Table S2. Mutants defective in ER degradation

Gene	Description	ER degradation	Macroautophagy
APQ12	Protein required for nuclear envelope	-	-
ATG1	Protein serine/threonine kinase required for	-	-
ATG3	Component of Atg8 conjugation system	-	-
ATG4	Component of Atg8 conjugation system	-	-
ATG5	Component of Atg12 conjugation system	-	-
ATG7	Component of Atg8 and Atg12 conjugation	-	-
ATG8	Component of Atg8 conjugation system	-	-
ATG9	Transmembrane protein required for	-	-
ATG10	Component of Atg12 conjugation system	-	-
ATG11	Adapter protein for selective autophagy	-	+
ATG12	Component of Atg12 conjugation system	-	-
ATG13	Component of Atg1 kinase complex	-	-
ATG14	Component of PI3K complex	-	-
ATG15	Lipase required for autophagy	-	-
ATG17	Scaffold protein for macroautophagy	-	-
ATG18	Component of Atg2-Atg18 complex	-	-
ATG40	Receptor for ER-phagy	-	+
BCH2	Protein involved in Golgi to plasma membrane trafficking	-	+
BEM2	Protein involved in actin cytoskeleton	-	+
CCZ1	Protein involved in membrane tethering and fusion at the late endosome and vacuole	-	-
DID4/VPS2	Protein involved in late endosome to vacuole	-	-
DOA4	Ubiquitin hydrolase required for endocytosis	-	+
EFM4	Protein involved in vesicle-mediated	-	+
END3	EH domain-containing protein involved in endocytosis and actin cytoskeletal	-	+
FMC1	Mitochondrial matrix protein required for assembly of mitochondrial F1F0 ATP	-	+
FPK1	Protein kinase regulating phospholipid translocation	-	+
GIC2	Cdc42p effector involved in initiation of budding and cellular polarization	-	+
IPK1	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase	-	+
LNP1	Protein involved in ER network organization	-	+

LST1	Subunit of the COPII coat	-	+
MFA2	Mating pheromone a-factor	-	+
NAS2	Proteasome-interacting protein involved in the assembly of proteasomal regulatory	-	+
PEP4	Vacuolar aspartyl protease	-	-
PEX34	Peroxisomal integral membrane protein regulates peroxisome populations	-	+
PLC1	Phospholipase C	-	-
PPZ1	Serine/threonine protein phosphatase Z	-	-
RIM15	Protein kinase involved in cell proliferation in response to nutrients	-	-
SEC66	Component of the Sec62/Sec63 complex that is involved in the posttranslational translocation of proteins to the ER	-	+
SHP1	UBX (ubiquitin regulatory X) domain-containing protein	-	-
SLM4	Subunit of the EGO complex involved in signal transduction and microautophagy	-	-
SST2	GTPase-activating protein that regulates desensitization to alpha factor pheromone	-	-
STE20	Cdc42p-activated signal transducing kinase	-	-
SWS2	Putative mitochondrial ribosomal protein	-	+
TRS85	Component of transport protein particle (TRAPP) complex III	-	-
VAC7	Integral vacuolar membrane protein involved in vacuole inheritance and morphology	-	+
VAM10	Protein involved in vacuole morphogenesis	-	-
VAM3	SNARE protein that mediates docking/fusion of transport intermediates with the vacuole	-	-
VAM7	SNARE protein that mediates docking/fusion of transport intermediates with the vacuole	-	-
VID28	protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase	-	+
VPS4	AAA-ATPase involved in multivesicular body (MVB) protein sorting	-	-
VPS5	Component of retromer complex	-	-
VPS8	Component of the CORVET complex	-	-

VPS13	Endosomal protein that localizes to multiple contact sites	-	+
VPS16	Component of CORVET and HOPS	-	-
VPS30	Subunit of PI3-kinase complexes I and II	-	-
VPS34	Subunit of PI 3-kinase complexes I and II	-	-
VPS35	Component of retromer complex	-	-
VPS38	Subunit of PI 3-kinase complex II	-	+
YPT6	Rab family GTPase required for fusion of endosome-derived vesicles with the late	-	-
YPT7	Rab family GTPase required for endocytosis and vacuole fusion	-	-

Legend: ER degradation was assayed in Sec61-GFP and Rtn1-GFP expressing cells that were incubated in SC-Ura medium with 400 ng/ml rapamycin for 18 hr at 30^{o}C. Macroautophagy was assayed in GFP-Atg8 expressing cells incubated in SD-N media for 1 hr at 30^{o}C. Phenotypes are indicated with the following signs: +, not defective; -, defective. Note: although *atg2Δ*, *atg16Δ*, *atg29Δ* and *atg31Δ* were not identified as defective by fluorescence, we later found a defect in Sec61-GFP degradation in these mutants (see Fig. S1B).