Table S1 – List of general autophagy genes that are targeted in the pilot autophagy gene screen. Related to Fig 1 and Supplemental Fig 1.

Gene Name	Ensembl No.
ULK1	ENSG00000177169
ULK2	ENSG00000083290
ATG13	ENSG00000175224
FIP200	ENSG00000023287
ATG101	ENSG00000123395
ATG9A	ENSG00000198925
ATG9B	ENSG00000181652
WIPI1	ENSG00000070540
WIPI2	ENSG00000157954
PIK3R4	ENSG00000196455
VPS34	ENSG00000078142
BECN	ENSG00000126581
ATG14	ENSG00000126775
UVRAG	ENSG00000198382
ATG3	ENSG00000144848
ATG4A	ENSG00000101844
ATG4B	ENSG00000168397
ATG4C	ENSG00000125703
ATG4D	ENSG00000130734
ATG5	ENSG00000057663
ATG7	ENSG00000197548
LC3A	ENSG00000101460
LC3B	ENSG00000140941
LC3B2	ENSG00000258102
GABARAP	ENSG00000170296
GABARAPL1	ENSG00000139112
GABARAPL2	ENSG00000034713
ATG10	ENSG00000152348
ATG12	ENSG00000145782
ATG16L1	ENSG00000085978
ATG16L2	ENSG00000168010

Table S2 – High confidence hits with Enhanced or Inhibited score of $P<0.01$. Related to Fig 1 and Supplemental Fig S1.

gene	**Localization**	**Enhanced(P-value)**	**Enhanced(log2 Fold change)**	**Inhibit (P-value)**	**Inhibit (log2 Fold change)**	**Enh/Inh (P-value)**	**Enh/Inh (Fold change)**
VPS16	lyso	0.077	-4.578	0.002	1.338	0.001	-5.368
PSMA5	cyto	0.263	-1.152	0.042	2.597	0.003	-4.701
PREB	ER/lyso	0.045	-1.513	0.023	2.902	0.006	-4.177
ATP5O	mito	0.156	-3.428	0.007	0.637	0.003	-3.862
CORO2A	cyto	0.238	-1.363	0.019	1.567	0.006	-3.796
LRRC34	nuc	0.473	-0.740	0.079	2.325	0.001	-3.783
PRPF4	nuc	0.018	-3.305	0.086	1.501	0.004	-3.662
RNF113A	nuc	0.018	-3.572	0.181	1.242	0.004	-3.607
RPL23	cyto	0.756	-2.475	0.328	3.792	0.000	-3.602
NDUFB2	mito	0.452	-2.580	0.003	1.051	0.001	-3.504
MMP24	golgi/extra	0.033	-3.140	0.096	0.358	0.003	-3.433
PSMB5	cyto	0.003	-2.790	0.140	0.381	0.003	-3.176
HSD17B10	mito	0.000	-2.930	0.039	0.492	0.000	-3.150
PAPSS1	cyto	0.066	-2.277	0.242	0.895	0.008	-3.114
PICK1	mito	0.030	-2.722	0.143	0.313	0.006	-3.041
TARS2	mito	0.035	-2.573	0.026	0.706	0.005	-2.983
DR1	nuc	0.019	-2.757	0.134	0.374	0.003	-2.967
DLD	mito	0.044	-0.800	0.046	1.446	0.004	-2.956
SERINC2	extracell	0.316	-1.540	0.065	0.553	0.009	-2.944
ATF5	cyto	0.183	-0.806	0.392	2.432	0.004	-2.895
RPS6KB2	cyto/nuc	0.099	-2.248	0.231	1.759	0.001	-2.780
