

Table SI. Primers for reverse transcription quantitative experiments with 8 disulfidptosis-related long non-coding RNAs.

Gene name	Primer sequence (5'-3')
AL390719.2	F: ATGGGATAGGGAAGGCAGGT R: CAGGGTCCTTCCTGTCACAC
ASMTL-AS1	F: TTGTGGACTTGTCTGTCTGG R: CTGACGGACGTATCTCGTTTT
AL031058.1	F: TCCCGTATACCTACACCTCTAT R: AATCTTAGGCATCAGCAACA
LINC02438	F: CCGCTGTGTGGAAAAGAGAATGTG R: CAAGGCACTATCACATTTGCCTGTA
LINC01788	F: ACCTAAGGGCTGATGGTGGG R: GTCCAGAGCTGACCTGTTCTAC
AC022613.2	F: AAGCCACAACTGACTGCATCT R: CATGATTCTGTGCGTCGGCA
RBMS3-AS3	F: GGAACCTGAACCTGAAGAACTCAA R: AGCTCTTGTGTGGGGTAGATG
AL122035.1	F: GGCAAACAACCTCCTTGAGC R: TGTGTCTCTTACCGCACTGG

F, forward; R, reverse.

Table SII. A total of 14 differentially expressed disulfidptosis-related lncRNAs.

lncRNA	Hazard ratio (95% confidence interval)	P-value
AL390719.2	0.839 (0.747-0.942)	0.003
ASMTL-AS1	0.776 (0.643-0.936)	0.008
AL031058.1	1.247 (1.095-1.421)	0.001
AC010487.1	0.819 (0.705-0.953)	0.009
LINC02223	22.786 (2.664-194.899)	0.004
LINC02438	2.042 (1.382-3.0174)	0.000
DEPDC1-AS1	2.499 (1.259-4.961)	0.009
LINC01788	2.358 (1.363-4.080)	0.002
AC022613.2	1.853 (1.256-2.733)	0.002
RBMS3-AS3	2.236 (1.443-3.466)	0.000
AL122035.1	1.771 (1.243-2.523)	0.002
AL590428.1	2.735 (1.569-4.770)	0.000
LINC02817	5.627 (1.856-17.059)	0.002
AC087564.1	14.961 (1.986-112.719)	0.009

lncRNA, long non-coding RNA.

Table SIII. A total of 8 differentially expressed disulfidptosis-related lncRNAs.

lncRNA	Coefficient
AL390719.2	-0.003727
ASMTL-AS1	-0.126979
AL031058.1	0.1324342
LINC02438	0.3540896
LINC01788	0.1858756
AC022613.2	0.1228996
RBMS3-AS3	0.1901772
AL122035.1	0.2711116

lncRNA, long non-coding RNA.

Table SIV. Gene set enrichment analysis pathways for different risk groups.

Pathways	Group
c2.cp.kegg.v7.4.symbols.gmt	
KEGG focal adhesion	High risk
KEGG WNT signaling pathway	High risk
KEGG regulation of actin cytoskeleton	High risk
KEGG cell cycle	High risk
KEGG bladder cancer	High risk
KEGG linoleic_acid_metabolism	Low risk
KEGG alpha_linolenic_acid_metabolism	Low risk
KEGG metabolism_of_xenobiotics_by_cytochrome_P450	Low risk
c2.cp.wikipathways.v7.4.symbols.gmt	
WP WNT signaling	High risk
WP regulation of actin cytoskeleton	High risk
WP focal adhesionpi3kaktmtorsignaling pathway	High risk
WP cell cycle	High risk
WP WNT signaling pathway and pluripotency	High risk
WP tamoxifen_metabolism	Low risk
WP estrogen_metabolism	Low risk
WP codeine_and_morphine_metabolism	Low risk
WP eicosanoid metabolism via cytochrome P450 monooxygenases cyp pathway	Low risk
c5.go.bp.v7.4.symbols.gmt	
GOBP focal adhesion assembly	High risk
GOBP regulation of cell cycle phase transition	High risk
GOBP WNT signaling pathway calcium modulating pathway	High risk
GOBP regulation of actin filament-based process	High risk
GOBP regulation of cell cycle	High risk
KEGG, Kyoto Encyclopedia of Genes and Genomes; GOBP, Gene Ontology Biological Process.	

