22.62	8.29	0.05
	AVERAGE	14.07	22.31	8.24	0.00
	STDEV	0.23	0.28	0.05	0.03
sh-BCYRN1	Replicate 1	13.31	21.76	8.45	0.25
	Replicate 2	13.47	21.95	8.48	0.25
	Replicate 3	14.43	22.83	8.40	0.11
	AVERAGE	13.74	22.18	8.44	0.20
	STDEV	0.61	0.57	0.04	0.05
sh-BCYRN1 + NC	Replicate 1	18.77	27.23	8.46	0.26
	Replicate 2	18.59	26.99	8.40	0.17
	Replicate 3	18.58	27.00	8.42	0.13
	AVERAGE	18.65	27.07	8.43	0.19
	STDEV	0.11	0.14	0.03	0.07
sh-BCYRN1 + inhibitor	Replicate 1	18.13	27.20	9.07	0.87
	Replicate 2	17.97	27.12	9.15	0.92
	Replicate 3	18.03	27.05	9.02	0.73
	AVERAGE	18.04	27.12	9.08	0.84
	STDEV	0.08	0.08	0.07	0.10



miR-330-5p inhibitor was transfected into HeLa/DDP cells with silenced BCYRN1, with inhibitor NC as NC. B and C, cell resistance assessed via MTT (B) assay and colony formation assay (C).

Sample		OD (490 nm)								Cell viability(%)							
		2.5 (μg/mL)	5 (μg/mL)	10 (μg/mL)	20 (μg/mL)	40 (μg/mL)	80 (μg/mL)	160 (μg/mL)	320 (μg/mL)	2.5 (μg/mL)	5 (μg/mL)	10 (μg/mL)	20 (μg/mL)	40 (μg/mL)	80 (μg/mL)	160 (μg/mL)	320 (μg/mL)
sh-BCYRN1	Replicate 1	0.483	0.461	0.385	0.343	0.301	0.221	0.168	0.089	100	95	80	71	62	46	35	18
	Replicate 2	0.473	0.444	0.405	0.357	0.329	0.239	0.124	0.105	100	94	86	75	70	51	26	22
	Replicate 3	0.479	0.430	0.430	0.334	0.288	0.215	0.168	0.136	100	90	90	70	60	45	35	28
	AVERAGE	0.478	0.445	0.407	0.345	0.306	0.225	0.153	0.110	100	93	85	72	64	47	32	23
	STDEV	0.01	0.02	0.02	0.01	0.02	0.01	0.03	0.02	0	5	5	3	5	3	5	5
sh-BCYRN1 + NC	Replicate 1	0.502	0.466	0.416	0.353	0.294	0.234	0.165	0.103	100	93	83	70	59	47	33	21
	Replicate 2	0.488	0.454	0.432	0.357	0.323	0.214	0.141	0.127	100	93	89	73	66	44	29	26
	Replicate 3	0.444	0.428	0.358	0.308	0.285	0.211	0.139	0.126	100	96	81	69	64	48	31	28
	AVERAGE	0.478	0.449	0.402	0.339	0.301	0.220	0.148	0.119	100	94	84	71	63	46	31	25
	STDEV	0.03	0.02	0.04	0.03	0.02	0.01	0.01	0.01	0	2	4	2	4	2	4	4
sh-BCYRN1 + inhibitor	Replicate 1	0.502	0.460	0.450	0.425	0.339	0.272	0.188	0.157	100	92	90	85	68	54	37	31
	Replicate 2	0.488	0.484	0.402	0.377	0.362	0.243	0.218	0.194	100	99	82	77	74	50	45	40
	Replicate 3	0.444	0.432	0.409	0.347	0.343	0.257	0.155	0.125	100	97	92	78	77	58	35	28
	AVERAGE	0.478	0.439	0.420	0.383	0.348	0.257	0.187	0.139	100	96	88	80	73	54	39	33
	STDEV	0.03	0.03	0.03	0.04	0.01	0.01	0.03	0.03	0	4	5	4	5	4	5	6



