FIG. 1

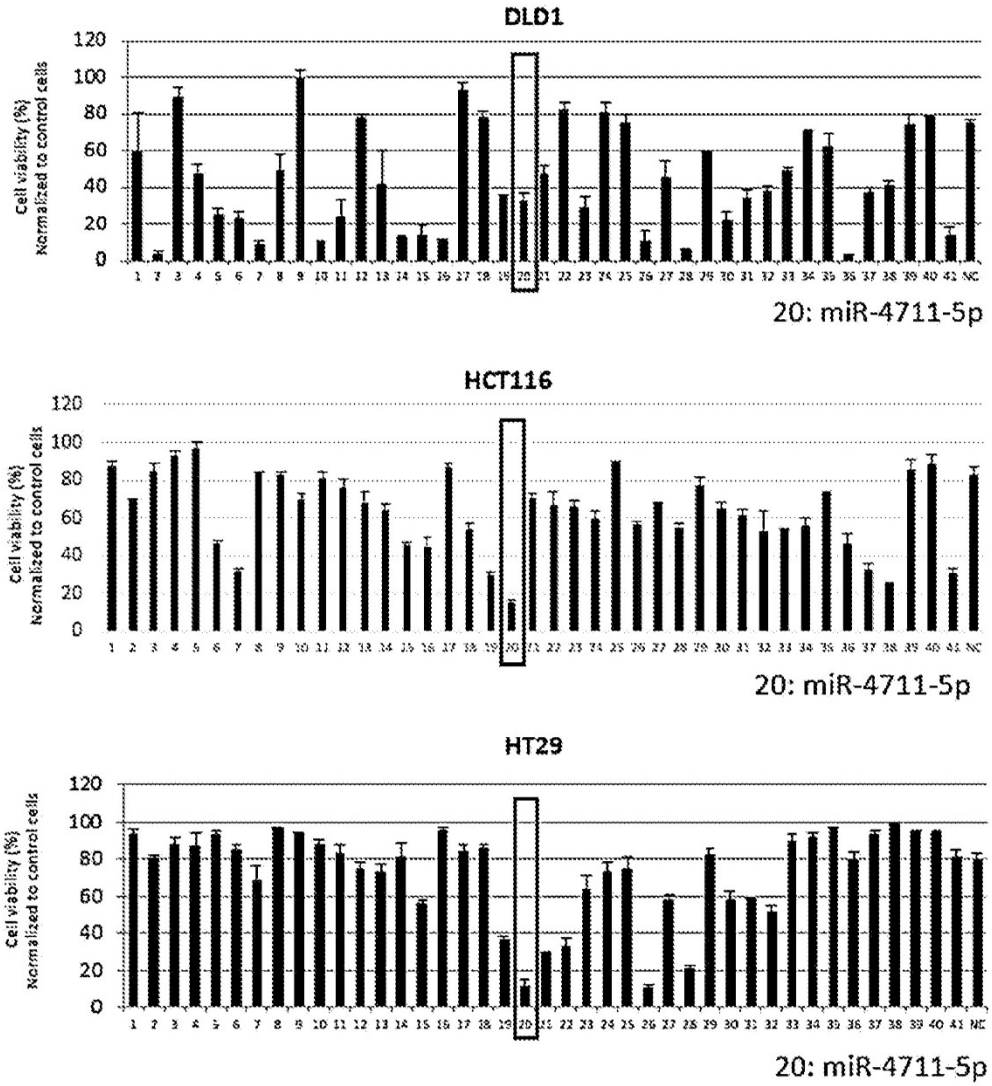

DLD1
Cell viability (%)
Normalized to control cells
120
100
80
60
40
20
0
20: miR-4711-5p
HCT116
Cell viability (%)
Normalized to control cells
20: miR-4711-5p
HT29
Cell viability (%)
Normalized to control cells
20: miR-4711-5p

FIG. 2

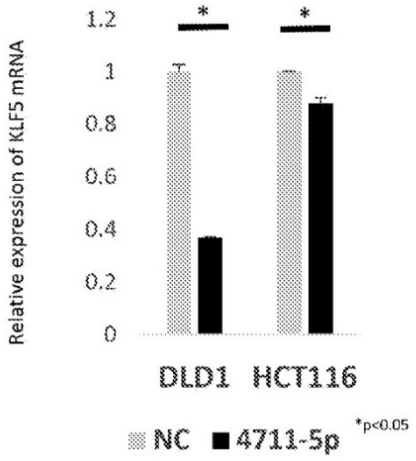

Relative expression of KLF5 mRNA
1.2
1
0.8
0.6
0.4
0.2
0
*
*
DLD1
HCT116
NC
4711-5p
*p<0.05

