

Appendix

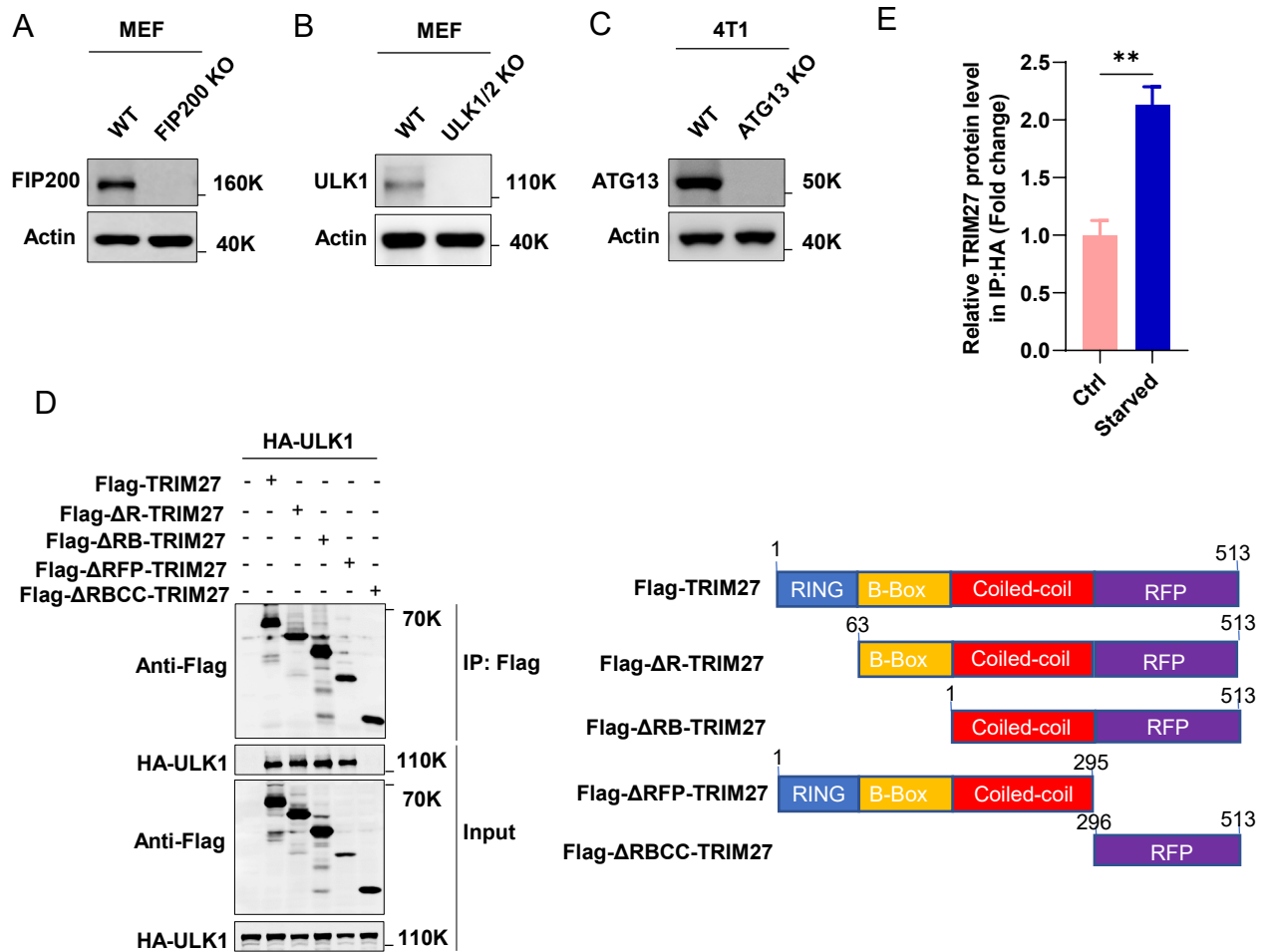
TRIM27 cooperates with STK38L to inhibit ULK1-mediated autophagy and promote tumorigenesis

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Appendix Fig S1



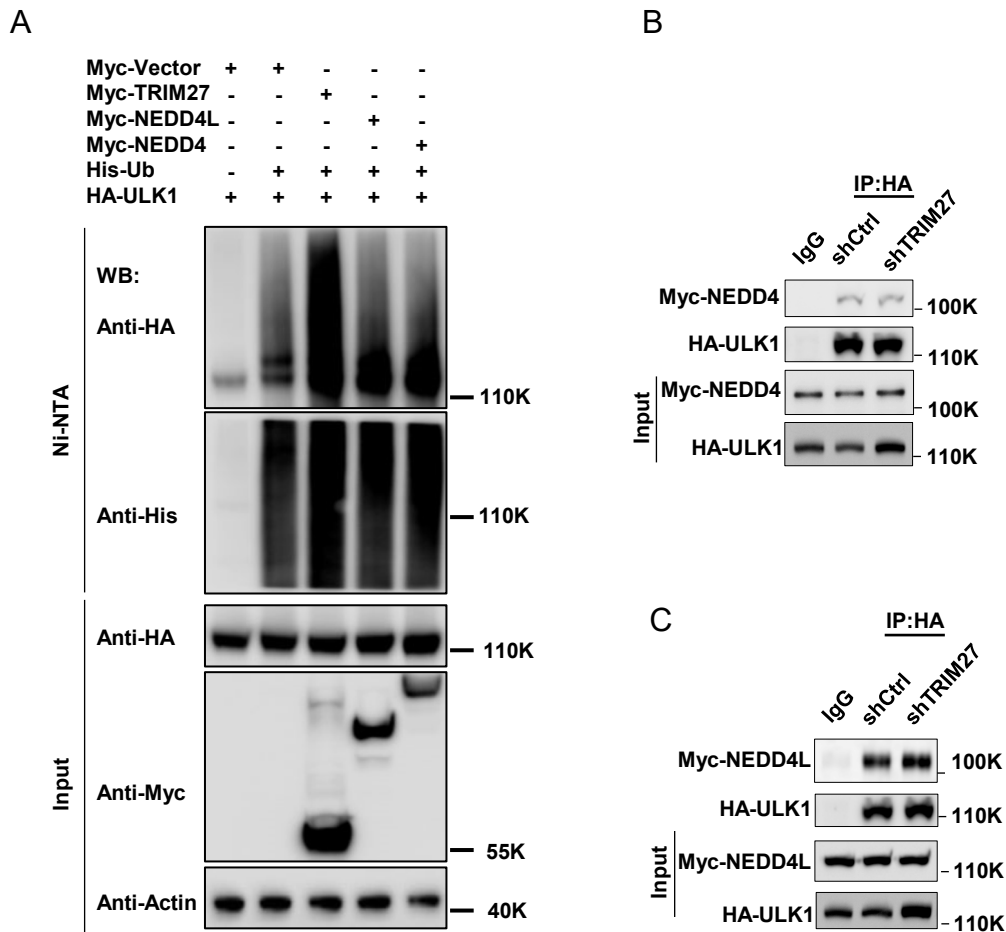
Appendix Figure S1. Removal of the RING-BOX-Coiled-coil domain of TRIM27 diminished its interaction with ULK1.