Sample	sh-BCYRN1	sh-BCYRN1 + NC	sh-BCYRN1 + inhibitor
Replicate 1	72.41	73.01	93.10
Replicate 2	77.13	76.36	97.71
Replicate 3	73.15	76.92	95.66
AVERAGE	74.23	75.43	95.49
STDEV	2.54	2.11	2.31

Sample	sh-BCYRN1	sh-BCYRN1 + NC	sh-BCYRN1 + inhibitor
Replicate 1	129	122	167
Replicate 2	125	124	164
Replicate 3	123	127	165
AVERAGE	125.67	124.33	165.33
STDEV	3.06	2.52	1.53

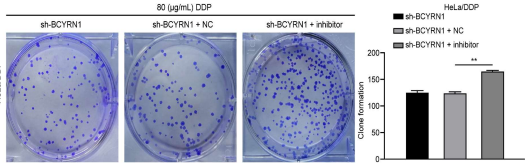
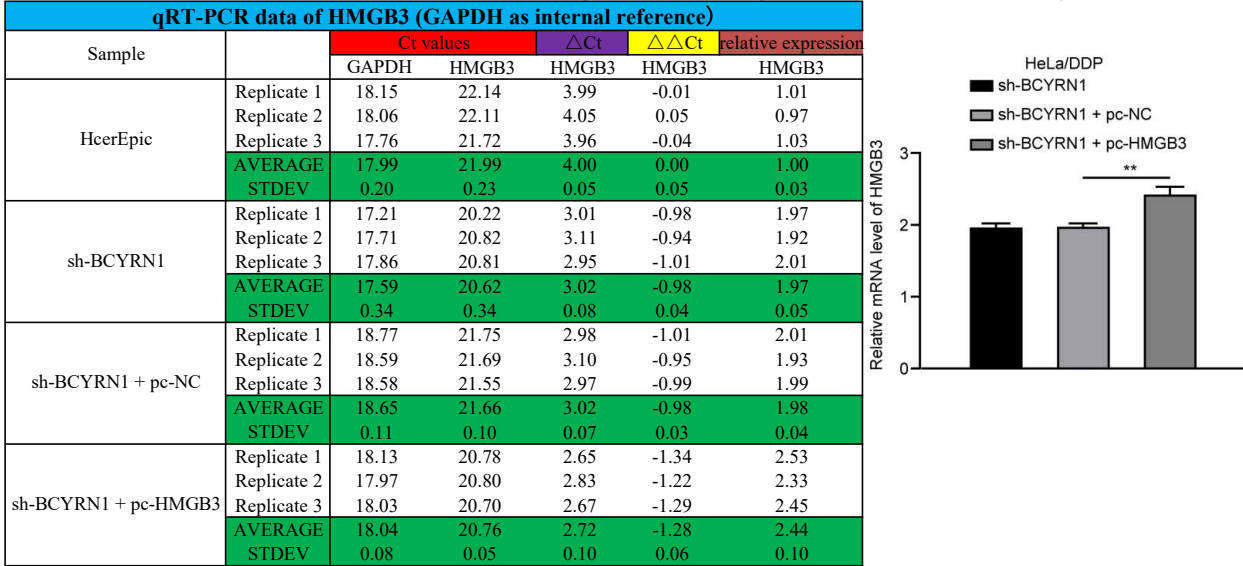


