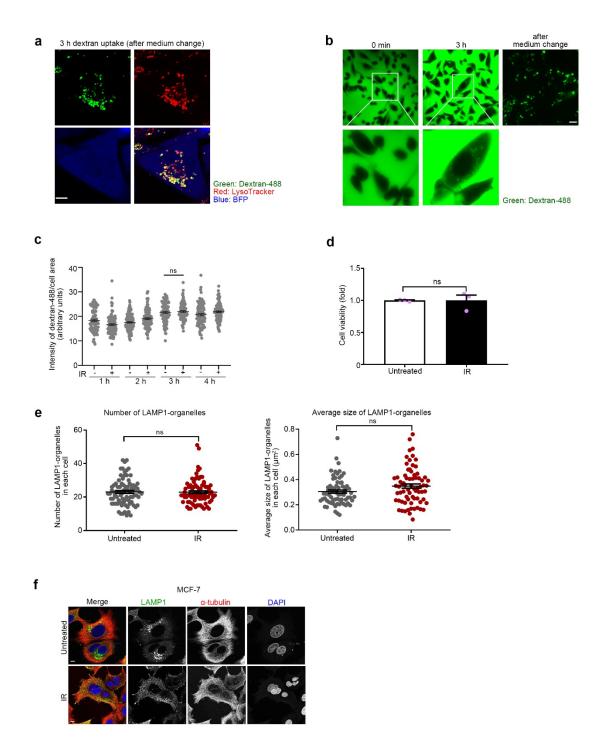
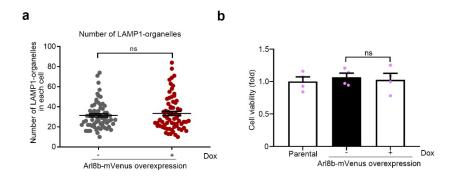


Supplementary Fig. 1 Cell viability, as detected using the Matrigel chemoinvasion assay, is not affected by treatment with lysosome inhibitors. a, b Cell viability of MDA-MB-231 (a) and Hs578T (b) cells after 0 Gy or 4 Gy IR treatment with or without a 12 h treatment with lysosome inhibitors (4 nM Baf A1 or 30 μ M CQ) were measured using the Cell Counting Kit-8 (CCK-8) assay. Data were collected from four independent experiments in duplicate and normalized to the control group. Columns, means (n=4); bars, SEMs. ns, not significant. c Immunofluorescence images of cells treated for 12 h with lysosome inhibitors. Green, LAMP1; red, LysoTracker Red DND-99. Bar, 10 μ m.

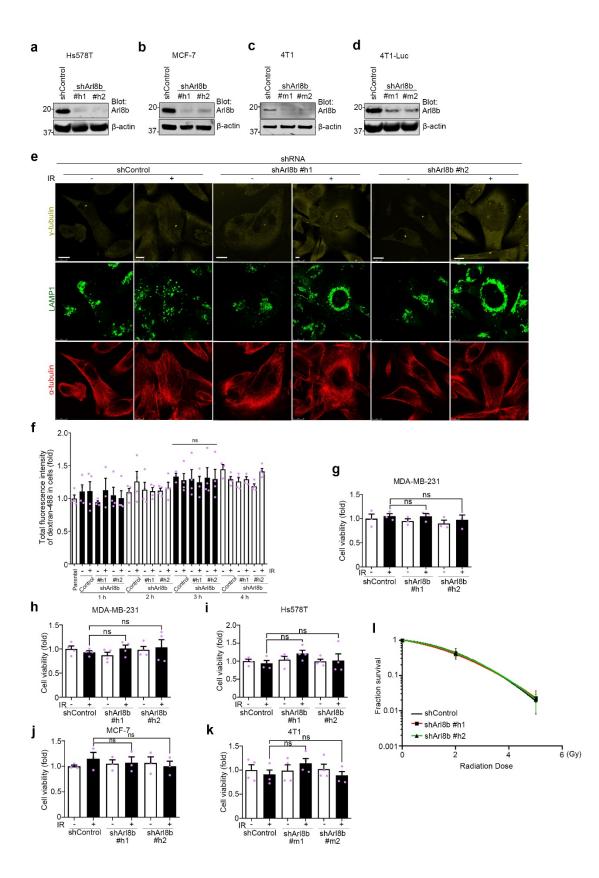


Supplementary Fig. 2 Lysosome exocytosis was quantified by dextran-488 uptake and release. a Immunofluorescence images showing the colocalization of dextran-488 and LysoTracker. Dextran-488 was incubated for 3 h, and the image was captured after a

