

## 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. 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, esophagus, lung, ovary, pancreas, and tongue, but not in corresponding normal tissues	chr2	47335315	47335314	+	Human	BC200; BC200a; LINC00004; NCRNA00004	NR_001568	Gene/RNA	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		$\Delta Ct$	$\Delta\Delta Ct$	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
carcinoma tissue	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

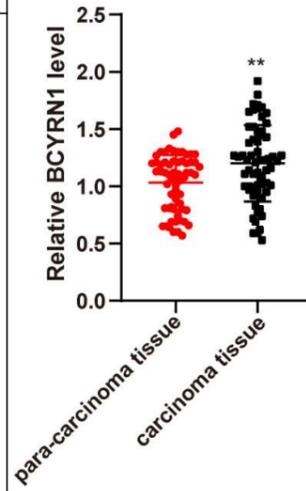
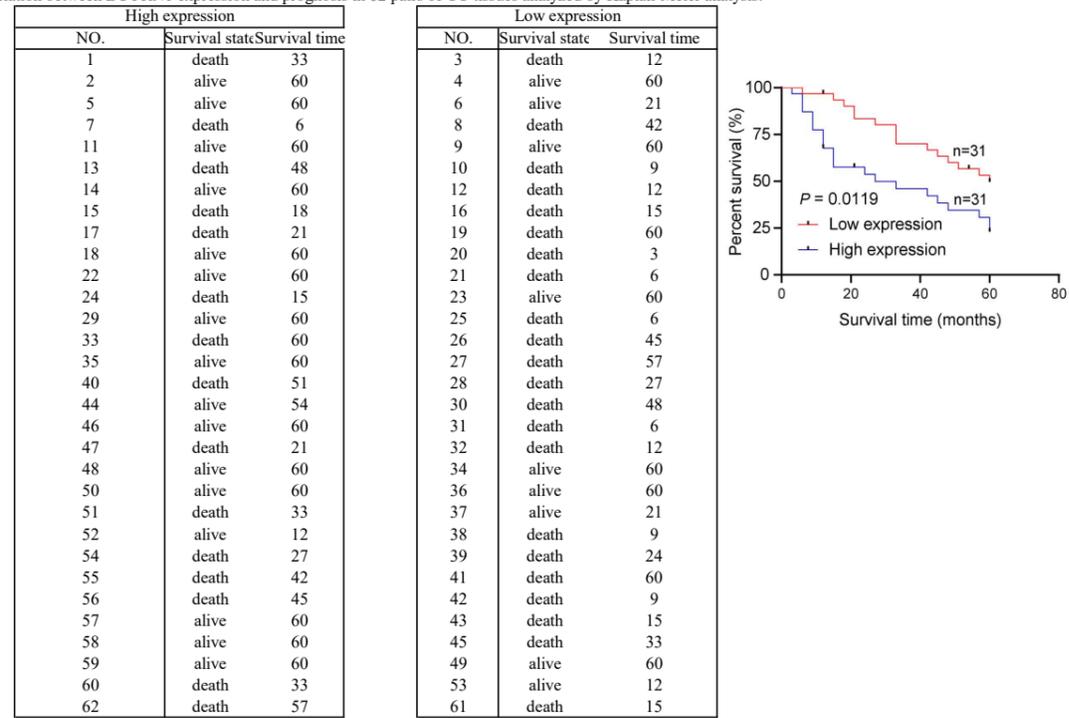


Fig. 1

	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
carcinoma tissue	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

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.

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)
Hela	Replicate 1	0.419	0.396	0.323	0.310	0.269	0.143	0.073	0.077	100	95	77	74	64	34	17	18
	Replicate 2	0.422	0.371	0.359	0.326	0.237	0.164	0.107	0.036	100	88	85	77	56	39	25	9
	Replicate 3	0.438	0.371	0.353	0.296	0.262	0.193	0.089	0.067	100	85	81	68	60	44	20	15
	AVERAGE	0.426	0.379	0.345	0.311	0.256	0.167	0.090	0.060	100	89	81	73	60	39	21	14
	STDEV	0.010	0.014	0.019	0.015	0.017	0.025	0.017	0.021	0	5	4	5	4	5	4	5
SiHa	Replicate 1	0.461	0.416	0.403	0.366	0.294	0.222	0.143	0.086	100	90	87	79	64	48	31	19
	Replicate 2	0.451	0.425	0.370	0.349	0.300	0.163	0.157	0.137	100	94	82	77	67	36	35	30
	Replicate 3	0.463	0.382	0.368	0.316	0.271	0.193	0.181	0.107	100	83	79	68	59	42	39	23
	AVERAGE	0.458	0.408	0.380	0.344	0.288	0.193	0.160	0.110	100	89	83	75	63	42	35	24
	STDEV	0.006	0.023	0.020	0.025	0.015	0.030	0.019	0.026	0	6	4	6	4	6	4	6
CaSki	Replicate 1	0.492	0.420	0.404	0.391	0.362	0.242	0.217	0.113	100	85	82	79	74	49	44	23
	Replicate 2	0.484	0.452	0.413	0.359	0.349	0.253	0.165	0.130	100	93	85	74	72	52	34	27
	Replicate 3	0.479	0.423	0.362	0.343	0.308	0.204	0.185	0.149	100	88	76	72	64	43	39	31
	AVERAGE	0.485	0.432	0.393	0.364	0.340	0.233	0.189	0.131	100	89	81	75	70	48	39	27
	STDEV	0.007	0.018	0.027	0.024	0.028	0.026	0.026	0.018	0	4	5	4	5	5	5	4
HeLa/DDP	Replicate 1	0.556	0.546	0.484	0.469	0.396	0.374	0.250	0.177	100	98	87	84	71	67	45	32
	Replicate 2	0.545	0.550	0.515	0.437	0.431	0.361	0.259	0.179	100	101	94	80	79	66	48	33
	Replicate 3	0.536	0.509	0.473	0.421	0.400	0.330	0.212	0.201	100	95	88	79	75	62	40	38
	AVERAGE	0.546	0.535	0.491	0.442	0.409	0.355	0.240	0.186	100	98	90	81	75	65	44	34
	STDEV	0.010	0.023	0.022	0.024	0.019	0.023	0.025	0.013	0	3	4	3	4	3	4	3
CaSki/DDP	Replicate 1	0.631	0.601	0.594	0.533	0.496	0.431	0.317	0.274	100	95	94	84	79	68	50	43
	Replicate 2	0.620	0.602	0.601	0.581	0.517	0.485	0.305	0.208	100	97	97	94	83	78	49	34
	Replicate 3	0.619	0.648	0.563	0.532	0.483	0.449	0.276	0.248	100	105	91	86	78	73	45	40
	AVERAGE	0.623	0.617	0.586	0.549	0.499	0.455	0.299	0.243	100	99	94	88	80	73	48	39
	STDEV	0.007	0.027	0.020	0.028	0.017	0.027	0.021	0.033	0	5	3	5	3	5	3	5

Sample	Hela	SiHa	CaSki	HeLa/DDP	CaSki/DDP
Replicate 1	59.31	63.41	76.85	126.78	155.91
Replicate 2	63.11	65.94	82.73	122.11	151.76
Replicate 3	58.87	67.60	76.66	126.93	158.61
AVERAGE	60.43	65.65	78.75	125.27	155.43
STDEV	2.33	2.11	3.45	2.74	3.45

