Figure S1, related to Figure 1 and Figure 2B

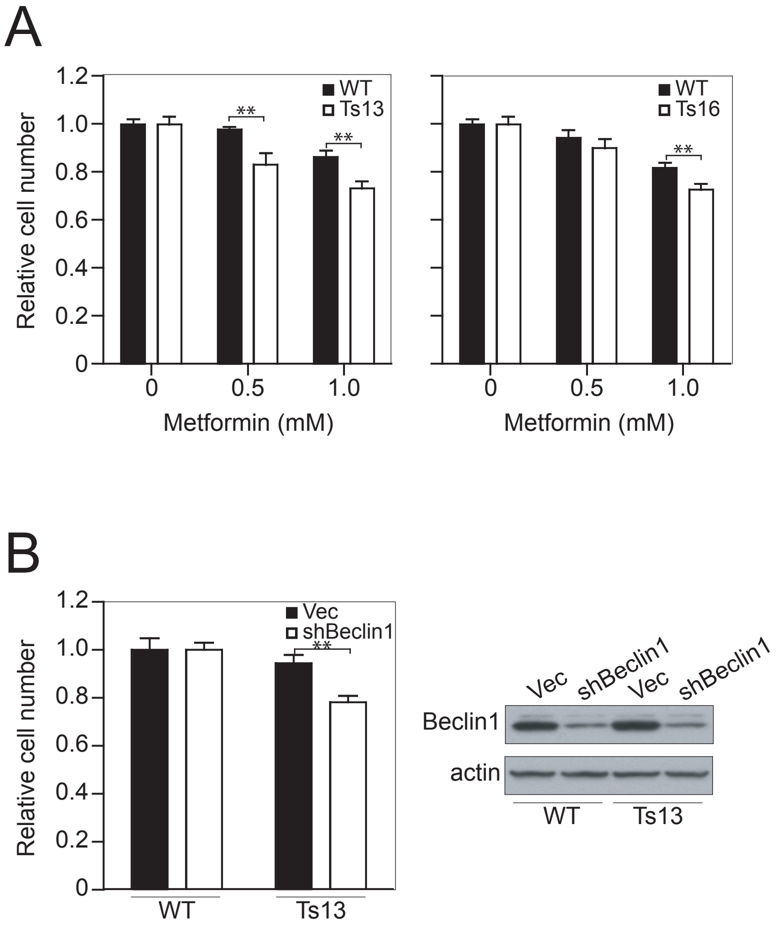