FIG. 3

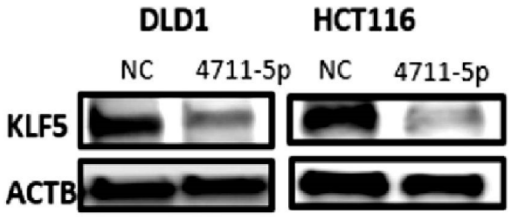


FIG. 4

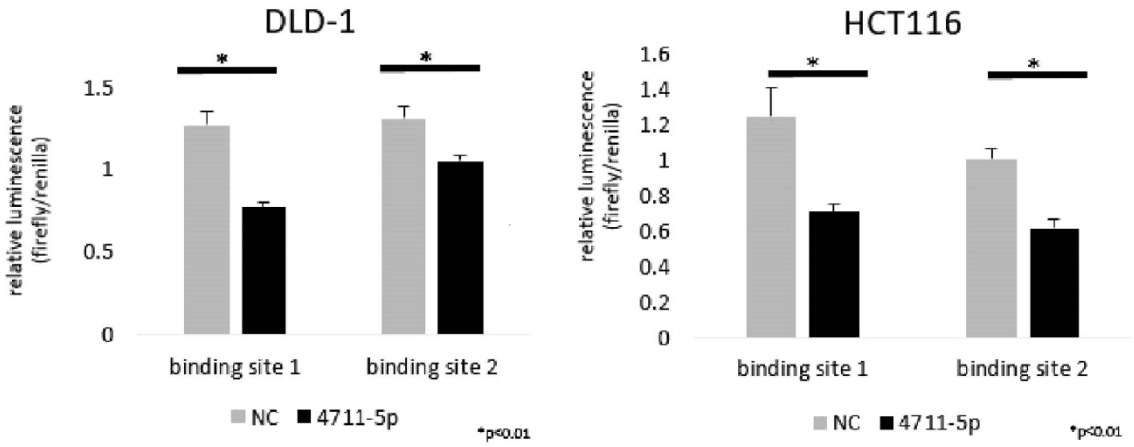


FIG. 5

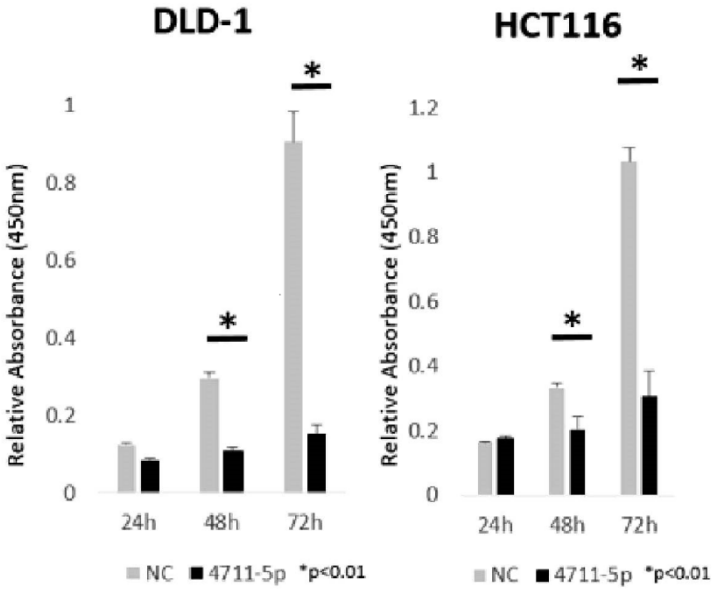


FIG. 6

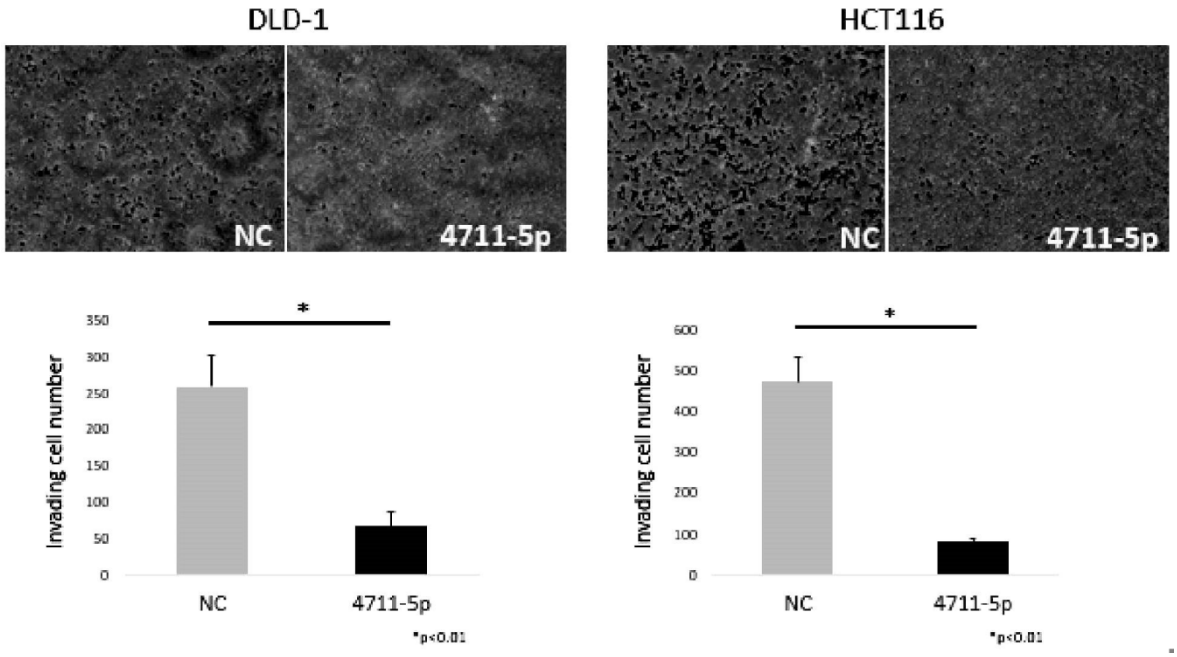

DLD-1
HCT116
NC
4711-5p
NC
4711-5p
Invading cell number
350
300
250
200
150
100
50
0
*
NC
4711-5p
*p<0.01
Invading cell number
600
500
400
300
200
100
0
*
NC
4711-5p
*p<0.01

FIG. 7

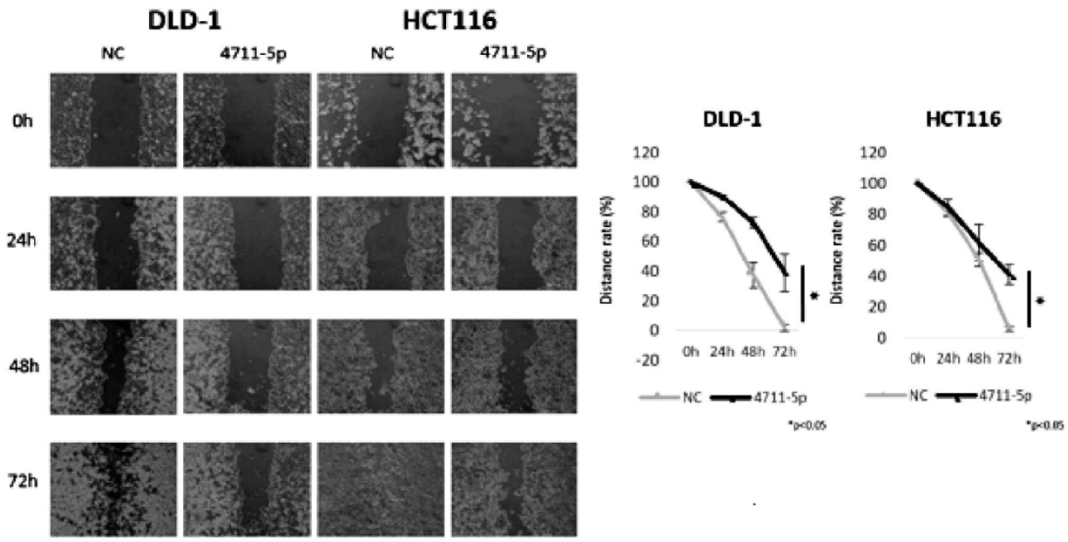

DLD-1
HCT116
NC
4711-5p
NC
4711-5p
0h
24h
48h
72h
DLD-1
HCT116
Distance rate (%)
120
100
80
60
40
20
0
-20
0h 24h 48h 72h
NC
4711-5p
*p<0.05
Distance rate (%)
120
100
80
60
40
20
0
0h 24h 48h 72h
NC
4711-5p
*p<0.05