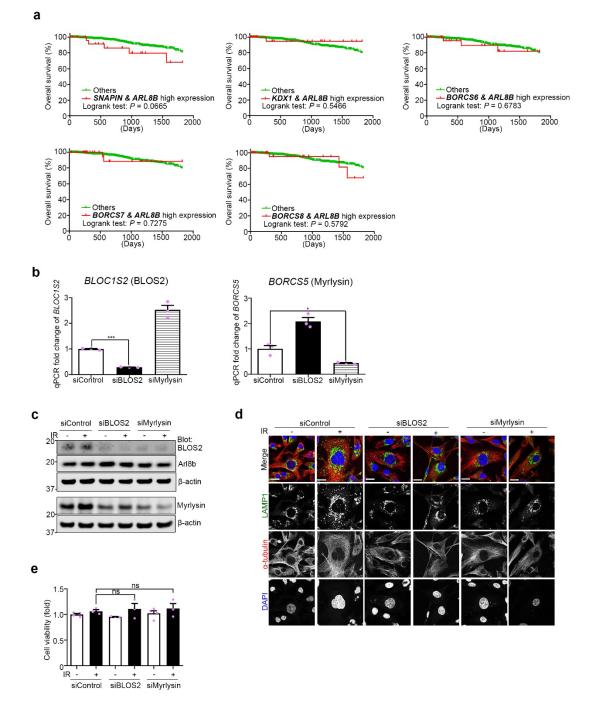
medium change. Green, dextran-488; red, LysoTracker; blue, blue fluorescent protein (BFP, cell margin). Bar, 10 μ m. **b** Representative fluorescent images showing dextran-488 in MDA-MB-231 cells. After 3 h of incubation, the medium was replaced with dextran-488-free medium. After exchange of the media, dextran-488 uptake into the cells was observed. **c** Fluorescence intensities of dextran-488 in MDA-MB-231 cells with or without 4 Gy IR treatment were normalized to each cell area. More than 20 cells per group were assessed in three independent experiments, and the results are shown as a scatter plot. Bars, SEMs. ns, not significant. **d** Cell viability in MDA-MB-231 cells with or without 4 Gy IR treatment during exocytosis assay was measured using the CCK-8 assay. Columns, means (n=3); bars, SEMs. ns, not significant. **e** Number and average size of LAMP1-organelles in each cell of MDA-MB-231 with or without IR treatment. More than 20 cells per group were assessed in three independent experiments, and the results are shown as a scatter plot. Bars, SEMs. ns, not significant. **e** Number and average size of LAMP1-organelles in each cell of MDA-MB-231 with or without IR treatment. More than 20 cells per group were assessed in three independent experiments, and the results are shown as a scatter plot. Bars, SEMs. ns, not significant. **f** Individual channels of the immunofluorescence images shown in Fig. 1i. Green, LAMP1; red, α -tubulin; blue, DAPI. Bar, 10 μ m.



Supplementary Fig. 3 Arl8b overexpression MDA-MB-231 cells. a Arl8b-mVenus overexpression was induced by doxycycline. The number of lysosomes in Arl8b-mVenus-overexpression cells was calculated. More than 20 cells per group were assessed in three independent experiments, and the results are shown as a scatter plot. Bars, SEMs. ns, not significant. **b** Cell viability in MDA-MB-231 cells stably overexpressing Arl8b-mVenus was measured by CCK-8 assay. Dox, doxycycline. Columns, means (n=4); bars, SEMs. ns, not significant.