Table SV. Antineoplastic drug sensitivity information (sensitive group: High-risk).

Target pathway	Low-risk group	High-risk group	P-value
	IC ₅₀ (25-75%)	IC ₅₀ (25-75%)	
Apoptosis regulation			
AZD5582	12.62 (6.65-23.8)	7.26 (2.41-18.66)	0.00
LCL161	171.54 (117.44-254.41)	111.94 (70.03-176.85)	0.00
MIM1	49.34 (38.96-68.96)	43.51 (30.65-63.26)	0.01
Obatoclox.Mesylate	5.04 (2.75-10.58)	3.08 (1.54-6.2)	0.00
UMI.77	14.6 (10.56-21.83)	10.89 (7.07-20.41)	0.00
Cell cycle			
BI.2536	1.49 (1.03-2.05)	1.25 (0.8-1.88)	0.01
CDK9_5576	0.72 (0.41-1.31)	0.5 (0.3-1.14)	0.03
Chromatin other			
AZD5153	6.72 (2.22-24.38)	3.71 (1.34-8.09)	0.00
LBET.762	37.96 (17.55-97.21)	18.66 (9.42-40.53)	0.00
LBRD9	85.6 (56.95-125.95)	75.91 (49.13-102.45)	0.01
JQ1	13.5 (9.73-20.49)	10.47 (5.71-14.73)	0.00
OTX015	21.96 (5.99-57.28)	7.02 (2.91-19.04)	0.00
DNA replication			
Camptothecin	0.11 (0.04-0.47)	0.06 (0.02-0.19)	0.00
Irinotecan	19.22 (4.63-76.59)	7.12 (2.05-30.61)	0.00
Mitoxantrone	2.04 (0.7-6.81)	1.47 (0.54-4.11)	0.02
Pyridostatin	30.28 (17.29-84)	17.84 (10.07-35.14)	0.00
Teniposide	1.98 (0.61-7.18)	1.2 (0.43-4.37)	0.02
Topotecan	1.33 (0.47-4.6)	0.81 (0.27-2.93)	0.00
EGFR signaling			
AZD3759	15.04 (10.68-23.84)	11.83 (7.46-22.62)	0.01
Osimertinib	8.04 (4.7-13.4)	4.73 (2.34-8.24)	0.00
Sapitinib	66.25 (43.77-107.96)	42.86 (16.6-95.84)	0.00
ERK MAPK signaling			
Trametinib	2.08 (0.61-7.31)	1.27 (0.48-4.04)	0.00
Genome integrity			
KU.55933	85.19 (70.15-109.07)	69.8 (54.07-92.64)	0.00
Niraparib	94.36 (47.29-191.56)	54.14 (25.15-107.49)	0.00
NU7441	15.28 (13.22-17.12)	12.82 (10.67-15.26)	0.00
Olaparib	86.77 (54.98-147.09)	54.97 (34.1-93.28)	0.00
Talazoparib	41.57 (13.01-124.58)	15.04 (3.97-49.85)	0.00
VE.822	30.11 (16.39-71.19)	27.79 (10.86-51.62)	0.02
IGF1R signaling			
BMS.754807	1.72 (1.14-2.44)	1.44 (0.71-2.09)	0.01
IGF1R_3801	8.85 (3.25-29.4)	3.35 (1.34-10.15)	0.00
Metabolism			
AGI.5198	108.44 (86.55-139.89)	101.45 (77.86-123.46)	0.01
GSK2606414	53.37 (33.51-85.13)	32.57 (19.59-50.85)	0.00
Mitosis			
Alisertib	16.69 (2.09-52.53)	2.81 (0.38-16.88)	0.00
Docetaxel_1819	0.14 (0.02-1.37)	0.07 (0.02-0.35)	0.01
Paclitaxel	0.07 (0.03-0.14)	0.05 (0.03-0.12)	0.05
Tozasertib	20.55 (16.47-26.34)	18.27 (12.51-24.38)	0.00
Vinorelbine	0.05 (0.02-0.22)	0.03 (0.02-0.09)	0.02
ZM447439	20.36 (16.89-24.89)	17.36 (14.21-22.39)	0.00
Other			