FIG. 8

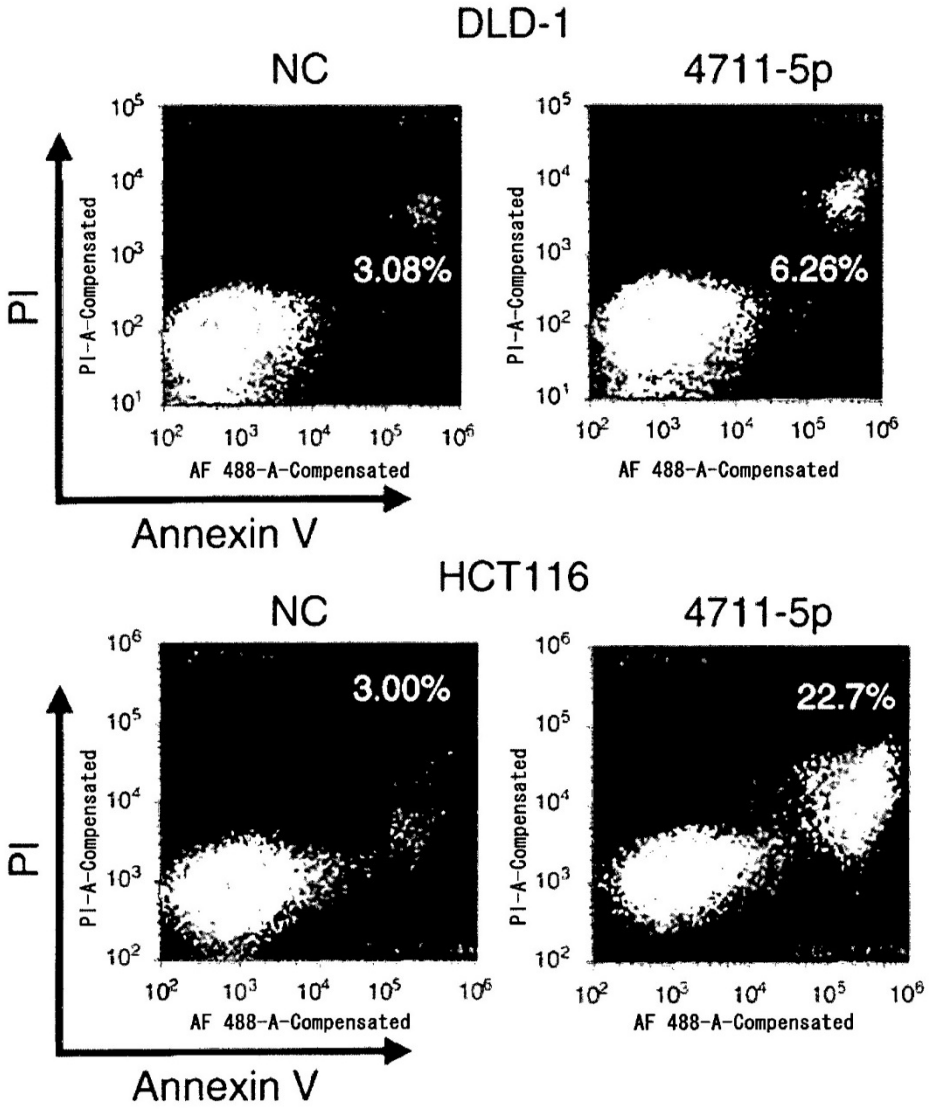

DLD-1
NC
4711-5p
3.08%
6.26%
PI
PI-A-Compensated
AF 488-A-Compensated
Annexin V
HCT116
NC
4711-5p
3.00%
22.7%
PI
PI-A-Compensated
AF 488-A-Compensated
Annexin V

