

Supplementary Table 1

Table S1

Yeast strains used in this study

Strain	Genotype	Reference
BY4742	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15</i>	Open Biosystems
<i>vms1Δ::HIS3</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3</i>	This study
<i>vms1Δ::KanMX</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::KanMX</i>	Open Biosystems
<i>vms1Δ</i>	<i>MATα/A, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::KanMX, vms1Δ::HIS3</i>	This study
<i>ufd2Δ::KanMX</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ufd2Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ufd2Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ufd2Δ::KanMX</i>	This study
<i>ubx1 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx1Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx1Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx1Δ::KanMX</i>	This study
<i>ubx2 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx2Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx2Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx2Δ::KanMX</i>	This study
<i>ubx3 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx3Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx3Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx3Δ::KanMX</i>	This study
<i>ubx4 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx4Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx4Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx4Δ::KanMX</i>	This study
<i>ubx5 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx5Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx5Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx5Δ::KanMX</i>	This study
<i>ubx6 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx6Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx6Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx6Δ::KanMX</i>	This study
<i>ubx7 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, ubx7Δ::KanMX</i>	Open Biosystems
<i>vms1Δ ubx7Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, ubx7Δ::KanMX</i>	This study
<i>npl4 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, npl4Δ::KanMX</i>	Open Biosystems
<i>vms1Δ npl4 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, npl4Δ::KanMX</i>	This study
<i>cdc48-3</i>	<i>MATα, his3 Δ1, leu2, ura3, lys2 Δ0, MET15, cdc48-3</i>	This study
<i>vms1Δ cdc48-3</i>	<i>MATα, his3 Δ1, leu2, ura3, lys2 Δ0, MET15, cdc48-3, vms1Δ::KanMX</i>	This study
<i>pdr5 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, pdr5Δ::KanMX</i>	Open Biosystems
<i>vms1Δ pdr5 Δ</i>	<i>MATα, his3 Δ1, leu2 Δ0, ura3 Δ0, lys2 Δ0, MET15, vms1Δ::HIS3, pdr5Δ::KanMX</i>	This study

Supplementary Table 1. List of strains used in this study. All strains were in the BY4742 background.

Supplementary Table 2
Table S2

Oligos used in this study

Oligo	Sequence
<i>VMS1Δ::KanMX-F</i>	ggattttcaaagatctgcagcctggtgacaagctccaatagcatctgtgcggattttcacaccg
<i>VMS1Δ::KanMX-R</i>	gcaaatgctaagaaaaatcctaaaaattgaatatgagatattccagattgtactgagagtgac
<i>VMS1Δ::His3-F</i>	ggattttcaaagatctgcagcctggtgacaagctccaatagcatcggatccccgggtaattaa
<i>VMS1Δ::His3-R</i>	gcaaatgctaagaaaaatcctaaaaattgaatatgagatattccgaattcgagctcgtttaa
<i>VMS1</i> screen-F	ttcttgaggagtgccacag
<i>VMS1</i> screen-R	ggcgtcattttcgcggtgag
<i>ufd2 Δ::His3-F</i>	ccaatagaaggtaaagttgaccacaagttgtaaggggaaaagtaactttgaaagtagaacccctattccatagatccggatccccgggtaattaa
<i>ufd2 Δ::His3-R</i>	aaatataagacacattgagcgtgaaataagccttattgattagggcaattttgcaatttatctatcacttattcatgaattcgagctcgtttaa
<i>UFD2</i> screen-F	ccagttcgagaatctagtctg
<i>UFD2</i> screen-R	gaagcaaatcgctttccacaa
<i>UBX1</i> screen-F	gtagtgacaacatgcctctggat
<i>UBX1</i> screen-R	gcagcagttattcatgatgctggt
<i>UBX2</i> screen-F	tggctgaggattgccccaagctg
<i>UBX2</i> screen-R	actataaaggtagccccagctcc
<i>UBX3</i> screen-F	agaccgcctaattggatcatcg
<i>UBX3</i> screen-R	aaactgatgcacgtgacactt
<i>UBX4</i> screen-F	aagatagcgggagcctcaaccgct
<i>UBX4</i> screen-R	gtacaagttacggaaggcggagct
<i>UBX5</i> screen-F	ctcgtgctctctgcagaagcga
<i>UBX5</i> screen-R	caacagcggcagatgcatcgt
<i>UBX6</i> screen-F	ggatttacctctagcgtcaacc
<i>UBX6</i> screen-R	aaccaggatttgcacgagcca
<i>UBX7</i> screen-F	gtgctgccatatacagcaact
<i>UBX7</i> screen-R	gctgagttctttcgcggtgat
<i>CDC48 -NotI-F1</i>	ttgcggcccggtggccagccaagaaacgga
<i>CDC48 -XhoI-R1</i>	agctcggagacgaccgaggtcctacagcct
<i>CDC48 -Cterm-BamHI-R1</i>	acggatccactatacaaatcatcatcttcc
<i>CDC48 -Myc-BamHI-F1</i>	acggatccGAACAAAACTCATCTCAGAAGAGGATCTGtagtagttatatgccaggtatatttttaaatcg
<i>CDC48 -HA-BamHI-F1</i>	acggatccTACCCATACGACGTCCAGACTACGCTtagtagttatatgccaggtatatttttaaatcg
<i>VMS1 -NotI-F</i>	ctgcggccgcttcttgaggagtgccacag
<i>VMS1 -Sall-R</i>	tcggctcagcggcgtcattttcgcggtgag
<i>VMS1 -Cterm-BamHI-R1</i>	acggatccgattttctttcatcctttctctg
<i>VMS1 -Myc-BamHI-F1</i>	acggatccGAACAAAACTCATCTCAGAAGAGGATCTGtagtagggaatctcatattcaatttttag
<i>VMS1 -HA-BamHI-F1</i>	acggatccTACCCATACGACGTCCAGACTACGCTtagtagggaatctcatattcaatttttag