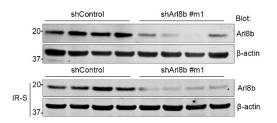


Supplementary Fig. 4 Effects of Arl8b knockdown on breast cancer cells. a-d Arl8b was knocked down using shRNA human #1 and human #2 in Hs578T cells (a) and MCF-7 cells (b); knocked down using shRNA mouse #1 and mouse #2 in 4T1 cells (c) and 4T1-Luc cells (d). Arl8b protein expression was detected by immunoblotting. e Individual channels of the immunofluorescence images shown in Fig. 4b. Yellow, y-tubulin (centrosome); green, LAMP1; red, α-tubulin. Bar, 10 μm. f Knockdown of Arl8b does not affect dextran-488 uptake in cells in an exocytosis assay. The fluorescence intensity of dextran-488 in MDA-MB-231 cells was measured by plate reader after medium change to Dextran-free PBS. Columns, means (n=3); bars, SEMs. ns, not significant. g Knockdown of Arl8b does not affect cell viability in an exocytosis assay (Fig. 4e). Cell viability in control or Arl8b-knockdown MDA-MB-231 cells with or without 4 Gy IR treatment during exocytosis assay was measured by CCK-8 assay. Columns, means (n=3); bars, SEMs. ns, not significant. h-k Knockdown of Arl8b does not affect cell viability in MDA-MB-231 (h), Hs578T (i) MCF-7 (j) and 4T1 (k) cells during the invasion assay (Fig. 4h-k). Cell viability in control or Arl8b-knockdown MDA-MB-231 cells with or without 4 Gy IR treatment during invasion assay was measured using the CCK-8 assay. Columns, means; bars, SEMs. ns, not significant. I Cell survival curves of control or Arl8b-knockdown MDA-MB-231 cells after IR were measured by colony formation assay. Arl8b did not involve in the radiosensitivity of MDA-MB-231 cells. Fractional survival is shown on a log axis, means (n=4); bars, SEMs.



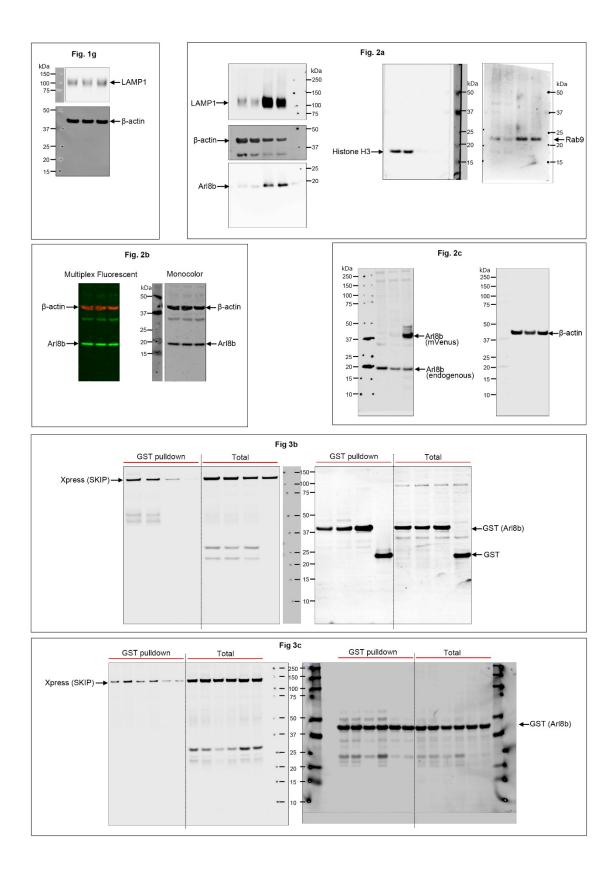
Supplementary Fig. 5 BORC-subunits. a Kaplan-Meier survival analysis based on the expression levels of *ARL8B* and BORC subunits. **b** MDA-MB-231 cells were transfected with siRNAs against BLOS2 or Myrlysin, and changes in expression were confirmed by qPCR. GAPDH was used as an internal control. Columns, means (n=3); bars, SEMs. *, *P*