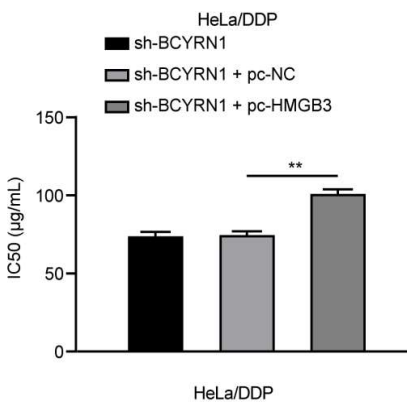
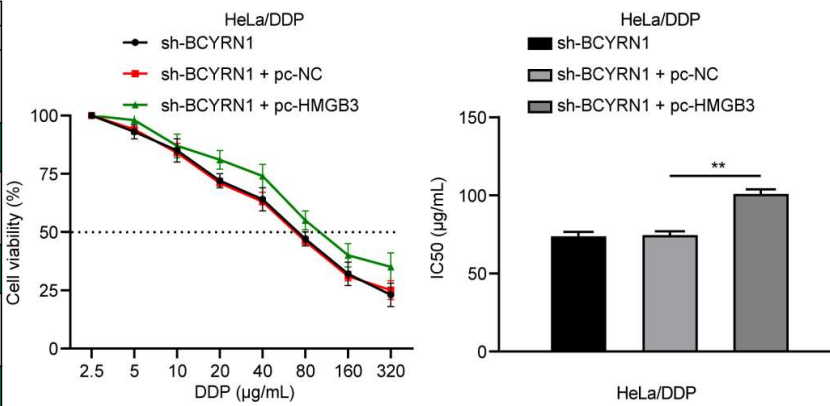
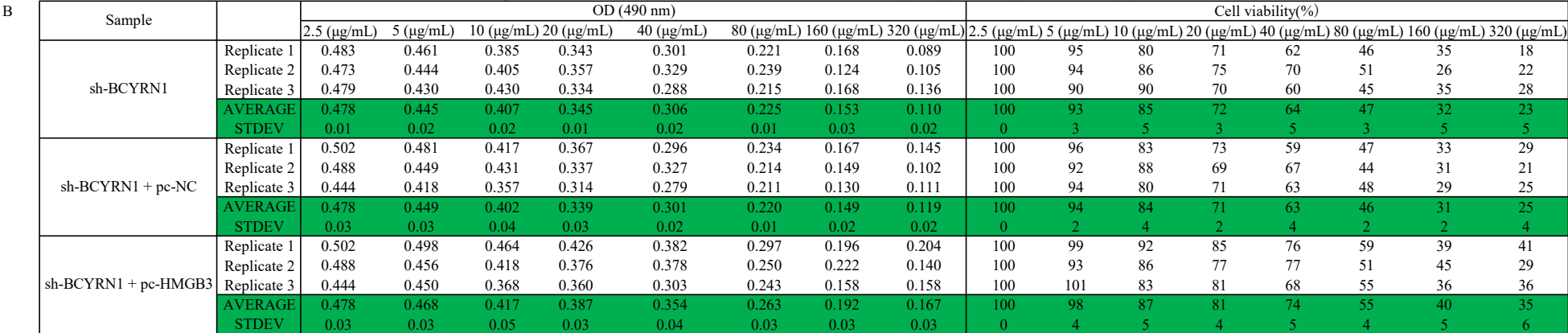
Fig. 5

Fig. 5. HMGB3 overexpression debilitates the suppressive function of BCYRN1 knockdown to DDP-resistance of CC cells.

pcDNA-HMGB3 was transfected into HeLa/DDP cells with silenced BCYRN1, with pcDNA-NC as NC. A, pcDNA-HMGB3 transfection efficiency in CC cells determined by RT-qPCR.



pcDNA-HMGB3 was transfected into HeLa/DDP cells with silenced BCYRN1, with pcDNA-NC as NC. B and C, cell resistance assessed via MTT (B) assay and colony formation assay (C).



Sample	sh-BCYRN1	sh-BCYRN1 + pc-NC	sh-BCYRN1 + pc-HMGB3
Replicate 1	72.41	72.79	103.29
Replicate 2	77.13	77.07	102.31
Replicate 3	73.15	75.08	98.48
AVERAGE	74.23	74.98	101.36
STDEV	2.54	2.14	2.54