MMAA	mito	0.004	-2.450	0.290	0.291	0.004	-2.736
MRPL24	mito	0.009	-2.653	0.350	0.206	0.002	-2.701
CYB5B	mito	0.017	-2.444	0.128	0.197	0.002	-2.647
NDUFS8	mito	0.025	-2.025	0.119	0.940	0.001	-2.514
MAP4	cyto	0.001	-1.838	0.452	0.647	0.001	-2.489
SGOL1	cyto/nuc	0.028	-2.509	0.598	0.969	0.007	-2.474
NDUFB4	mito	0.002	-2.233	0.057	0.379	0.000	-2.449
CCAR1	nuc	0.071	-2.976	0.230	0.047	0.003	-2.418
DDX52	nuc	0.127	-1.969	0.215	0.228	0.008	-2.408
SLC7A9	PM	0.019	-2.104	0.225	0.390	0.010	-2.404
PLD4	ER	0.125	-2.144	0.073	0.601	0.003	-2.238
MGLL	ER	0.032	-2.244	0.252	0.197	0.002	-2.235
VARS2	mito	0.002	-1.740	0.003	0.660	0.000	-2.184
LOC441155	nuc	0.059	-1.866	0.984	0.169	0.004	-2.163
PIK3C3	cyto/lyso	0.115	-1.250	0.046	1.094	0.002	-2.135
ABHD8	extracell	0.018	-2.204	0.988	0.056	0.008	-2.129
DFFA	cyto/nuc	0.058	-2.106	0.221	0.215	0.003	-2.122
ADAM18	PM	0.070	-2.343	0.969	0.045	0.002	-2.113
RACGAP1	cyto	0.009	-1.760	0.750	1.216	0.003	-2.110
OXA1L	mito	0.008	-1.531	0.008	0.772	0.001	-2.107
GNAS	cyto/nuc	0.037	-1.752	0.179	0.296	0.005	-2.102
FGFBP3	extracell	0.096	-1.818	0.047	0.466	0.006	-2.078
NUDCD1	cyto	0.021	-0.913	0.276	0.589	0.002	-2.031
RBM28	nuc	0.011	-1.583	0.210	0.360	0.009	-2.025
MTNR1A	PM	0.146	-1.006	0.057	1.024	0.007	-1.962
SUPV3L1	mito	0.120	-0.848	0.043	0.937	0.007	-1.929
GDI1	cyto	0.071	-1.422	0.117	0.202	0.007	-1.920
NR2C1	nuc	0.030	-1.907	0.801	0.028	0.005	-1.903
FMOD	lyso	0.329	-0.293	0.119	1.756	0.008	-1.870
NDUFA8	mito	0.003	-1.696	0.314	0.422	0.000	-1.853
RPL10L	cyto	0.265	-1.688	0.508	0.285	0.006	-1.844
LEO1	nuc	0.102	-1.726	0.184	0.414	0.005	-1.801
HLTF	nuc	0.142	-1.838	0.534	0.396	0.003	-1.773
MRPL33	mito	0.001	-1.516	0.418	0.262	0.001	-1.771
KCNN3	PM	0.297	-1.476	0.095	0.464	0.009	-1.728
MRPL34	mito	0.012	-1.232	0.013	0.521	0.001	-1.698
CUL9	cyto	0.031	-2.430	0.200	0.668	0.007	-1.675
GDAP2	lyso	0.080	-1.519	0.338	0.477	0.007	-1.635
RIMBP2	PM	0.705	-0.817	0.003	0.836	0.006	-1.551
MS4A3	PM	0.456	-1.309	0.441	0.496	0.009	-1.541
ENPP3	PM	0.014	-1.139	0.089	0.521	0.003	-1.527
SLMO2	mito	0.059	-1.359	0.287	0.148	0.007	-1.513
ARL6IP1	ER	0.218	-0.601	0.002	0.669	0.006	-1.493

NDUFS2	mito	0.068	-1.181	0.024	0.577	0.002	-1.485
CAPN3	cyto	0.022	-1.076	0.024	0.605	0.004	-1.474