Dactinomycin_1811	0.1 (0.03-0.31)	0.06 (0.03-0.15)	0.01
X5.Fluorouracil	118.25 (42.64-597.63)	58.1 (17.6-188.61)	0.00
YK.4.279	12.34 (6.3-23.53)	8.08 (3.74-16.2)	0.00
Other, kinases			
AZ960	8.46 (5.34-18.4)	6 (3.12-12.17)	0.00
AZD5363	22.6 (15.46-33.01)	17.23 (9.84-26.75)	0.00
Entospletinib	47.78 (33.62-73.7)	35.68 (22.32-52.26)	0.00
JAK_8517	26.81 (13.92-48.27)	16.28 (8.6-33.81)	0.00
Ruxolitinib	149.32 (109.04-195.77)	113.38 (79.33-158.3)	0.00
PI3K MTOR signaling			
Alpelisib	52.03 (30.93-88.58)	28.11 (13.95-50.33)	0.00
AMG.319	171.78 (108.81-267.69)	97.61 (60.12-158.33)	0.00
AZD2014	9.15 (4.08-23.3)	5.75 (2.8-11.16)	0.00
AZD8186	36.58 (15.89-93.08)	15.56 (6.54-38.35)	0.00
Buparlisib	2.9 (2.12-3.99)	2.53 (1.91-3.24)	0.01
Pictilisib	5.77 (2.67-11.21)	3.07 (1.68-6.02)	0.00
Taselisib	14.77 (4.09-70.9)	3.1 (0.68-11.56)	0.00
Uprosertib_1553	23.97 (5.59-140.97)	7.18 (2.16-23.05)	0.00
Protein stability and degradation			
Luminespib	0.17 (0.06-0.61)	0.06 (0.02-0.17)	0.00
RTK signaling			
Foretinib	3.01 (2.01-4.44)	2.57 (1.56-4.07)	0.01
Savolitinib	17.73 (10.2-29.08)	10.14 (6.52-16.25)	0.00
Staurosporine	0.07 (0.04-0.21)	0.03 (0.01-0.08)	0.00
Unclassified			
Acetalax	156.47 (83.52-272.69)	104.1 (39.96-238.52)	0.00
WNT signaling			
Carmustine	493.32 (351.27-670.93)	415.26 (302.8-567.6)	0.01
XAV939	86.69 (61.97-120.26)	75.62 (53.6-101.73)	0.01

Table SVI. Antineoplastic drug sensitivity information (sensitive group: Low-risk).