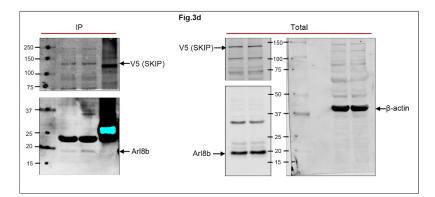
< 0.01, ***, P < 0.001. **c** Protein levels of BLOS2 and Myrlysin were suppressed by knockdown of either Myrlysin or BLOS2. The BLOS2 and Myrlysin protein expression levels were detected by western blotting. **d** Individual channels of the immunofluorescence images shown in Fig. 5f. Green, LAMP1; red, α -tubulin; blue, DAPI. Bar, 20 µm. **e** Cell viability in MDA-MB-231 cells following the siRNA-mediated knockdown of BLOS2 or Myrlysin treated with or without 4 Gy IR used during the invasion assay was measured by CCK-8 assay. Columns, means (n=3); bars, SEMs. ns, not significant.

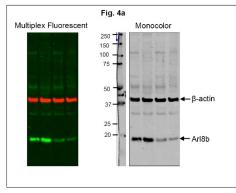


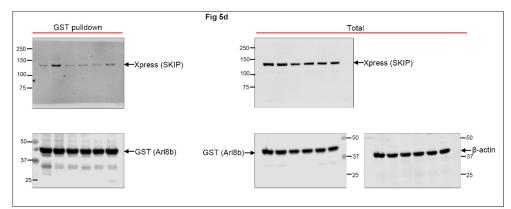
Supplementary Fig. 6 Protein levels of Arl8b in *in vivo* tumors were suppressed by shRNA knockdown. Arl8b protein expression in *in vivo* tumors was detected by

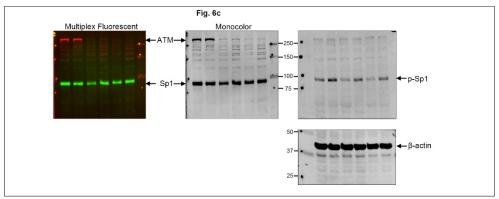
immunoblotting.

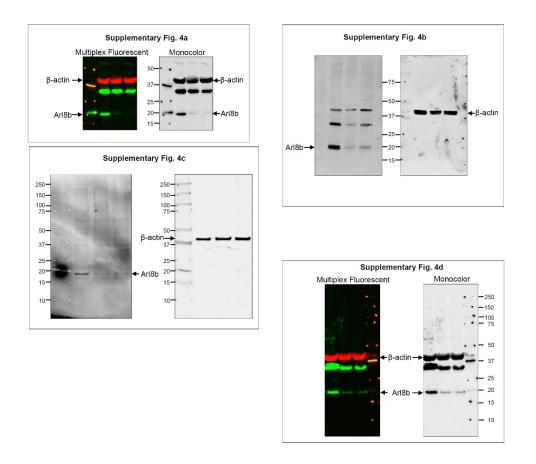


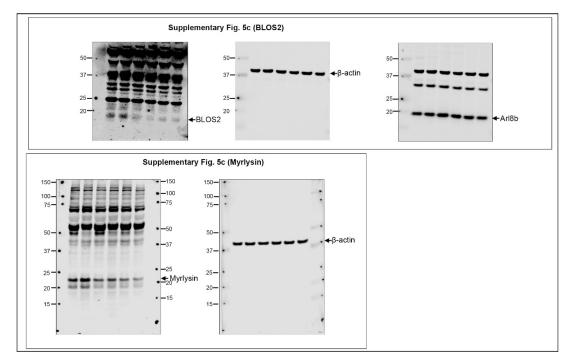


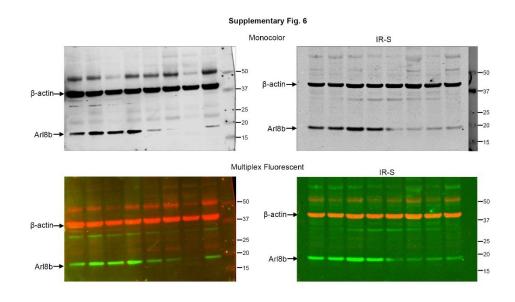












Supplementary Fig. 7 Uncropped scans of western blots.