ARSA	lyso/ER	0.007	-1.156	0.197	0.292	0.003	-1.454
MRPL16	mito	0.005	-1.000	0.008	0.552	0.001	-1.446
ZNF711	nuc	0.009	-1.308	0.949	0.216	0.008	-1.443
TOR3A	ER	0.005	-1.319	0.642	0.057	0.003	-1.413
AARS2	mito	0.003	-1.298	0.376	0.144	0.001	-1.410
ANAPC10	cyto/nuc	0.229	-0.551	0.706	0.501	0.006	-1.408
COA3	mito	0.021	-0.827	0.204	0.540	0.007	-1.374
MAGEA11	cyto	0.005	-2.550	0.055	1.000	0.004	-1.342
BCS1L	mito	0.201	-0.613	0.504	0.849	0.004	-1.327
EI24	ER/golgi	0.504	-0.567	0.002	0.765	0.005	-1.322
MRPL30	mito	0.005	-0.976	0.090	0.512	0.001	-1.307
CHMP2A	endosome	0.255	-0.076	0.483	1.185	0.009	-1.274
ZNF333	nuc	0.067	-0.822	0.042	0.635	0.004	-1.249
RNF146	cyto	0.013	-1.152	0.390	0.181	0.006	-1.245
ATG10	lyso/cyto	0.143	-0.541	0.023	0.876	0.006	-1.240
POLG2	mito	0.100	-0.877	0.009	0.675	0.001	-1.229
SULT1C2	cyto	0.019	-0.804	0.136	0.696	0.001	-1.217
NDUFS5	mito	0.020	-1.036	0.048	0.458	0.001	-1.214
KCNK13	PM	0.012	-0.702	0.047	0.563	0.002	-1.201
CHAF1A	nuc	0.099	-1.101	0.170	0.731	0.003	-1.195
TECPR1	lyso	0.060	-0.795	0.454	0.507	0.009	-1.187
MRPL41	mito	0.053	-1.291	0.248	0.337	0.001	-1.175
TRMT10C	mito	0.196	-0.640	0.041	0.716	0.009	-1.168
WBSCR16	mito	0.005	-0.784	0.272	0.371	0.002	-1.165
ZNF414	nuc	0.030	-0.745	0.211	0.331	0.007	-1.163
GP9	PM	0.835	-0.388	0.011	1.073	0.003	-1.142
GRSF1	mito	0.012	-1.033	0.523	0.184	0.005	-1.138
ALYREF	cyto/nuc	0.031	-1.353	0.798	0.191	0.003	-1.118
COA4	mito	0.082	-1.005	0.184	0.334	0.006	-1.100
MRPL55	mito	0.088	-0.616	0.007	0.571	0.002	-1.039
CNTF	extracell	0.004	-0.881	0.479	0.165	0.003	-1.023
ETV1	nuc	0.027	-1.217	0.784	0.210	0.002	-1.018
MRPL17	mito	0.065	-1.030	0.921	0.152	0.008	-0.991
WIPI1	endosome	0.012	-0.993	0.651	0.242	0.002	-0.991
PTCD1	mito	0.010	-0.835	0.412	0.184	0.003	-0.980
C16orf45	nuc	0.017	-0.900	0.611	0.197	0.004	-0.979
PRUNE2	cyto	0.404	-0.392	0.079	0.931	0.009	-0.957
MRPL22	mito	0.149	-0.378	0.024	0.641	0.008	-0.950
ATP5J2	mito	0.028	-0.771	0.276	0.184	0.007	-0.949
SLC26A4	PM	0.004	-0.823	0.881	0.009	0.008	-0.949
DDRGK1	ER	0.014	-0.794	0.578	0.166	0.006	-0.944
POLE2	nuc	0.136	-0.715	0.117	0.388	0.009	-0.929
ZDHHC2	ER/golgi	0.716	-0.239	0.003	0.777	0.005	-0.924
EPG5	nuc	0.188	-0.368	0.066	0.708	0.005	-0.914
TMEM74	lyso	0.025	-0.566	0.535	0.182	0.005	-0.905
