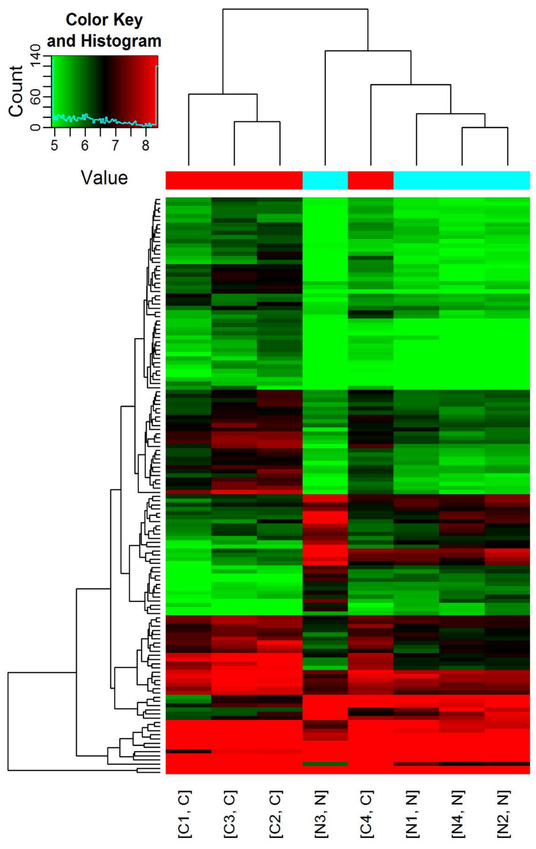
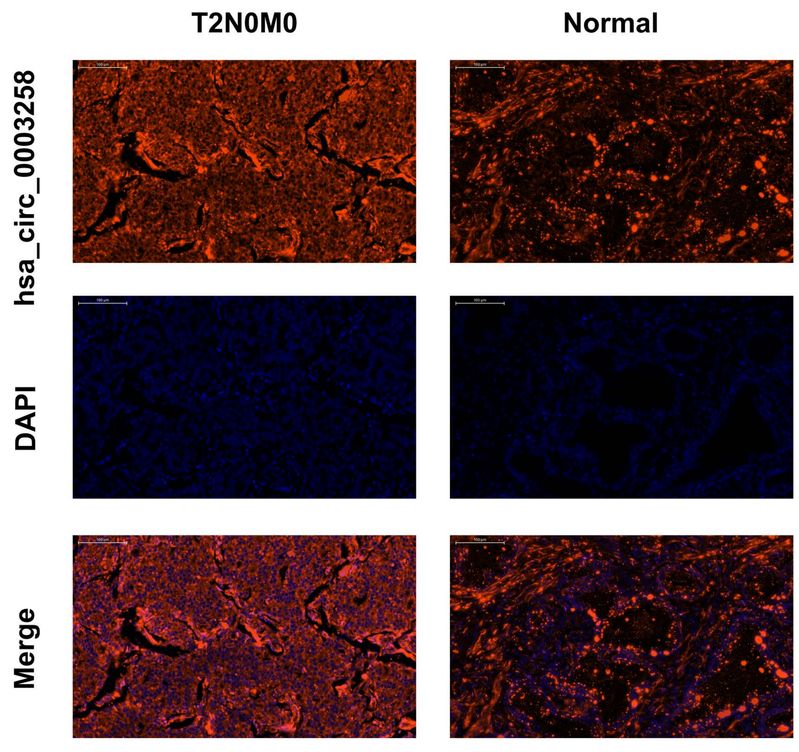
Fig.S1

A



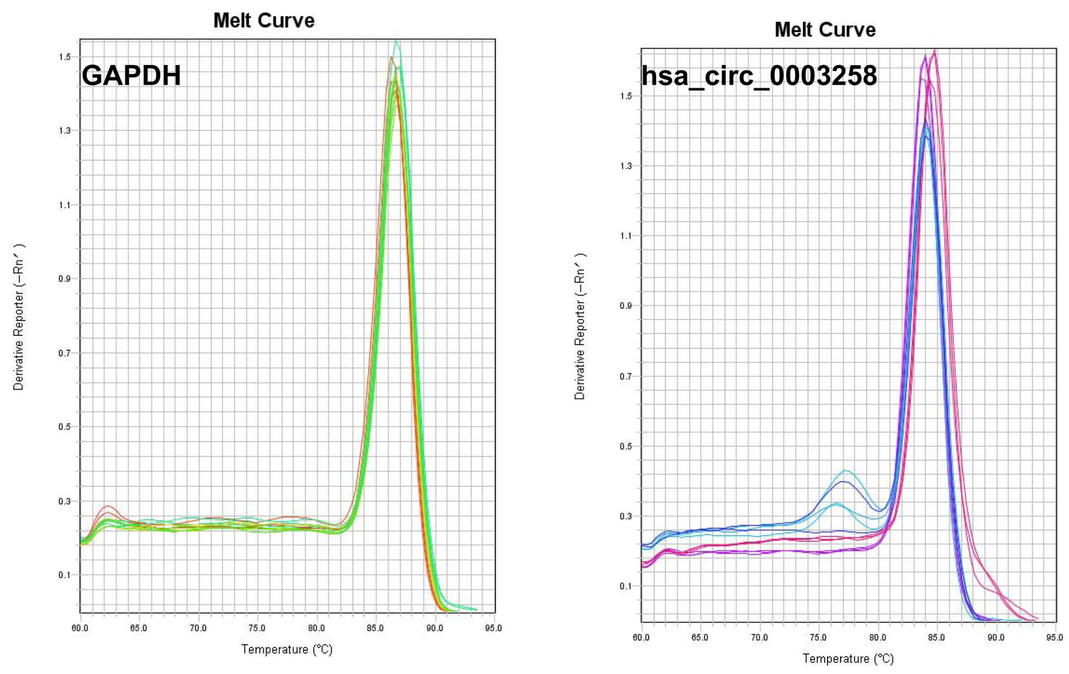
B



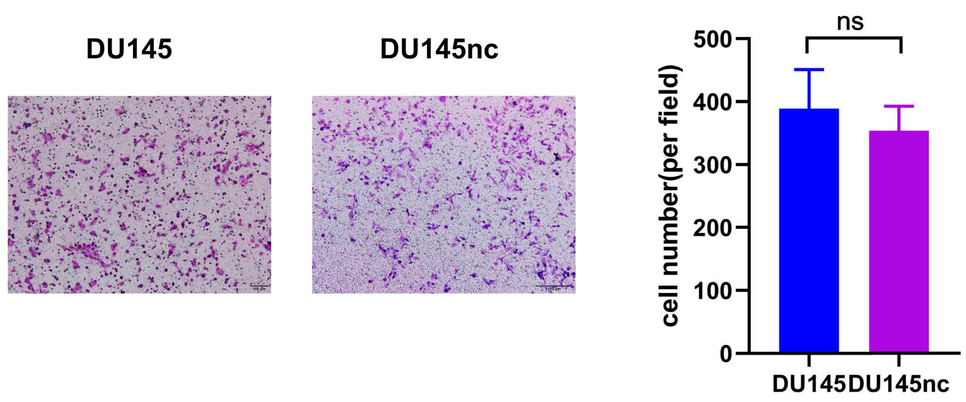
C

Protein coding potential			
IRES Elements	Parameter Index		
	Position (start--end)	R Score	With Pseudoknot (Y/N)
	119--247	1.319271	N
Open Reading Frame (ORF)	No open reading frame was found ! (Protein length less than 100aa)		
Protein Features	The possibility of encoding protein is relatively low(R<1.6 or it has no open reading frame), so no protein features was predicted!		