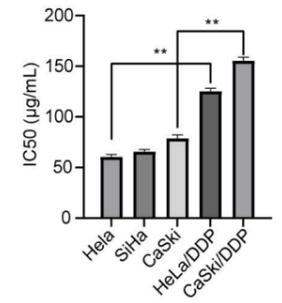
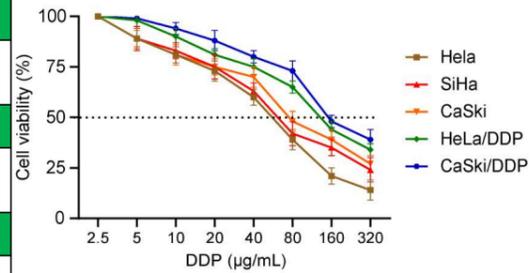


Fig. 1

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

qRT-PCR data of BCYRN1 (GAPDH as internal reference)						
Sample		Ct values		$\Delta$ Ct	$\Delta\Delta$ Ct	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

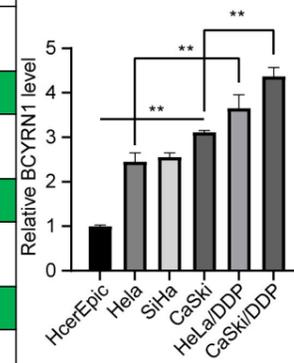
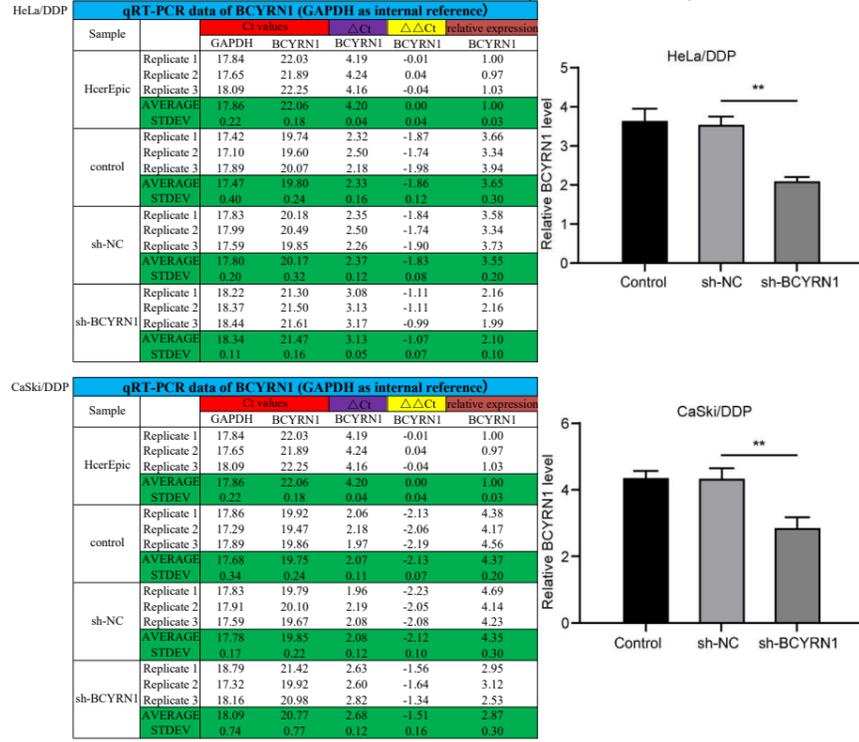
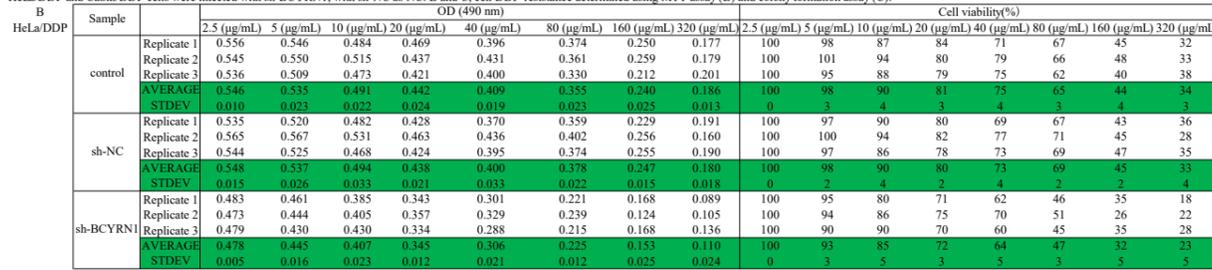


Fig. 2. BCYRN1 knockout reduces DDP-resistance of CC cells.

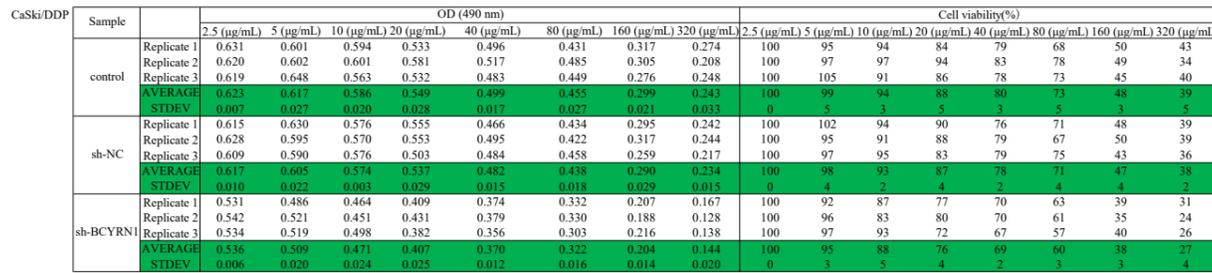
HeLa/DDP and CaSki/DDP cells were infected with sh-BCYRN1, with sh-NC as NC. A. Interference efficiency of sh-BCYRN1 tested via RT-qPCR.



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

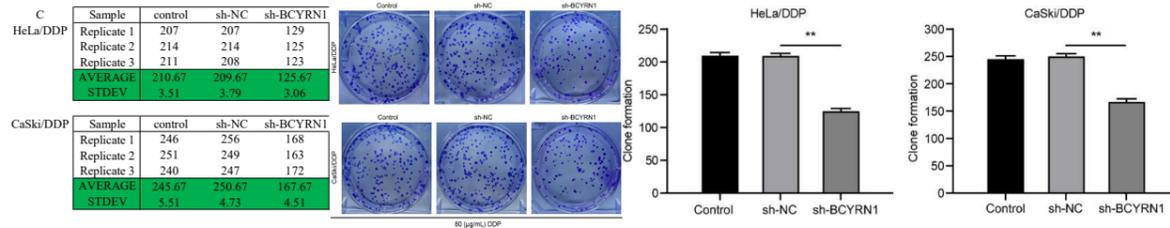


Fig. 3. BCYRN1 competitively binds to miR-330-5p to improve HMGB3 mRNA level.