Figure S2, related to Figure 3

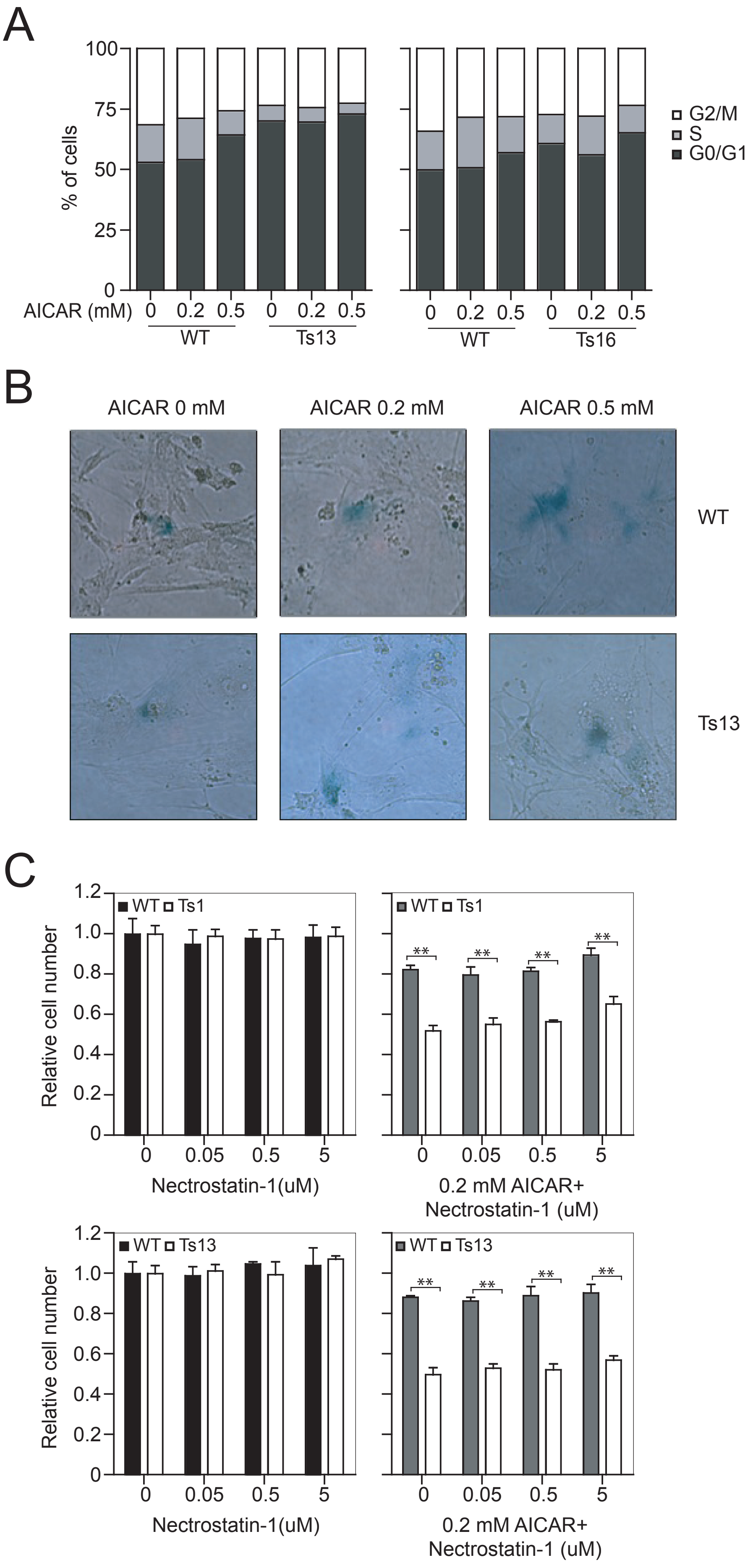