D



E



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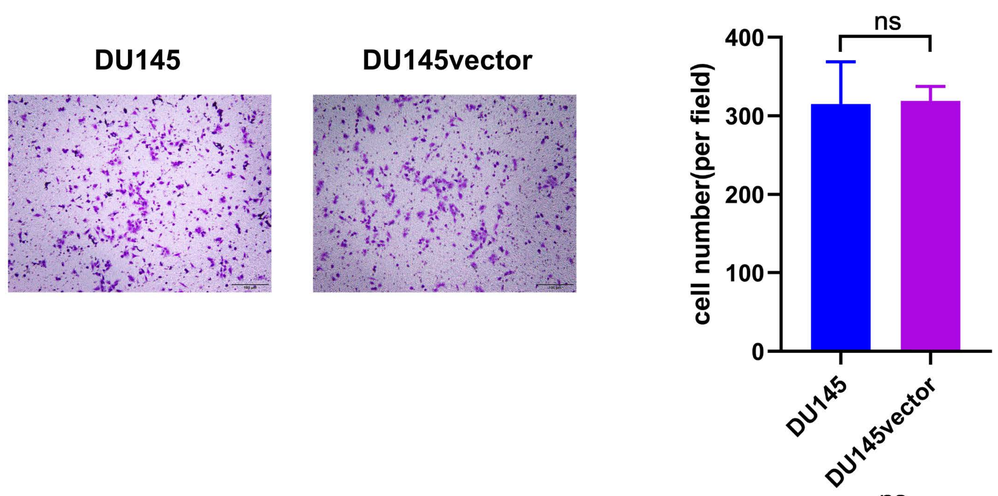

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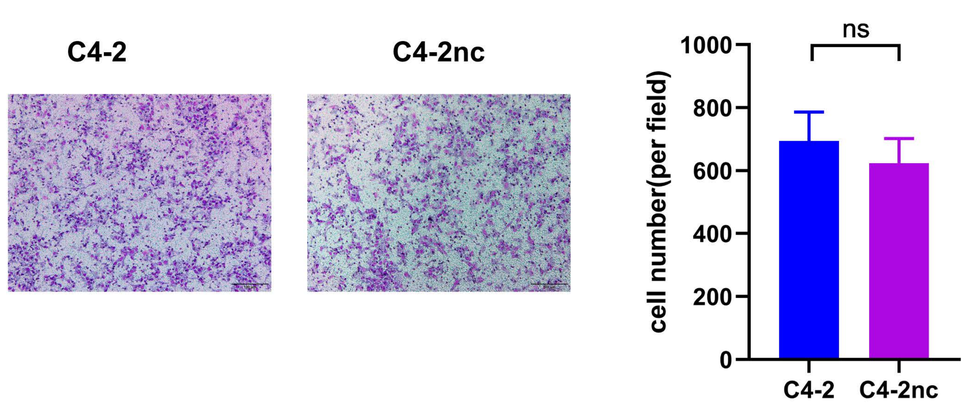

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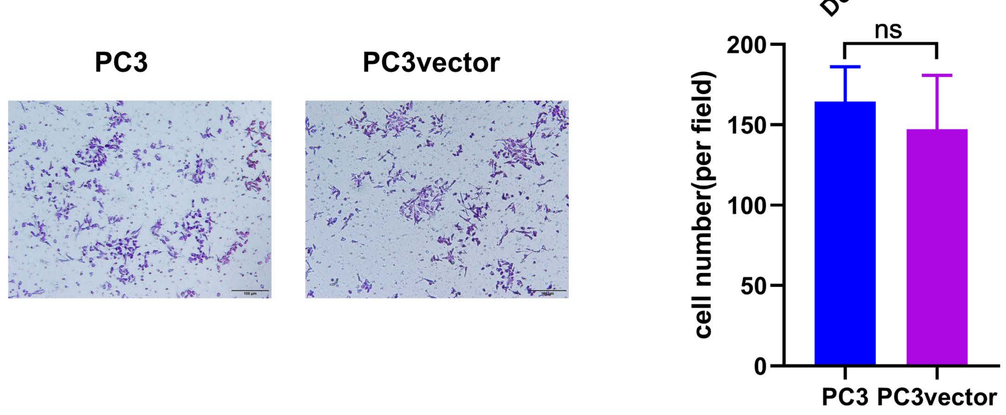

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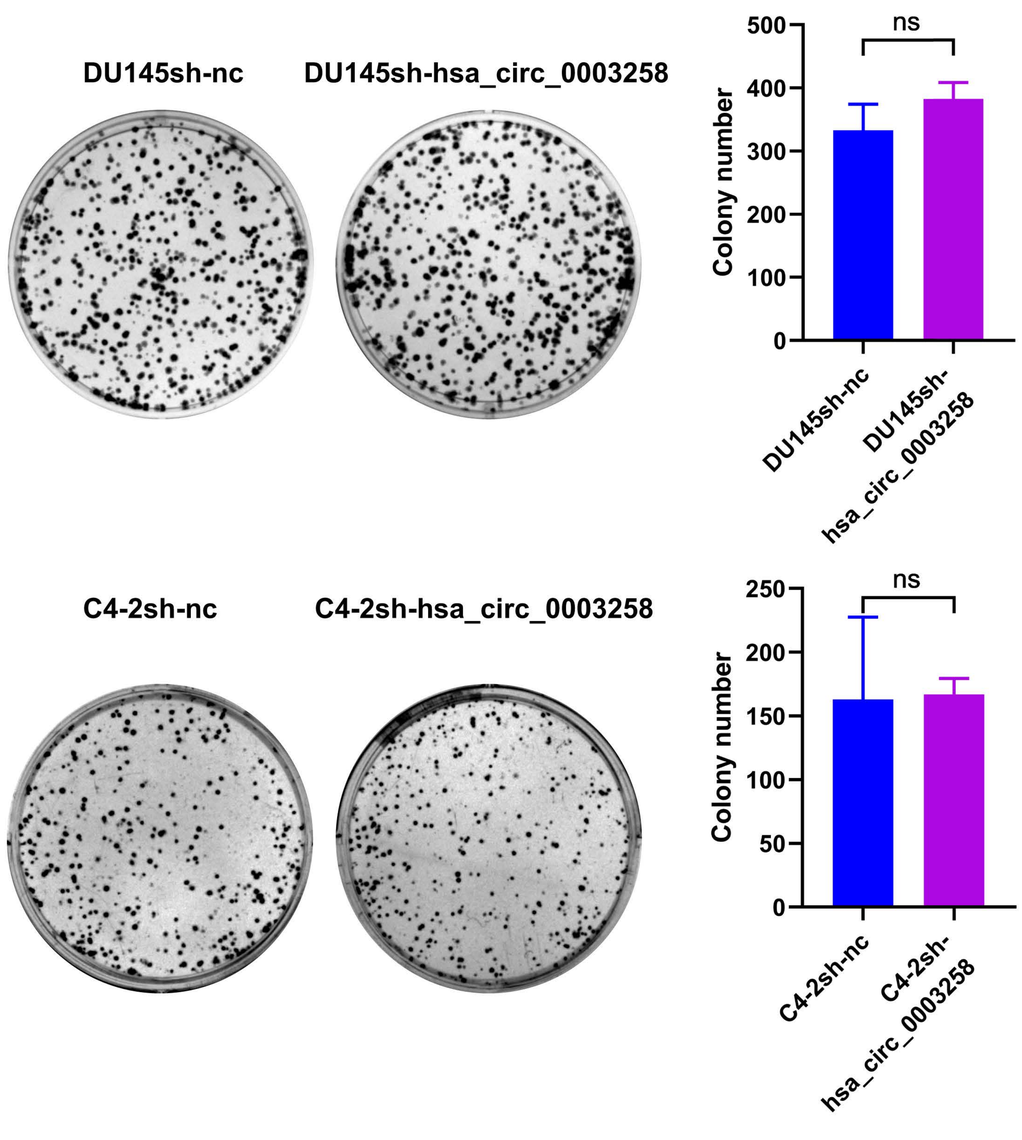