Target pathways	Low-risk group	High-risk group	P-value
	IC ₅₀ (25-75%)	IC ₅₀ (25-75%)	
ABL signaling			
Nilotinib	27.84 (9.18-61.13)	61.73 (24.41-132.81)	0.00
Apoptosis regulation			
ABT737	10.15 (1.04-36.97)	15.55 (4.92-37.85)	0.01
AZD5991	69.7 (17.51-198.7)	75.38 (27.97-246.47)	0.04
Navitoclax	5.37 (0.35-42.76)	15.3 (3.95-62.87)	0.00
Sabutoclax	0.49 (0.32-1.01)	0.8 (0.51-1.44)	0.00
Sepantronium.bromide	0.01 (0-0.02)	0.02 (0.01-0.05)	0.00
Venetoclax	8.73 (3.39-15.89)	12.59 (6.37-19.48)	0.00
WEHI.539	30.48 (14.23-64.53)	41.47 (22.86-74.11)	0.00
Cell cycle			
AZD7762	1.02 (0.46-1.83)	1.29 (0.67-2.24)	0.01
CDK9_5038	0.06 (0.04-0.15)	0.09 (0.04-0.27)	0.03
MK.1775	1.4 (0.9-2.62)	2.05 (1.12-3.48)	0.00
Palbociclib	35.04 (18.41-72.66)	45.79 (26.64-71.69)	0.02
Wee1.Inhibitor	4.99 (2.73-12.61)	10.79 (4.77-23.58)	0.00
Chromatin histone acetylation			
Entinostat	9.04 (1.75-36.41)	18.02 (5.56-65.34)	0.00
OF.1	53.78 (28.06-102.64)	68.98 (37.13-113.06)	0.02
PCI.34051	67.64 (41.78-117.95)	109.36 (60.45-201.91)	0.00
Vorinostat	3.67 (0.79-13.41)	9.8 (3.25-41.56)	0.00
Chromatin histone methylation			
EPZ004777	151.58 (67.64-289.16)	242.39 (113.53-455.49)	0.00
EPZ5676	229.35 (111.55-433.29)	353.66 (196.44-568.1)	0.00
GSK343	14.54 (9.79-22.42)	20.42 (14.13-28)	0.00
Chromatin other			
PFI3	182.75 (122.03-287.55)	217.77 (148.48-301.86)	0.03
Cytoskeleton			
BDP.00009066	9.34 (5.97-13.74)	12 (8.81-17.41)	0.00
PAK_5339	9.72 (5.2-14.48)	14.73 (9.15-20.29)	0.00
DNA replication			
Cyclophosphamide	160.55 (81.27-300.55)	231.24 (135.81-365.56)	0.00
Epirubicin	0.27 (0.17-0.51)	0.38 (0.22-0.76)	0.00
Gemcitabine	0.41 (0.12-1.01)	0.66 (0.24-2.14)	0.00
Leflunomide	122.1 (99.24-159.19)	159.47 (124.38-221.71)	0.00
Nelarabine	386.1 (183.02-685.25)	436.82 (281.36-760.79)	0.01
Oxaliplatin_1806	143.92 (75.3-246.57)	175.41 (98.68-305.04)	0.04
Temozolomide	359.26 (193.6-662.76)	474.53 (293.25-707.63)	0.01
EGFR signaling			
Lapatinib	16.35 (7.86-31.15)	23.16 (8.97-61.1)	0.04
ERK MAPK signaling			
Dabrafenib	78.05 (38.57-141)	135.23 (83.32-201.55)	0.00
ERK_2440	10.51 (4.77-24.7)	15.13 (6.41-34.56)	0.01
ERK_6604	23.72 (11.53-48.48)	38.87 (19.58-68.62)	0.00
KRAS.G12C.Inhibitor.12	52.41 (29.45-97.79)	93.58 (49.88-217.59)	0.00
Ulixertinib_2047	6.28 (1.37-16.25)	17.07 (5.8-38.1)	0.00
Genome integrity			
AZD6738	5.73 (2.94-11.86)	10.71 (5.34-18.83)	0.00
BIBR.1532	117.76 (78.16-185.95)	153.92 (115.72-231.42)	0.00