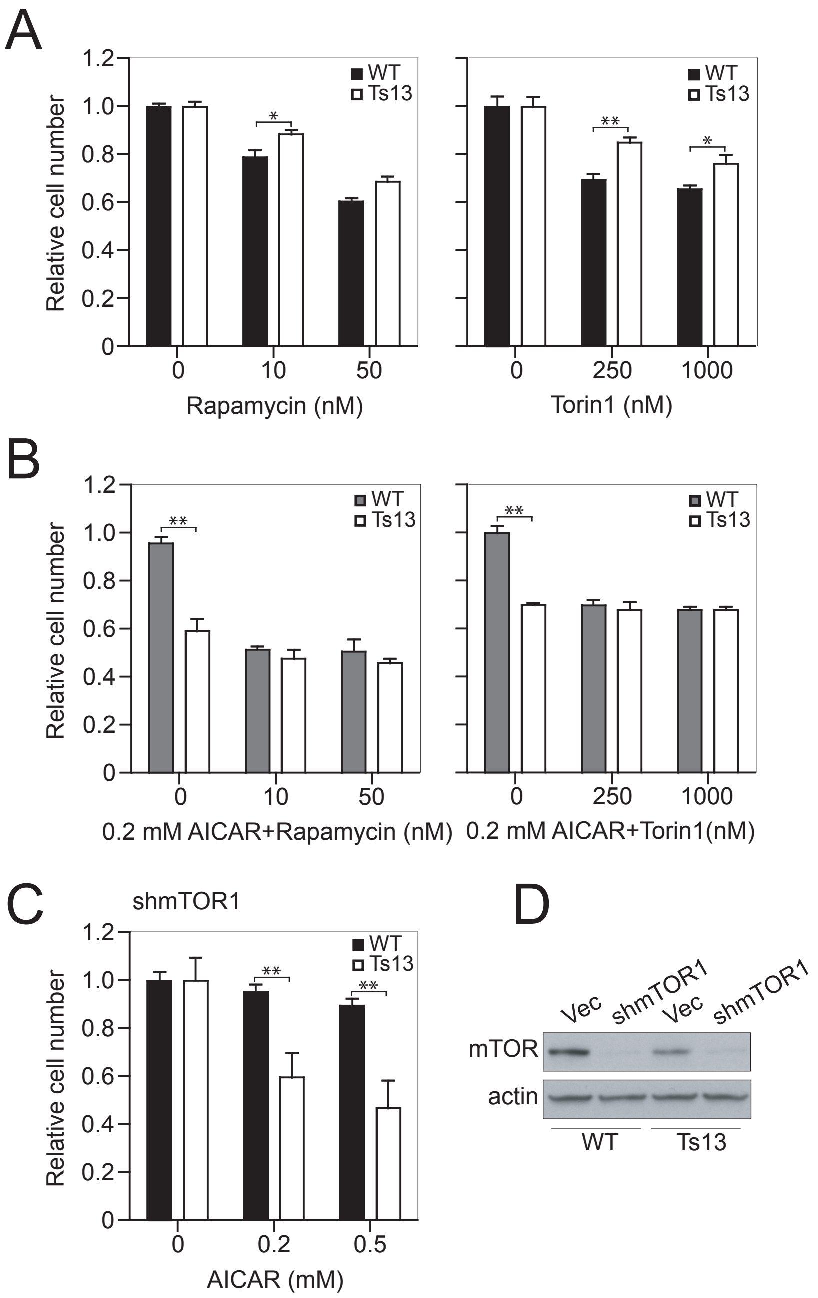
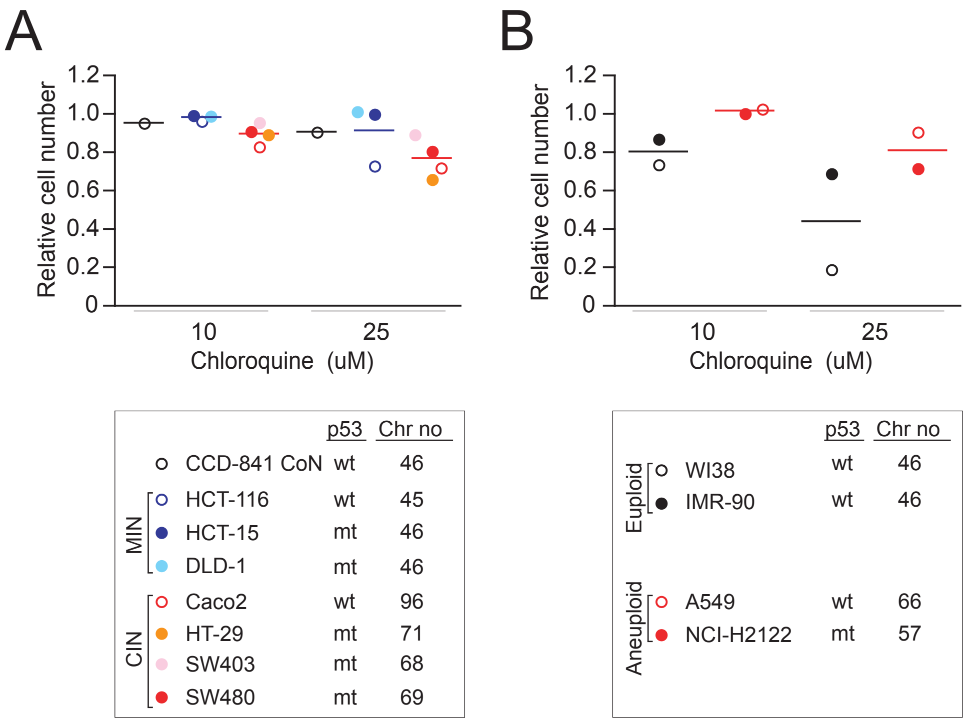