J

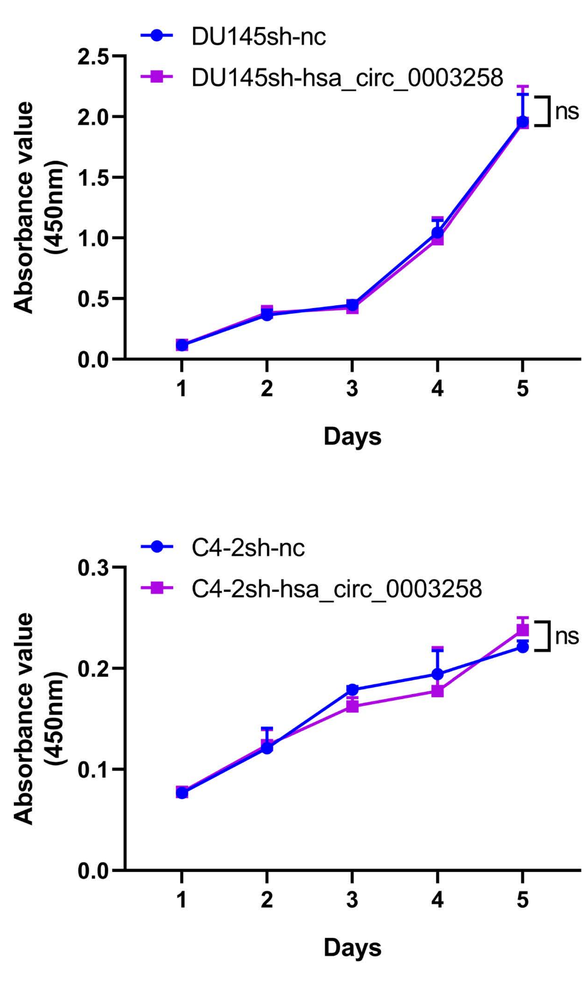
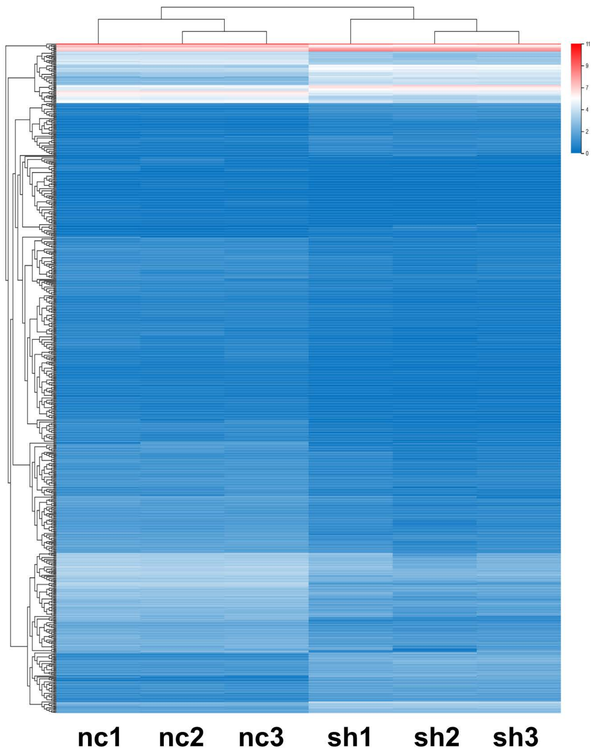
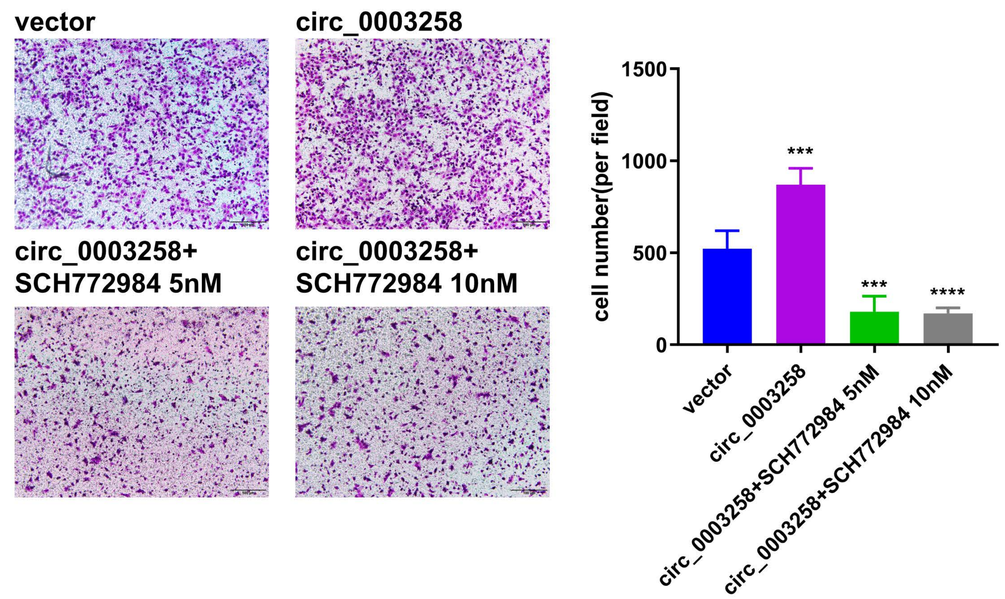