(A-C) Verification of gene knockout of FIP200 and ULK1/2 in MEF cells and ATG13 in the 4T1 cell line, respectively, using Western blot. Actin was used as a loading control.

(D) Co-immunoprecipitation assays between HA-ULK1 and the indicated truncated Flag-TRIM27 mutants transfected in HEK293T cells.

(E) Quantification of data presented in Figure 1H shows mean \pm s.e.m. of three independent experiments, P values were determined by a two-tailed unpaired t -test, $**P < 0.01$.

Appendix Fig S2



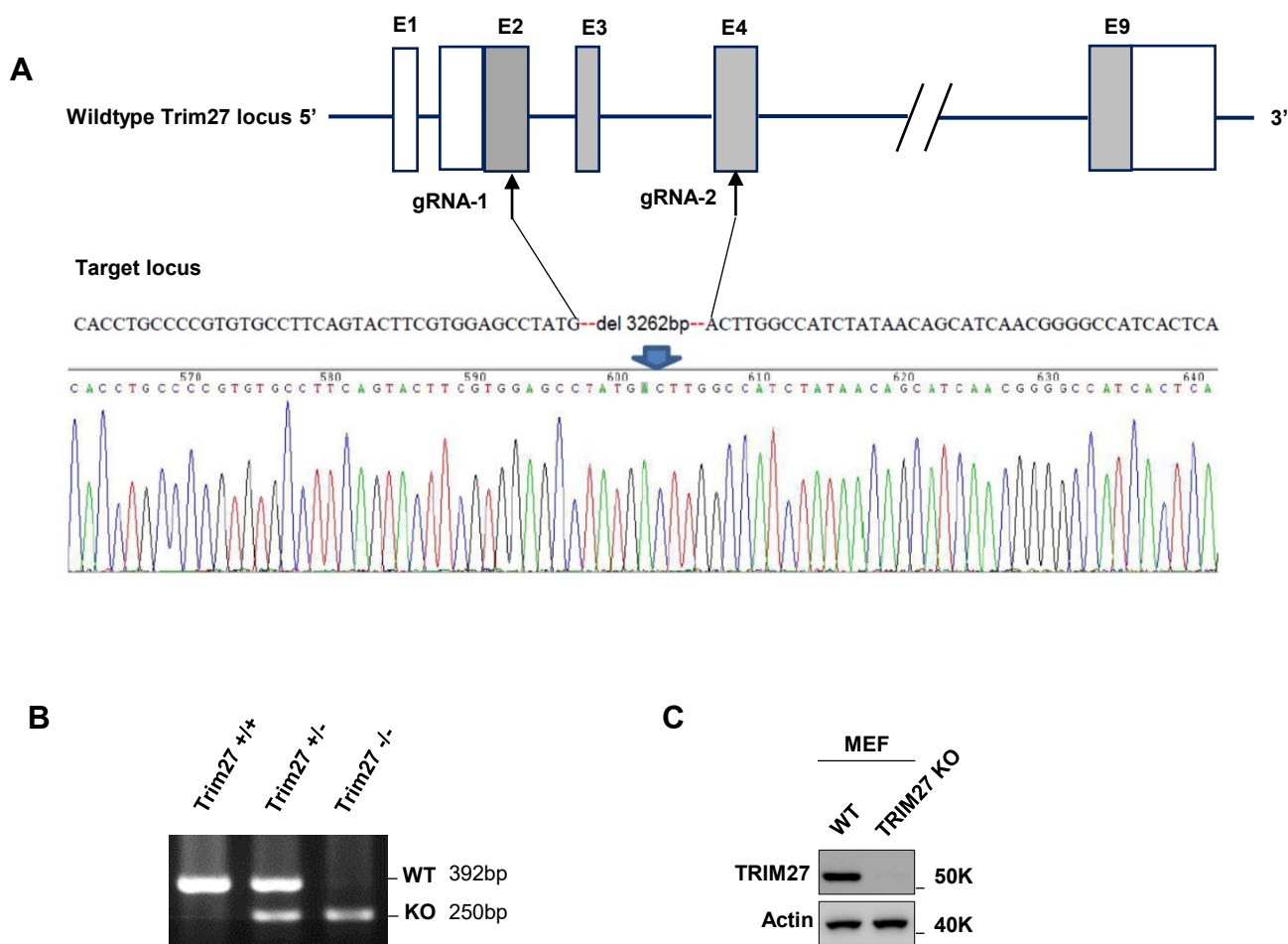
Appendix Figure S2. TRIM27 functions independently of NEDD4 and NEDD4L.

(A) Ubiquitination analysis of HA-ULK1 in HEK293T cells after co-transfection with indicated constructs.

(B) Co-immunoprecipitation assays in HEK293T cells after co-transfection with HA-ULK1 and Myc-NEDD4 in the presence or absence of TRIM27 followed by Western blotting as indicated.

(C) Co-immunoprecipitation assays in HEK293T cells after co-transfection with HA-ULK1 and Myc-NEDD4L in the presence or absence of TRIM27 followed by Western blot as indicated.