Figure S3, related to Figure 3



Supplemental Figure

Figure S4, related to Figure 6C and D



Supplemental Figure

Figure S5, related to Figure 7

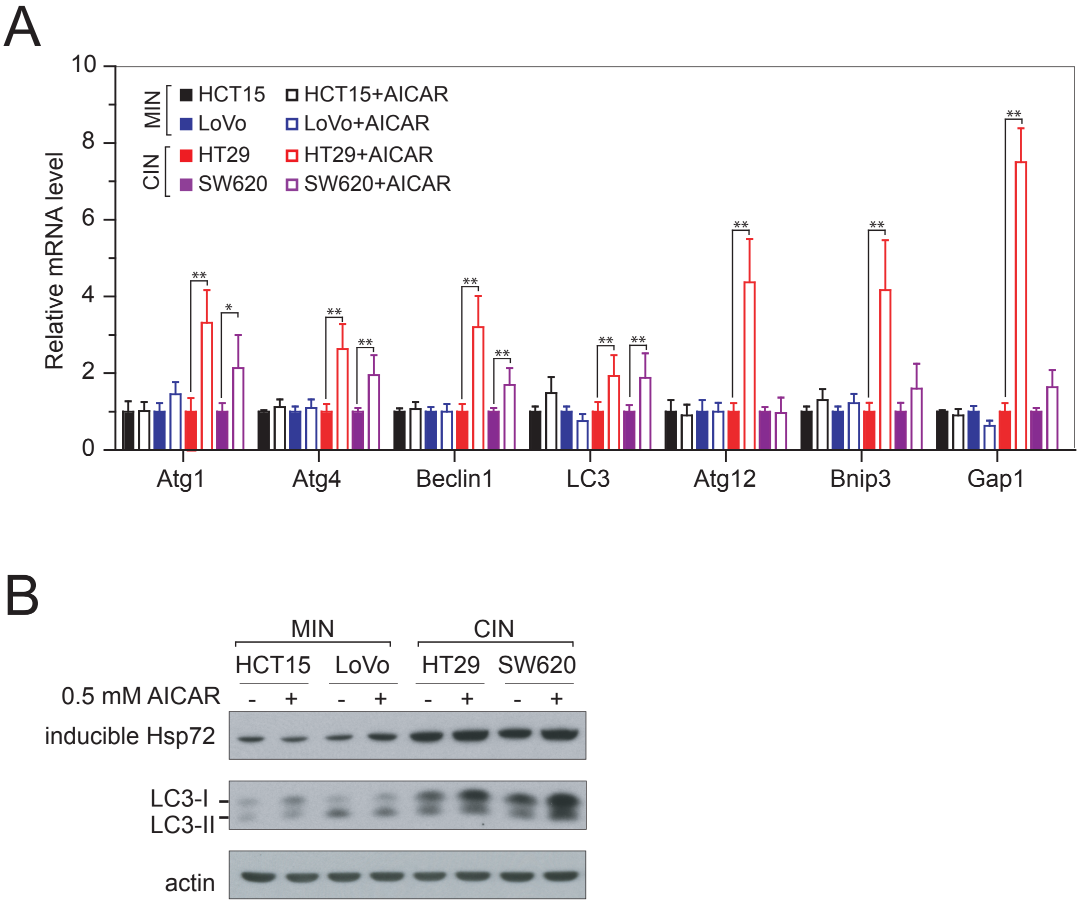


Figure S6, related to Figure 4