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

Subcellular locations	score
Cytoplasm	0.544372743239
Nucleus	0.0901740969514
Ribosome	0.0477896199333
Cytosol	0.28132948281
Exosome	0.291529204539

Predicted location
Cytoplasm

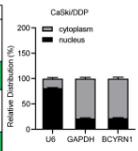
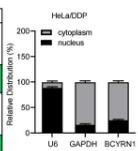
B. BCYRN1 expression in DDP-resistant CC cells measured by RT-qPCR following the fractionation of nuclear and cytoplasmic RNA assay.

Sample		qRT-PCR data of U6 (GAPDH as internal reference)					
		Ct values	ΔCt	ΔΔCt	relative expression	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	0.58	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		

Sample		qRT-PCR data of GAPDH (GAPDH as internal reference)					
		Ct values	ΔCt	ΔΔCt	relative expression	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		
CaSki/DDP	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	0.21	0.17	0.07	0.07	0.05	
	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		

Sample		qRT-PCR data of BCYRN1 (GAPDH as internal reference)					
		Ct values	ΔCt	ΔΔCt	relative expression	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		
CaSki/DDP	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	
	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		

Sample		HeLa/DDP			CaSki/DDP			
		U6	GAPDH	BCYRN1	U6	GAPDH	BCYRN1	
HeLa/DDP	cytoplasm	Replicate 1	1.06	0.90	11.39	87.47	77.08	
		Replicate 2	0.98	1.13	1.04	83.35	76.47	
		Replicate 3	0.97	0.98	1.07	82.86	73.21	
	AVERAGE	1.00	1.00	1.00	84.56	75.58		
	STDEV	0.05	0.11	0.09	2.53	2.08		
	nucleus	Replicate 1	8.22	0.13	0.27	88.61	12.53	22.92
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		
CaSki/DDP	cytoplasm	Replicate 1	0.97	0.96	0.96	22.23	82.26	77.69
		Replicate 2	1.03	0.98	1.09	19.49	80.48	81.09
		Replicate 3	1.00	1.06	0.96	18.01	77.25	78.98
	AVERAGE	1.00	1.00	1.00	19.91	79.99	79.25	
	STDEV	0.03	0.05	0.07	2.14	2.54	0.71	
	nucleus	Replicate 1	3.41	0.21	0.28	77.77	17.74	22.31
Replicate 2		4.26	0.24	0.25	80.51	19.52	18.91	
Replicate 3		4.53	0.31	0.26	81.99	22.75	21.02	
AVERAGE	4.07	0.25	0.26	80.09	20.01	20.75		
STDEV	0.58	0.05	0.01	2.14	2.54	1.71		



C. The binding sites of BCYRN1 and 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-330-5p	NC_000022.4:393811..473951+1	21	-18.80	GGCTGTATCCACCCATCCATCCAGGA 3'HE3	3.1E-3

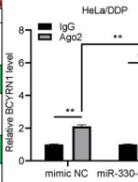
  

Binding Site of hsa-miR-330-5p on HMGB3:

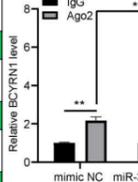
Binding Site	Class	Alignment
chrX:150158480-150158487[+]	7mer-m8	Target: 5' ggAUGAGGAGGUAUGCCAGAGG 3' miR-330-5p: 3' ggAUGAGGAGGUAUGCCAGAGG 5'

D. The binding relation between BCYRN1 and miR-330-5p verified through RIP assay.

Sample		qRT-PCR data of BCYRN1 (GAPDH as internal reference)					
		Ct values	ΔCt	ΔΔCt	relative expression	BCYRN1	
HeLa/DDP	mimic NC	Replicate 1	18.15	20.61	2.46	-0.05	1.04
		Replicate 2	17.88	20.42	2.54	0.03	0.98
		Replicate 3	18.06	20.59	2.53	0.02	0.99
	AVERAGE	18.03	20.54	2.53	0.00	1.00	
	STDEV	0.14	0.10	0.04	0.04	0.03	
	Ago2	Replicate 1	18.05	19.51	1.46	-1.00	2.00
Replicate 2		18.33	19.78	1.45	-1.09	2.13	
Replicate 3		17.50	18.89	1.39	-1.14	2.20	
AVERAGE	17.96	19.39	1.43	-1.08	2.11		
STDEV	0.42	0.46	0.04	0.07	0.10		
CaSki/DDP	mimic NC	Replicate 1	18.04	20.67	2.63	0.04	0.97
		Replicate 2	17.75	20.33	2.58	-0.01	1.00
		Replicate 3	17.88	20.43	2.55	-0.04	1.03
	AVERAGE	17.89	20.48	2.59	0.00	1.00	
	STDEV	0.15	0.17	0.04	0.04	0.03	
	Ago2	Replicate 1	17.71	17.94	0.23	-2.40	5.28
Replicate 2		18.09	18.24	0.15	-2.43	5.39	
Replicate 3		17.73	17.78	0.05	-2.50	5.66	
AVERAGE	17.84	17.99	0.14	-2.44	5.44		
STDEV	0.21	0.23	0.09	0.05	0.19		



Sample		qRT-PCR data of BCYRN1 (GAPDH as internal reference)					
		Ct values	ΔCt	ΔΔCt	relative expression	BCYRN1	
HeLa/DDP	mimic NC	Replicate 1	18.43	20.09	1.66	-0.05	1.04
		Replicate 2	17.96	19.67	1.71	0.00	1.00
		Replicate 3	17.74	19.51	1.77	0.06	0.96
	AVERAGE	18.04	19.76	1.71	0.00	1.00	
	STDEV	0.35	0.40	0.06	0.06	0.04	
	Ago2	Replicate 1	17.38	17.81	0.43	-1.23	2.35
Replicate 2		17.91	18.66	0.75	-0.96	1.95	
Replicate 3		17.74	18.38	0.64	-1.13	2.19	
AVERAGE	17.68	18.28	0.61	-1.11	2.16		
STDEV	0.27	0.43	0.16	0.14	0.20		
CaSki/DDP	mimic NC	Replicate 1	18.34	20.07	1.73	0.02	0.98
		Replicate 2	18.29	19.93	1.64	-0.07	1.05
		Replicate 3	17.86	19.61	1.75	0.04	0.97
	AVERAGE	18.16	19.87	1.71	0.00	1.00	
	STDEV	0.26	0.24	0.06	0.06	0.04	
	Ago2	Replicate 1	17.78	16.82	-0.96	-2.69	6.45
Replicate 2		18.92	17.95	-0.97	-2.61	6.11	
Replicate 3		17.79	17.00	-0.79	-2.54	5.82	
AVERAGE	18.16	17.26	-0.91	-2.61	6.12		
STDEV	0.66	0.61	0.10	0.08	0.32		



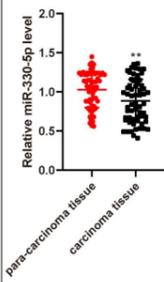
E. The target relation of BCYRN1 and miR-330-5p and of miR-330-5p and HMGB3 confirmed via dual-luciferase reporter gene assay.