Fig.S2

A



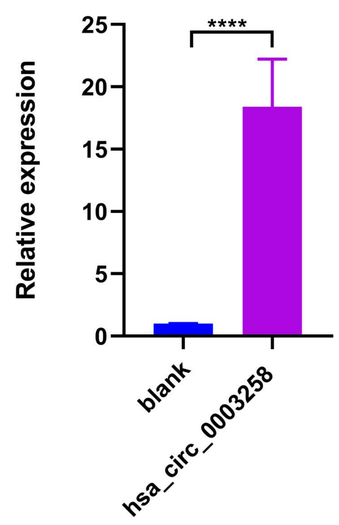
B



C

Mirbase ID											percentile
hsa_circ_0003258 (5' ... 3') hsa-miR-1278 (3' ... 5')	GAUUUCAACAUGAAGCAGUACUU ||||||| UAUCUACUAUACGUGUCAUGAU	7mer-m8	228	234	0.003	0.018	-0.058	-0.024	0.012	-0.169	91
hsa_circ_0003258 (5' ... 3') hsa-miR-203 (3' ... 5')	AGUGGUGUGGCAAGGAUUUCAAC |||||| |||||| GAUCACCAGGAUUUG--UAAAGUG	7mer-1a	214	220	-0.013	0.026	-0.046	0.031	0.074	-0.002	88
hsa_circ_0003258 (5' ... 3') hsa-miR-502-5p (3' ... 5')	UGUGCCAGUGGUGUGGCAAGGAU ||||||| AUCGUGGGUCUAUCGUUCCUA	7mer-m8	208	214	-0.007	0.003	-0.055	0.005	-0.034	-0.208	94
hsa_circ_0003258 (5' ... 3') hsa-miR-599 (3' ... 5')	NNNNNNNNNNNNNNCACACAAAA |||||| CAAACUAUUUGACUGUGUUG	7mer-1a	4	10	too_close	too_close	too_close	too_close	too_close	too_close	NA
hsa_circ_0003258 (5' ... 3') hsa-miR-653 (3' ... 5')	UGGUGUGGCAAGGAUUUCAACAU ||||||| GUCAUCUCUAACAAAGUUGUG	7mer-m8	216	222	0.003	-0.018	-0.056	-0.005	0.053	-0.143	94
hsa_circ_0003258 (5' ... 3') hsa-miR-766 (3' ... 5')	ACUCCUUGCAGCAUUCUGGAGAG |||||| CGACUCCGACACCCCGACCUCA	7mer-1a	91	97	0.001	0.020	-0.040	0.031	-0.048	-0.11	81
hsa_circ_0003258 (5' ... 3') hsa-miR-942 (3' ... 5')	CUUGCAGCAUUCUGGAGAGAAGC ||||||| GUGUACCGGUUUUGUCUCUUCU	7mer-m8	95	101	0.003	0.071	-0.048	0.023	0.016	-0.055	75

D



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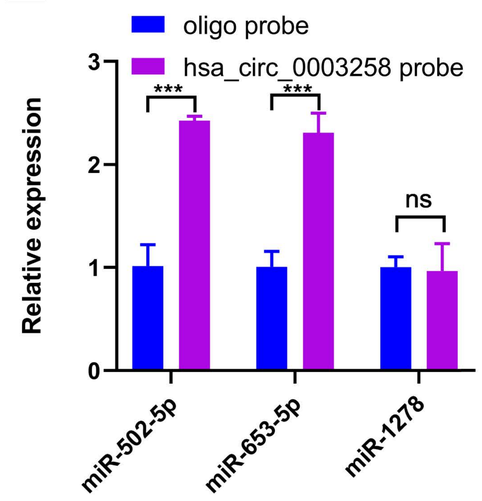

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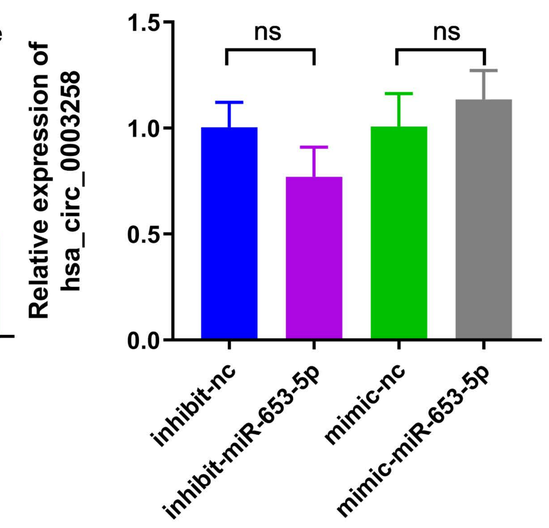

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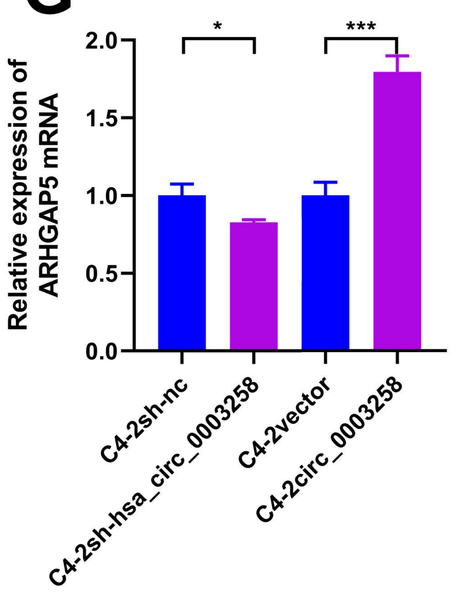

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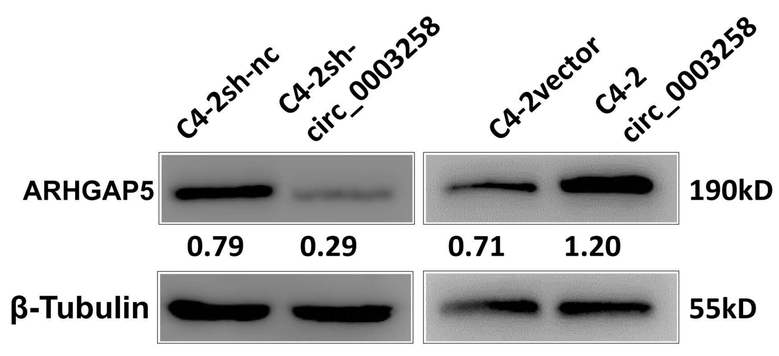

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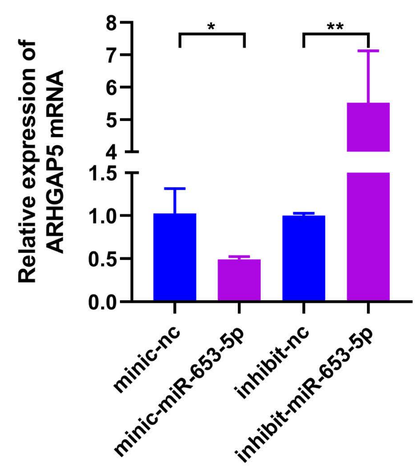