FIG. 9

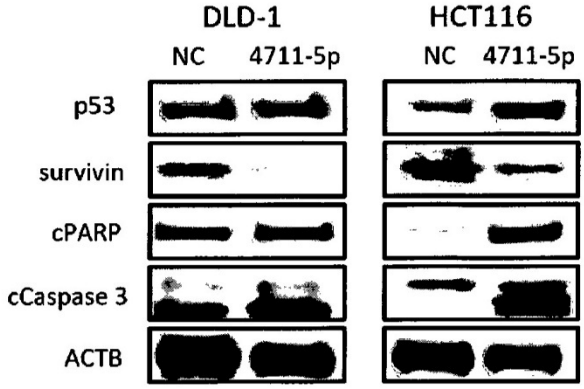

DLD-1
HCT116
NC
4711-5p
NC
4711-5p
p53
survivin
cPARP
cCaspase 3
ACTB

FIG. 10

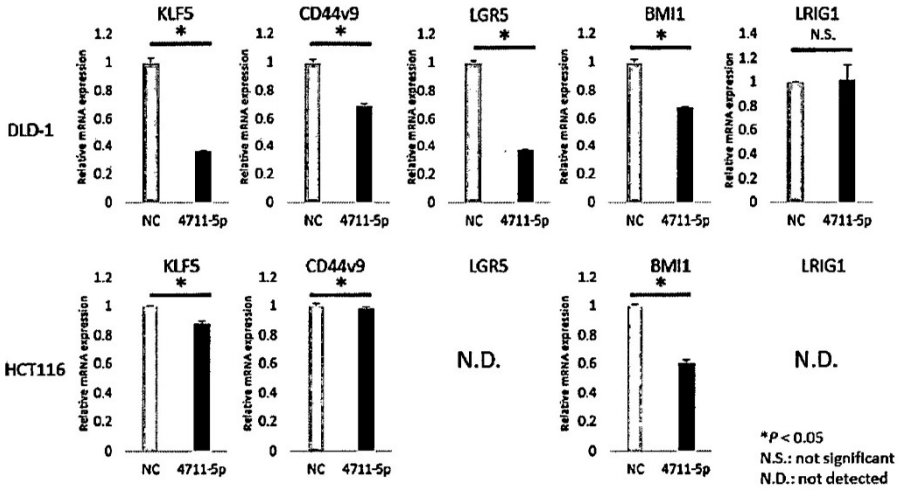


FIG. 11

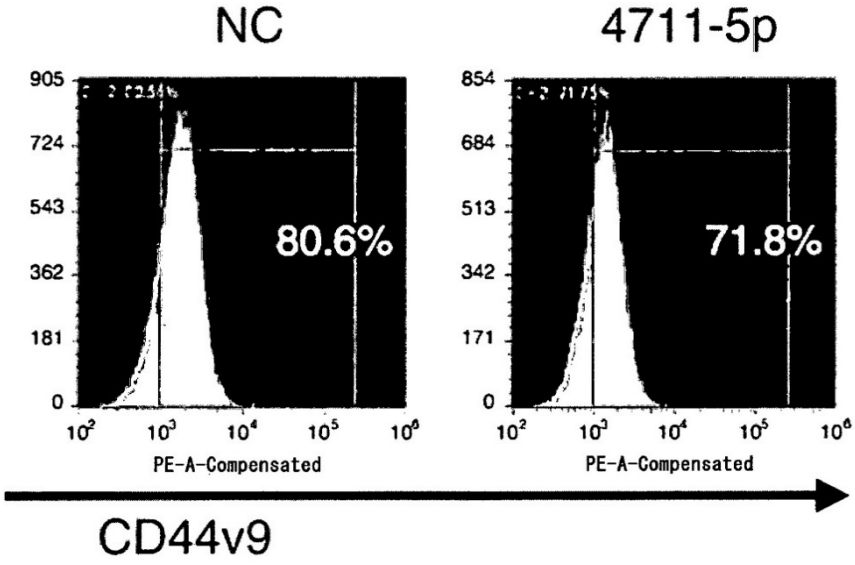


FIG. 12

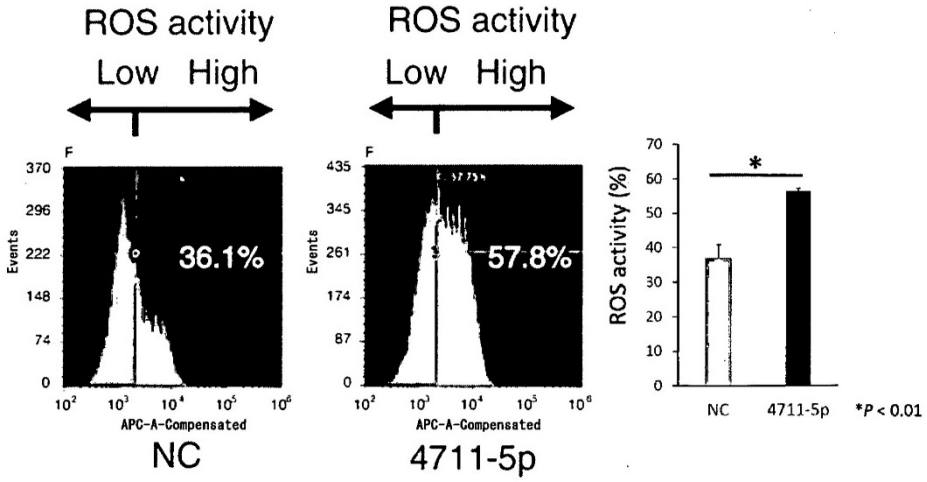


FIG. 13

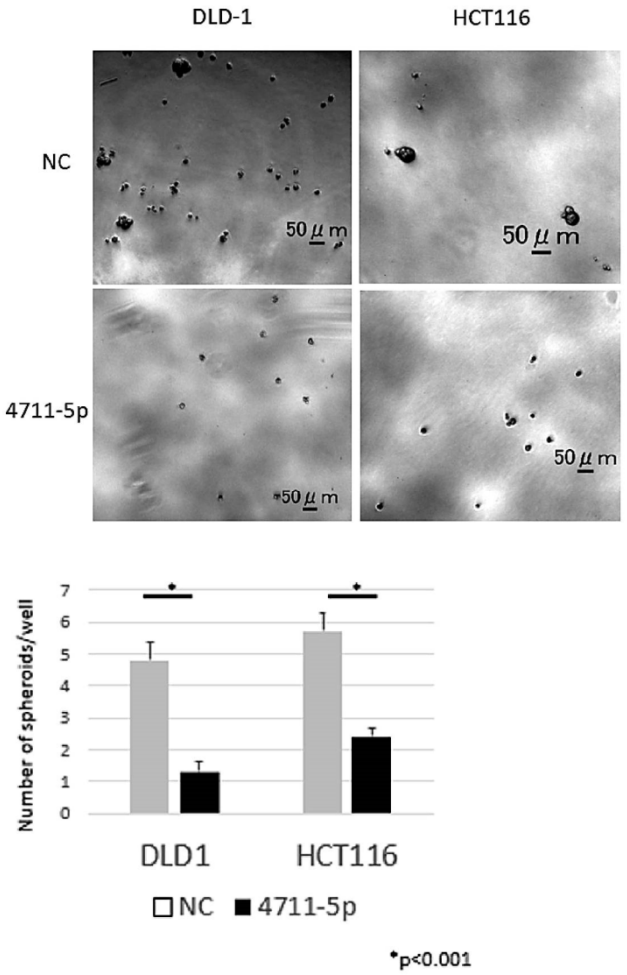

DLD-1
HCT116
NC
4711-5p
50 μm
Number of spheroids/well
DLD1
HCT116
NC
4711-5p
*p<0.001