Sample		Relative luciferase activity		Relative luciferase activity of NC		
		mimic NC	miR-330-5p mimic	mimic NC	miR-330-5p mimic	
HeLa/DDP	BCYRN1 WT	Replicate 1	0.63	0.27	1.00	0.44
		Replicate 2	0.66	0.27	1.05	0.40
		Replicate 3	0.60	0.32	0.95	0.54
	AVERAGE	0.63	0.29	1.00	0.46	
	STDEV	0.03	0.03	0.05	0.07	
	BCYRN1 MUT	Replicate 1	0.57	0.59	1.00	1.02
Replicate 2		0.52	0.48	0.91	0.93	
Replicate 3		0.59	0.65	1.03	1.11	
AVERAGE	0.56	0.57	0.98	1.02		
STDEV	0.04	0.09	0.06	0.09		

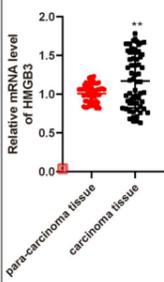


Sample		Relative luciferase activity		Relative luciferase activity of NC	
		mimic NC	miR-330-5p mimic	mimic NC	miR-330-5p mimic
CaSki/DDP	BCYRN1 WT				

	6	14.10	22.64	8.54	0.33	0.79
	7	14.22	22.14	7.92	-0.28	1.22
	8	14.42	22.81	8.39	0.19	0.88
	9	14.22	22.54	8.32	0.12	0.92
	10	14.67	22.56	7.89	-0.31	1.24
	11	13.42	21.54	8.12	-0.08	1.06
	12	14.67	22.44	7.77	-0.43	1.35
	13	13.33	22.36	9.03	0.83	0.56
	14	14.66	22.58	7.92	-0.28	1.22
	15	14.43	23.45	9.02	0.82	0.57
	16	13.44	21.45	8.01	-0.19	1.14
	17	14.20	23.14	8.94	0.74	0.60
	18	14.40	22.43	8.03	-0.17	1.13
	19	13.65	21.56	7.91	-0.29	1.22
	20	13.76	22.31	8.55	0.35	0.79
	21	13.11	21.11	8.00	-0.20	1.15
	22	14.56	22.67	8.11	-0.09	1.07
	23	13.22	21.12	7.90	-0.30	1.23
	24	13.78	22.49	8.71	0.51	0.70
	25	14.42	22.44	8.02	-0.18	1.13
	26	12.90	21.26	8.36	0.16	0.90
	27	14.67	23.56	8.89	0.69	0.62
	28	14.54	22.42	7.88	-0.32	1.25
	29	13.65	22.41	8.76	0.56	0.68
	30	14.32	22.81	8.49	0.29	0.82
	31	12.78	20.76	7.98	-0.22	1.17
	32	12.67	21.16	8.49	0.29	0.82
	33	14.54	22.46	7.92	-0.28	1.22
	34	14.42	22.81	8.39	0.19	0.88
	35	13.56	21.67	8.11	-0.09	1.07
	36	14.54	22.77	8.23	0.03	0.98
	37	13.78	21.61	7.83	-0.37	1.29
	38	14.54	23.14	8.60	0.40	0.76
	39	14.65	22.82	8.17	-0.03	1.02
	40	14.51	22.54	8.03	-0.17	1.13
	41	13.56	21.45	7.89	-0.31	1.24
	42	14.56	22.91	8.35	0.15	0.90
	43	14.43	22.55	8.12	-0.08	1.06
	44	14.43	22.83	8.40	0.20	0.87
	45	14.57	22.34	7.77	-0.43	1.35
	46	13.55	21.42	7.87	-0.33	1.26
	47	14.43	22.81	8.38	0.18	0.88
	48	13.54	21.43	7.89	-0.31	1.24
	49	14.21	22.41	8.20	0.00	1.00
	50	13.67	21.56	7.89	-0.31	1.24
	51	13.54	22.36	8.82	0.62	0.65
	52	14.44	22.56	8.12	-0.08	1.06
	53	13.54	22.16	8.62	0.42	0.75
	54	13.50	21.25	7.75	-0.45	1.37
	55	12.67	20.68	8.01	-0.19	1.14
	56	13.86	21.67	7.81	-0.39	1.31
	57	13.52	21.42	7.90	-0.30	1.23
	58	12.86	21.61	8.75	0.55	0.68
	59	13.83	21.87	8.04	-0.16	1.12
	60	13.88	22.46	8.58	0.38	0.77
	61	13.64	21.64	8.00	-0.20	1.15
	62	14.24	22.14	7.90	-0.30	1.23
	<b>AVERAGE</b>	<b>13.96</b>	<b>22.16</b>	<b>8.20</b>	<b>0.00</b>	<b>1.03</b>
	<b>STDEV</b>	<b>0.56</b>	<b>0.65</b>	<b>0.35</b>	<b>0.35</b>	<b>0.23</b>
para-carcinoma tissue	1	12.67	21.38	8.71	0.58	0.67
	2	13.86	23.08	9.22	1.04	0.49
	3	13.52	21.62	8.10	0.43	0.74
	4	12.86	21.05	8.19	-0.14	1.10
	5	13.83	22.51	8.68	0.76	0.59
	6	13.56	21.88	8.32	-0.22	1.16
	7	14.22	23.43	9.21	1.29	0.41
	8	13.56	21.84	8.28	-0.11	1.08
	9	12.78	20.75	7.97	-0.35	1.27
	10	14.56	22.15	7.59	-0.30	1.23
	11	14.67	23.43	8.76	0.64	0.64
	12	13.80	21.51	7.71	-0.06	1.04
	13	14.54	23.93	9.39	0.36	0.78
	14	13.22	20.76	7.54	-0.38	1.30
	15	14.42	24.08	9.66	0.64	0.64
	16	14.42	22.21	7.79	-0.22	1.16
	17	14.67	24.53	9.86	0.92	0.53
	18	14.42	22.38	7.96	-0.07	1.05
	19	13.65	22.60	8.95	1.04	0.49
	20	13.54	21.78	8.24	-0.31	1.24
	21	14.11	21.79	7.68	-0.32	1.25
	22	14.44	22.36	7.92	-0.19	1.14
	23	14.55	22.01	7.46	-0.44	1.36
	24	14.42	23.70	9.28	0.57	0.67
	25	13.54	22.19	8.65	0.63	0.65
	26	14.24	22.62	8.38	0.02	0.99
	27	14.36	22.97	8.61	-0.28	1.21
	28	14.45	22.22	7.77	-0.11	1.08
	29	14.55	23.71	9.16	0.40	0.76
	30	14.50	23.01	8.51	0.02	0.99
	31	14.56	22.44	7.88	-0.10	1.07
	32	12.77	21.32	8.55	0.06	0.96
	33	13.88	21.84	7.96	0.04	0.97
	34	14.66	23.01	8.35	-0.04	1.03
	35	14.56	23.39	8.83	0.72	0.61
	36	14.55	23.00	8.45	0.22	0.86
	37	13.42	21.31	7.89	0.06	0.96
	38	14.43	22.66	8.23	-0.37	1.29
	39	14.66	22.80	8.14	-0.03	1.02
	40	12.44	21.17	8.73	0.70	0.62
	41	14.21	23.13	8.92	1.03	0.49
	42	14.65	23.07	8.42	0.07	0.95
	43	13.56	21.31	7.75	-0.37	1.29
	44	14.55	23.88	9.33	0.93	0.52
	45	14.45	22.48	8.03	0.26	0.84
	46	13.43	21.61	8.18	0.31	0.81
	47	14.55	23.47	8.92	0.54	0.69
	48	13.54	21.48	7.94	0.05	0.97
	49	14.65	22.42	7.77	-0.43	1.35
	50	14.60	22.72	8.12	0.23	0.85
	51	13.65	23.02	9.37	0.55	0.68
	52	14.65	23.97	9.32	1.20	0.44
	53	13.76	22.70	8.94	0.32	0.80
	54	14.65	22.79	8.14	0.39	0.76
	55	13.65	22.60	8.95	0.94	0.52
	56	14.54	22.65	8.11	0.30	0.81
	57	14.44	23.09	8.65	0.75	0.59
	58	14.55	23.76	9.21	0.46	0.73
	59	14.21	21.86	7.65	-0.39	1.31
	60	13.50	22.63	9.13	0.55	0.68
	61	14.54	22.34	7.80	-0.20	1.15
	62	14.44	23.26	8.82	0.92	0.53
	<b>AVERAGE</b>	<b>14.07</b>	<b>22.53</b>	<b>8.45</b>	<b>0.25</b>	<b>0.88</b>
	<b>STDEV</b>	<b>0.59</b>	<b>0.87</b>	<b>0.59</b>	<b>0.48</b>	<b>0.27</b>