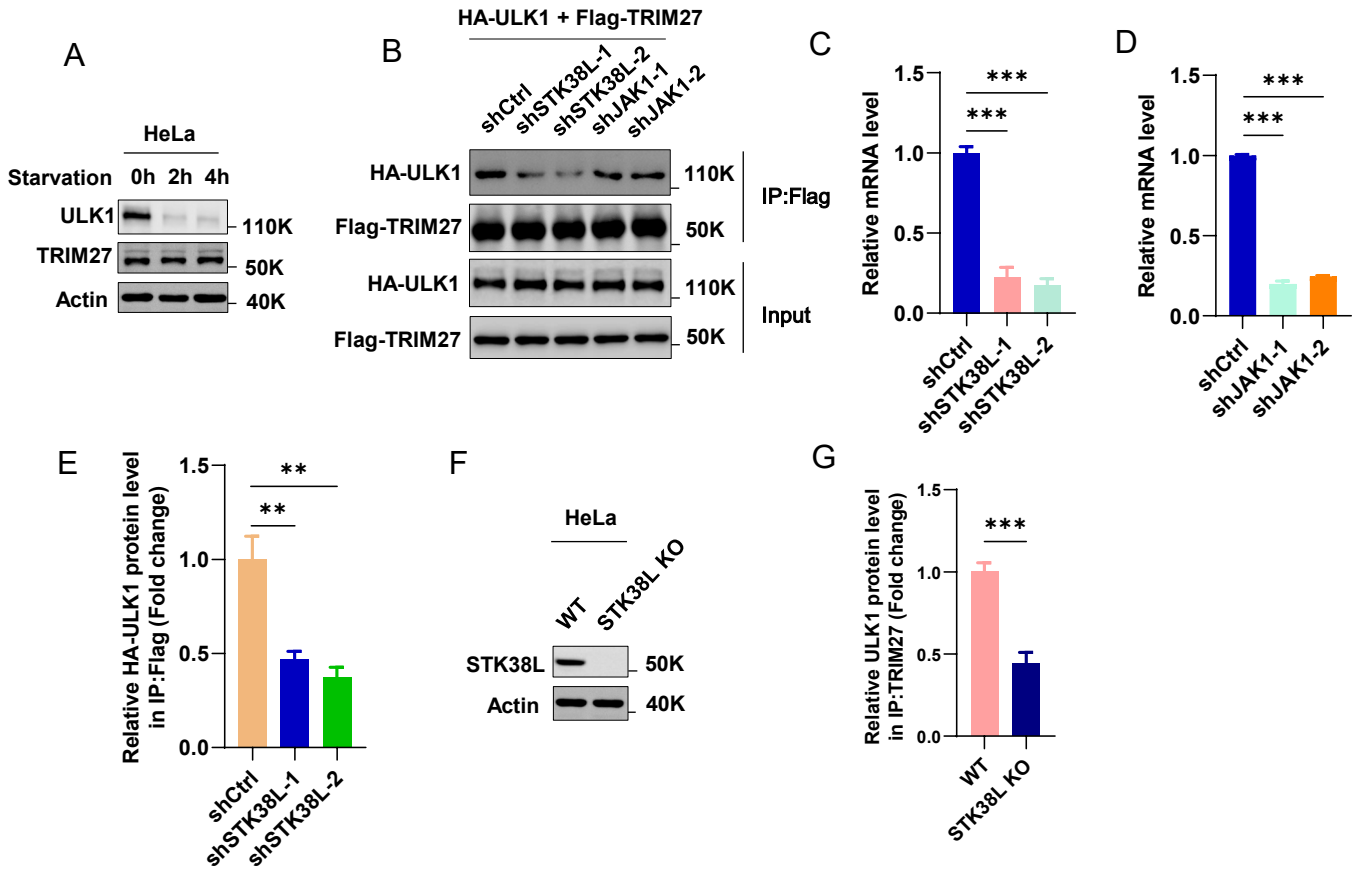
Appendix Fig S3



Appendix Figure S3. Verification of gene editing approaches using CRISPR/Cas9 technology in cell lines and mice.

(A) Schematic diagram of Trim27^{-/-} mice construction strategy to create a 3262bp deletion between exon-2 and exon-4. (B) Representative genotyping analysis used to indicate Trim27 knockout (-/-) mice by PCR. (C) Verification of TRIM27 knockout in MEFs isolated from Trim27^{-/-} mice by Western blot.

Appendix Fig S4



Appendix Figure S4. Knockdown of STK38L reduces binding between TRIM27 and ULK1.

(A) ULK1 protein levels in HeLa cells starved in HBSS for the indicated times.

(B) Co-immunoprecipitation between Flag-TRIM27 with HA-ULK1 in HEK293T cells after knockdown of the indicated genes. The cells were starved for 1h before immunoprecipitation of Flag-TRIM27 with Flag antibodies before detection of bound HA-ULK1 using Western blotting against HA.

(C-D) Relative gene knockdown efficiency of STK38L (C), JAK1 (D) in HEK293T cells. Data are mean \pm s.e.m. of three independent experiments. *P* values were determined by a one-way ANOVA with Dunnett's multiple comparisons test. ****P* < 0.001.

(E) Quantification of data presented in Figure 4E shows mean \pm s.e.m. of three independent experiments. *P* values were determined by a one-way ANOVA with Dunnett's multiple comparisons test, ***P* < 0.01.

(F) Verification of STK38L knockout in HeLa cells by Western blot.

(G) Quantification of data presented in Figure 4H shows mean \pm s.e.m. of five independent experiments. *P* values were determined by a two-tailed unpaired *t*-test, ****P* < 0.001.