FIG. 14

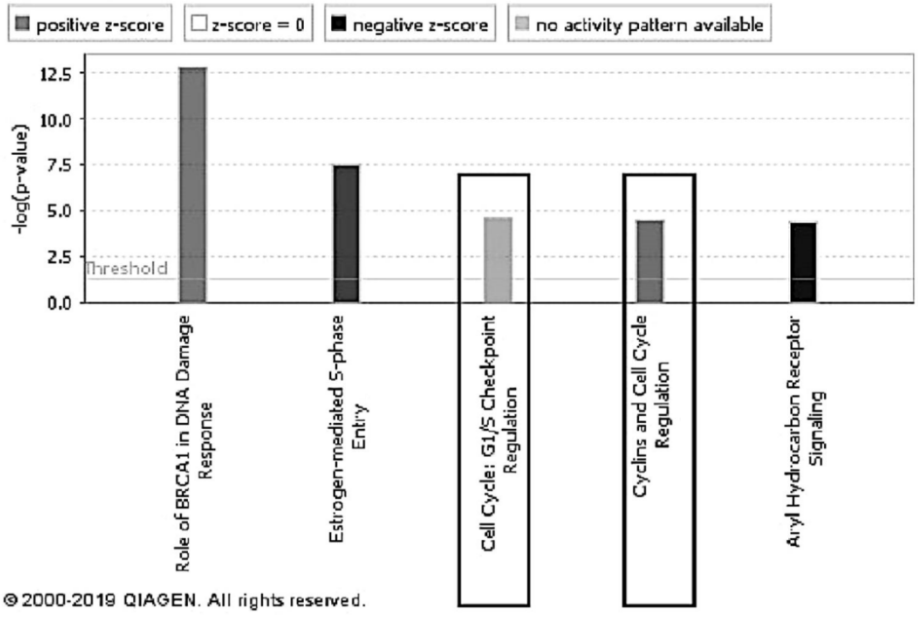

positive z-score
z-score = 0
negative z-score
no activity pattern available
-log(p-value)
Threshold
Role of BRCA1 in DNA Damage Response
Estrogen-mediated S-phase Entry
Cell Cycle: G1/S Checkpoint Regulation
Cyclins and Cell Cycle Regulation
Aryl Hydrocarbon Receptor Signaling
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FIG. 15

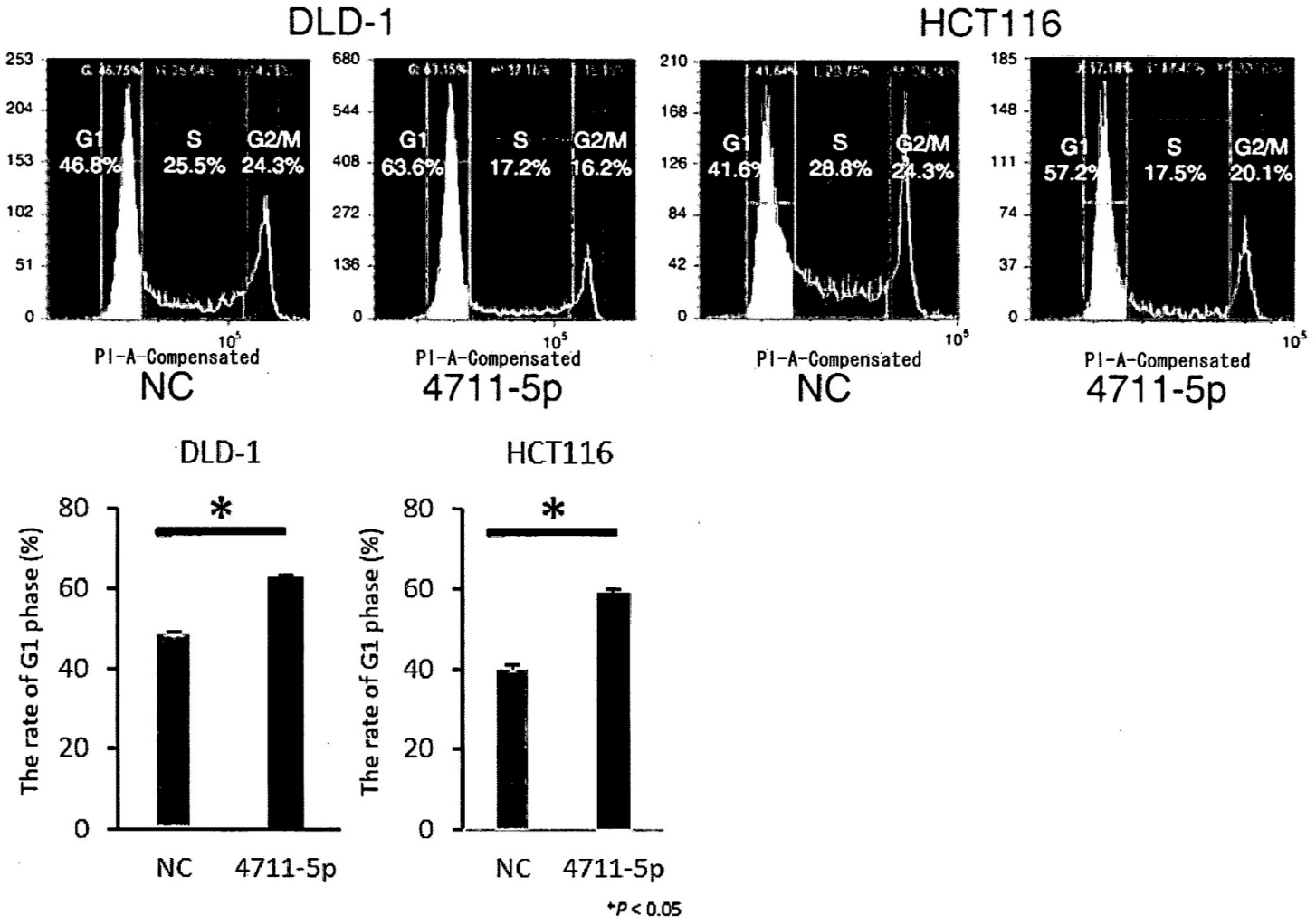

DLD-1
HCT116
G1
46.8%
S
25.5%
G2/M
24.3%
G1
63.6%
S
17.2%
G2/M
16.2%
G1
41.6%
S
28.8%
G2/M
24.3%
G1
57.2%
S
17.5%
G2/M
20.1%
PI-A-Compensated
NC
4711-5p
The rate of G1 phase (%)
*
NC
4711-5p
*P < 0.05