Target	Company	Catalog	Host	Application/ dilution
Arl8b	Proteintech (Rosemont, USA)	13049-1-AP	Rabbit	WB (1:1000)
ATM	Sigma-Aldrich	A1106-25UL	Mouse	WB (1:1000)
BLOC1S2	Abnova (Taipei, Taiwan)	H00282991- M01	Mouse	WB (1:500)
Cathepsin B (D1C7Y)	Cell Signaling Technology	#31718s	Rabbit	IF (1:400)
Cathepsin D	Abcam	ab134169	Rabbit	IF (1:400)
GST tag (EPR4236)	Abcam	ab111947	Rabbit	WB (1:2000) IF (1:400)
HA tag	Medical and Biological Laboratories	M180-3	Mouse	IF (1:400)
Histone H3 (MABI0301)	Medical and Biological Laboratories (Nagoya, Japan)	300-34783	Mouse	WB (1:1000)
Ki67 (D3B5)	Cell Signaling Technology	#12202	Rabbit	IHC (1:400)
LAMP1	Cell Signaling Technology	#9091	Rabbit	WB (1:1000) IF (1:400)
LOH12CR1 (Myrlysin)	Proteintech	17169-1-AP	Rabbit	WB (1:500)
MMP3 (D7f5b)	Cell Signaling Technology	#14351T	Rabbit	IF (1:400)
MT1-MMP (D1E4)	Cell Signaling Technology	#131 30	Rabbit	IF (1:400)
p-Sp1 (Ser101)	Active Motif (Carlsbad, USA)	39758	Rabbit	WB (1:1000)
Rab9	Cell Signaling Technology	#5118	Rabbit	WB (1:1000)
Sp1 (D4C3)	Cell Signaling Technology	#9389	Rabbit	WB (1:1000) ChIP
V5 tag	Thermo Fisher Scientific	R960-25	Mouse	WB (1:1000)
V5 tag (D3H8Q)	Cell Signaling Technology	#13202	Rabbit	WB (1:1000)
Xpress tag	Thermo Fisher Scientific	R910-25	Mouse	WB (1:1000) IF (1:400)
α-tubulin	Cell Signaling Technology	#3873	Mouse	IF (1:400)
β-actin	Sigma-Aldrich	A5441	Mouse	WB (1:5000)
β-actin	Cell Signaling Technology	#4970	Rabbit	WB (1:5000)
γ-tubulin-Alexa Fluor® 647	Abcam (Cambridge, UK)	ab191114	Mouse	IF (1:400)