Appendix Fig S5

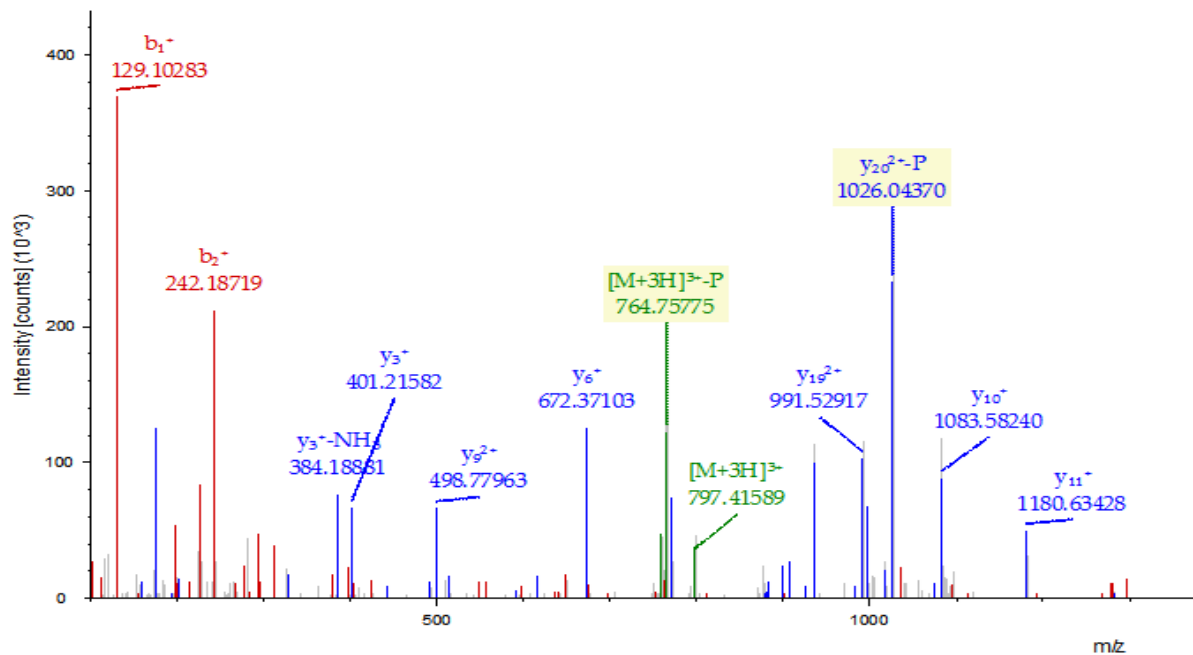
A

Position ^c	Peptide score ^c	Modified sequence ^c	Mass error [ppm] ^c	#PSMs ^c
S 774 ^c	88.48 ^c	mFsVGSSSSSLGSGSSSAR ^c	-1.29166398650567 ^c	36 ^c
S 405 ^c	83.3 ^c	TPSPsPTcSSSPSPSGR ^c	-1.56674100843157 ^c	21 ^c
S 450 ^c	70.88 ^c	IEQLQsPTQQQTAR ^c	-1.46697365847086 ^c	8 ^c
T 754 ^c	50.36 ^c	GGGASSPAPVVFtVGsPPSGATPPQSTR ^c	-0.297675900911386 ^c	3 ^c
S 757 ^c	50.36 ^c	GGGASSPAPVVFtVGsPPSGATPPQSTR ^c	-0.297675900911386 ^c	3 ^c
T 653 ^c	49.98 ^c	QGVVmtPPR ^c	-0.382470715124909 ^c	1 ^c
S 494 ^c	49.71 ^c	KLsLGGGRPYTPSPQVGTIPER ^c	1.44765022583157 ^c	4 ^c
S 465 ^c	43.47 ^c	sGSTSPLGFGR ^c	0.0825802896974214 ^c	16 ^c
S 614 ^c	40.47 ^c	sPLPILGSPTK ^c	-0.234505543237274 ^c	13 ^c
S 543 ^c	33.83 ^c	PGSsVPEHsPR ^c	-1.72472095407573 ^c	2 ^c

B

Sequence: **KLsLGGGRPYTPSPQVGTIPER**, Phospho (79.9663 Da)

FTMS, HCD, z=+3, Mono m/z=797.41364 Da, M⁺H⁺=2390.22635 Da, Match Tol.=0.02 Da

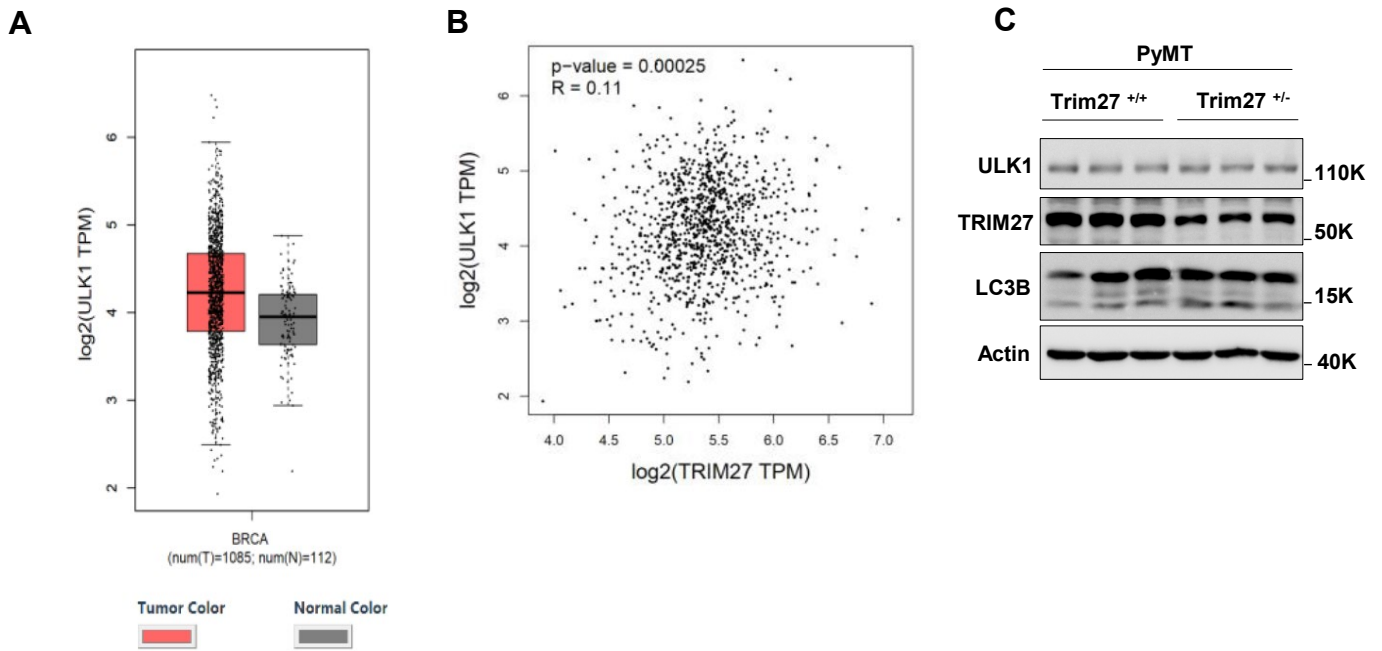


Appendix Figure S5. Mass spectrometry analysis of the phosphorylation sites of ULK1 mediated by STK38L.

(A) Summary table of potential ULK1 phosphorylation site(s) based on mass spectrographic analysis of HA-ULK1 precipitated from HEK293T cells co-transfected with HA-ULK1 and Flag-STK38L.

(B) MS/MS spectra of the HA-ULK1 tryptic peptide containing the serine 494 residue showing a mass shift of 79.9663 Da consistent with phosphorylation.