FIG. 16

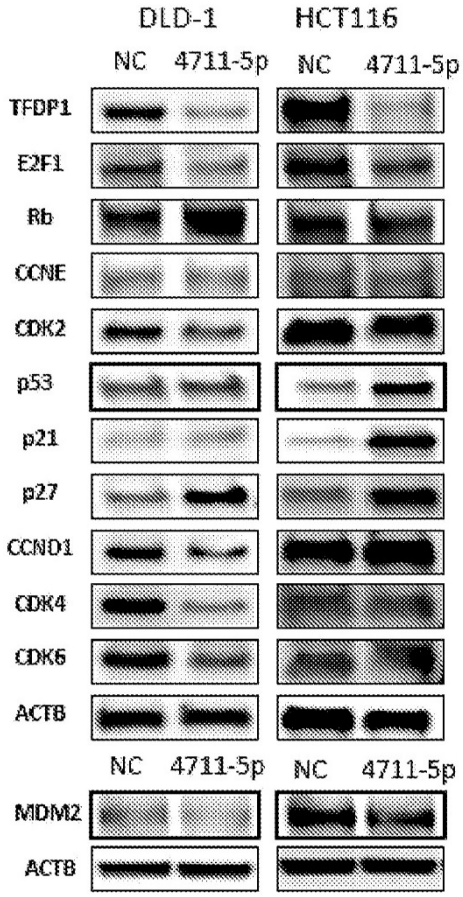

DLD-1
HCT116
NC
4711-5p
NC
4711-5p
TFDP1
E2F1
Rb
CCNE
CDK2
p53
p21
p27
CCND1
CDK4
CDK6
ACTB
NC
4711-5p
NC
4711-5p
MDM2
ACTB

FIG. 17

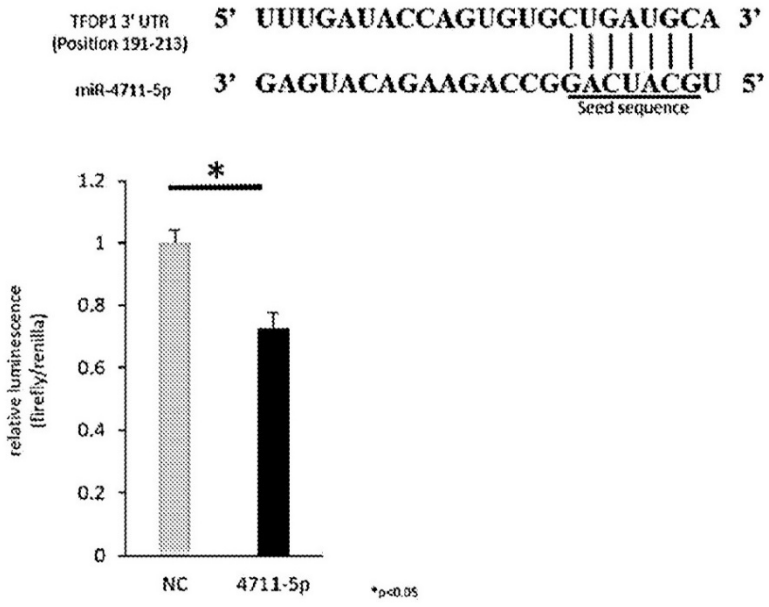
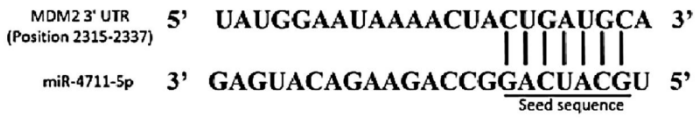

TFDP1 3' UTR
(Position 191-213)
5' UUUGAUACCAGUGUGCUGAUGCA 3'
miR-4711-5p
3' GAGUACAGAAGACCGGACUACGU 5'
Seed sequence
*
1.2
1
0.8
0.6
0.4
0.2
0
relative luminescence
(firefly/renilla)
NC
4711-5p
*p<0.05