WDFY3	cyto/nuc	0.118	-0.650	0.430	0.456	0.008	-0.902
KLK6	mito/nuc	0.119	-1.015	0.922	0.318	0.006	-0.868
RNF183	ER	0.031	-0.635	0.129	0.445	0.004	-0.866
TRAPPC12	cyto/nuc	0.116	-0.533	0.044	0.449	0.008	-0.838
LIPT2	mito	0.052	-0.848	0.473	0.106	0.007	-0.829
ASB16	cyto	0.320	-0.103	0.103	0.739	0.009	-0.821
FZD6	PM	0.196	-0.559	0.202	0.469	0.006	-0.808
RAB5C	lyso	0.073	-0.573	0.100	0.263	0.009	-0.796
CDK5RAP3	cyto	0.043	-0.764	0.308	0.208	0.004	-0.785
DCLK2	cyto	0.361	-0.278	0.175	0.580	0.010	-0.782
PIGF	ER	0.181	-0.254	0.133	0.461	0.008	-0.758
KIAA0391	mito	0.030	-0.609	0.362	0.210	0.009	-0.700
CEACAM5	PM	0.084	-0.827	0.358	0.015	0.007	-0.679
LRR1	nuc	0.282	-0.199	0.129	0.523	0.009	-0.594
LILRB4	PM	0.060	0.810	0.140	-0.358	0.010	0.616
SCUBE1	PM	0.039	0.637	0.693	-0.112	0.010	0.620
TMC4	PM	0.168	0.506	0.184	-0.485	0.010	0.649
LOH12CR1	lyso	0.014	0.813	0.893	-0.014	0.009	0.726
PNISR	cyto/nuc	0.007	0.645	0.536	-0.255	0.002	0.748
C1orf194	nuc	0.024	0.884	0.846	-0.170	0.009	0.751
FUCA2	ER/lyso	0.100	0.485	0.064	-0.425	0.005	0.754

WDR64	cyto	0.030	0.822	0.812	-0.119	0.009	0.767
UQCRC2	mito	0.016	0.779	0.927	-0.008	0.010	0.770
DOCK2	cyto	0.552	0.176	0.029	-0.787	0.005	0.771
CSTB	cyto	0.420	0.265	0.073	-0.776	0.008	0.795
C10orf32	lyso	0.462	0.377	0.045	-0.705	0.007	0.818
ITIH3	extracell	0.146	0.619	0.056	-0.599	0.003	0.824
FOXK2	nuc	0.008	0.658	0.710	-0.180	0.007	0.832
OR5A2	PM	0.025	0.470	0.047	-0.372	0.002	0.835
LYVE1	extracell	0.226	0.399	0.008	-0.520	0.005	0.841
ZPBP2	nuc	0.320	0.092	0.010	-0.669	0.006	0.842
DMXL2	extracell	0.794	0.028	0.010	-0.904	0.008	0.848
SHOC2	cyto/nuc	0.141	0.498	0.037	-0.687	0.001	0.856
COG7	golgi/nuc	0.699	0.046	0.056	-1.041	0.006	0.858
THOC6	nuc	0.974	0.188	0.012	-0.898	0.009	0.867
CRYGS	cyto/nuc	0.054	0.444	0.158	-0.646	0.004	0.871
TMTC4	PM	0.015	0.625	0.335	-0.477	0.003	0.871
TRABD2B	extracell	0.051	0.797	0.864	-0.449	0.006	0.873
PRSS33	extracell	0.015	0.780	0.714	-0.124	0.010	0.876
TC2N	nuc	0.074	0.491	0.128	-0.536	0.007	0.879
SERPINA3	lyso	0.031	0.677	0.277	-0.443	0.002	0.889
S100A6	cyto	0.062	0.664	0.215	-0.392	0.010	0.903
OR7E24	PM	0.497	0.239	0.128	-0.881	0.008	0.919
CBLB	cyto/nuc	0.590	0.182	0.007	-1.475	0.003	0.924
IRS1	cyto	0.460	0.229	0.163	-1.056	0.007	0.926