J

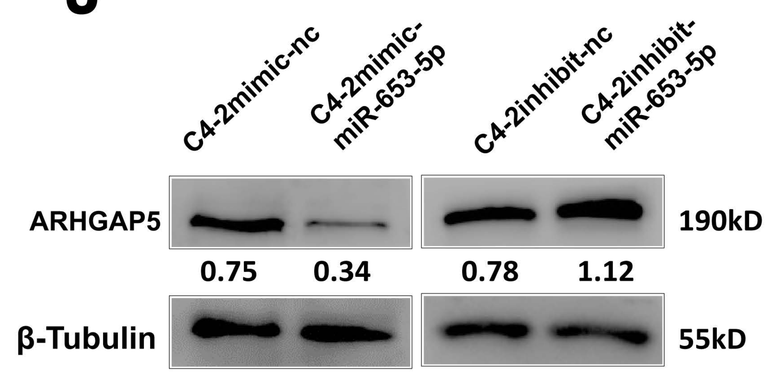
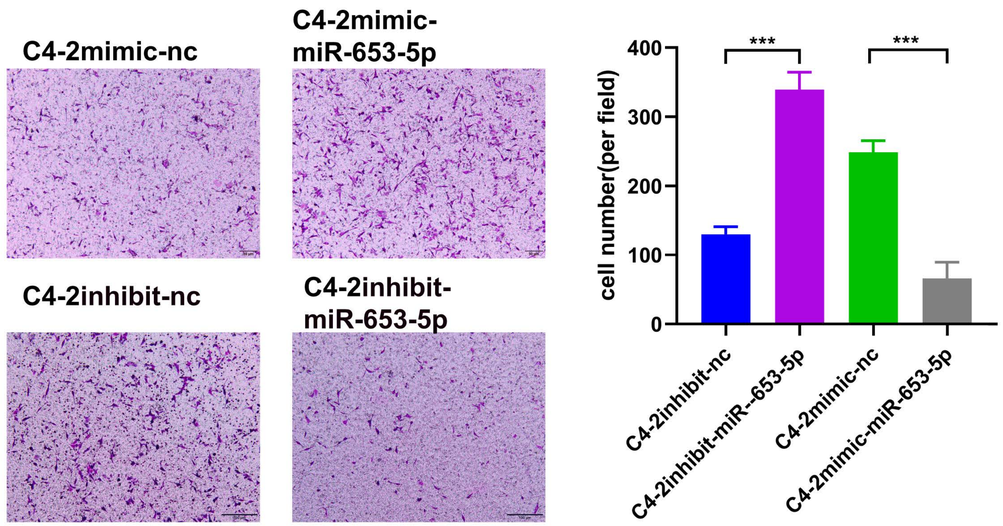
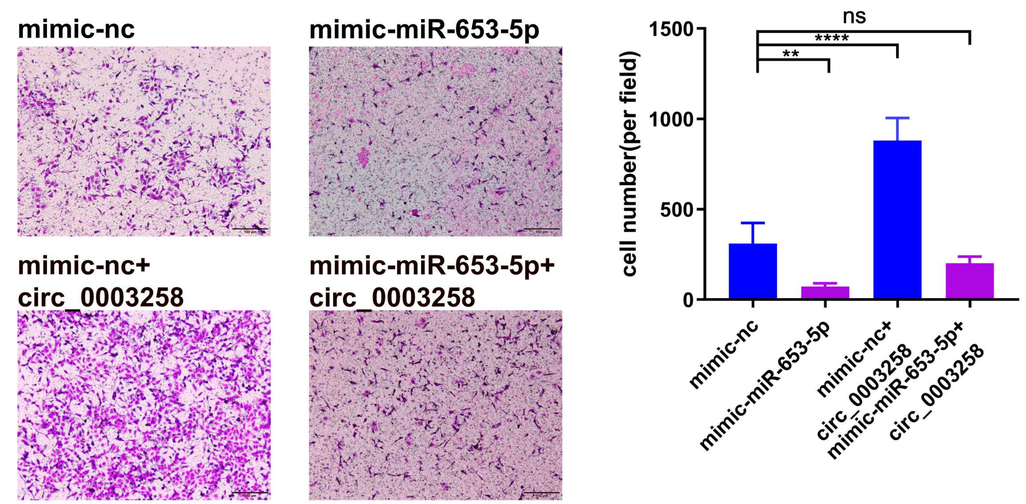


Fig.S3

A


C4-2mimic-nc
C4-2mimic-miR-653-5p
C4-2inhibit-nc
C4-2inhibit-miR-653-5p
cell number(per field)
400
300
200
100
0
***
***
C4-2inhibit-nc
C4-2inhibit-miR--653-5p
C4-2mimic-nc
C4-2mimic-miR-653-5p

B


mimic-nc
mimic-miR-653-5p
mimic-nc+ circ_0003258
mimic-miR-653-5p+ circ_0003258
cell number(per field)
1500
1000
500
0
ns
****
**
mimic-nc
mimic-miR-653-5p
mimic-nc+ circ_0003258
mimic-miR-653-5p+ circ_0003258

C

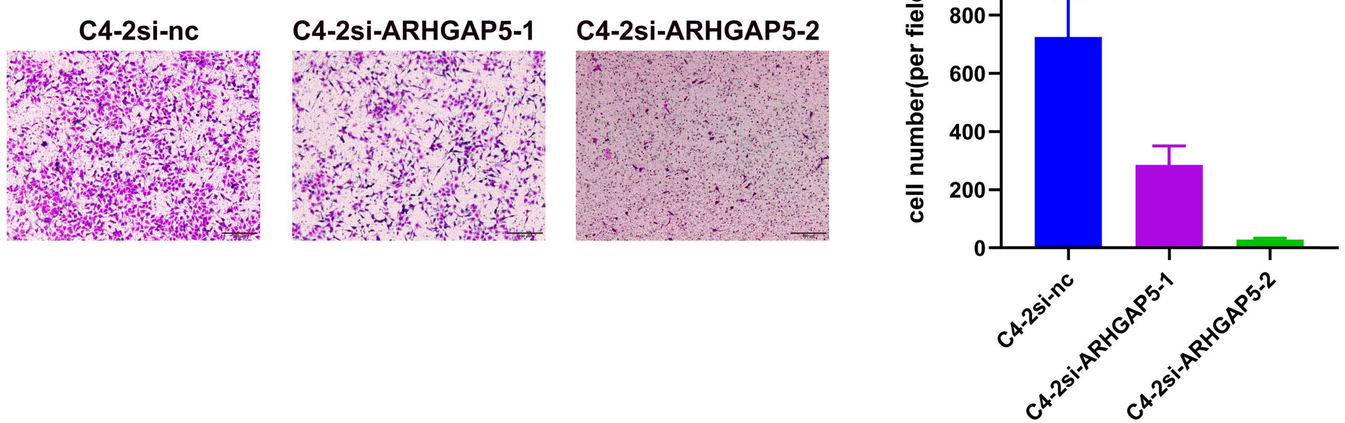
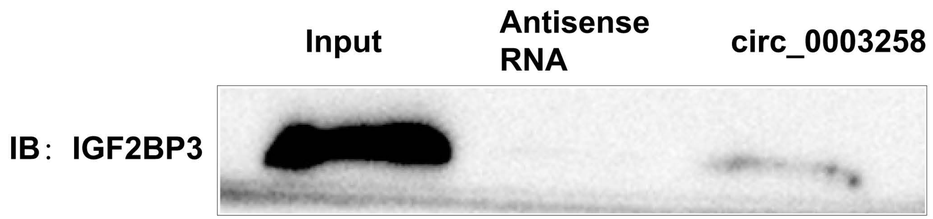
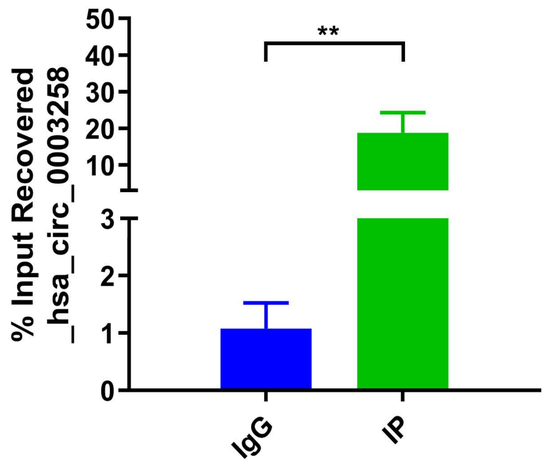

C4-2si-nc
C4-2si-ARHGAP5-1
C4-2si-ARHGAP5-2
cell number(per field)
1000
800
600
400
200
0
**
**
C4-2si-nc
C4-2si-ARHGAP5-1
C4-2si-ARHGAP5-2