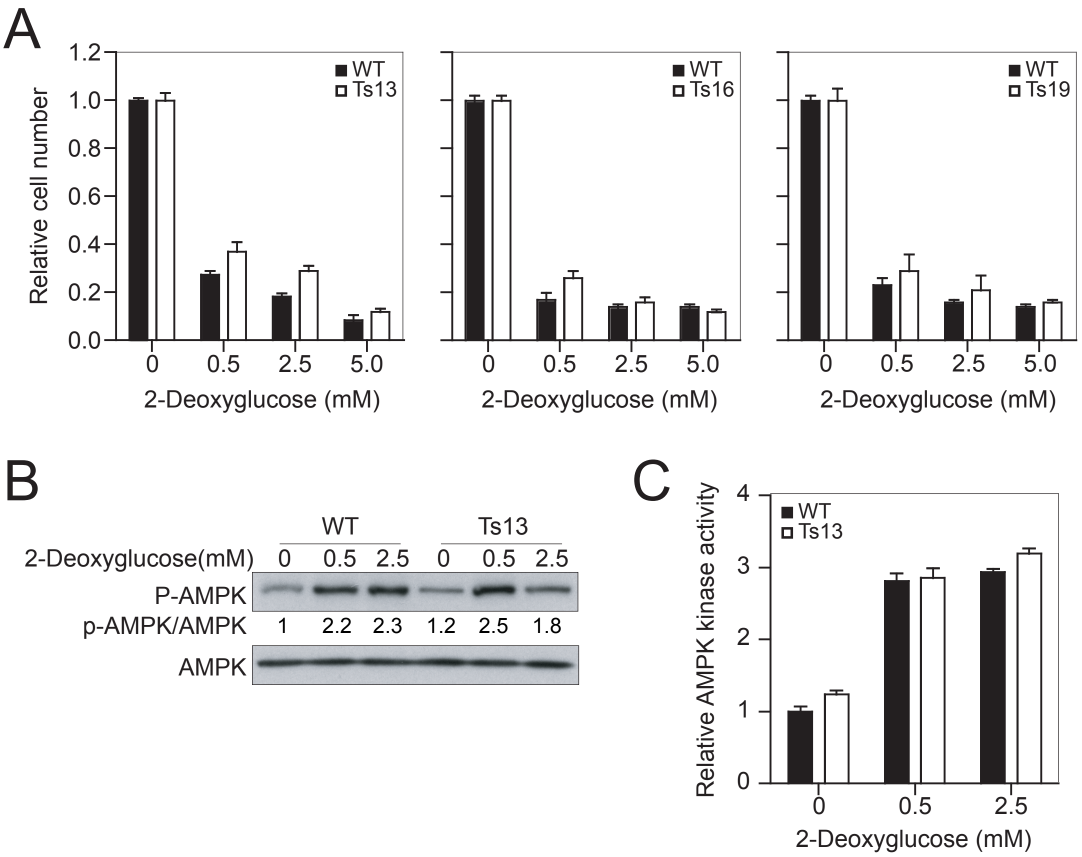


Figure S7, related to Figure 3

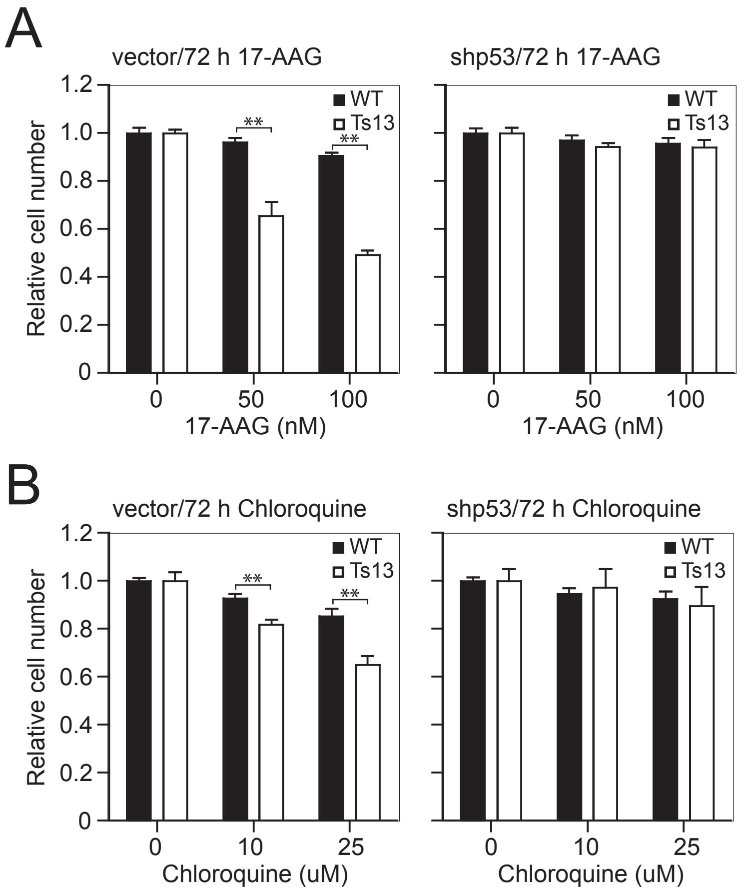


Table S1, related to Figure 1 and 2

Effects of selected compounds on euploid (WT) and trisomic (Ts) MEFs.