Supplementary Table 2. List of oligonucleotide primers used in this study. Restriction enzyme recognition sites are underlined and epitope tags are capitalized.

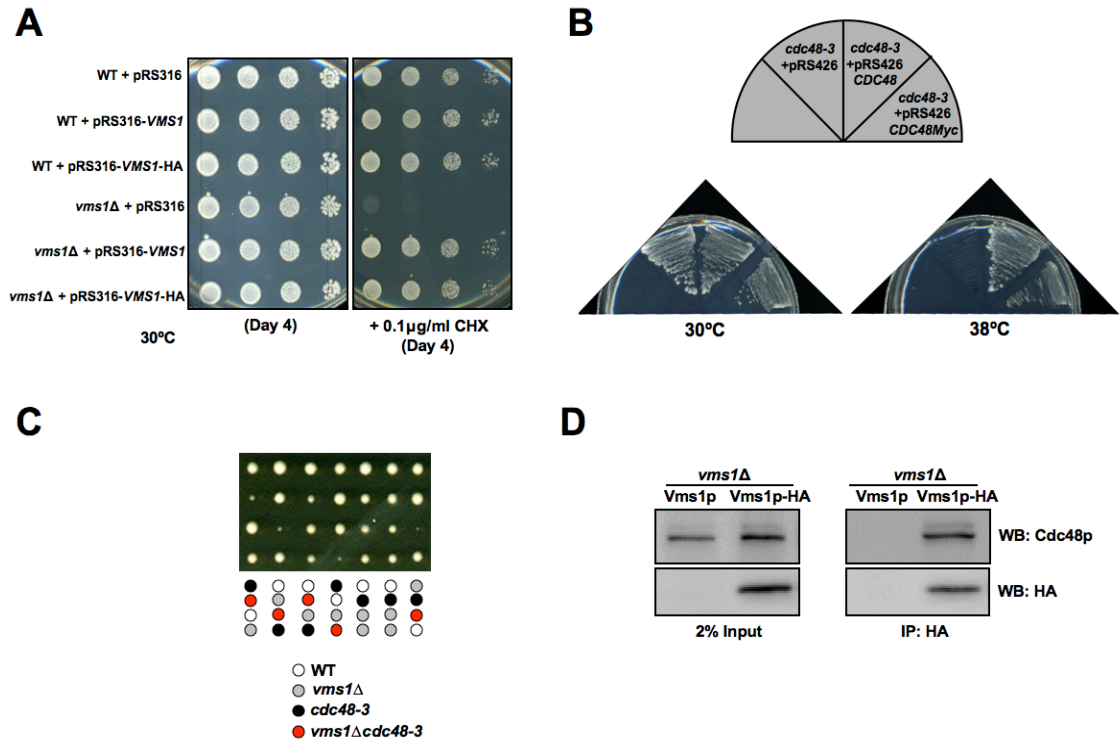
Supplementary Table 3

Table S3**Plasmids used in this study**

Plasmid name	Description	Reference
pSM1152	PGK1 promoter, CFTR-HA expression plasmid, 2 micron	Zhang, et al., 2002
pSM1911	PGK1 promoter, Ste6p*-HA expression plasmid, 2 micron	Huyer, et al., 2006
pUB23-Ub-Pro	GAL promoter, Ubiquitin-Proline β galactosidase, 2 micron	Bachmair, et al., 1986
CPY*-3xHA	Endogenous promoter, CPY* 3xHA expression plasmid, CEN	Bhamidipati, et al., 2005
pRS316- <i>CDC48</i>	Endogenous promoter, untagged <i>CDC48</i> , CEN	This study
pRS426- <i>CDC48</i>	Endogenous promoter, untagged <i>CDC48</i> , 2 micron	This study