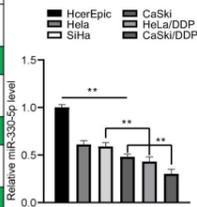
qRT-PCR data of HMGB3 (GAPDH as internal reference)						
Sample	NO.	Ct values		ΔCt		Relative expression
		GAPDH	HMGB3	ΔCt	ΔΔCt	
	1	17.92	21.70	-3.78	-0.19	1.14
	2	18.23	22.11	-3.88	-0.09	1.06
	3	18.43	22.43	-4.00	0.03	0.98
	4	18.22	22.32	-4.10	0.13	0.91
	5	17.99	22.15	-4.16	0.19	0.88
	6	18.23	22.49	-4.26	0.29	0.82
	7	18.10	21.98	-3.88	-0.09	1.07
	8	18.22	22.43	-4.21	0.24	0.85
	9	18.42	22.43	-4.01	0.04	0.97
	10	18.67	22.56	-3.89	-0.08	1.06
	11	17.78	22.00	-4.22	0.25	0.84
	12	18.67	22.89	-4.22	0.25	0.84
	13	18.43	22.14	-3.71	-0.26	1.20
	14	17.44	21.43	-3.99	0.02	0.99
	15	18.20	22.08	-3.88	-0.09	1.06
	16	18.40	22.54	-4.14	0.17	0.89
	17	17.65	21.42	-3.77	-0.20	1.15
	18	17.76	21.67	-3.91	-0.06	1.04
	19	18.54	22.67	-4.13	0.16	0.89
	20	17.76	22.00	-4.24	0.27	0.83
	21	17.54	21.56	-4.02	0.05	0.97
	22	18.42	22.67	-4.25	0.28	0.82
	23	16.90	20.65	-3.75	-0.22	1.16
	24	18.67	22.76	-4.09	0.12	0.92
	25	18.54	22.41	-3.87	-0.10	1.07
	26	17.55	21.54	-3.99	0.02	0.99
	27	18.67	22.45	-3.78	-0.19	1.14
	28	19.66	23.56	-3.90	-0.07	1.05
	29	19.65	23.54	-3.89	-0.08	1.06
	30	17.55	21.67	-4.12	0.15	0.90
	31	16.78	21.00	-4.22	0.25	0.84
	32	16.67	20.49	-3.82	-0.15	1.11
	33	18.54	22.46	-3.92	-0.05	1.04
	34	17.86	22.07	-4.21	0.24	0.85
	35	17.56	21.67	-4.11	0.14	0.91
	36	18.54	22.77	-4.23	0.26	0.83
	37	17.78	21.45	-3.67	-0.30	1.23
	38	18.65	22.67	-4.02	0.05	0.97
	39	18.65	22.82	-4.17	0.20	0.87
	40	18.56	22.54	-3.98	0.01	0.99
	41	17.56	21.45	-3.89	-0.08	1.06
	42	18.42	22.59	-4.17	0.20	0.87
	43	18.43	22.56	-4.13	0.16	0.89
	44	18.56	22.36	-3.80	-0.17	1.12
	45	18.57	22.34	-3.77	-0.20	1.15
	46	18.56	22.56	-4.01	0.04	0.98
	47	18.43	22.54	-4.11	0.14	0.91
	48	17.56	21.43	-3.87	-0.10	1.07
	49	18.22	22.11	-3.89	-0.08	1.06
	50	17.56	21.56	-4.00	0.03	0.98
	51	16.78	20.55	-3.77	-0.20	1.15
	52	18.56	22.45	-3.89	-0.08	1.06
	53	18.67	22.56	-3.89	-0.08	1.06
	54	16.67	20.65	-3.98	0.01	0.99
	55	17.86	21.54	-3.68	-0.29	1.22
	56	17.86	21.56	-3.70	-0.27	1.21
	57	18.65	22.45	-3.80	-0.17	1.12
	58	17.56	21.42	-3.86	-0.11	1.08
	59	18.65	22.42	-3.77	-0.20	1.15
	60	17.88	21.87	-3.99	0.02	0.99
	61	18.21	22.11	-3.90	-0.07	1.05
	62	18.24	22.11	-3.87	-0.10	1.07
	<b>AVERAGE</b>	<b>18.12</b>	<b>22.09</b>	<b>-3.97</b>	<b>0.00</b>	<b>1.01</b>
	<b>STDEV</b>	<b>0.62</b>	<b>0.65</b>	<b>0.17</b>	<b>0.17</b>	<b>0.12</b>



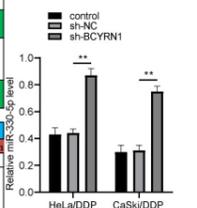
	1	17.83	20.89	3.06	-0.72	1.64
	2	17.56	21.63	4.07	0.19	0.88
	3	18.22	22.27	4.05	0.05	0.97
	4	17.56	21.76	4.20	0.10	0.93
	5	16.78	20.28	3.50	-0.66	1.58
	6	17.56	21.10	3.54	-0.72	1.65
	7	18.22	21.27	3.05	-0.83	1.77
	8	17.56	21.35	3.79	-0.42	1.34
	9	16.78	20.15	3.37	-0.64	1.56
	10	18.56	21.83	3.27	-0.62	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.