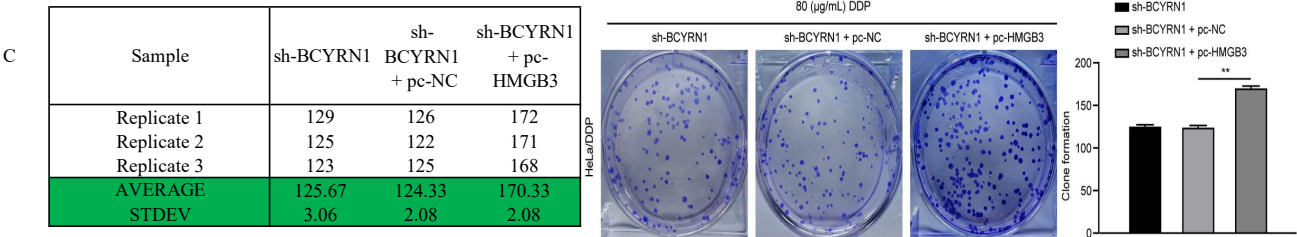
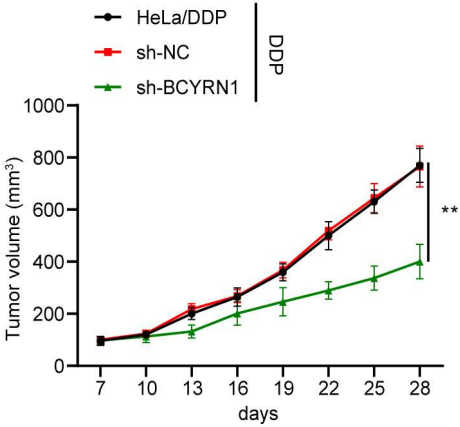


Fig. 6. BCYRN1 knockdown suppresses DDP-resistance of CC cells in vivo.

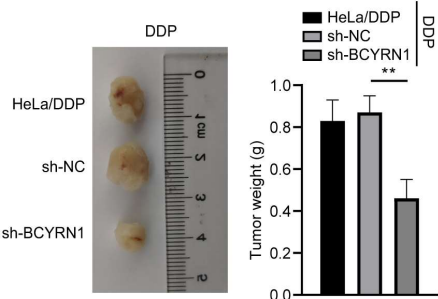
A, tumor volume in transplanted tumor model.

Sample		7 (days)	10 (days)	13 (days)	16 (days)	19 (days)	22 (days)	25 (days)	28 (days)
HeLa/DDP	Replicate 1	91.98	102.30	208.40	257.49	373.78	468.51	647.42	638.39
	Replicate 2	98.82	143.05	247.23	268.50	345.28	499.19	603.99	861.54
	Replicate 3	104.36	119.28	227.79	273.47	330.98	502.95	575.25	812.96
	Replicate 4	100.06	127.10	207.09	277.70	413.16	534.54	658.67	747.89
	Replicate 5	116.99	121.92	186.90	226.41	354.65	538.51	738.70	802.81
	Replicate 6	87.80	126.88	228.43	301.67	387.39	568.20	637.15	728.98
	AVERAGE	100.00	123.42	217.64	267.54	367.54	518.65	643.53	765.43
	STDEV	10.22	13.24	21.15	24.89	30.04	35.33	55.80	78.32
sh-NC	Replicate 1	103.63	108.27	163.55	248.88	346.06	439.33	565.95	774.27
	Replicate 2	103.82	118.27	235.33	313.76	360.46	425.29	605.40	723.84
	Replicate 3	107.08	126.37	193.45	281.28	366.95	544.42	610.23	690.47
	Replicate 4	115.06	120.09	207.23	246.69	372.48	512.91	650.85	787.33
	Replicate 5	73.94	144.83	198.10	212.95	305.44	539.97	655.96	880.25
	Replicate 6	77.03	102.16	206.84	282.34	403.81	538.08	694.13	762.34
	AVERAGE	96.76	120.00	200.75	264.32	359.20	500.00	630.42	769.75
	STDEV	17.02	14.94	23.32	35.34	32.53	53.76	45.43	64.79
sh-BCYRN1	Replicate 1	99.00	137.29	112.36	129.07	222.61	302.90	284.63	293.60
	Replicate 2	87.82	121.86	129.37	268.66	321.55	313.27	272.54	481.45
	Replicate 3	80.43	125.44	143.16	187.23	272.01	261.52	375.12	440.55
	Replicate 4	101.90	79.53	132.47	214.02	219.27	237.95	347.99	385.78
	Replicate 5	122.49	86.28	174.57	196.27	167.82	295.33	371.29	432.01
	Replicate 6	96.36	128.87	101.97	213.27	273.63	326.86	369.66	369.85
	AVERAGE	98.00	113.21	132.32	201.42	246.15	289.64	336.87	400.54
	STDEV	14.36	24.12	25.42	45.35	53.89	33.51	46.29	65.93



B, representative images and weights of tumors.