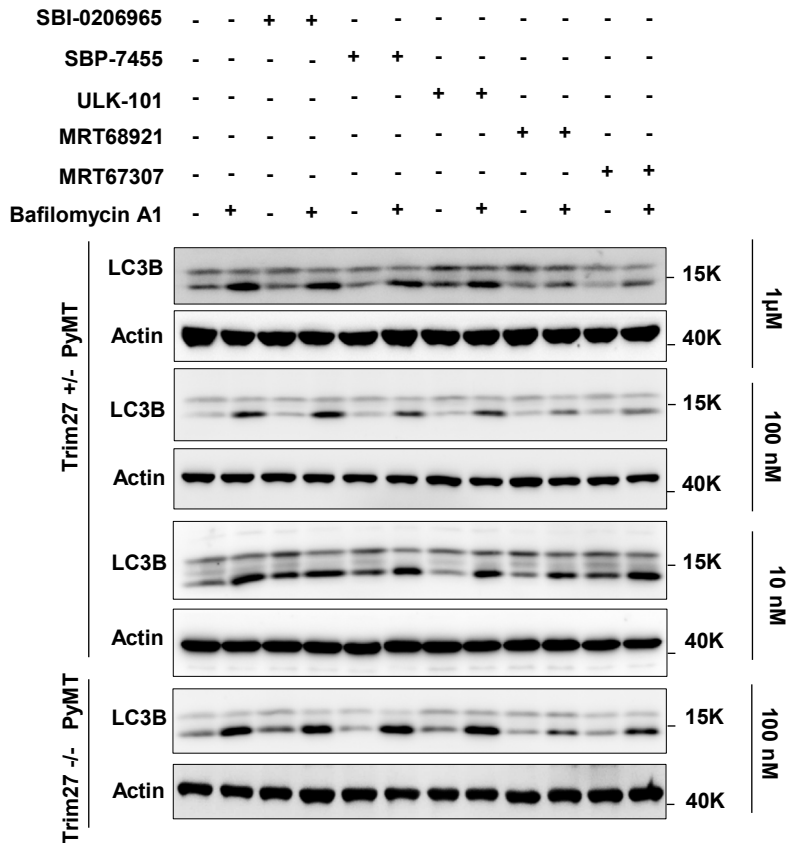
Appendix Fig S6



Appendix Figure S6. Bioinformatics analysis of the ULK1 or TRIM27 mRNA level in TCGA database.

- (A) Relative mRNA levels of ULK1 in normal breast tissues and breast tumors in the TCGA database.
- (B) Analysis of the correlation between ULK1 and TRIM27 mRNA in the TCGA database.
- (C) Western blot analysis of indicated proteins in the mammary tumors of PyMT Trim27^{+/+} or Trim27^{+/-} mice. Each lane represents a different mouse.

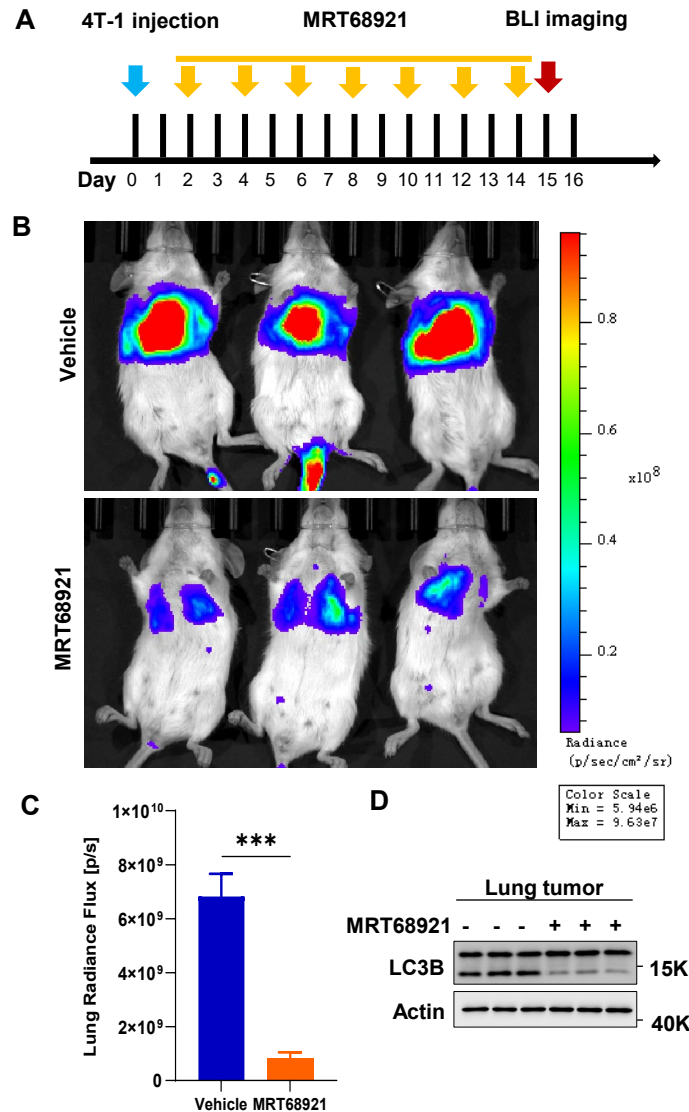
Appendix Figure S7



Appendix Figure S7. Titration of ULK1 inhibitors to determine effective minimal concentrations that inhibit autophagy.

PyMT-derived mammary cells from Trim27^{+/-} and Trim27^{-/-} mice were treated with the indicated ULK1 inhibitors or vehicle controls for 24hr. Afterwards, cell lysates were subjected to Western blot analysis against LC3B with actin used as a loading control.

Appendix Figure S8



Appendix Figure S8. Inhibition of Ulk1 with MRT68921 inhibits 4T1 cell lung metastasis in vivo. (A-B) 4T1 cells bearing luciferase (2×10^5) were injected intravenously into the tail veins of female BALB/c mice before initiation of treatments one day later by intravenously injection with either DMSO or MRT68921 (20 mg/kg/d) every two days as indicated for seven consecutive treatments ($n = 8$ per group) (A). On the 15th day after tumor inoculation, the mice were subjected to a lung tumor bioluminescence imaging (B) and radiance flux levels quantitated (C). Data are presented as mean \pm s.e.m. from 12 mice with either DMSO treatment ($n=6$) or MRT68921 treatment ($n=6$). P values were determined by a two-tailed unpaired t -test, *** $P < 0.001$. (D) After humane sacrifice, lung tumors were dissected and subjected to Western blotting analysis against LC3B with actin a loading control.