C21orf91	MTs	0.159	0.418	0.184	-0.656	0.007	0.928
TMEM170A	ER	0.110	0.665	0.180	-0.403	0.009	0.941
NLRP1	cyto	0.118	0.411	0.021	-0.621	0.004	0.945
UBE2O	nuc	0.017	0.818	0.380	-0.264	0.006	0.979
CUL3	cyto	0.013	1.047	0.888	-0.058	0.004	0.993
KRTAP2-3	cyto	0.056	0.740	0.244	-0.278	0.009	0.998
C17orf85	nuc	0.337	0.416	0.062	-0.856	0.009	1.018
NOL11	nuc	0.361	0.448	0.062	-0.921	0.001	1.024
ITPK1	cyto	0.599	0.022	0.008	-0.948	0.005	1.026
SEMA4G	PM	0.072	0.648	0.033	-0.483	0.007	1.052
LACTBL1	cyto	0.105	0.651	0.263	-0.500	0.009	1.057
PTK2	cyto	0.010	0.940	0.436	-0.188	0.005	1.068
NMD3	nuc	0.025	1.211	0.841	-0.051	0.005	1.069
ASCC3	cyto/nuc	0.038	0.815	0.121	-0.625	0.002	1.073
MED21	nuc	0.611	0.160	0.002	-1.058	0.001	1.074
CDR2	nuc	0.499	0.451	0.007	-0.620	0.007	1.114
E2F8	cyto	0.476	0.256	0.005	-0.866	0.004	1.117
GPR133	PM	0.039	0.651	0.032	-0.743	0.001	1.121
SCG5	extracell	0.230	0.229	0.003	-0.722	0.003	1.122
UBE2J1	ER	0.573	0.139	0.018	-1.086	0.002	1.144
TWIST2	nuc	0.024	0.776	0.248	-0.509	0.006	1.187
PFDN5	nuc	0.002	0.950	0.791	-0.279	0.006	1.192
LY96	endosome	0.073	0.750	0.073	-0.822	0.005	1.214
SCD	ER	0.351	0.334	0.091	-1.164	0.008	1.228
BIK	mito	0.052	1.192	0.383	-0.248	0.008	1.285
C17orf82	nuc	0.231	0.424	0.117	-1.260	0.004	1.362
CALCOCO2	cyto/nuc	0.175	0.707	0.030	-1.057	0.009	1.398
GCA	cyto	0.216	0.484	0.017	-1.217	0.001	1.410
OR56A1	PM	0.012	0.685	0.305	-0.734	0.007	1.476
CCDC130	nuc	0.012	0.935	0.188	-0.734	0.006	1.494
CHERP	ER	0.062	0.909	0.037	-1.199	0.000	1.497
INTS7	cyto/nuc	0.211	0.391	0.022	-1.201	0.008	1.513
TPTE2	ER	0.195	0.546	0.151	-0.701	0.003	1.545
ABCB9	lyso	0.276	0.222	0.194	-0.287	0.007	1.633
NUCKS1	nuc	0.250	0.442	0.143	-1.325	0.008	1.709
JUNB	nuc	0.004	0.764	0.055	-1.155	0.001	1.783
FAP	PM	0.013	1.166	0.812	-1.038	0.001	1.855
MMS22L	nuc	0.180	0.307	0.015	-1.753	0.002	1.923
RPL7A	cyto	0.428	0.927	0.004	-2.293	0.004	2.152
CCNC	nuc	0.006	1.945	0.576	-0.172	0.002	2.172
RAF1	mito	0.011	1.290	0.059	-1.414	0.002	3.005
SNW1	nuc	0.017	3.081	0.209	-0.269	0.003	3.204
RSRC2	nuc	0.017	0.661	0.019	-2.794	0.002	3.355
RPS5	cyto	0.271	1.632	0.034	-1.594	0.010	3.619

Table S3 – Immunopreciptation-mass spectrometry analysis of DDRGK1 interactors. Related to Fig 6.