Sample	U6	miR-330-5p		relative expression		
		ΔCt	ΔΔCt	miR-330-5p	miR-330-5p	
HeerEpic	Replicate 1	13.89	22.09	8.20	-0.04	1.03
	Replicate 2	13.98	22.21	8.23	-0.01	1.01
	Replicate 3	14.33	22.62	8.29	0.05	0.97
	AVERAGE	14.07	22.31	8.24	0.00	1.00
STDEV	0.23	0.28	0.05	0.05	0.03	
Hela	Replicate 1	13.72	22.63	8.91	0.71	0.61
	Replicate 2	13.62	22.66	9.04	0.81	0.57
	Replicate 3	13.50	22.41	8.91	0.62	0.65
	AVERAGE	13.61	22.57	8.95	0.71	0.61
STDEV	0.11	0.14	0.08	0.10	0.04	
SiHa	Replicate 1	13.69	22.59	8.90	0.70	0.62
	Replicate 2	13.50	22.61	9.11	0.88	0.54
	Replicate 3	14.13	23.13	9.00	0.71	0.61
	AVERAGE	13.77	22.78	9.00	0.76	0.59
STDEV	0.32	0.31	0.11	0.10	0.04	
CaSki	Replicate 1	13.64	22.98	9.34	1.14	0.45
	Replicate 2	13.22	22.53	9.31	1.08	0.47
	Replicate 3	14.16	23.41	9.25	0.96	0.51
	AVERAGE	13.67	22.97	9.30	1.06	0.48
STDEV	0.47	0.44	0.05	0.09	0.03	
HeLa/DDP	Replicate 1	14.53	24.06	9.53	1.33	0.40
	Replicate 2	14.74	24.01	9.27	1.04	0.49
	Replicate 3	13.63	23.22	9.59	1.30	0.41
	AVERAGE	14.30	23.76	9.46	1.22	0.43
STDEV	0.59	0.47	0.17	0.16	0.05	
CaSki/DDP	Replicate 1	13.73	23.63	9.90	1.70	0.31
	Replicate 2	13.41	23.17	9.76	1.53	0.35
	Replicate 3	13.77	24.08	10.31	2.02	0.25
	AVERAGE	13.64	23.63	9.99	1.75	0.30
STDEV	0.20	0.46	0.29	0.25	0.05	

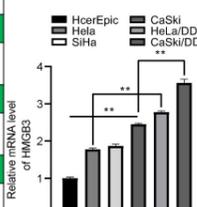


Sample	U6	miR-330-5p		relative expression		
		ΔCt	ΔΔCt	miR-330-5p	miR-330-5p	
HeerEpic	Replicate 1	13.89	22.09	8.20	-0.04	1.03
	Replicate 2	13.98	22.21	8.23	-0.01	1.01
	Replicate 3	14.33	22.62	8.29	0.05	0.97
	AVERAGE	14.07	22.31	8.24	0.00	1.00
STDEV	0.23	0.28	0.05	0.05	0.03	
control	Replicate 1	14.53	24.06	9.53	1.33	0.40
	Replicate 2	14.74	24.01	9.27	1.04	0.49
	Replicate 3	13.63	23.22	9.59	1.30	0.41
	AVERAGE	14.30	23.76	9.46	1.22	0.43
STDEV	0.59	0.47	0.17	0.16	0.05	
sh-NC	Replicate 1	13.86	23.35	9.49	1.29	0.41
	Replicate 2	13.56	22.88	9.32	1.09	0.47
	Replicate 3	14.38	23.85	9.47	1.18	0.44
	AVERAGE	13.93	23.36	9.43	1.19	0.44
STDEV	0.41	0.49	0.09	0.10	0.03	
sh-BCYRN1	Replicate 1	13.31	21.76	8.45	0.25	0.84
	Replicate 2	13.47	21.95	8.48	0.25	0.84
	Replicate 3	14.43	22.83	8.40	0.11	0.93
	AVERAGE	13.74	22.18	8.46	0.20	0.87
STDEV	0.61	0.57	0.04	0.08	0.05	



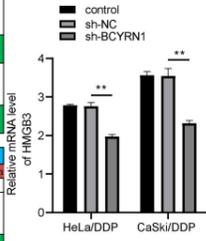
Sample	U6	miR-330-5p		relative expression		
		ΔCt	ΔΔCt	miR-330-5p	miR-330-5p	
HeerEpic	Replicate 1	13.89	22.09	8.20	-0.04	1.03
	Replicate 2	13.98	22.21	8.23	-0.01	1.01
	Replicate 3	14.33	22.62	8.29	0.05	0.97
	AVERAGE	14.07	22.31	8.24	0.00	1.00
STDEV	0.23	0.28	0.05	0.05	0.03	
control	Replicate 1	13.73	23.63	9.90	1.70	0.31
	Replicate 2	13.41	23.17	9.76	1.53	0.35
	Replicate 3	13.77	24.08	10.31	2.02	0.25
	AVERAGE	13.64	23.63	9.99	1.75	0.30
STDEV	0.20	0.46	0.29	0.25	0.05	
sh-NC	Replicate 1	14.10	23.88	9.78	1.58	0.33
	Replicate 2	14.04	23.86	9.82	1.59	0.33
	Replicate 3	14.32	24.53	10.21	1.92	0.26
	AVERAGE	14.15	24.09	9.94	1.70	0.31
STDEV	0.15	0.38	0.24	0.19	0.04	
sh-BCYRN1	Replicate 1	13.97	22.53	8.56	0.36	0.78
	Replicate 2	13.98	22.71	8.73	0.50	0.71
	Replicate 3	13.57	22.25	8.68	0.39	0.76
	AVERAGE	13.84	22.50	8.66	0.42	0.75
STDEV	0.23	0.23	0.09	0.07	0.04	

Sample	GAPDH	HMGB3		relative expression		
		ΔCt	ΔΔCt	HMGB3	HMGB3	
HeerEpic	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	
Hela	Replicate 1	17.25	20.42	3.17	-0.82	1.77
	Replicate 2	17.80	21.03	3.23	-0.82	1.77
	Replicate 3	18.37	21.47	3.10	-0.86	1.82
	AVERAGE	17.81	20.97	3.17	-0.83	1.78
STDEV	0.56	0.53	0.07	0.02	0.03	
SiHa	Replicate 1	17.18	20.26	3.08	-0.91	1.88
	Replicate 2	18.00	21.19	3.19	-0.86	1.82
	Replicate 3	18.31	21.34	3.03	-0.93	1.91
	AVERAGE	17.83	20.93	3.10	-0.90	1.87
STDEV	0.58	0.59	0.06	0.04	0.04	
CaSki	Replicate 1	18.28	20.96	2.68	-1.31	2.48
	Replicate 2	17.70	20.47	2.77	-1.28	2.43
	Replicate 3	18.22	20.90	2.68	-1.28	2.43
	AVERAGE	18.07	20.78	2.71	-1.29	2.45
STDEV	0.32	0.27	0.05	0.02	0.03	
HeLa/DDP	Replicate 1	17.87	20.39	2.52	-1.47	2.77
	Replicate 2	17.61	20.17	2.56	-1.49	2.81
	Replicate 3	17.66	20.16	2.50	-1.46	2.75
	AVERAGE	17.71	20.24	2.53	-1.47	2.78
STDEV	0.14	0.13	0.03	0.02	0.03	
CaSki/DDP	Replicate 1	17.62	19.74	2.12	-1.87	3.66
	Replicate 2	19.04	21.26	2.22	-1.83	3.56
	Replicate 3	17.57	19.74	2.17	-1.79	3.46
	AVERAGE	18.08	20.25	2.17	-1.83	3.56
STDEV	0.83	0.88	0.05	0.04	0.10	



Sample	GAPDH	HMGB3		relative expression		
		ΔCt	ΔΔCt	HMGB3	HMGB3	
HeerEpic	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	