VE821	48.38 (30.46-90.22)	73.76 (39.52-110.56)	0.00
Hormone-related			
Fulvestrant_1200	16.91 (11.86-23.14)	19.78 (14.66-26.17)	0.00
GDC0810	130.86 (79.44-201.49)	146.75 (99.38-223.31)	0.03
Tamoxifen	32 (20.96-49.74)	36.96 (27.16-55.92)	0.02
IGF1R signaling			
GSK1904529A	60.55 (35.79-107.4)	84.41 (48.47-147.02)	0.00
Linsitinib	34.85 (13.53-74.87)	70.77 (33.21-122.81)	0.00
JNK and p38 signaling			
Doramapimod	77.73 (62.24-110.48)	104.08 (74-143.05)	0.00
Mitosis			
Vincristine	0.1 (0.04-0.31)	0.18 (0.07-0.73)	0.00
Other			
Cytarabine	4.54 (1.79-10.24)	6.64 (2.91-15.61)	0.00
Dactinomycin_1911	0.01 (0-0.01)	0.01 (0-0.02)	0.00
LY2109761	152.04 (72.21-272.97)	207.68 (123.09-450.65)	0.00
Picolinici.acid	155.83 (97.07-239.22)	187.16 (130.3-283.11)	0.00
VSP34_8731	9.79 (3.96-16.29)	11.89 (6.97-29.37)	0.00
Zoledronate	38.09 (23.51-62.37)	54.26 (31.63-85.42)	0.00
Other, kinases			
AZD1208	167.88 (118.5-277.57)	209.84 (146.42-329.2)	0.00
IRAK4_4710	117 (43.91-232.03)	211.02 (112.11-351.43)	0.00
JAK1_8709	58.15 (40.75-84.79)	66.71 (46.95-93.94)	0.04
PRT062607	22.39 (15.24-31.95)	29.42 (20.34-41.88)	0.00
Sorafenib	11.58 (4-22.08)	23.22 (11.93-45.43)	0.00
p53 pathway			
MIRA.1	191.59 (110.75-353.34)	270.33 (156.9-387.36)	0.00
Nutlin.3a....	77.15 (12.9-274.91)	223.8 (59.92-470.65)	0.00
PI3K MTOR signaling			
AT13148	27 (13.24-52.54)	52.72 (26.42-97.45)	0.00
MK.2206	17.47 (13.29-27.54)	22.17 (13.82-32.96)	0.02
PF.4708671	44.82 (35.1-55.68)	51.22 (41.65-62.4)	0.00
Protein stability and degradation			
ML323	76.8 (43.94-128.03)	105.41 (63.47-171.52)	0.00
P22077	64.84 (27.76-137.2)	114.24 (58.6-236.65)	0.00
RTK signaling			
Axitinib	20.06 (15.71-28.1)	22.85 (16.93-31.3)	0.02
AZD4547	13.95 (10.04-20.46)	19.19 (12.8-33.61)	0.00
Cediranib	7.75 (3.5-12.7)	10.77 (6.11-17.59)	0.00
PD173074	45.82 (15.5-91.01)	78.23 (34.47-183.73)	0.00
SB505124	9.39 (7.69-10.89)	10.07 (8.4-11.99)	0.01
Unclassified			
Elephantin	15.63 (6.93-43.26)	41.55 (20.98-115.94)	0.00
Gallibiscoquinazole	11.66 (8.38-16.93)	14.17 (10.29-20.93)	0.00
Podophyllotoxin.bromide	0.35 (0.15-0.83)	0.72 (0.35-2.17)	0.00
Sinularin	31.91 (7.21-69.28)	64.23 (28.57-136.6)	0.00
WNT signaling			
MN.64	101.75 (47.04-188.37)	133.48 (74.47-236.27)	0.00

Table SVII. Antineoplastic drug sensitivity information (no obviously sensitive group).