FIG. 18



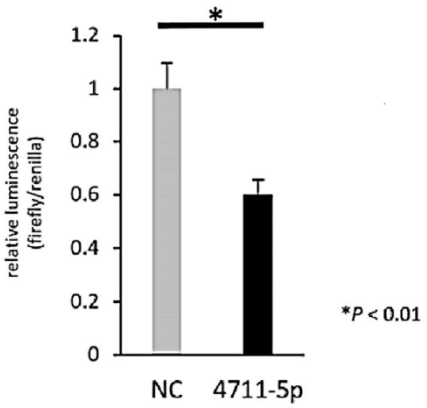


FIG. 19

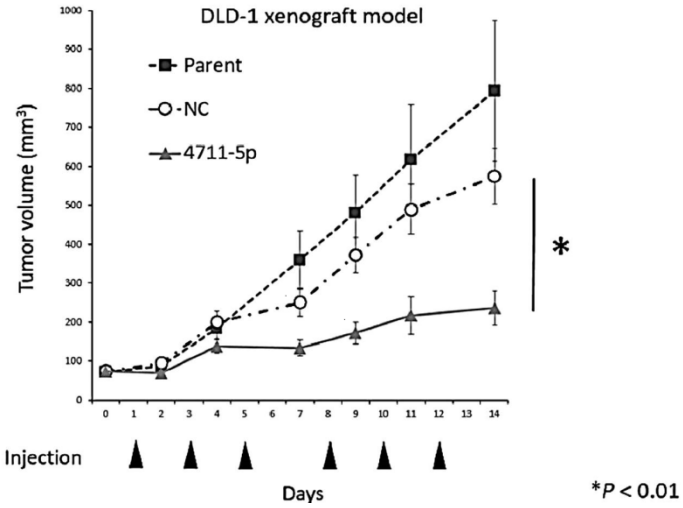


FIG. 20

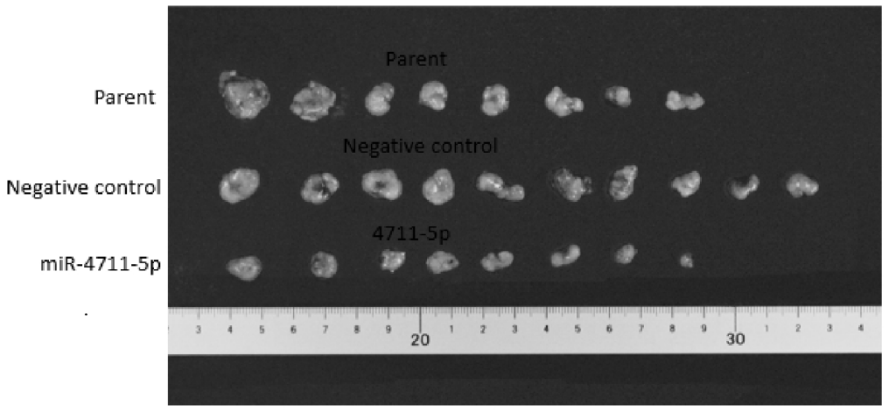


FIG. 21

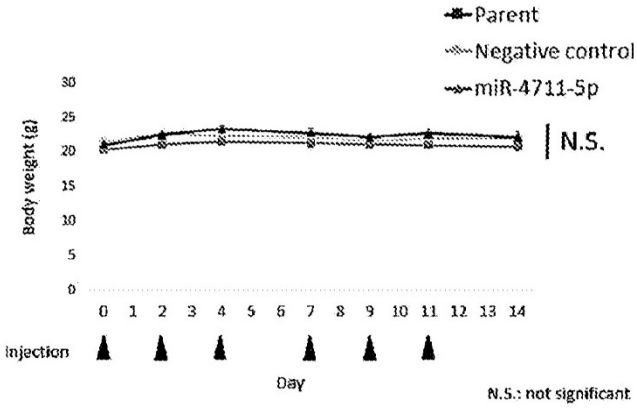


FIG. 22

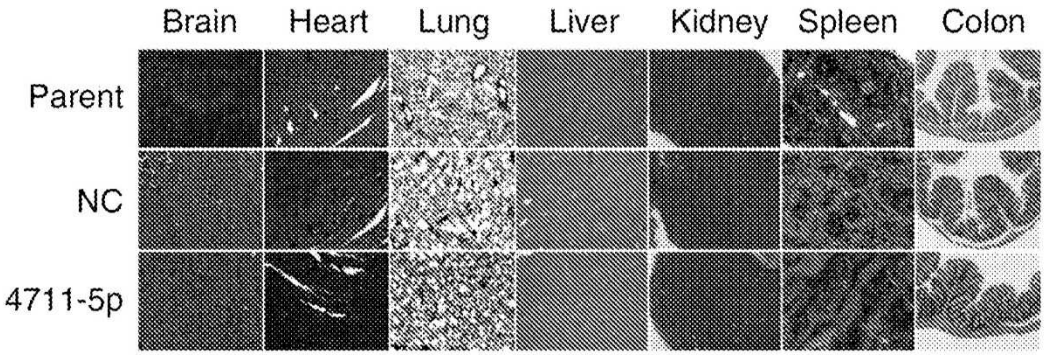


FIG. 23

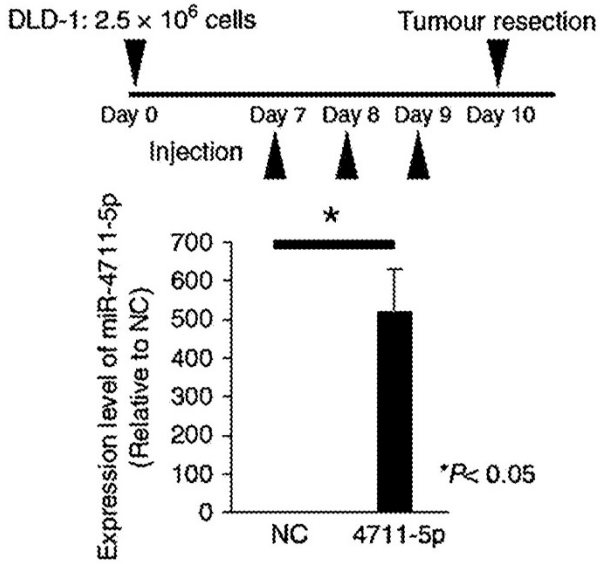


FIG. 24

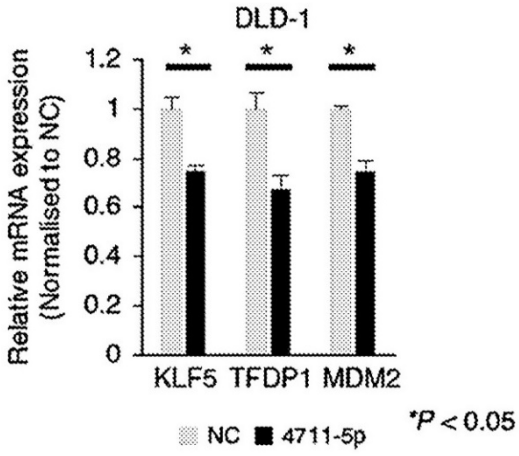


FIG. 25

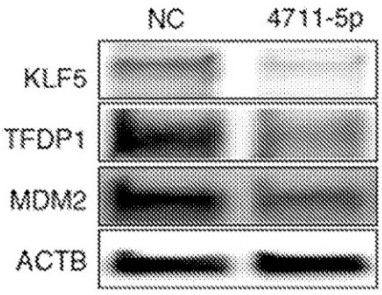


FIG. 26