Sample	Replicate	17.87	20.39	2.52	-1.47	2.77
control	Replicate 1	17.87	20.39	2.52	-1.47	2.77
	Replicate 2	17.61	20.17	2.56	-1.49	2.81
	Replicate 3	17.66	20.16	2.50	-1.46	2.75
	AVERAGE	17.71	20.24	2.53	-1.47	2.78
	STDEV	0.14	0.13	0.03	0.02	0.03
sh-NC	Replicate 1	17.56	20.10	2.54	-1.45	2.73
	Replicate 2	17.69	20.32	2.63	-1.42	2.68
	Replicate 3	17.11	19.55	2.44	-1.52	2.87
	AVERAGE	17.45	19.99	2.54	-1.46	2.76
	STDEV	0.30	0.40	0.10	0.05	0.10
sh-BCYRN1	Replicate 1	17.21	20.22	3.01	-0.98	1.97
	Replicate 2	17.71	20.82	3.11	-0.94	1.92
	Replicate 3	17.86	20.81	2.95	-1.01	2.01
	AVERAGE	17.59	20.62	3.02	-0.98	1.97
	STDEV	0.34	0.34	0.08	0.04	0.05

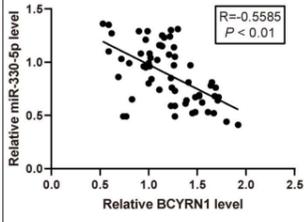


CaSki/DDP

qRT-PCR data of HMGB3 (GAPDH as internal reference)						
Sample	Replicate	CaSki			Relative expression	
		GAPDH	HMGB3	HMGB3	ΔΔCt	HMGB3
HeerEpic	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
control	Replicate 1	17.62	19.74	2.12	-1.87	3.66
	Replicate 2	19.04	21.26	2.22	-1.83	3.56
	Replicate 3	17.57	19.74	2.17	-1.79	3.46
	AVERAGE	18.08	20.25	2.17	-1.83	3.56
	STDEV	0.83	0.88	0.05	0.04	0.10
sh-NC	Replicate 1	18.01	20.19	2.18	-1.81	3.51
	Replicate 2	17.67	19.97	2.30	-1.75	3.36
	Replicate 3	18.09	20.14	2.05	-1.91	3.76
	AVERAGE	17.92	20.10	2.18	-1.82	3.54
	STDEV	0.22	0.15	0.13	0.08	0.20
sh-BCYRN1	Replicate 1	18.46	21.19	2.73	-1.26	2.39
	Replicate 2	17.31	20.15	2.84	-1.21	2.31
	Replicate 3	17.89	20.68	2.79	-1.17	2.25
	AVERAGE	17.89	20.67	2.79	-1.21	2.32
	STDEV	0.58	0.52	0.06	0.05	0.07

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

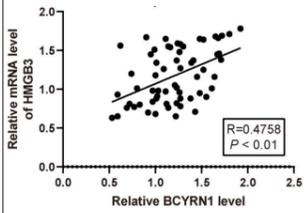
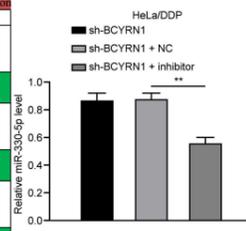


Fig. 4. miR-330-5p depletion neutralizes the suppressive function of BCYRN1 knockdown to DDP-resistance of CC cells.

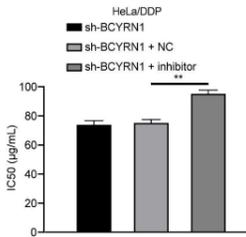
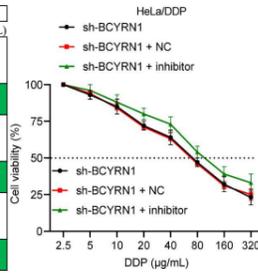
miR-330-5p inhibitor was transfected into HeLa/DDP cells with silenced BCYRN1, with inhibitor NC as NC. A, miR-330-5p inhibitor transfection efficiency in CC cells determined by RT-qPCR.

Sample	qRT-PCR data of miR-330-5p (U6 as internal reference)					
	U6	miR-330-5p	miR-330-5p	miR-330-5p	miR-330-5p	
HeerEpic	Replicate 1	13.89	22.09	8.20	-0.04	1.03
	Replicate 2	13.98	22.21	8.23	-0.01	1.01
	Replicate 3	14.33	22.62	8.29	0.05	0.97
	AVERAGE	14.07	22.31	8.24	0.00	1.00
	STDEV	0.23	0.28	0.05	0.05	0.03
sh-BCYRN1	Replicate 1	13.31	21.76	8.45	0.25	0.84
	Replicate 2	13.47	21.95	8.48	0.25	0.84
	Replicate 3	14.43	22.83	8.40	0.11	0.93
	AVERAGE	13.74	22.18	8.44	0.20	0.87
	STDEV	0.61	0.57	0.04	0.08	0.05
sh-BCYRN1 + NC	Replicate 1	18.77	27.23	8.46	0.26	0.84
	Replicate 2	18.59	26.99	8.40	0.17	0.89
	Replicate 3	18.58	27.00	8.42	0.13	0.91
	AVERAGE	18.65	27.07	8.43	0.19	0.88
	STDEV	0.11	0.14	0.03	0.07	0.04
sh-BCYRN1 + inhibitor	Replicate 1	18.13	27.20	9.07	0.87	0.55
	Replicate 2	17.97	27.12	9.15	0.92	0.53
	Replicate 3	18.03	27.05	9.02	0.73	0.60
	AVERAGE	18.04	27.12	9.08	0.84	0.56
	STDEV	0.08	0.08	0.07	0.10	0.04



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	0.02	0.02	0	3	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	0.230	0.148	0.119	100	94	84	71	63	48	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

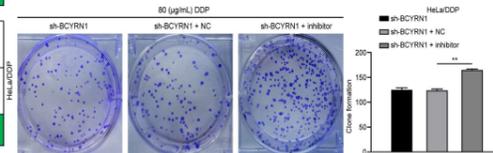
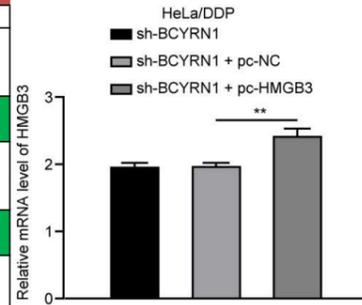


Fig. 5. HMGB3 overexpression debilitates the suppressive function of BCYRN1 knockdown to DDP-resistance of CC cells.