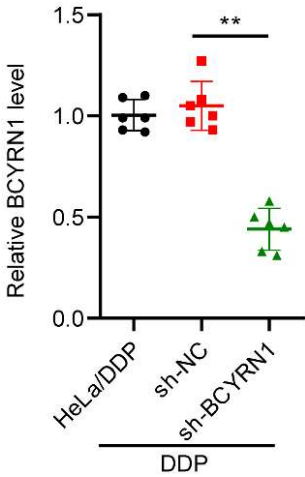
Sample	HeLa/DDP	sh-NC	sh-BCYRN1
Replicate 1	0.75	0.90	0.39
Replicate 2	0.91	0.93	0.45
Replicate 3	0.86	0.82	0.50
Replicate 4	1.04	0.66	0.46
Replicate 5	0.80	0.78	0.61
Replicate 6	0.86	0.89	0.35
AVERAGE	0.87	0.83	0.46
STDEV	0.10	0.10	0.09



C, D and E, expression of BCYRN1 (C) , miR-330-5p (D) and HMGB3 (E) mRNA detected by RT-qPCR.

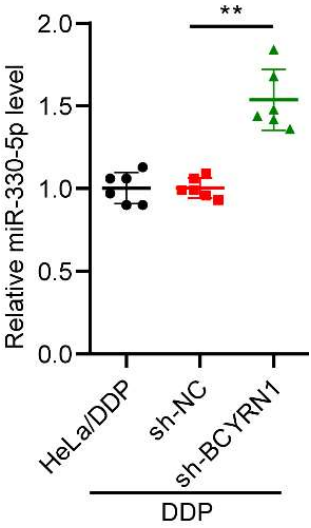
C

qRT-PCR data of BCYRN1 (GAPDH as internal reference)						
Sample		Ct values		△Ct	△△Ct	relative expression
		GAPDH	BCYRN1	BCYRN1	BCYRN1	BCYRN1
HeLa/DDP	Replicate 1	17.12	21.34	4.22	0.10	0.93
	Replicate 2	18.43	22.56	4.13	0.01	0.99
	Replicate 3	17.43	21.43	4.00	-0.12	1.09
	Replicate 4	18.23	22.21	3.98	-0.14	1.10
	Replicate 5	17.54	21.68	4.14	0.02	0.99
	Replicate 6	18.54	22.78	4.24	0.12	0.92
	AVERAGE	17.88	22.00	4.12	0.00	1.00
	STDEV	0.59	0.60	0.11	0.11	0.08
sh-NC	Replicate 1	18.43	22.54	4.11	-0.11	1.08
	Replicate 2	17.65	21.89	4.24	0.11	0.93
	Replicate 3	18.65	22.65	4.00	0.00	1.00
	Replicate 4	17.87	21.78	3.91	-0.07	1.05
	Replicate 5	18.43	22.61	4.18	0.04	0.97
	Replicate 6	18.54	22.43	3.89	-0.35	1.27
	AVERAGE	18.26	22.32	4.06	-0.06	1.05
	STDEV	0.40	0.38	0.14	0.16	0.12
sh-BCYRN1	Replicate 1	17.44	22.44	5.00	0.78	0.58
	Replicate 2	18.40	24.23	5.83	1.70	0.31
	Replicate 3	17.43	22.53	5.10	1.10	0.47
	Replicate 4	18.22	23.36	5.14	1.16	0.45
	Replicate 5	17.44	23.16	5.72	1.58	0.33
	Replicate 6	18.54	23.79	5.25	1.01	0.50
	AVERAGE	17.91	23.25	5.34	1.22	0.44
	STDEV	0.53	0.70	0.35	0.35	0.10