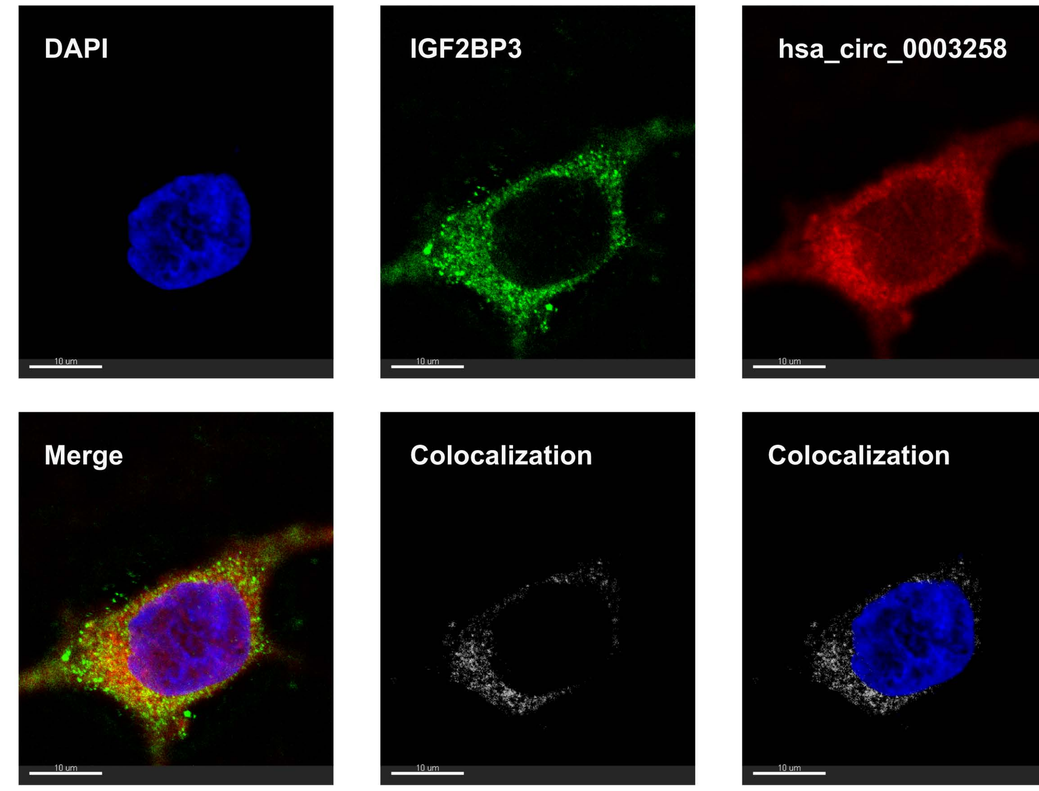
Fig.S4

A

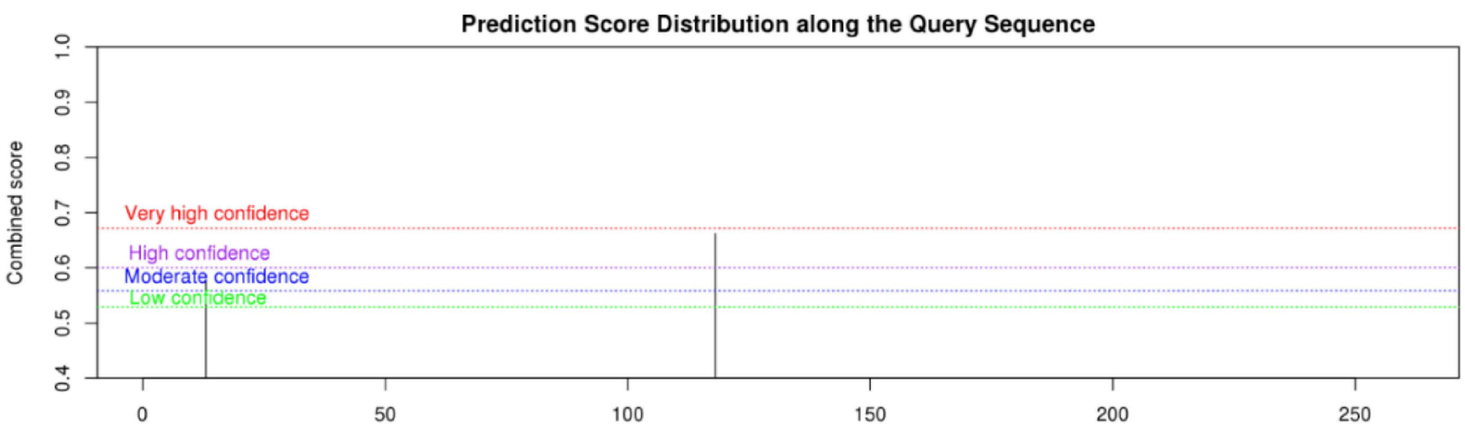

Input
Antisense RNA
circ_0003258
IB：IGF2BP3


% Input Recovered _hsa_circ_0003258
50
40
30
20
10
3
2
1
0
**
IgG
IP

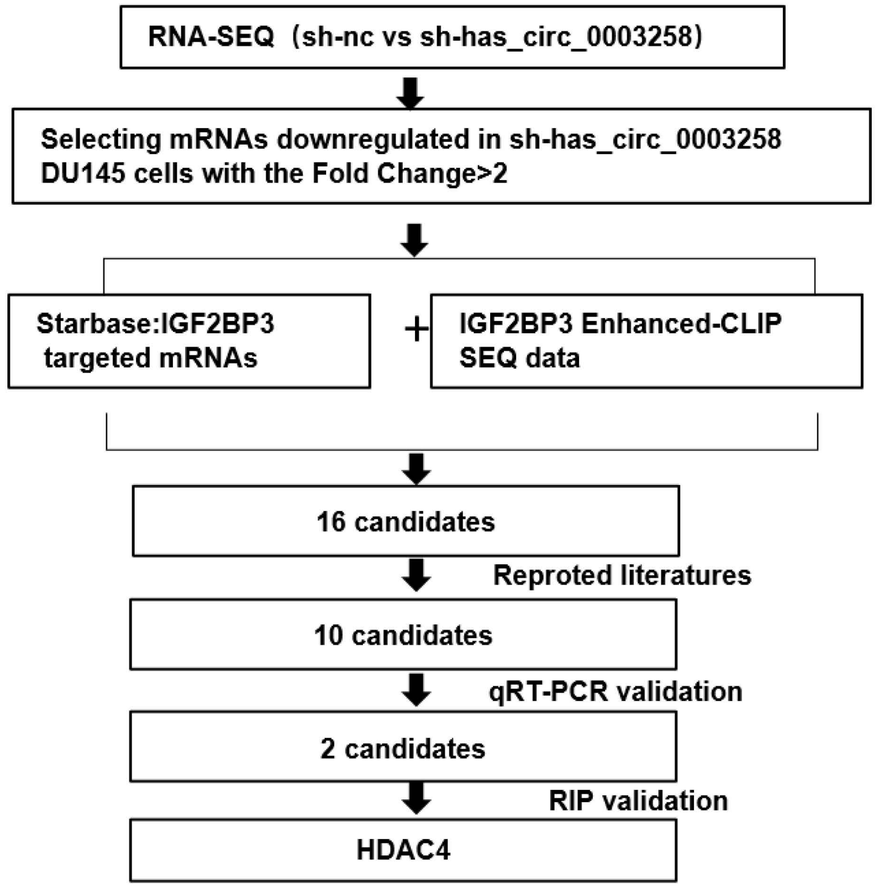
B


DAPI
IGF2BP3
hsa_circ_0003258
Merge
Colocalization
Colocalization

C


Prediction Score Distribution along the Query Sequence
Combined score
1.0
0.9
0.8
0.7
0.6
0.5
0.4
Very high confidence
High confidence
Moderate confidence
Low confidence
0
50
100
150
200
250