pRS316- <i>CDC48Myc</i>	Endogenous promoter, C-terminal 1xmyc tagged <i>CDC48</i> , CEN	This study
pRS316- <i>CDC48HA</i>	Endogenous promoter, C-terminal 1xHA tagged <i>CDC48</i> , CEN	This study
pRS426- <i>CDC48Myc</i>	Endogenous promoter, C-terminal 1xmyc tagged <i>CDC48</i> , 2 micron	This study
pRS426- <i>VMS1</i>	Endogenous promoter, untagged <i>VMS1</i> , CEN	This study
pRS315- <i>VMS1HA</i>	Endogenous promoter, C-terminal 1xHA tagged <i>VMS1</i> , CEN	This study
pRS316- <i>VMS1HA</i>	Endogenous promoter, C-terminal 1xHA tagged <i>VMS1</i> , CEN	This study
pRS426- <i>VMS1HA</i>	Endogenous promoter, C-terminal 1xHA tagged <i>VMS1</i> , 2 micron	This study

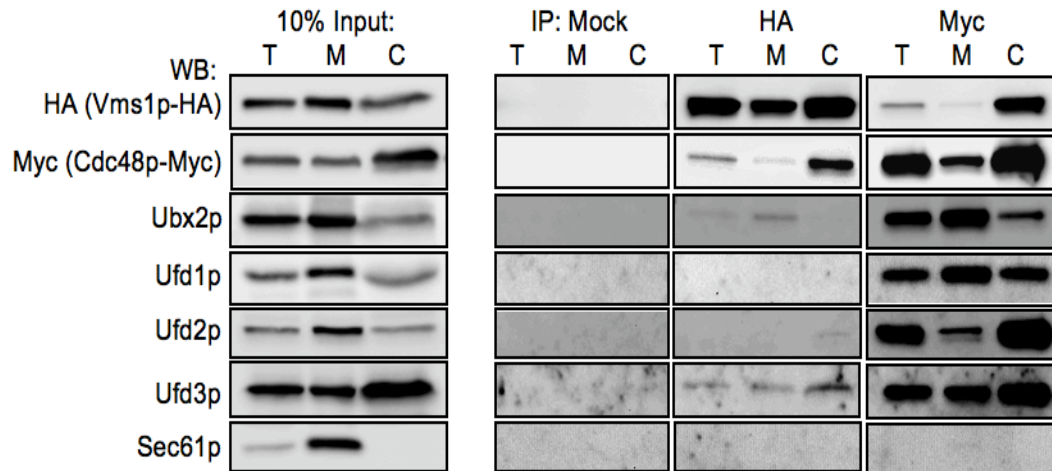
Supplementary Table 3. Plasmids used in the study. Unless referenced, all plasmids were constructed by PCR amplification and cloning as detailed in the Experimental Procedures section.

