Table S3. **Details of CRISPR sequences, genotyping results of all knockout cell lines in this study**

Gene Symbol	Uniprot	GeneID/ Location	Targeting strategy	CRISPR gRNA (PAM)	Main clone	Depth/ Unique Alleles	Mutation	Protein impact
STX17	P56962	55014/ NC_000009.12	Targets the fourth exon.	ACCAGATCCATGACTGTTGGTGG	#13	5/3	c.[411_412insT]; [411del]; [411_414del]	p.[G138Wfs*11]; [G138Wfs*19]; [G138Efs*18]
VPS39	Q96JC1	23339/ NC_000015.10	Targets the first exon.	ATCGACTGTCTGGCTGCCTGGGG	#20	5/2	c.[68_69insAGTCAGATGTTGGAACCTGGAGTCCATTTAGAAGACGTCTGGGGAGCGGCCGCAGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAC]; [68_69insACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCG	p.[W24Vfs*10]; [W24Rfs*42]
LC3 TKO								
MAP1LC3A	Q9H492	84557/ NC_000020.11	Targets the third exon.	TCAAGATCATCCGGTGCGTGG	#39	5/2	c.[203+2_203+3insT];[203+2_203+3del]	p.[?];[?] (affecting splicing)
MAP1LC3B	Q9GZQ8	81631/ NC_000016.10	Targets the second exon.	ATCCAACCAAAATCCCGGTAGG		5/2	c.[95del];[85_96+3del]	p.[P32Rfs*2];[?] (affecting splicing)
MAP1LC3C	Q9BXW4	440738/ NC_000001.11	Targets the third exon.	CACTCTTGACAGGTGGTAGTGG	#15 (made from LC3A/B DKO #39)	5/3	c.[118_127del];[114_117del];[115_123del]	p.[V40Afs*61]; [V39*]; [V39_V41del]
GBRP TKO								
GABARAP	O95166	11337/ NC_000017.11	Targets the first exon.	GATCTTCTCGCCCTCAGAGCGG	#54	5/2	c.[25_57del];[63_64insA]	p.[H9_E19del]; [R22Tfs*33]
GABARAPL1	Q9H0R8	23710/ NC_000012.12	Targets the second exon.	ATTACCAGTAAGGTCAGAGG		5/2	c.[165_169+4del];[160_161del]	p.[T56Wfs*16]; [N54Pfs*19]
GABARAPL2	P60520	11345/ NC_000016.1	Targets the second exon.	CGACAGGGTTCCGGTGAGTGG	#7 (made from GABARAP/GABARAPL1 DKO #54)	5/3	c.[90+1_90+3del];[89_90del];[90+2del]	p.[?]; [?];[?] (affecting splicing)
Hexa KO								
GABARAP	O95166	11337/ NC_000017.11	Targets the first exon.	GATCTTCTCGCCCTCAGAGCGG	#54	5/2	c.[25_57del];[63_64insA]	p.[H9_E19del]; [R22Tfs*33]
GABARAPL1	Q9H0R8	23710/ NC_000012.12	Targets the second exon.	ATTACCAGTAAGGTCAGAGG		5/2	c.[165_169+4del];[160_161del]	p.[T56Wfs*16]; [N54Pfs*19]
MAP1LC3A	Q9H492	84557/ NC_000020.11	Targets the third exon.	TCAAGATCATCCGGTGCGTGG	#2 (made from GABARAP/L1 DKO #54)	5/2	c.[203+1G>T;203+2_203+7del];[200_201insG;203_203+2GGT>CAC]	p.[?]; p.[I71Mfs*60;?] (affecting splicing)

MAP1LC3B	Q9GZQ8	81631/ NC_000016.10	Targets the second exon.	ATCCAACCAAAATCCCGGTAGG		5/1	c.[95_96+360del]	p.[P32Rfs*2]
MAP1LC3C	Q9BXW4	440738/ NC_000001.11	Targets the third exon.	CACTCTTGACAGGTGGTAGTGG	#51 (made from GABARAP/L1/ LC3A/B tetra KO #2)	9/2	c.[117_118insCCAGGTCGAAGTTGCTCTTGAAGTTGGGGGTCAGGCCCAGGCTCAGGGCAATCAGGTTTCCGAACAGGCCATTCTTCTTCTCGCCGGGCAGCTGGGCGATCAGATTTTCCGGCCGTCTGCTCTTGCTCAGTCTGGCAGACAGGATGGCCTTGGCGTCCACGCCGCTGGCGTTGATGGGGTTTTCCTCGAACAGCTGGTTGTAGGTCTGCACCAGCTGGATGAACAGCTTGTCCACGTCGCTGTTGTCGGGGTTCAGGTCGCCCTCGATCAGGAAGTGGCTCCGGAACTTGATCATGTGGGCCAGGGCCAGATAGATCAGCCGCAGGTCGGCCTTGTCGGTGCTGTCCACCAGTTTCTTTCTCAGGTGGTAGATGGTGGGGTACTTCTCG]; [118_123del]	p.[V40Afs*68];[V40_V41del]
GABARAPL2	P60520	11345/ NC_000016.1	Targets within the second exon.	CGACAGGGTTCCGGTGAGTGG		5/2	c.[89_90+2del];[90_90+1del]	p.[P30Rfs*13];[V31*]

The indels detected in the knockout cell lines (Mutation column) and their resulting proteins (Protein impact column) are formatted according to Human Genome Variation Society (http://varnomen.hgvs.org/). For genes with multiple splice variants, mutation positions are determined using the variant that encodes for the canonical isoform annotated in Uniprot. The numbers after the asterisks represent the number of amino acids made from the first amino acid changed to the first stop codon encountered. del, deletion; ins, insertion; c., coding DNA; p., protein; fs, frame shift; *, stop codon; [?], affecting splicing.