A

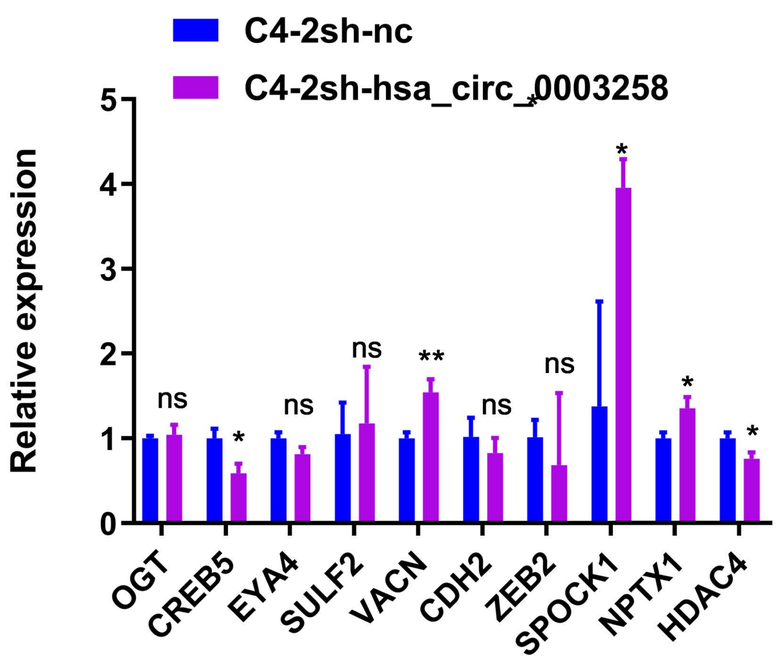


B

Fig.S5

Characteristics	Gene Name
Genes downregulated in has_circ_0003258 knockdown PC cells with Fold Change>2.0 and bound by IGF2BP3	VCAN、PHACTR2、NPTX1、PELI2、CREB5、EYA4、CDH2、OGT、ZEB2、SAMD11、HDAC4、SPOCK1、RUNX1T1、CCND1、SULF2、PHF21B
Genes associated with metastasis	SULF2、VCAN、ZEB2、CDH2、SPOCK1、EYA4、NPTX1、HDAC4、CREB5、OGT

C



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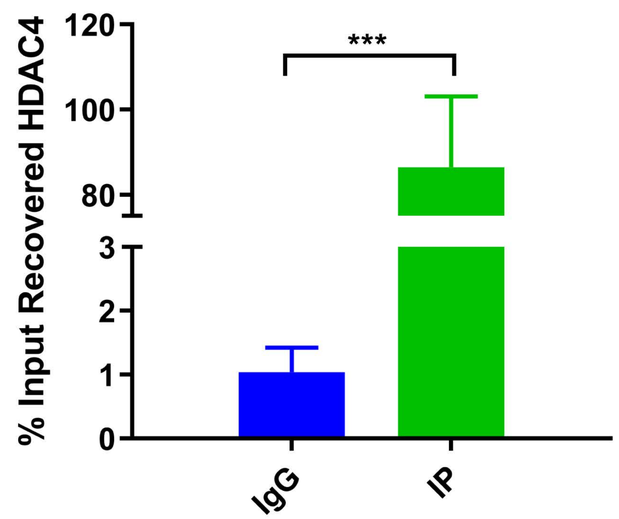
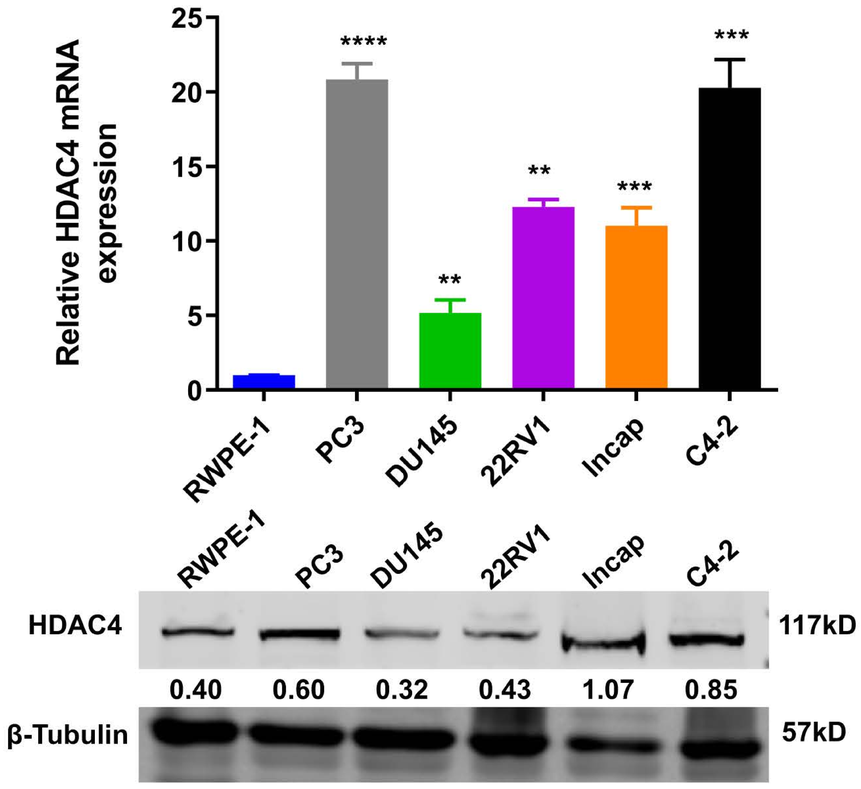
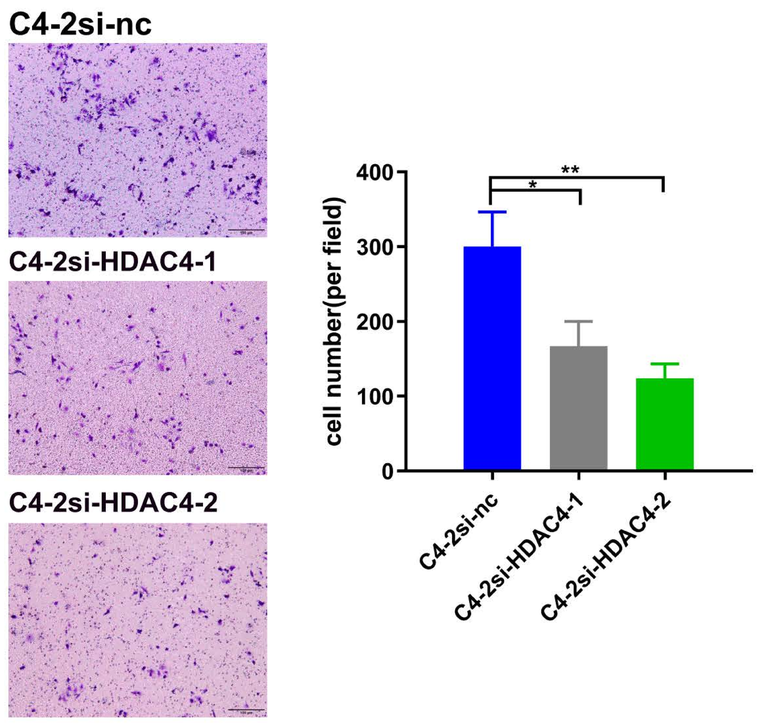


