Supplemental Materials Molecular Biology of the Cell

Kama et al.



CDC48 - peptide coverage

MGEEHKPLIDASGVDPREEDKTATATIRRKKK<u>dnmllvddainddn</u>SVIAINSNTMDKLELF R<u>gdtvlvk</u>GKKRK<u>dtvlivliddeledgac</u>RINRVWRNNLRIR<u>lgdlvtihpcpdi</u>KYATRI SVLFIADTIGTTCHLFDVFIKGYFVEAYRBVRKGDHFVVRGCMQVEFKVUDVEPEEYAVV AQDTIHHEGEPINREDEENNMEVGYDIGGCRKQMAQIREMVEIGHFVVRGCMQVEFKVUDVEPEEYAVV AQDTIHHEGEPINREDEENNMEVGYDIGGCRKQMAQIREMVEIGHFVURGCMRQVEFKVUDVEPEEYAVV AQDTIHHEGEPINREDEENNMEVGYDIGGCRKQMAQIREMVEIGHFVDIGFDAIRRFGR <u>gvlmygpgigktiMARAVANETGAFFFLINGPEVMSKMACSESSNIRKaf6eaeknapai</u> <u>ifideidsiapkRDKTNGEVERRvsglltlmdgmKARSNVVIAATNRPNSIDFAIRRFGR</u> <u>ekmdlidideeutaevurthrtNMKKIADDVDLEALAAFTHGYWGADIASLSEEAAMQQIE</u> <u>EELKetveypvlhpdqytk</u>FGLSPSKgvlfygppgtgtTLLAKavatevsanfisvKGPELL SMMYGESESNIRDIFDKAR<u>aaaptvvfldeldsiakARggslgdaggasdrvvnqlltemdg</u> <u>makKNVFVIGATNRBDQIDDAILRPGRLDQLIYVPLDEDEARR]sinagIrKtplegglel</u> <u>taiakatqffsgadllyivq</u>TAAXYAIKDSIEAHRQHEAEKEVK<u>vogedeventdega</u>KAEQE PEVDPVPYIKHFFAEAMKTAKR<u>svsdaelr</u>YEAYSQOMKASGGFSNFNFNDADLGTTAT DNANSNASSGCAAFGSNAEEDDDLYS

В.		26°C	33°C	35° (37°C
cdc48-3 cdc48-3+DDi cdc48-3+DDi cdc48-3+DDi cdc48-3+DDi cdc48-3+DDi cdc48-3+DDi cdc48-3+DDi cdc48-3+CDi	1 11-389 1D220A 178-428 14202-299 14323-390 C48-GFP				
cdc48-10 cdc48-10+DDI cdc48-10+DDI cdc48-10+DDI cdc48-10+DDI cdc48-10+DDI cdc48-10+DDI cdc48-10+DDI cdc48-10+CD	1 11-389 1D220A 178-428 15202-299 15323-390 C48-GFP	• • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • •	• •		
C. WT (303 ddi1∆ WT (cdc cdc48-10 ddi1∆ cd npI4∆ ddi1∆ np WT (ufd: ufd1-1 vps27∆	α) 48-10) 0 c48-10 i4Δ 1-1)	26°C		35°C	37'C 37'C
D.	GFP-CPS1	FM4-64	merge	light	%
WT	5 0	Q Q	() ()	H CO	97 (lumen)
wt	🧶 🏇	0 *	🥏 🗞		3 (lumen & memb)
ddi1∆	* 80	8°.	8°	H	69 (memb)
ddi1∆	ی ۲	0-00		H CO	31 (lumen & memb)
dsk2∆	۵.	Ör	0,	H S S S S S S S S S S S S S S S S S S S	64 (memb)
dsk2∆	é 🤗	Ő. Ø	()	H TH COO	36 (lumen & memb)
rad23∆		° 00.		H tum	92 (lumen)
rad23∆		00		H	8 (lumen & memb)

Figure S1. Ddi1 interacts physically with Cdc48. (A) Cdc48 coverage. The primary sequence of *S. cerevisiae* Cdc48 protein is presented. Underlined and lowercase amino acid designations

indicate peptide sequences identified by mass spectrometry in bands excised from SDS-PAGEresolved and Coomassie-labeled HA-Ddi1 and HA-Ddi1^{D220A} precipitates. (B). Over-expression of Ddi1 or Ddi1 truncation mutants do not ameliorate the growth defects of the cdc48-3 or cdc48-10 alleles. cdc48-3 and cdc48-10 cells were transformed with vector alone (pAD54) or pAD54-based plasmids expressing HA-tagged Ddi1 or Ddi1 truncation mutants (e.g. Ddi1¹⁻³⁸⁹, Ddi1^{D220A}, Ddi1⁷⁸⁻⁴²⁸, Ddi1^{Δ202-299}, and Ddi1^{Δ323-390}) or a single-copy plasmid expressing Cdc48-GFP. Cells were grown to mid-log phase on glucose-containing medium at 26°C before serial dilution (10-fold each) and plating by drops onto pre-warmed solid medium. Plates were grown for 2 to 3 days at the indicated temperatures before photo-documentation. (C) The deletion of **DDI1** has no effect upon the growth of *cdc48* and *npl4* mutants. WT control cells (e.g. W303 and the background strains for the cdc48-10 and ufd1-1 mutations), $ddi1\Delta$, cdc48-10, $ddi1\Delta$ cdc48-10, $npl4\Delta$, $ddi1\Delta$ $npl4\Delta$, ufd1-1, and $vps27\Delta$ cells were grown to mid-log phase on glucose-containing medium at 26°C before serial dilution (10-fold each) and plating by drops onto pre-warmed solid medium. Plates were grown for 2-3 days at the indicated temperatures before photo-documentation. (D) Cps1 trafficking to the vacuole lumen is inhibited in cells lacking DDI1 or DSK2, but not RAD23. WT (W303 background) control cells and cells lacking DDII, DSK2, or RAD23 (i.e. $ddi1\Delta$; $dsk2\Delta$ rad23 Δ cells; W303 background) were transformed with a plasmid expressing GFP-Cps1. Cells were grown to mid-log at 26°C, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. Light indicates the DIC window. % indicates the percentage of cells having GFP-Cps1 localized to the vacuolar limiting membrane (memb), vacuolar lumen (lumen), or both (lumen & memb). Statistics are presented in Table 1. Size bar = $1\mu m$.