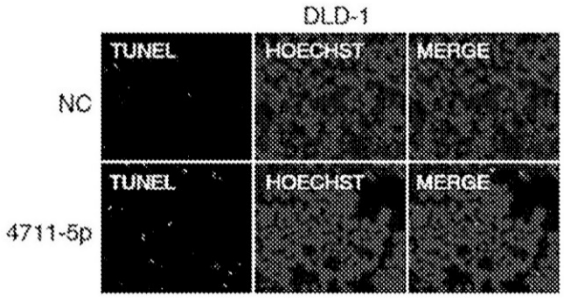


FIG. 27

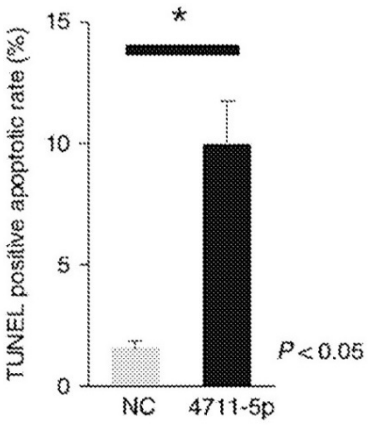


FIG. 28

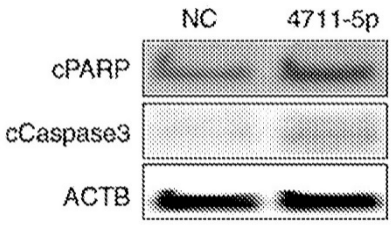


FIG. 29

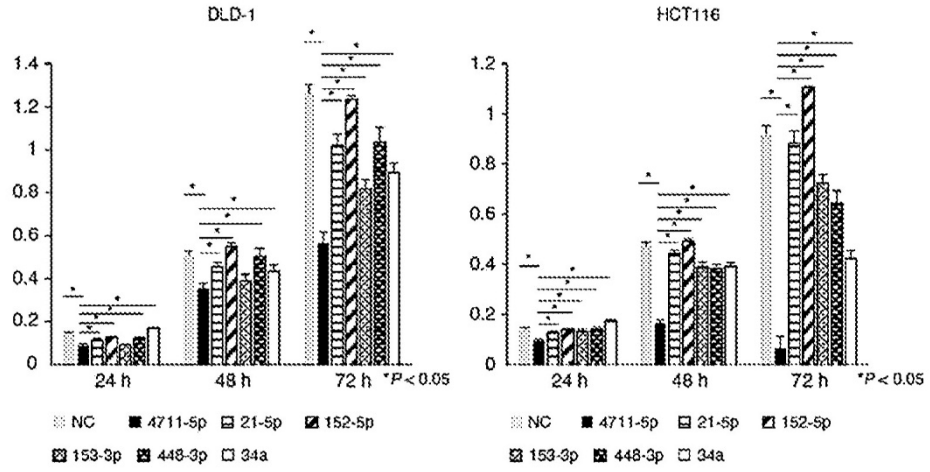


FIG. 30

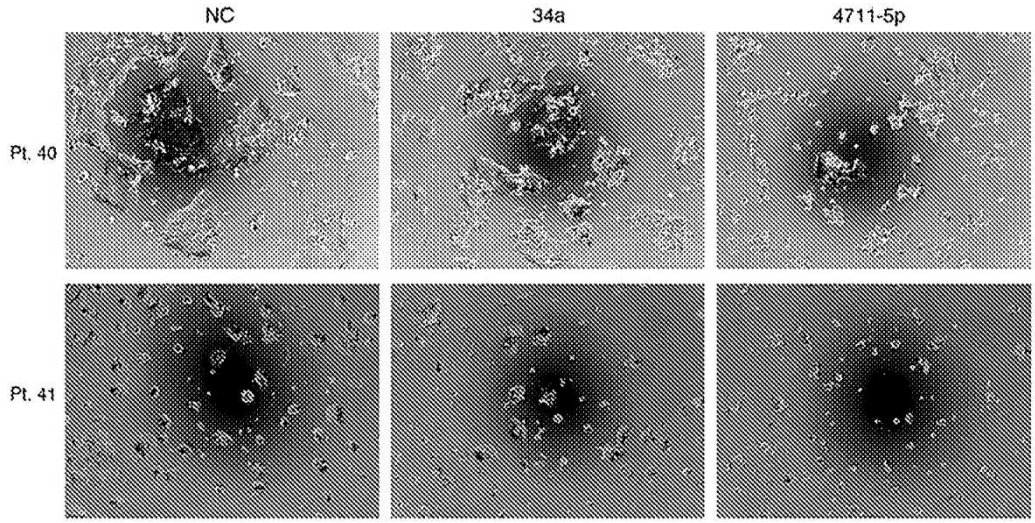
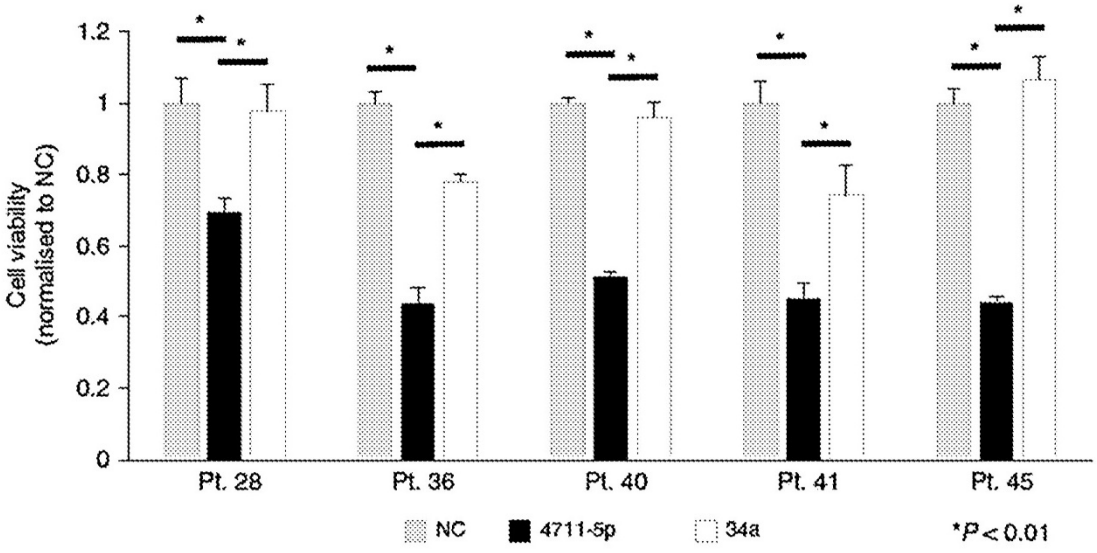


FIG. 31


Cell viability
(normalised to NC)
1.2
1
0.8
0.6
0.4
0.2
0
Pt. 28
Pt. 36
Pt. 40
Pt. 41
Pt. 45
NC
4711-5p
34a
*P < 0.01