Fig.S6

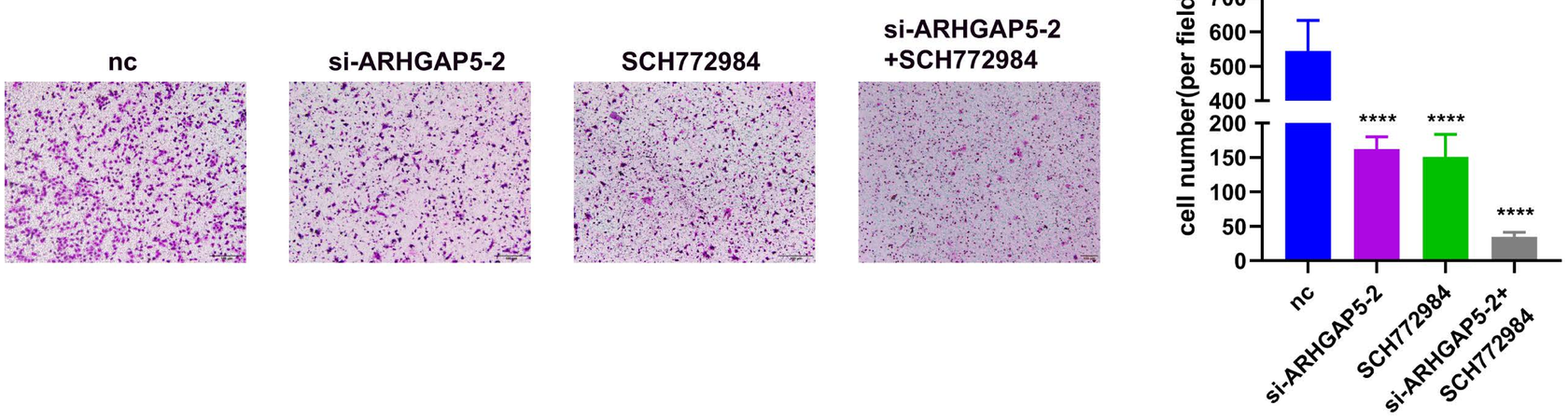
A


Relative HDAC4 mRNA expression
25
20
15
10
5
0
****
**
**
***
***
RWPE-1
PC3
DU145
22RV1
lncap
C4-2
HDAC4
117kD
0.40
0.60
0.32
0.43
1.07
0.85
β-Tubulin
57kD

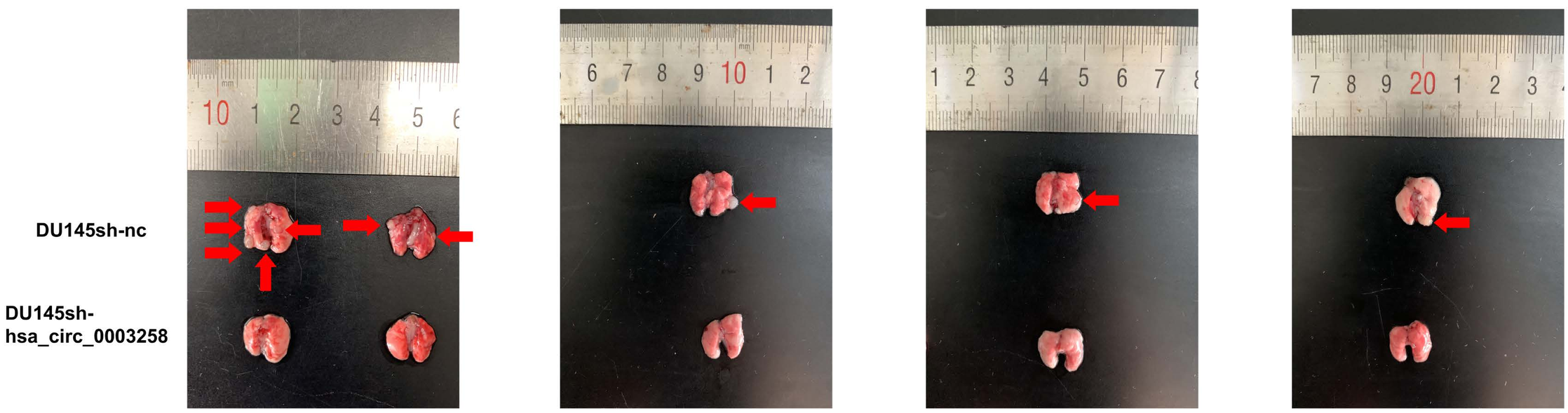
B


C4-2si-nc
C4-2si-HDAC4-1
C4-2si-HDAC4-2
cell number(per field)
400
300
200
100
0
**
*
C4-2si-nc
C4-2si-HDAC4-1
C4-2si-HDAC4-2

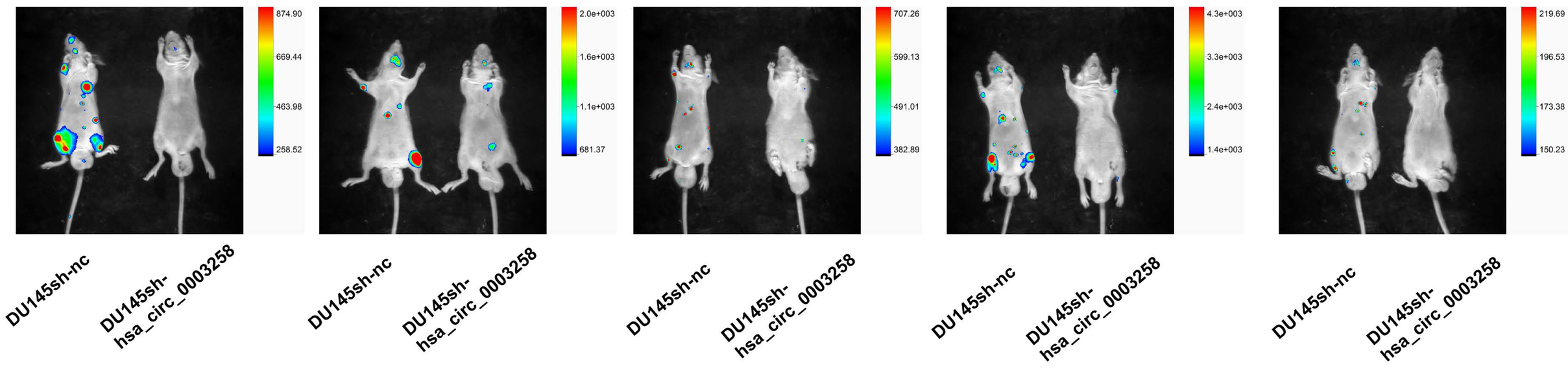
C


nc
si-ARHGAP5-2
SCH772984
si-ARHGAP5-2
+SCH772984
cell number(per field)
800
700
600
500
400
200
150
100
50
0
****
****
****
nc
si-ARHGAP5-2
SCH772984
si-ARHGAP5-2+
SCH772984

D


DU145sh-nc
DU145sh-
hsa_circ_0003258

E


874.90
669.44
463.98
258.52
2.0e+003
1.6e+003
1.1e+003
681.37
707.26
599.13
491.01
382.89
4.3e+003
3.3e+003
2.4e+003
1.4e+003
219.69
196.53
173.38
150.23
DU145sh-nc
DU145sh-
hsa_circ_0003258