Supplementary Figure S1



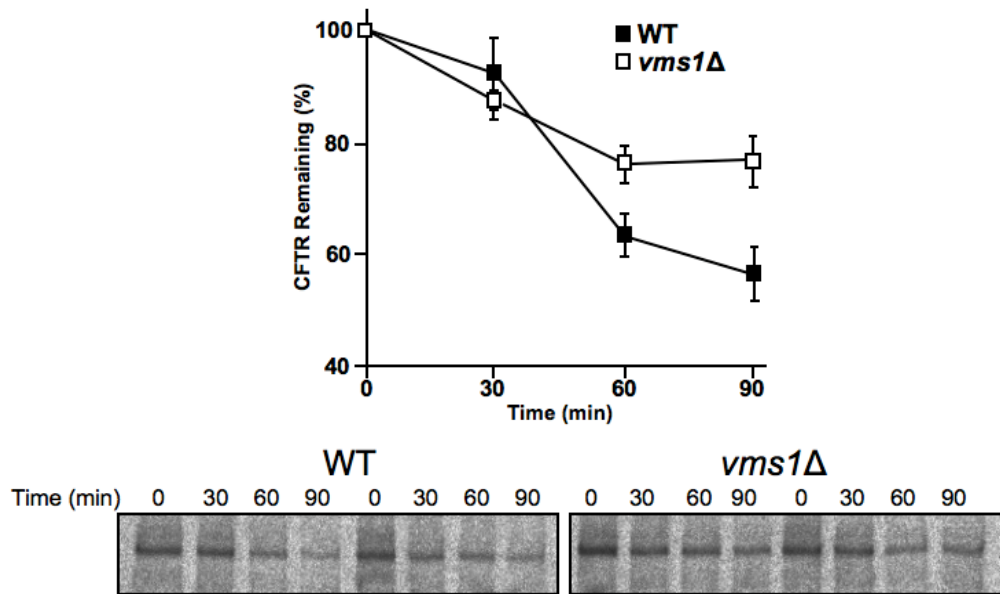
Supplementary Figure S1. *A*. An epitope-tagged form of Vms1p is functional. WT BY4742 and *vms1*Δ strains were transformed with an empty vector or a CEN plasmid containing either the untagged or HA-tagged form of Vms1p. Serial dilutions were spot plated on selective media lacking or containing 0.1 μg/ml cycloheximide. *B*. An epitope-tagged form of Cdc48p is functional. The indicated strains were transformed with an empty vector or untagged or Myc-tagged forms of Cdc48p. Serial dilutions of the transformants were spot plated on selective media and then incubated at 30°C or 38°C. *C*. *VMS1* genetically interacts with a mutant allele of *CDC48*. A temperature sensitive mutant allele of *CDC48*, *cdc48-3*, was genetically crossed with strains lacking the *VMS1* gene. Tetrads were sporulated, dissected, and grown at 30°C. *D*. Cdc48p coimmunoprecipitates with Vms1p from ER-enriched fractions. ER-membranes were prepared as described in the Experimental Procedures, solubilized and immunoprecipitated with anti-HA agarose. Immunoprecipitates were resolved by SDS-PAGE and immunoblotted for anti-HA and Anti-Cdc48p.