Alternate ID	Molecular Weight	DDKO-1	DDKO-2	DDKO-3	DD-HA-1	DD-HA-2	DD-HA-3	DDKO/DD-HA*
UFL1	90 kDa	0	0	0	61	53	50	0
DDRGK1	36 kDa	0	0	0	50	42	41	0
MYBBP1A	149 kDa	2	0	0	17	15	17	0.666666667
IRS4	134 kDa	0	0	0	6	5	3	0
PABPC1	71 kDa	0	0	0	8	3	2	0
RPL7A	30 kDa	2	0	2	11	13	10	1.333333333
GNL2	84 kDa	0	0	0	6	4	2	0
LTV1	55 kDa	0	0	0	6	2	4	0
NAT10	116 kDa	0	0	0	5	5	2	0
EMD	29 kDa	2	0	0	6	8	6	0.666666667
DHX9	141 kDa	0	0	0	8	2	0	0
CHMP4B	25 kDa	0	0	0	3	4	3	0
RRP12	144 kDa	0	0	0	3	3	4	0
RPLP0	34 kDa	0	0	2	7	5	6	0.666666667
BANF1	10 kDa	0	0	0	3	3	3	0
RCN2	37 kDa	0	0	0	6	3	0	0
HSPA1A	70 kDa	0	2	0	7	5	4	0.666666667
NOP56	66 kDa	0	0	2	7	4	5	0.666666667
LYAR	44 kDa	0	0	0	3	2	3	0
RPL10A	25 kDa	2	2	2	9	9	9	2
RFC1	128 kDa	0	0	0	3	2	2	0
RRP1	53 kDa	0	0	0	3	2	2	0
FCF1	23 kDa	0	0	0	2	2	3	0
RPL15	24 kDa	2	0	2	7	7	6	1.333333333
TEX10	106 kDa	0	2	0	5	3	5	0.666666667
NOP58	60 kDa	0	0	2	5	4	3	0.666666667
RPL22L1	15 kDa	0	0	0	4	2	0	0
RPL30	13 kDa	0	0	0	2	2	2	0
AIMP1	34 kDa	0	0	0	2	2	2	0
CDC20	55 kDa	0	0	0	2	2	2	0
TUBG1	51 kDa	0	0	0	2	2	2	0
HNRNPF	46 kDa	3	0	2	7	7	6	1.666666667
KPNB1	97 kDa	2	0	2	7	2	7	1.333333333
HEATR3	75 kDa	0	0	0	3	0	2	0
KIFC1	74 kDa	0	0	0	3	0	2	0
BRIX1	41 kDa	0	0	0	5	0	0	0
USP10	87 kDa	0	0	0	2	0	3	0
MYH9	227 kDa	3	0	0	4	0	9	1
PNO1	28 kDa	0	0	2	3	2	5	0.666666667
HNRNPM	78 kDa	7	5	8	25	18	13	6.666666667
RPL8	28 kDa	4	0	2	8	6	6	2
NPM1	33 kDa	0	2	0	9	0	0	0.666666667
SREK1IP1	18 kDa	0	0	2	3	2	4	0.666666667

Table S4 – Immunoprecipitation-mass spectrometry analysis of DDRGK1-dependent UFMylation substrates. Related to Fig 6.

Alternate ID	Molecular Weight	HEK293T Neg Ctrl	UFSP2+DDRGK1 KO-Biorep1	UFSP2+DDRGK1 KO-Biorep2	UFSP2+DDRGK1 KO-Biorep3	UFSP2 KO-Biorep1	UFSP2 KO-Biorep2	UFSP2 KO-Biorep3	UFSP2 KO/ UFSP2+DDRGK1 KO*
ACLY	121 kDa	0	2	0	0	7	9	10	5.8
EPRS	171 kDa	0	0	0	0	6	2	5	5.333333333
ASNS	64 kDa	0	0	0	0	5	4	2	4.666666667
RACK1	35 kDa	0	0	0	2	4	3	4	2.8
RPN1	69 kDa	0	3	4	3	8	10	10	2.384615385
CLTC	192 kDa	4	5	8	7	17	17	16	2.304347826
GOT2	48 kDa	0	2	2	3	4	5	4	1.6
RPL26	17 kDa	2	9	9	9	14	14	13	1.466666667
GANAB	107 kDa	2	7	10	7	13	13	13	1.555555556
HNRNPU	91 kDa	4	6	7	5	11	10	13	1.761904762
FASN	273 kDa	11	18	16	14	24	21	25	1.431372549
UFM1	9 kDa	0	14	12	12	13	14	13	1.048780488
RPL7A	30 kDa	4	6	7	8	7	8	10	1.166666667
RPL10A	25 kDa	0	2	3	2	3	2	3	1.1
UFC1	19 kDa	0	4	5	5	4	3	4	0.823529412
STRAP	38 kDa	0	3	2	2	2	2	2	0.9
UBA5	45 kDa	0	9	8	10	8	9	8	0.933333333

* +1 inflation was performed for the average peptide count of both UFSP2+DDRGK1 KO and UFSP2 KO conditions before ratio count.