Supplementary Table 1. List of antibodies

Supplementary Table 2. List of sequences

shRNA	Sequence $(5'-3')$			
Scrambled	ATCTCGCTTGGGCGAGAGTAAG			
control				
Arl8b #h1	GCTGAAGATGAATATCCCTAA			
Arl8b #h2	AGGTAACGTCACAATAAAGAT			
Arl8b #m1	CGAGGAGTCAATGCAATTGTT			
Arl8b #m2	GCCTCTCGAAATGAACTGCAT			
siRNA	Sequence (5'-3')			
	Sense	Antisense		
Scrambled	GUUUAUUGACAAGUUAAGAdTdT	UCUUAACUUGUCAAUAAACdTdT		
control				
BLOS2	GAUCGGAAUGGUGGAGAACUUdTdT	AAGUUCUCCACCAUUCCGAUCdTdT		
Myrlysin	GACCAGAAUGCUUUGGUUAAAdTdT	UUUAACCAAAGCAUUCUGGUCdTdT		
Sp1 #1	AAUGAGAACAGCAACAACUCCdTdT	GGAGUUGUUGCUGUUCUCAUUdTdT		
Sp1 #2	GAGUCACCCAAUGAGAACAdTdT	UGUUCUCAUUGGGUGACUCdTdT		
ATM #1	CAUCUAGAUCGGCAUUCAGdTdT CUGAAUGCCGAUCUAGAUGdTdT			
ATM #2	GCCUCCAAUUCUUCACAGUAAdTdT	UUACUGUGAAGAAUUGGAGGCdTdT		
qPCR primers	Sequence (5'-3')			
	Forward	Reverse		
GAPDH	ACAACTTTGGTATCGTGGAAGG	GCCATCACGCCACAGTTTC		
18S rRNA	TCGGAACTGAGGCCATGATT	CCTCCGACTTTCGTTCTTGATT		
BLOC1S2	AGCTGAGGAAGCAAAGGAGCCT	CCAGGAGCTTATAGTCTTCACTG		
BORCS5	GCCGTTGCTTTTGACCAGAATGC	TGCTCGGCATACTTGGCGTATC		
SP1	ACGCTTCACACGTTCGGATGAG	TGACAGGTGGTCACTCCTCATG		
Negative	TTTTGACCTACCGTTGCTGA	TCATCTCACCTTGGGTTCACATT		
control for				
ChIP-qPCR				
(Chromosome				
13 gene desert)				
BLOC1S2	GCTCCTGGACACCCAAAATCT	GGGTGGAGACAGTCAGGGTA		
promoter				
(-1237/-1108)				
BORCS5	GAGAACGCTAGAGCCAGCTAAC	GGGACCTTGGCAGTTATCAACA		
promoter				
(-669/-518)				

Supplementary Table 3. *P*-value

		gure 1a	
<i>t</i> -test		Significant	P value
Control	Control IR	**	0.009
Baf A1	Baf A1 IR	ns	0.6033
CQ	CQ IR	ns	0.2994
Control IR	Baf A1 IR	**	0.0011
Control IR	CQ IR	**	0.0022
	Fi	gure 1b	
t-te	est	Significant	<i>P</i> value
Control	Control IR	*	0.0100
Baf A1	Baf A1 IR	ns	0.4674
CQ	CQ IR	ns	0.5841
Control IR	Baf A1 IR	**	0.002
Control IR	CQ IR	**	0.0013
		gure 1c	
t-te		Significant	<i>P</i> value
Untreated	IR	**	0.0059
	Fi	gure 1d	
t-te	<i>t</i> -test		<i>P</i> value
Untreated	IR	Significant *	0.0411
	Fi	gure 1e	
<i>t</i> -test		Significant	<i>P</i> value
Untreated	IR	*	0.0463
	Fi	gure 1j	
Mann-Whitney test		Significant	<i>P</i> value
Untreated	IR	***	< 0.001
	Fi	gure 1k	
<i>t</i> -test		Significant	<i>P</i> value
Untreated	IR	*	0.0268
	Fi	gure 1n	
Mann-Wh		Significant	P value
Untreated	IR	*	0.0371
		gure 2a	
t-te		Significant	<i>P</i> value
Untreated	IR	*	0.0258
		gure 2b	
<i>t</i> -test		Significant	<i>P</i> value
0Gy	4Gy	ns	0.4112
0Gy	8Gy	ns	0.6459
		gure 2g	
Mann-Wh		Significant	<i>P</i> value
Dox -	Dox +	***	< 0.001
		gure 2h	