D

qRT-PCR data of miR-330-5p (U6 as internal reference)						
Sample		Ct values		Δ Ct	$\Delta\Delta$ Ct	relative expression
		U6	miR-330-5p	miR-330-5p	miR-330-5p	miR-330-5p
HeLa/DDP	Replicate 1	14.43	22.54	8.11	-0.09	1.06
	Replicate 2	13.54	21.78	8.24	0.04	0.97
	Replicate 3	13.54	21.89	8.35	0.15	0.90
	Replicate 4	14.42	22.54	8.12	-0.08	1.06
	Replicate 5	13.64	21.99	8.35	0.15	0.90
	Replicate 6	14.40	22.43	8.03	-0.17	1.13
	AVERAGE	14.00	22.20	8.20	0.00	1.00
	STDEV	0.46	0.35	0.13	0.13	0.09
sh-NC	Replicate 1	14.54	22.56	8.02	-0.09	1.06
	Replicate 2	14.42	22.76	8.34	0.10	0.93
	Replicate 3	13.42	21.79	8.37	0.02	0.99
	Replicate 4	13.60	21.78	8.18	0.06	0.96
	Replicate 5	14.65	22.88	8.23	-0.12	1.09
	Replicate 6	14.45	22.50	8.05	0.02	0.99
	AVERAGE	14.18	22.38	8.20	0.00	1.00
	STDEV	0.53	0.48	0.14	0.09	0.06
sh-BCYRN1	Replicate 1	14.60	22.20	7.60	-0.51	1.42
	Replicate 2	14.42	22.09	7.67	-0.57	1.48
	Replicate 3	13.42	21.33	7.91	-0.44	1.36
	Replicate 4	13.52	20.76	7.24	-0.88	1.84
	Replicate 5	14.52	22.34	7.82	-0.53	1.44
	Replicate 6	14.64	21.92	7.28	-0.75	1.68
	AVERAGE	14.19	21.77	7.59	-0.61	1.54
	STDEV	0.56	0.61	0.28	0.17	0.18



E

qRT-PCR data of HMGB3 (GAPDH as internal reference)						
Sample		Ct values		Δ Ct	$\Delta\Delta$ Ct	relative expression
		GAPDH	HMGB3	HMGB3	HMGB3	HMGB3
HeLa/DDP	Replicate 1	18.40	22.54	4.14	-0.07	1.05
	Replicate 2	17.54	22.00	4.46	0.25	0.84
	Replicate 3	17.54	21.78	4.24	0.03	0.98
	Replicate 4	18.21	22.32	4.11	-0.10	1.07
	Replicate 5	18.11	22.31	4.20	-0.01	1.01
	Replicate 6	17.42	21.54	4.12	-0.09	1.07
	AVERAGE	17.87	22.08	4.21	0.00	1.00
	STDEV	0.42	0.38	0.13	0.13	0.09
sh-NC	Replicate 1	18.42	22.42	4.00	-0.14	1.10
	Replicate 2	17.42	21.98	4.56	0.10	0.93
	Replicate 3	18.42	22.69	4.27	0.03	0.98
	Replicate 4	17.54	21.69	4.15	0.04	0.97
	Replicate 5	18.11	22.60	4.49	0.29	0.82
	Replicate 6	17.54	21.69	4.15	0.03	0.98
	AVERAGE	17.91	22.18	4.27	0.06	0.96
	STDEV	0.46	0.45	0.22	0.14	0.09
sh-BCYRN1	Replicate 1	18.54	23.44	4.90	0.76	0.59
	Replicate 2	18.21	23.76	5.55	1.09	0.47
	Replicate 3	17.54	22.90	5.36	1.12	0.46
	Replicate 4	17.65	22.59	4.94	0.83	0.56
	Replicate 5	18.33	23.49	5.16	0.96	0.51
	Replicate 6	18.42	22.89	4.47	0.35	0.78
	AVERAGE	18.12	23.18	5.06	0.85	0.56
	STDEV	0.42	0.45	0.38	0.28	0.12