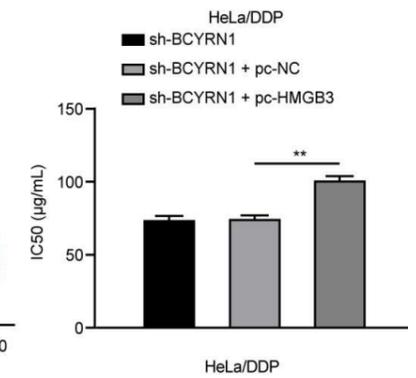
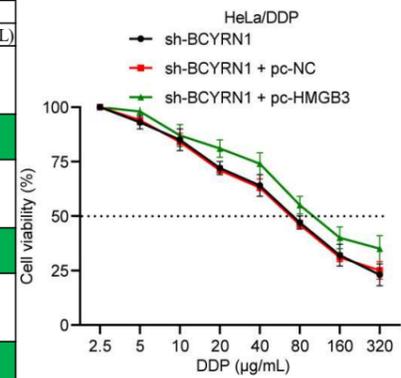
pcDNA-HMGB3 was transfected into HeLa/DDP cells with silenced BCYRN1, with pcDNA-NC as NC. A, pcDNA-HMGB3 transfection efficiency in CC cells determined by RT-qPCR.

qRT-PCR data of HMGB3 (GAPDH as internal reference)						
Sample		Ct values		$\Delta\Delta Ct$		relative expression
		GAPDH	HMGB3	HMGB3	HMGB3	
HcerEpic	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
sh-BCYRN1	Replicate 1	17.21	20.22	3.01	-0.98	1.97
	Replicate 2	17.71	20.82	3.11	-0.94	1.92
	Replicate 3	17.86	20.81	2.95	-1.01	2.01
	AVERAGE	17.59	20.62	3.02	-0.98	1.97
	STDEV	0.34	0.34	0.08	0.04	0.05
sh-BCYRN1 + pc-NC	Replicate 1	18.77	21.75	2.98	-1.01	2.01
	Replicate 2	18.59	21.69	3.10	-0.95	1.93
	Replicate 3	18.58	21.55	2.97	-0.99	1.99
	AVERAGE	18.65	21.66	3.02	-0.98	1.98
	STDEV	0.11	0.10	0.07	0.03	0.04
sh-BCYRN1 + pc-HMGB3	Replicate 1	18.13	20.78	2.65	-1.34	2.53
	Replicate 2	17.97	20.80	2.83	-1.22	2.33
	Replicate 3	18.03	20.70	2.67	-1.29	2.45
	AVERAGE	18.04	20.76	2.72	-1.28	2.44
	STDEV	0.08	0.05	0.10	0.06	0.10



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		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	3	5	3	5	3	5	5		
sh-BCYRN1 + pc-NC	Replicate 1	0.502	0.481	0.417	0.367	0.296	0.234	0.167	0.145	100	96	83	73	59	47	33	29		
	Replicate 2	0.488	0.449	0.431	0.337	0.327	0.214	0.149	0.102	100	92	88	69	67	44	31	21		
	Replicate 3	0.444	0.418	0.357	0.314	0.279	0.211	0.130	0.111	100	94	80	71	63	48	29	25		
	AVERAGE	0.478	0.449	0.402	0.339	0.301	0.220	0.149	0.119	100	94	84	71	63	46	31	25		
	STDEV	0.03	0.03	0.04	0.03	0.02	0.01	0.02	0.02	0	2	4	2	4	2	2	4		
sh-BCYRN1 + pc-HMGB3	Replicate 1	0.502	0.498	0.464	0.426	0.382	0.297	0.196	0.204	100	99	92	85	76	59	39	41		
	Replicate 2	0.488	0.456	0.418	0.376	0.378	0.250	0.222	0.140	100	93	86	77	77	51	45	29		
	Replicate 3	0.444	0.450	0.368	0.360	0.303	0.243	0.158	0.158	100	101	83	81	68	55	36	36		
	AVERAGE	0.478	0.468	0.417	0.387	0.354	0.263	0.192	0.167	100	98	87	81	74	55	40	35		
	STDEV	0.03	0.03	0.05	0.03	0.04	0.03	0.03	0.03	0	4	5	4	5	4	5	6		



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

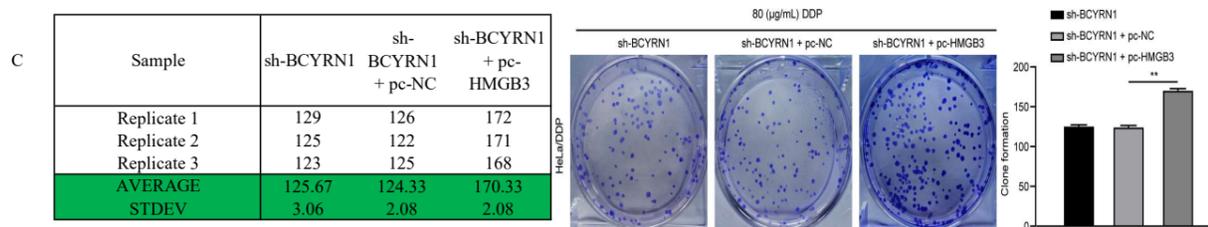
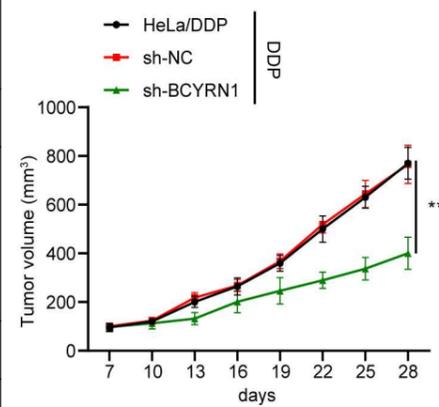


Fig. 6. BCYRN1 knockdown suppresses DDP-resistance of CC cells in vivo.

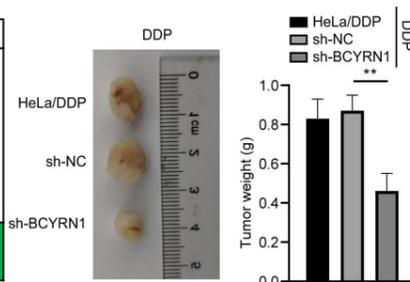
A, tumor volume in transplanted tumor model.

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.

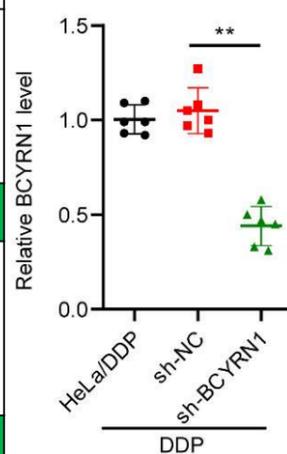
Sample	HeLa/DDP	sh-NC	sh-BCYRN1
Replicate 1	0.75	0.90	0.39
Replicate 2	0.91	0.93	0.45
Replicate 3	0.86	0.82	0.50
Replicate 4	1.04	0.66	0.46
Replicate 5	0.80	0.78	0.61
Replicate 6	0.86	0.89	0.35
AVERAGE	0.87	0.83	0.46
STDEV	0.10	0.10	0.09



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

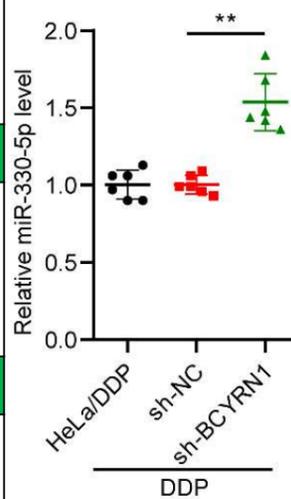
C

qRT-PCR data of BCYRN1 (GAPDH as internal reference)						
Sample		Ct values		$\Delta$ Ct	$\Delta\Delta$ 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		$\Delta$ 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		$\Delta$ 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	