t-te	est	Significant	P value	
Dox -	Dox +	*	0.0373	
		ure 3c		
<i>t</i> -test		Significant	<i>P</i> value	
WT	WT IR	**	0.0085	
		ure 4d		
Mann-Wh	U	Significant	<i>P</i> value	
shControl IR	shArl8b #h1 IR	***	< 0.001	
shControl IR	shArl8b #h2 IR	***	< 0.001	
	Fig	ure 4e		
t-te	est	Significant	<i>P</i> value	
shControl IR	shArl8b #h1 IR	*	0.0464	
shControl IR	shArl8b #h2 IR	*	0.0375	
	Fig	gure 4f		
t-te	est	Significant	P value	
shControl IR	shArl8b #h1 IR	*	0.0127	
shControl IR	shArl8b #h2 IR	*	0.0124	
	Fig	ure 4g		
t-te	est	Significant	<i>P</i> value	
shControl IR	shArl8b #h1 IR	*	0.0101	
shControl IR	shArl8b #h2 IR	*	0.0377	
	Fig	ure 4h		
t-te	est	Significant	<i>P</i> value	
shControl	shControl IR	*	0.0150	
shControl IR	shArl8b #h1 IR	*	0.0105	
shControl IR	shArl8b #h2 IR	*	0.0481	
	L L	gure 4i		
t-te	1	Significant	<i>P</i> value	
shControl	shControl IR	*	0.0185	
shControl IR	shArl8b #h1 IR	**	0.0044	
shControl IR	shArl8b #h2 IR	*	0.0323	
		gure 4j		
t-te	1	Significant	<i>P</i> value	
shControl	shControl IR	*	0.0253	
shControl IR	shArl8b #h1 IR	*	0.0397	
shControl IR	shArl8b #h2 IR	*	0.0177	
Figure 4k				
t-te		Significant	<i>P</i> value	
shControl	shControl IR	*	0.0225	
shControl IR	shArl8b #m1 IR	*	0.0496	
shControl IR	shArl8b #m2 IR		0.0299	
N. A	0	ure 4m	D	
Mann-Wh		Significant *	<i>P</i> value	
shControl IR	shArl8b #h1 IR	***	0.0113	
shControl IR	shArl8b #h2 IR	ጥጥጥ	< 0.001	

	Fig	ure 5a		
Logrank test		Significant	P value	
ARL8B Others		**	0.0058	
BLOCISI/ARL8B	Others	*	0.0253	
BLOC1S2/ARL8B	Others	***	<0.001	
BORCS5/ARL8B	Others	*	0.0454	
	Fig	ure 5b		
Brunner-M		Significant	<i>P</i> value	
BLOC1S2/ARL8B Others		*	0.0326	
	Fig	ure 5d		
t-te	st	Significant	<i>P</i> value	
siControl IR	siBLOS2 IR	*	0.0498	
	Fig	ure 5h		
Mann-Wh	itney test	Significant	<i>P</i> value	
siControl IR	siBLOS2 IR	*	0.0257	
siControl IR	siMyrlysin IR	*	0.0304	
	Fig	ure 5i		
t-te	st	Significant	<i>P</i> value	
siControl	siControl IR	*	0.0265	
siControl IR	siBLOS2 IR	*	0.0326	
siControl IR	siMyrlysin IR	*	0.0204	
	Fig	ure 6a		
t-te		Significant	<i>P</i> value	
siControl	siSp1 #1	**	0.0025	
siControl	siSp1 #2	**	0.0027	
	U	(BLOC1S2)	_	
t-te		Significant	<i>P</i> value	
siControl IR	siSp1 #1 IR	**	0.0069	
siControl IR	siSp1 #2 IR	**	0.0034	
	Č	(BORCS5)	D 1	
t-te		Significant	<i>P</i> value	
siControl IR	siSp1 #1 IR	***	<0.001	
siControl IR	siSp1 #2 IR	**	0.0074	
Figure 6d (<i>BLOC1S2</i>)				
t-te		Significant *	<i>P</i> value	
Anti-Sp1	Anti-Sp1 IR	-	0.0430	
		(BORCS5)	D 1	
t-te		Significant *	<i>P</i> value	
Anti-Sp1 Anti-Sp1 IR		ure 7c	0.0174	
		Significant	<i>P</i> value	
<i>t</i> -test		Significant *		
sucontrol IK-S	ShCohuoi hC-S ShAhoo #hili hC-S 0.0207			
Figure 7e t-test Significant P value				
t-test shControl IR-S shArl8b #m1 IR-S		significant *	<i>P</i> value 0.0321	
SIICOIIIIOI IK-S	511/1100 #1111 IK-S		0.0321	

Figure 7h			
t-test		Significant	P value
shControl IR-S	shArl8b #m1 IR-S	***	< 0.001