Table S5 – CRISPR cutting and CRISPRi sgRNA sequences used in this study. Related to STAR methods in the generation of cell lines with gene knockout or knockdown.

Construct	Protospacer	Source
AMPKα1-sgRNA1(RNP cutting guide)	GGCTGTCGCCATCTTTCTCC	This study
AMPKα1-sgRNA2 (RNP cutting guide)	GAAGATCGGCCACTACATTC	This study
AMPKα2-sgRNA1 (RNP cutting guide)	TCAGCCATCTTCGGCGCGCG	This study
AMPKα2-sgRNA2 (RNP cutting guide)	GAAGATCGGACACTACGTGC	This study
pX458-DDRGK1*sgRNA1	ATGAGATCCCGGCCTCAGGG	This study
pX458- UFL1-sgRNA1	TAGGAGATGCCGCTGCACCA	This study
pX458- UFL1-sgRNA2	CTGACTCGCAGTAGACGCGG	This study
pX458-UFSP2-sgRNA	GCCTAATT TGGGCTCCACAA	This study
pX458-pLG1-puro NT sgRNA	AATAAGAGGAGGCCTTGATT	Walczak et al. 2019
pLG1-puro NT sgRNA	GCGCCAAACGTGCCCTGACGG	Addgene #109002
pLG1-puro ULK1 sgRNA	GGCGGCGGCACAGAGACCGT	Addgene #109004
pLG1-puro ATG10 sgRNA	GAGGCCGCGGACCTGACTGA	Horlback et al. 2016
pLG1-puro VPS16 sgRNA	GAAAGGCAGAGTCCCCGAGT	Horlback et al. 2016
pLG1-puro EI24 sgRNA	GACGGGGCCGCTGGGAAGTC	Horlback et al. 2016
pLG1-puro NDUFB4 sgRNA	GGGCCTCCCAGGCGGGAATA	Horlback et al. 2016
pLG1-puro NDUFB2 sgRNA	GGGGGAAGCGAAGTAGGCAG	Horlback et al. 2016
pLG1-puro ATP5O sgRNA	GGTCCCCCGGGATGCCTACG	Horlback et al. 2016
pLG1-puro DDRGK1 sgRNA-1	GCCGCTACCAAGTACCACAC	Horlback et al. 2016
pLG1-puro DDRGK1 sgRNA-2	GGCGGCGCGACGGTCCACAA	Horlback et al. 2016
pLG1-puro DDRGK1 sgRNA-3	GTGCACTGAGGCCCTCGTCA	Horlback et al. 2016
pLG1-hygro DDRGK1 sgRNA-3	GTGCACTGAGGCCCTCGTCA	Horlback et al. 2016
pLG1-puro UFL1 sgRNA-1	GGCCTGACTCGCAGTAGACG	Horlback et al. 2016
pLG1-puro UFL1 sgRNA-2	GCGCCTGGGAAGAGATTAGG	Horlback et al. 2016
pLG1-puro UFM1 sgRNA-1	GAAGAGATGAAGACTGCGTG	Horlback et al. 2016
pLG1-puro UFM1 sgRNA-2	GGGAAGTCGTGCTACCCCCG	Horlback et al. 2016
pLG1-puro UBA5 sgRNA-1	GCGCTGGGTGCACGTCCCCA	Horlback et al. 2016
pLG1-puro IRE1a sgRNA-1	GGGCGGTGACCGAGCCTCAG	Horlback et al. 2016