Appendix Table S1. FIP200 interaction proteins identified by mass spectrometry

Accession Number	Molecular Weight	Peptide number	Peptide number	Percent coverage	Percent coverage
		Normal Condition	Starved condition	Normal Condition	Starved condition
RBCC1_MOUSE	182 kDa	108	99	55.00%	53.10%
ATG13_MOUSE	56 kDa	19	19	42.40%	39.30%
ULK1_MOUSE	112 kDa	33	26	39.50%	30.00%
VTI1B_MOUSE	27 kDa	4	6	19.40%	29.30%
ATGA1_MOUSE	25 kDa	4	2	18.80%	6.88%
ULK2_MOUSE	113 kDa	15	14	17.80%	16.40%
DREB_MOUSE	77 kDa	9	14	17.30%	14.40%
PRDX1_MOUSE	22 kDa	3	5	15.60%	24.60%
M2OM_MOUSE	34 kDa	4	20	14.00%	49.00%
DPM1_MOUSE	29 kDa	2	2	12.70%	12.70%
CDC42_MOUSE	21 kDa	2	2	12.60%	11.00%
CHCH3_MOUSE	26 kDa	3	1	12.30%	3.96%
RAC1_MOUSE	21 kDa	2	3	8.85%	16.10%
CCPG1_MOUSE	86 kDa	6	6	7.84%	7.44%
IRGM1_MOUSE	47 kDa	3	2	6.60%	4.89%
CY1_MOUSE	35 kDa	2	2	5.85%	8.62%
RPN2_MOUSE	69 kDa	2	6	5.07%	15.70%
MFGM_MOUSE	51 kDa	2	4	4.75%	9.72%
GRB10_MOUSE	71 kDa	2	2	3.70%	3.70%
CC127_MOUSE	31 kDa	1	3	3.08%	12.30%
PP1B_MOUSE	37 kDa	1	5	3.06%	19.90%
UN45A_MOUSE	103 kDa	2	7	2.75%	9.22%
TAXB1_MOUSE	94 kDa	2	0	2.70%	0
FIL1L_MOUSE	130 kDa	2	0	2.56%	0
OST48_MOUSE	49 kDa	1	3	2.04%	4.99%
RPN1_MOUSE	69 kDa	1	2	1.97%	3.62%
SDPR_MOUSE	47 kDa	1	3	1.91%	8.37%
K1199_MOUSE	153 kDa	2	5	1.76%	3.38%
DPYL3_MOUSE	62 kDa	1	2	1.75%	4.04%
LONP2_MOUSE	95 kDa	1	3	1.41%	3.76%
SYNPO_MOUSE	100 kDa	1	3	1.40%	4.31%
RGRF1_MOUSE	144 kDa	2	1	1.03%	0.56%
MYPT1_MOUSE	115 kDa	0	8	0.00%	7.19%
PHLB2_MOUSE	141 kDa	0	3	0.00%	1.60%
ECHA_MOUSE	83 kDa	0	6	0	9.04%
MOSC2_MOUSE	38 kDa	0	5	0	11.80%
EHD2_MOUSE	61 kDa	0	6	0	11.20%
PP12C_MOUSE	85 kDa	0	4	0	3.45%
LETM1_MOUSE	83 kDa	0	2	0.00%	4.88%
SRPRB_MOUSE	30 kDa	0	4	0	20.80%
SSRA_MOUSE	32 kDa	0	3	0	11.90%
TRI27_MOUSE	59 kDa	0	2	0	4.29%
PALLD_MOUSE	152 kDa	0	2	0.00%	1.99%
NEDD4_MOUSE	103 kDa	0	3	0	2.59%
ILVBL_MOUSE	68 kDa	0	3	0	10.30%
PM34_MOUSE	34 kDa	0	3	0	11.40%
PP1A_MOUSE	38 kDa	0	3	0	20.00%
ARM10_MOUSE	33 kDa	0	2	0	9.15%
DPYL2_MOUSE	62 kDa	0	2	0	4.02%
EHD4_MOUSE	61 kDa	0	2	0	3.51%
KC1A_MOUSE	39 kDa	0	2	0	6.53%
PHB_MOUSE	30 kDa	0	2	0	7.72%
SGPL1_MOUSE	64 kDa	0	2	0	4.05%
SRC8_MOUSE	61 kDa	0	2	0	3.66%
STML2_MOUSE	38 kDa	0	2	0	7.93%
SUN2_MOUSE	82 kDa	0	2	0	2.74%

Appendix Table S2 Antibodies and Reagents

Antibodies	SOURCE	Catalogue
Rabbit anti-FIP200	PTGLAB	Cat#17250
Rabbit anti-ATG13	CST	Cat#13273
Rabbit anti-ULK1 human	SCBT	Cat#8054
Rabbit anti-mouse-ULK1	Sigma	Cat# sc33182
Rabbit polyclonal TRIM27	Sigma	Cat#SAB2700796
Rabbit polyclonal anti-p-S495 ULK1	PTM-BIO	N/A
Anti-p-S318-ATG13	NOVUS	Cat#NBP2-19127SS
β -Actin	CST	Cat#3700
Rabbit anti-p62/SQSTM1	CST	Cat#5114
p-Ser (16B4)	SCBT	Cat#sc-81514
p-Thr (14B3)	SCBT	Cat# sc-81526
Mouse Monoclonal anti-STK38L	ORIGENE	Cat#TA505176
Rabbit monoclonal anti-LC3B	CST	Cat#3868
Mouse monoclonal anti-Flag-Tag	Sigma	Cat#F3040
Rabbit polyclonal anti-Myc-Tag	PTGLAB	Cat#16286-1-AP
Mouse monoclonal anti-HA-Tag	Sigma	Cat#H9658
Rabbit-anti-GST	CST	Cat#2625
Rabbit IgG Isotype control	CST	Cat #3900
Mouse IgG1 Isotype Control	CST	Cat#5415
Mouse anti-Ubiquitin	CST	Cat#3936
Rabbit anti-Atg5	CST	Cat#12994
Rabbit anti-Atg7	CST	Cat#8558
Rabbit anti-ULK2	SCBT	Cat#sc-293453
Anti-rabbit IgG (H+L), F(ab') ₂ Fragment (Alexa Fluor® 647 Conjugate)	CST	Cat#4414
Normal Rabbit IgG	CST	Cat#2729
Dynabeads™ His-Tag Isolation and Pulldown	Invitrogen™	Cat#10103D
Cycloheximide	Sigma	Cat#C1988
MG-132	Calbiochem	Cat#474790
Plasmocure™ - Mycoplasma Elimination Reagent	Invivogen	Cat#ant-pc
Blasticidine S hydrochloride	Sigma	Cat#15205
Puromycin	Sigma	Cat#P8833
MycoStrip™ - Mycoplasma Detection Kit	Invivogen	Cat#rep-mys-50
HA Peptides	APEX BIO	Cat#A6004
Urea	Sigma	Cat#8.18710
Hoechst 33342	Sigma	Cat#B2261
Corning® Costar® ultra-low attachment plate	Corning®	Cat#CLS3471
Pierce™ HA-Tag Magnetic IP/Co-IP Kit	Thermo Scientific™	Cat#88838
Clean-Blot™ IP detection reagent (HRP)	Thermo Scientific™	Cat#21230