Target pathway	Low-risk group	High-risk group	P-value
	IC ₅₀ (25-75%)	IC ₅₀ (25-75%)	
Cell cycle			
AZD5438	8.29 (4.14-17.23)	8.69 (4.55-18.99)	0.15
Dinaciclib	0.06 (0.04-0.12)	0.05 (0.03-0.1)	0.08
MK.8776	22.77 (13.22-39.77)	26.35 (13.04-44.58)	0.34
Ribociclib	46.39 (42.72-50.22)	46.76 (42.91-50.07)	0.49
RO.3306	15.16 (11.93-20.43)	15.85 (11.4-21.87)	0.70
Chromatin histone methylation			
GSK591	85.67 (66.05-132.49)	98.76 (71.6-145.48)	0.22
Chromatin other			
RVX.208	112.46 (85.67-153.93)	114.95 (81.69-154.27)	0.50
Cytoskeleton			
GSK269962A	18.51 (15.07-21.65)	18.44 (15.09-22.68)	0.63
DNA replication			
Cisplatin	26.64 (13.02-54.32)	20.33 (9.71-67.08)	0.62
Fludarabine	151.98 (77.15-264.48)	151.67 (96.4-328.35)	0.16
Oxaliplatin_1089	45.55 (20.3-117.48)	35.19 (17.02-85.32)	0.08
EGFR signaling			
Afatinib	6.21 (3.56-9.83)	5.97 (3.15-12.31)	0.87
Erlotinib	14.5 (8.15-23.44)	12.44 (6.66-24.7)	0.38
Gefitinib	24.33 (7.79-51.86)	27.56 (12.04-63.4)	0.10
ERK MAPK signaling			
PD0325901	1.92 (0.98-3.58)	1.5 (0.87-3.31)	0.09
PLX.4720	82.92 (45.64-149.45)	85.44 (50.69-148.02)	0.50
SCH772984	17.22 (5.53-34.35)	13.22 (5.97-27.78)	0.17
Selumetinib	53.99 (31.03-118.43)	63.99 (34.22-134.65)	0.18
Ulixertinib_1908	17.81 (8.81-29.49)	16.34 (8.85-25.91)	0.28
VX.11e	18.23 (7.19-39.55)	18.36 (9.86-29.67)	0.50
Genome integrity			
Mirin	1.36 (0.92-2.38)	1.66 (0.99-2.83)	0.13
Telomerase.Inhibitor.IX	115.01 (75.56-177.85)	98.41 (68.63-169.91)	0.20
Hormone-related			
Fulvestrant_1816	95.11 (64.38-129.59)	95.96 (66.42-133.01)	0.81
IGF1R signaling			
BMS.536924	8.4 (6.22-12.58)	8.36 (5.47-11.52)	0.16
NVP.ADW742	13.69 (9.46-23.67)	16.7 (11.13-25.54)	0.08
Metabolism			
AGL.6780	58.05 (44.93-76.66)	59.13 (45.27-85.68)	0.80
Daporinad	0.01 (0-0.06)	0.01 (0-0.02)	0.12
Mitosis			
Docetaxel	0.01 (0-0.02)	0.01 (0.01-0.02)	0.05
Vinblastine	0.02 (0.01-0.05)	0.02 (0.01-0.05)	0.76
Other			
BMS.345541	29.11 (13.02-86.62)	26.88 (13.33-52.34)	0.18
BPD.00008900	87.57 (59.45-138.13)	96.69 (61.18-141.03)	0.55
Eg5_9814	0.05 (0.02-0.1)	0.04 (0.02-0.09)	0.07
IAP_5620	174.77 (113.86-247.85)	166.86 (88.96-283.76)	0.57
Pevonedistat	2.2 (0.82-5.05)	2.6 (0.66-6.08)	0.51
TAF1_5496	43.42 (24.44-78.09)	46.33 (26.42-82.92)	0.43
Other, kinases			
Dasatinib	5.35 (1.55-15.49)	4.98 (1.81-10.85)	0.69