Supplementary Figure S2



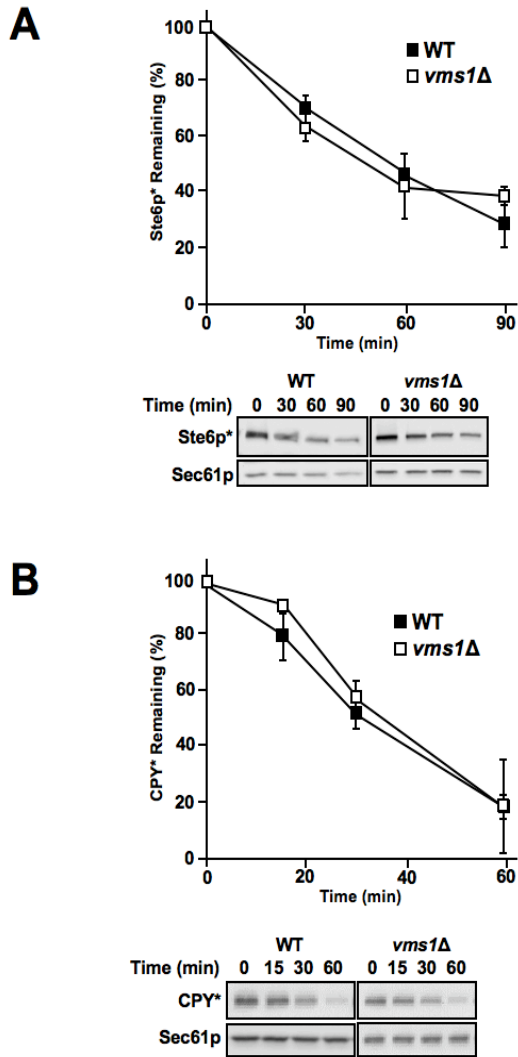
Supplementary Figure S2. Vms1p physically associates with other members of the Cdc48p complex. Total lysate (T), membrane (M), and cytosolic (C), fractions were prepared from cells expressing Vms1p-HA from a 2 μ plasmid the under control of its endogenous promoter. Vms1p-HA was immunoprecipitated with anti-HA agarose and Cdc48p-Myc was immunoprecipitated with anti-Myc agarose as described in the Experimental Procedures. Immunoprecipitated material was resolved by SDS-PAGE followed by immunoblot analysis with the indicated antibodies.

Supplementary Figure S3



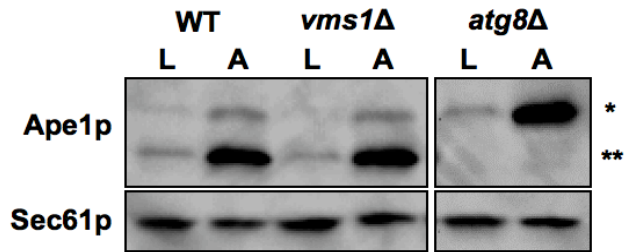
Supplementary Figure S3. Loss of *VMS1* affects the ERAD of CFTR as assessed by pulse-chase analysis. Wild type and *vms1Δ* cells expressing CFTR-HA were radio-labeled for 1 hour and chased with cold methionine and cysteine. The indicated time points were taken, the cells were lysed and CFTR-HA was immunoprecipitated with anti-HA agarose. The immunoprecipitate was resolved on a 10% SDS-polyacrylamide gel and subject to radiography. Data were quantitated relative to the zero time point. N = 10, +/- SEM. Wild-type (WT) cells are denoted by the filled squares and *vms1Δ* cells are represented by the unfilled squares.

Supplementary Figure S4



Supplementary Figure S4. Loss of *VMS1* has no effect on the degradation of two other model ERAD substrates, (A.) Ste6p* and (B.) CPY*, as assessed by cycloheximide chase. For both (A.) and (B.), wild-type is represented by filled squares and *vms1Δ* is represented by open squares.

Supplementary Figure S5



L: Log-phase

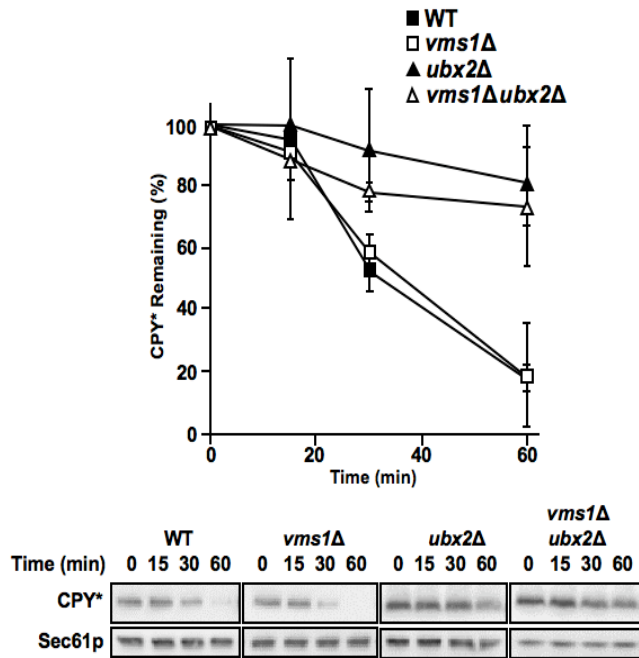
A: Nitrogen starvation/Autophagic induction