Gibco™ DMEM, high glucose	Gibco™	Cat#11584486
GlutaMAX™ Supplement	Gibco™	Cat#35050061
Trypsin-EDTA (0.25%)	Gibco™	Cat#25200056
Alkaline Phosphatase, Calf Intestinal (CIP)	NEW ENGLAND BioLabs	Cat#M0290S
Lambda Protein Phosphatase	NEW ENGLAND BioLabs	Cat#P0753S
UBE1	R & D SYSTEMS	Cat#E-305-025
UBE2D3	R & D SYSTEMS	Cat#E2-627-100
HIS-Ubiquitin	R & D SYSTEMS	Cat#U-530-02M
HIS-Ubiquitin K48	R & D SYSTEMS	Cat#UM-HK480
HIS-Ubiquitin K63	R & D SYSTEMS	Cat#UM-HK630
Pierce™ Protein A/G Agarose	Thermo Scientific™	Cat#20421
cOmplete™, Mini, EDTA-free Protease Inhibitor Cocktail	Roche	Cat#4693159001
Anti-FLAG® M2 Magnetic Beads	Millipore	Cat#M8823
D-PBS	Gibco™	Cat#14040141
2-Mercaptoethanol	Sigma	Cat#M7522
Sodium Pyruvate (100 mM)	Gibco™	Cat#11360070
DMEM/F12 ((without HEPES, with L-glutamine))	Gibco™	Cat#11320033
HBSS, calcium, magnesium, no phenol red	Gibco™	Cat#14025076
Penicillin-Streptomycin (10,000 U/mL)	Gibco™	Cat# 15140122
BSA fraction V	ThermoFisher	Cat#15260037
FBS	Gibco™	Cat#26140087
TRIzol™ Reagent	Invitrogen	Cat# 15596026
PrimeScript™ RT reagent kit	Takara	Cat#DRR037A
SYBR™ Green PCR Master Mix	Applied Biosystems™	Cat# 4309155
ULK1 101	Selleck	Cat#S8793
SBI-0206965	Selleck	Cat#S7885
SBP-7455	Selleck	Cat#S3393
MRT68921	Selleck	Cat#S7949
MRT67307	Selleck	Cat#S7948

Appendix Table S3. Recombinant DNA constructs

Recombinant DNA Constructs		
Flag-TRIM27	This Paper	N/A
Flag-ΔR-TRIM27	This Paper	N/A
Flag-ΔRB-TRIM27	This Paper	N/A
Flag-ΔRFP-TRIM27	This Paper	N/A
Flag-ΔRBCC-TRIM27	This Paper	N/A
Myc-TRIM27	This Paper	N/A
HA-TRIM27	This Paper	N/A
HA-ULK1	This Paper	N/A
HA-ULK1 150-1051AA	This Paper	N/A
HA-ULK1 278-1051AA	This Paper	N/A
HA-ULK1 330-1051AA	This Paper	N/A
HA-ULK1 500-1051AA	This Paper	N/A
HA-ULK1 600-1051AA	This Paper	N/A
HA-ULK1 828-1051AA	This Paper	N/A
HA-ULK1 1-500AA	This Paper	N/A
HA-ULK1 1-600AA	This Paper	N/A
HA-ULK1 1-828AA	This Paper	N/A
HA-ULK1 K568R	This Paper	N/A
HA-ULK1 K571R	This Paper	N/A
HA-ULK1 K568/571R	This Paper	N/A
HA-hULK1 S495A	This Paper	N/A
HA-ULK1 S494A	This Paper	N/A
HA-ULK1 T754A	This Paper	N/A
HA-ULK1 S405A	This Paper	N/A
HA-ULK1 S774A	This Paper	N/A
HA-ULK1 S543A	This Paper	N/A
HA-ULK1 S465A	This Paper	N/A
HA-ULK1 S614A	This Paper	N/A
HA-ULK1 S450A	This Paper	N/A
HA-ULK1 T653A	This Paper	N/A
HA-ULK1 S757A	This Paper	N/A
HA-FIP200	This Paper	N/A
HA-ATG13	This Paper	N/A
GST-TRIM27	This Paper	N/A
GST-STK38L	This Paper	N/A
GST-STK38L K119A	This Paper	N/A
Flag-STK38L	This Paper	N/A
Myc-STK38L	This Paper	N/A
Myc-STK38L K119A	This Paper	N/A

Myc-STK38L K432/K434R	This Paper	N/A
Myc-STK38L K1-13R	This Paper	N/A
Myc-STK38L K14-27R	This Paper	N/A
Myc-STK38L K28-38R	This Paper	N/A
Myc-STK38L K1-38R	This Paper	N/A
Myc-STK38L K1-16R	This Paper	N/A
Myc-STK38L K1-19R	This Paper	N/A
Myc-STK38L K432/K434	This Paper	N/A
Myc-STK38L K181/K432/K434	This Paper	N/A
Myc-STK38L K182/K432/K434	This Paper	N/A
Myc-STK38L K215/K224/K432/K434	This Paper	N/A
Myc-STK38L K181/K215/K224/K432/K434R	This Paper	N/A
Myc-STK38L R181/215/224/432/434K	This Paper	N/A
GFP-TRIM27	This Paper	N/A
Cherry-ULK1	This Paper	N/A
His-Ub	This Paper	N/A
His-Ub K6	This Paper	N/A
His-Ub K11	This Paper	N/A
His-Ub K27	This Paper	N/A
His-Ub K29	This Paper	N/A
His-Ub K33	This Paper	N/A
His-Ub K48	This Paper	N/A
His-Ub K63	This Paper	N/A
His-Ub K48	This Paper	N/A
His-Ub K63	This Paper	N/A
His-Ub K6R	This Paper	N/A
Myc-NEDD4	This Paper	N/A
Myc-NEDD4L	This Paper	N/A
HA-ULK2	This Paper	N/A