GSK2578215A	126.82 (100.37-168.88)	135.99 (104.66-189.69)	0.12
Ibrutinib	94.14 (57.72-159.46)	80.23 (39.28-179.45)	0.12
ULK1_4989	9.02 (5.83-14.36)	9.13 (5.98-15.14)	0.63
WZ4003	42.97 (32.86-62.35)	40.57 (26.02-59.69)	0.19
p53 pathway			
PRIMA.1MET	89.9 (58.83-149.05)	93.42 (52.36-173.9)	0.76
PI3K MTOR signaling			
Afuresertib	11.79 (7.91-18.17)	12.74 (8.51-20.84)	0.22
AZD6482	25.18 (21.03-30.21)	24.3 (19.6-29.28)	0.18
AZD8055	0.81 (0.75-0.9)	0.83 (0.75-0.93)	0.39
CZC24832	153.15 (109.14-230.54)	162.24 (117.13-225.56)	0.34
Dactolisib	0.2 (0.09-0.56)	0.18 (0.11-0.35)	0.39
GNE.317	1.84 (1.2-2.81)	1.65 (1.1-2.58)	0.19
Ipatasertib	32.13 (22.71-49)	31.83 (22.19-52.92)	0.71
LJI308	156.03 (106.58-222.88)	157.67 (125.22-237.63)	0.17
OSI.027	115.29 (60.99-198.14)	122.21 (73.29-199.8)	0.27
Rapamycin	0.12 (0.06-0.21)	0.1 (0.07-0.16)	0.13
Uprosertib_2106	16.74 (11-31.88)	16.05 (7.9-27.34)	0.13
Protein stability and degradation			
Bortezomib	0.01 (0.01-0.01)	0.01 (0.01-0.01)	0.73
MG.132	0.2 (0.15-0.25)	0.18 (0.15-0.25)	0.68
RTK signaling			
AZD1332	40.95 (26.22-72.36)	46.79 (30.15-76.67)	0.19
Crizotinib	23.59 (14.3-36.37)	26.01 (17.51-40.79)	0.09
Unclassified			
Dihydrorotenone	2.5 (1.64-3.78)	2.4 (1.35-4)	0.52
WNT signaling			
AZ6102	11.01 (8.17-15)	11.81 (8.14-16.49)	0.24
IWP.2	15.88 (11.15-21.8)	15.64 (11.71-20.82)	1.00
LGK974	55.24 (35.24-81.36)	52.19 (34.88-89.71)	0.84
SB216763	166.6 (117.71-280.1)	191.35 (130-258.09)	0.14
WIKI4	41.8 (27.77-60.02)	43.32 (33.35-58.32)	0.20
Wnt.C59	67.46 (53.33-82.34)	69.63 (51.42-89.55)	0.56

Table SVIII. Summary of antineoplastic drug target pathways.

Target pathway	A: Number of high-risksensitive	B: Number of low-risk sensitive	C: Total quantity of drugs	A/C	B/C
ABL signaling	0	1	1	0%	100%
Apoptosis regulation	5	7	12	42%	58%
Cell cycle	2	5	12	17%	42%
Chromatin histone acetylation	0	4	4	0%	100%
Chromatin histone methylation	0	3	4	0%	75%
Chromatin other	5	1	7	71%	14%
Cytoskeleton	0	2	3	0%	67%
DNA replication	6	7	16	38%	44%
EGFR signaling	3	1	7	43%	14%
ERK MAPK signaling	1	5	12	8%	42%
Genome integrity	6	3	11	55%	27%
Hormone-related	0	3	4	0%	75%
IGF1R signaling	2	2	6	33%	33%
JNK and p38 signaling	0	1	1	0%	100%
Metabolism	2	0	4	50%	0%
Mitosis	6	1	9	67%	11%
Other	3	6	15	20%	40%
Other, kinases	5	5	15	33%	33%
p53 pathways	0	2	3	0%	67%
PI3K/MTOR signaling	8	3	22	36%	14%
Protein stability and degradation	1	2	5	20%	40%
RTK signaling	3	5	10	30%	50%
Unclassified	1	4	6	17%	67%
WNT signaling	2	1	9	22%	11%

Table SIX. Survival analysis from the Human Protein Atlas database.

Gene	Expression group	Number of patients	5-year survival rate	P-value
SLC2A1	High	83	24%	<0.001
	Low	323	46%	
SLC3A2	High	114	26%	<0.001
	Low	292	47%	
WASF2	High	162	32%	0.08
	Low	244	48%	
NCKAP1	High	136	32%	0.04
	Low	270	46%	
RAC1	High	112	30%	0.01
	Low	294	45%	