pLG1-puro IRE1a sgRNA-2	GAGCGGACGCAGAACTGACT	Horlback et al. 2016
pLG1-puro FAM134B sgRNA-1	GGGACTGGAGAGAGAATGCG	Horlback et al. 2016
pLG1-puro FAM134B sgRNA-2	GAGGTGAAGTCATCCAATGA	Horlback et al. 2016
pLG1-puro FAM134B sgRNA-3	GTCCTAGCTTCATTCAAGGG	Horlback et al. 2016
pLG1-puro FAM134B sgRNA-4	GCTCCCAGTACTGTGACAGG	Horlback et al. 2016
pLG1-puro FAM134B sgRNA-5	GGCACGAACTCACTCAAGAG	Horlback et al. 2016
pLG1-puro CDK5RAP3 sgRNA-1	GGAGTCGAGATGCTGACCAC	Horlback et al. 2016
pLG1-puro CDK5RAP3 sgRNA-2	GGGAGGGAGACCGGAGACAC	Horlback et al. 2016
pLG1-puro Sox9 sgRNA-3	GGGAGTTGGAGAGCCGAAAG	Horlback et al. 2016
pLG1-puro Sox9 sgRNA-4	GGTCCGAGCCGGAGCCCGAC	Horlback et al. 2016
pLG1-puro ASC1 sgRNA-1	GTAGTCCGGTGCAGGACGTG	Horlback et al. 2016
pLG1-puro ASC1 sgRNA-2	GTGGTTCCGGCTGGGGAAGA	Horlback et al. 2016

Table S6 - qRT-PCR primers used in this study. Related STAR methods for the quantitative measurement of cDNA.

Target	**Primer 1**	**Primer 2**
EI24	AGTGTTGTGCTTGGAATGGTGG	GCCACGACCAAACATCTCCATG
VPS16	ACTCGGGGACTCTGCCTTTTAC	GGCAATCCCTGAGTTCCTCCTT
ULK1	GTCGCCGTCAAGTGCATTAACA	CGTACAGGGCCACGATGTTTTC
ATG10	GTGATAGTTGGGAATGGAGACC	GGTAGATGCTCCTAGATGTGAC
sXBP1	TGCTGAGTCCGCAGCAGGTG	GCTGGCAGGCTCTGGGGAAG
ACTB	GGGTCAGAAGGATTCCTATG	GGTCTCAAACATGATCTGGG
IRE1A	ACTTTGTCATCGGCCTTTGCAG	AGTGAGGCCGCATAGTCAAAGT
PERK	TGGTGTCATCCAGCCTTAGCAA	CATGCTTTCACGGTCTTGGTCC
DDRGK1	AAGGAGGAGGAGGAGAGGAAGG	CTCTGTCAGGAAGCTCTGGGAC
UFL1	TCGGTTGGCAGAAGAGGTCAAT	AAGTCGCTGAGTTAGTGCCTGT
FAM134B	CCAGATGAAAGACCCAGGCTCA	TGCACACACTACAGACCAGGAG
CDK5RAP3	TGCTGGAGGATCTGATTGGCAA	ACTCGGTCCACATACCTTGGTG
SOX9	GGCAAGCTCTGGAGACTTCTGA	GGCTGGTACTTGTAATCCGGGT
ASC1	CCCACAGAGGACGACTTTGGAT	CCCAGAAGACAACCTGACGGAT
BiP	TCTGTGCAGCAGGACATCAAGT	GTCTTTGTTTGCCCACCTCCAA
CANX	CACTGCTCCTCCTTCATCTCCC	TCCACCCTGACAGAGTTCCTCT
CLIMP63	CAGGACTTCTCCCGGCAGAG	TCCAAATGTGGCTTGCAAAGACT
REEP5	GTTCCTGCACGAGAAGAACTGC	AGAGGCTCCATAACCGAACACC