Appendix Table S4 Oligonucleotide sequences

lentiCRISPR sequences	v2	gRNA	Sequence (5'→3')
TRIM27 KO-human			ATGGCCGCAGTCGAGCATCA
ULK1 KO-human			CGAAGGCGCCGTGGCCGATC
ATG13 KO-mouse			CGCTCATCATCTTCCCCGAC
STK38L KO-human			GACTGTAGCCAAGCTCACAT

shRNA sequences	Sequence (5'→3')
shTRIM27-1 human	GGACCATAGGTGTCTGTGA
shTRIM27-2 human	GCGGTACAGTTACCTCAA
shSTK38L-1 human	GAACCGGACTACAAATCCA
shSTK38L-2 human	GCAGACTGGTTACAACAAA
shJAK1-1 human	GCGATATATTCCAGAAACATT
shJAK1-2 human	GACAGTCACAAGACTTGTGAA
shULK2-1 human	GTCAGTGGTATTCGCATCAA
shULK2-2 human	GCAGACCGAAGATATTGTTTA
shATG5-1 human	GCAGAACCATACTATTGCTT
shATG5-2 human	GATTCATGGAATTGAGCCAAT
shATG7-1 human	GCCTGCTGAGGAGCTCTCCAT
shATG7-2 human	CCCAGCTATTGGAACACTGTA
shAtg5-1 mouse	GCATCTGAGCTACCCAGATAA
shAtg7-1 mouse	CCAGCTCTGAACTCAATAATA
shULK1-1 human	ACATCGAGAACGTCACCAAGT
shULK1-2 human	GCCCTTTGCGTTATATTGTAT

qRT-PCR Primers	Forward (5'→3')	Reverse (5'→3')
qRT-β-actin	GTGGCCGAGGACTTTGATTG	CCTGTAACAACGCATCTCATATT
qRT-TRIM27	TTCATCGCCGGGAGACATTA	GGCTGAGGTTACTCCACCTT
qRT-ULK1	GAGAGGCTCATCTTCAGCCA	TTGCACTTGGTGACGTTCTC
qRT-STK38L	ACCAGACTTGGCTTGGATGA	ATATGGGCCACCTGCTCTTT
qRT-JAK1	TTGATGCCAGCTCACTGGAG	AGCCATCCCTAGACACTCGT

Appendix Table S5. TRIM27 interaction proteins identified by mass spectrometry

Number	Accession	Score	Mass	Matched Peptide Sequences	emPAI
1	A0A1U9X8R9_HUMAN	419	59763	13 (10)	0.9
2	YBOX1_HUMAN	400	35903	13 (8)	1.03
3	A0A024RAQ1_HUMAN	149	40066	5 (3)	0.27
4	B4DEP6_HUMAN	377	66146	18 (11)	0.97
5	ST38L_HUMAN	108	54196	11 (5)	0.42
6	ANM5_HUMAN	311	73322	20 (15)	1.2
7	A0A024RCA7_HUMAN	277	11658	5 (5)	5.11
8	GGOB1_HUMAN	267	377215	28 (11)	0.1
9	EF2_HUMAN	254	96246	14 (12)	0.54
10	A0A024RBH2_HUMAN	249	66097	9 (5)	0.27
11	RS3A_HUMAN	245	30154	9 (5)	0.87
12	EF1A1_HUMAN	206	50451	9 (6)	0.66
13	Q3MIH3_HUMAN	190	15004	7 (5)	2.41
14	ICLN_HUMAN	188	26370	4 (4)	0.81
15	SYTL2_HUMAN	174	105150	13 (9)	0.32
16	A0A0D9SGF6_HUMAN	165	288226	15 (6)	0.08
17	AT1A1_HUMAN	161	114135	6 (4)	0.12
18	TKT_HUMAN	152	68519	10 (7)	0.39
19	D0PNI1_HUMAN	152	27899	5 (5)	0.76
20	A0A0A0MRM8_HUMAN	151	146293	5 (3)	0.07
21	LAP2A_HUMAN	150	76016	6 (4)	0.18
22	A0A024R8S5_HUMAN	149	57480	7 (4)	0.25
23	ALDOA_HUMAN	141	39851	4 (4)	0.49
24	A0A109NGN6_HUMAN	144	26565	3 (3)	0.61
25	ASPH_HUMAN	144	86266	1 (1)	0.08
26	SYEP_HUMAN	141	172080	9 (5)	0.1
27	A0A1U9X972_HUMAN	126	229209	9 (3)	0.04
28	MBD4_HUMAN	124	66808	12 (6)	0.33
29	TR150_HUMAN	117	108658	10 (5)	0.19
30	H0Y4R1_HUMAN	116	51549	4 (2)	0.13
31	TCPQ_HUMAN	113	60153	8 (5)	0.3
32	H0Y7A7_HUMAN	103	20863	2 (1)	0.35
33	H0UI66_HUMAN	102	118485	7 (3)	0.09
34	A0A0F7NGI8_HUMAN	102	83266	4 (1)	0.04
35	A0A024RDG1_HUMAN	101	108740	3 (1)	0.03
36	A0A0U1RQF0_HUMAN	101	275649	10 (5)	0.06
37	A0A087WVQ6_HUMAN	97	193703	4 (3)	0.05
38	PSB6_HUMAN	96	25570	5 (3)	0.45
39	EFTU_HUMAN	96	49852	8 (3)	0.21
40	A0A087WZK9_HUMAN	95	39736	2 (2)	0.17
41	COPG1_HUMAN	94	98967	7 (3)	0.1
42	PCM1_HUMAN	94	230057	7 (4)	0.06
43	A0A024R652_HUMAN	94	102152	6 (2)	0.07
44	F262_HUMAN	92	58953	6 (2)	0.11
45	Q6IAX2_HUMAN	86	18610	4 (2)	0.65
46	A0A090N8Y2_HUMAN	86	73229	4 (2)	0.09
47	A0A0A0N0M2_HUMAN	85	134831	7 (1)	0.02
48	COPA_HUMAN	85	139797	6 (3)	0.1
49	CAMP3_HUMAN	85	135464	9 (4)	0.1
50	CALX_HUMAN	84	67982	3 (2)	0.1