*** Unprocessed Ape1p**

**** Processed Ape1p**

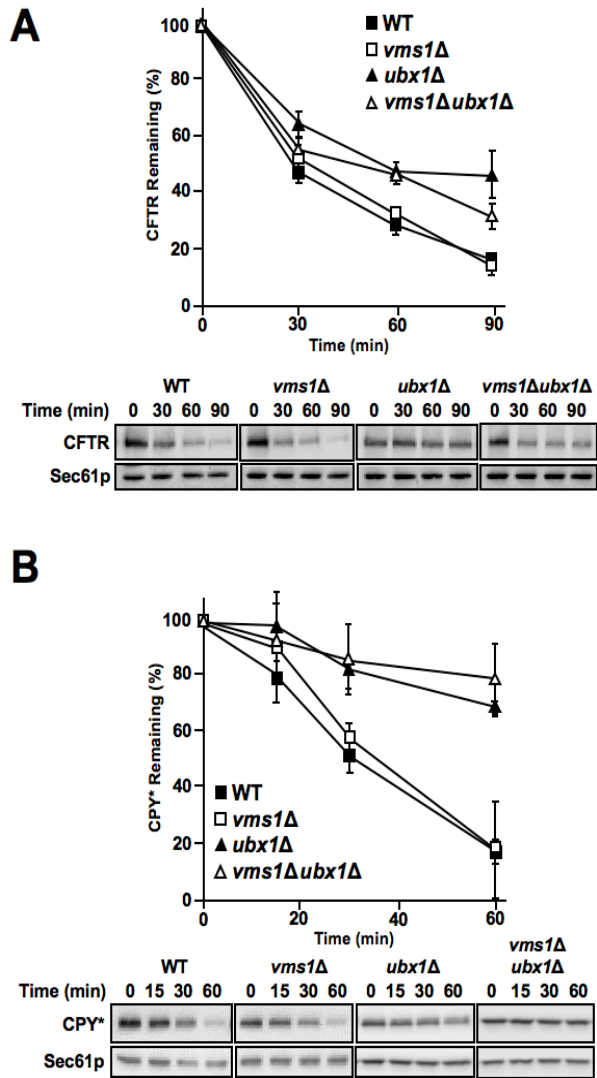
Supplementary Figure S5. Strains lacking *VMS1* do not exhibit a defect in the Cytoplasmic-to-Vacuole Transport (CVT) pathway. Wild-type (WT), *vms1Δ*, and *atg8Δ* cells were grown in rich medium or in nitrogen-poor medium. Total lysates were prepared, and equal amounts of lysate were separated by SDS-PAGE for immunoblotting with a marker of CVT activity, Ape1p. Sec61p was analyzed as a loading control.

Supplementary Figure S6



Supplementary Figure S6. The simultaneous loss of *UBX2* and *VMS1* does not result in a synthetic ERAD defect for CPY*. Wild-type is denoted by filled squares, *vms1Δ* by open squares, *ubx2Δ* by filled triangles, and *vms1Δubx2Δ* by open triangles.

Supplementary Figure S7

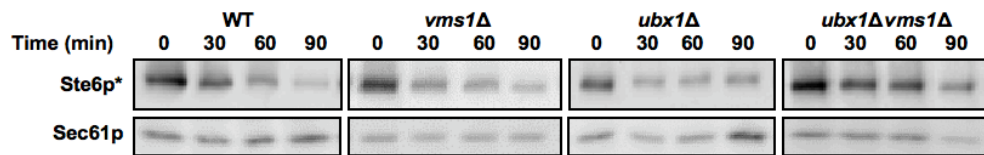


Supplementary Figure S7. The loss of *UBX1* results in an ERAD defect for CFTR and CPY*. For (A.) and (B.), wild-type is denoted by filled squares, *vms1*Δ by open squares, *ubx1*Δ by filled triangles, and *vms1*Δ*ubx1*Δ by open triangles.