	Agent	Target	[C]	Ratio of treated/ untreated							
				WT	Ts1	WT	Ts13	WT	Ts16	WT	Ts19
DNA damage	Aphidicolin	DNA Polymerase α,δ,ε	1 μM	22±0.7	43±3.9**	41±3.4	67±1.4**	48±3.2	47±1.6	34±1.8	31±2.6
	Camptothecin	Topoisomerase 1	100 nM	93±4.3	99±5.6	98±3.7	94±1.4	86±2.9	92±2.5**	n.a.	n.a.
	Cisplatin	DNA	10 μM	n.a.	n.a.	26±2.8	18±2.4	23±3.6	22±1.7	n.a.	n.a.
	Doxorubicin	DNA	50 ng/ml	n.a.	n.a.	35±2.0	54±1.8**	39±2.9	46±3.6**	38±4.3	36±3.0
	Hydroxyurea	ribonucleoside diphosphate reductase	100 μM	n.a.	n.a.	68±3.9	65±4.2	n.a.	n.a.	n.a.	n.a.
Proteotoxic stress	**17-AAG**	Hsp90	100 nM	87±2.4	35±3.5**	90±5.0	70±2.4**	86±4.0	78±1.9**	92±4.0	78±3.7*
	Cycloheximide	Ribosome	50 ng/ml	n.a	n.a	68±3.1	62±2.9*	60±0.5	69±2.6**	58±1.5	44±2.0**
	Chloroquine	Lysosome	25 μM	69±6.0	15±6.4**	90±1.5	70±2.5**	89±2.6	79±3.6**	79±1.4	66±2.4*
	Lactacystin	Proteasome	10 μM	n.a	n.a	77±0.5	70±5.2*	63±3.6	79±3.2**	63±2.1	33±1.3**
	MG132	Proteasome	0.5 μM	31±1.6	42±2.2**	40±1.8	48±1.1*	47±2.7	51±3.7	30±1.6	32±1.8
	Puromycin	Ribosome	0.2 μg/ml	n.a	n.a	83±4.3	54±4.0**	73±2.8	83±3.1**	77±3.8	69±4.4*
	Tunicamycin	GlcNAc phospho-transferase (GPT)	50 ng/ml	n.a	n.a	80±4.1	77±3.5	88±5.0	87±6.7	75±1.9	76±3.8
Energy stress	**AICAR**	AMPK	0.5 mM	77±2.8	29±2.3**	64±4.1	30±4.1**	70±4.1	47±7.8**	77±2.3	70±2.2*
	Compound C	AMPK	5 μM	73±2.4	98±6.3**	45±3.3	78±6.3**	60±2.2	72±3.2**	61±3.	62±3.0
	2-Deoxyglucose	hexokinase	2.5 mM	n.a	n.a	18±1.4	29±2.2**	14±1.0	16±2.0	16±0.1	21±6.0
	Metformin	AMPK	1 mM	n.a	n.a	86±2.4	73±2.9**	82±2.1	72±2.4**	n.a.	n.a.
	Rapamycin	mTOR	10 nM	48±3.4	61±1.2**	60±1.5	69±2.1*	51±1.4	55±1.6	53±3.0	54±2.4
	Torin1	mTOR	250 nM	73±1.4	86±5.4**	69±2.4	85±2.0**	n.a.	n.a.	n.a.	n.a.

**P*<0.05, ***P*<0.005, t test

Growth improvement ≥ 5% is shown in green

Growth inhibition ≥ 5% is shown in red

Table S2

shRNA sequences used in this study

shRNA	Sense squence
AMPKα.1623	CCAGGAAGTCATACAATAGAA
Beclin1.1147	CTGGAGTCTCTGACAGACAAA
mTOR.6309	CAGGCATATGGCCGAGATTTA
p53.1224	CCACTACAAGTACATGTGTAA

Table S3, related to Figure 5

Primers used for quantitative Real-Time PCR

Gene	Forward primer	Reverse primer
Atg1	5’-agccctggatgagatgtttc	5’-atgggtgacagaaccaagac
Atg4	5’-attgctgtggggtttttctg	5’-aaccccaggattttcagagg
Beclin1	5’-tggccaataagatgggtctg	5’-tgcctccagtgtcttcaatc
LC3	5’-tggacaagaccaagttcctg	5’-agccattgctgtcccgaatg
Atg12	5’-ttccttaaactggtggcctc	5’-acagcaccgaaatgtctctg
Bnip3	5’-tccactagcaccttctgatg	5’-caggaacaccgcatttacag
Gaprapl1	5’-cgtggagaaggctcctaaag	5’-atacagctggcccatggtag
Rpl19	5’-aagcctgtgactgtccattc	5’-cttcttggattcccggtatc