Supplementary Figure S8

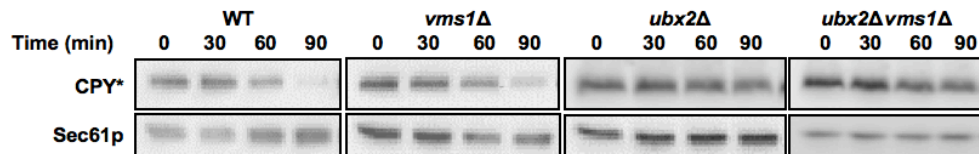
A

Strain	Ste6p*	
	Single	+ <i>vms1</i> Δ
<i>ubx1</i> Δ	-	+
<i>ubx2</i> Δ	-	-
<i>ubx3</i> Δ	-	-
<i>ubx4</i> Δ	-	-
<i>ubx5</i> Δ	-	-
<i>ubx6</i> Δ	-	-
<i>ubx7</i> Δ	-	-
<i>ufd2</i> Δ	+	+



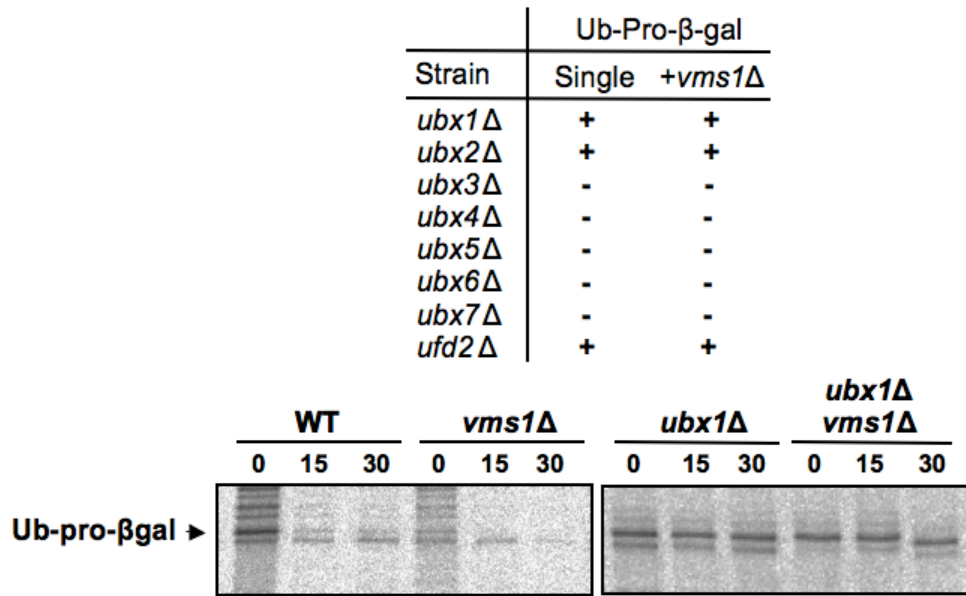
B

Strain	CPY*	
	Single	+ <i>vms1</i> Δ
<i>ubx1</i> Δ	+	+
<i>ubx2</i> Δ	+	+
<i>ubx3</i> Δ	-	-
<i>ubx4</i> Δ	-	+
<i>ubx5</i> Δ	-	-
<i>ubx6</i> Δ	-	-
<i>ubx7</i> Δ	-	-
<i>ufd2</i> Δ	-	-



Supplementary Figure S8. A summary of degradation assays for the ERAD substrates Ste6p* (*A*) and CPY* (*B*). Strains listed in the tables in (*A*) and (*B*) were transformed with a plasmid engineered to express Ste6p*-HA or the CPY*-HA, respectively. Cycloheximide chase analyses were performed and data were quantitated relative to the zero time point. Beneath each table are representative images from select experiments.

Supplementary Figure S9



Supplementary Figure S9. A summary of degradation assays for the N-end rule substrate, Ub-Pro- β -gal. A radio-labeling pulse cycloheximide chase was performed and data were quantitated relative to the zero time point. A representative image corresponding to a select experiment is shown.