Figure S2. Trafficking of Fur4 and Ste2 to the vacuole is unaffected in cells bearing mutations in *CDC48* or the yeast ubiquilins. (A) Localization of Fur4-GFP to the plasma membrane and vacuole is not affected in cells bearing the *cdc48-10* allele or in *ddi1* Δ cells and cells lacking all three ubiquilins. WT control (W303) and *cdc48-10*, *vps27* Δ , *ddi1* Δ , and *ddi1* Δ *rad23* Δ *dsk2* Δ cells were transformed with a single-copy plasmid expressing Fur4-GFP. Cells were grown to mid-log phase on glucose-containing medium at 26°C at, pulse-chase labeled with FM4-64, and examined by confocal microscopy. White arrows indicate the position of the class E compartment wherein GFP-Fur4 and FM4-64 accumulate in *vps27* Δ cells (a class E *vps* mutant). *Merge* indicates merger of the GFP and FM4-64 windows. *Light* indicates the DIC window. Size bar = 1µm. Additional WT control cells of the *cdc48-10*, *vps27* Δ , and *ddi1* Δ backgrounds (*e.g.* KFY100 and BY4741, respectively) were examined, but gave identical results to that shown for the WT cells in the figure (data not shown). (B) The intracellular localization of Ste2-GFP was not affected in *cdc48-10*, *vps27* Δ , *ddi1* Δ , and *ddi1* Δ *rad23* Δ *dsk2* Δ cells

were transformed with a single-copy plasmid expressing Ste2-GFP. Cells were grown to mid-log phase on glucose-containing medium at 26°C at, pulse-chase labeled with FM4-64, and examined by confocal microscopy. White arrows indicate the position of the class E compartment wherein Ste2-GFP and FM4-64 accumulate in $vps27\Delta$ cells (a class E vps mutant). *Merge* indicates merger of the GFP and FM4-64 windows. *Light* indicates the DIC window. Size bar = 1µm. Additional WT control cells of the *cdc48-10*, $vps27\Delta$, and *ddi1* Δ backgrounds (*e.g.* KFY100 and BY4741, respectively,) were examined, but gave identical results to that shown for the WT cells in the figure (data not shown).



Figure S3. Individual mutations in DD11, DSK2, RAD23, CDC48, NPL4, and UFD1 do not affect CPY secretion, but combined $ddi1\Delta$ $dsk2\Delta$ $rad23\Delta$ and $ddi1\Delta$ cdc48-10 mutations show a partial secretion effect. (A) Localization of GFP-Yif1 in WT, cdc48-3, cdc48-10, $npl4\Delta$, npl4-1, npl4-2, and ufd1-1 cells. WT control (e.g. BY4741 and W303 backgrounds and background strains for the cdc48-3, cdc48-10 and ufd1-1 mutations), cdc48-3, cdc48-10, $npl4\Delta$, npl4-1, npl4-2, and ufd1-1 cells were transformed with a single-copy plasmid expressing GFP-Yif1. Cells were grown to mid-log phase cells on glucose containing medium at 26°C, pulsechase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. Light indicates the DIC window. Size bar = 1 μ m. (B) Localization of GFP-Yif1, GFP-CPY, and Vps10-GFP in WT and $ddi1\Delta$ cells. WT control (W303), and $ddi1\Delta$ cells were transformed with a single-copy plasmid expressing GFP-Yif1, Cells were grown to mid-log phase on glucose-containing medium at 26°C, pulsechase labeled with FM4-64 windows. Light indicates the DIC window. Size bar = 1 μ m. (B) Localization of GFP-Yif1, GFP-CPY, and Vps10-GFP in WT and $ddi1\Delta$ cells. WT control (W303), and $ddi1\Delta$ cells were transformed with a single-copy plasmid expressing GFP-Yif1, Cells were grown to mid-log phase on glucose-containing medium at 26°C, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. Light indicates the DIC window. Size bar = 1 μ m. (C) Localization of GFP-CPY in WT and ddi1 Δ cells. WT control (W303), and ddi1 Δ cells were transformed with a

single-copy plasmid expressing CPY¹⁻⁵⁰GFP. Cells were grown to mid-log phase on glucosecontaining medium at 26°C, shifted to galactose-containing medium for 12h at 26°C to induce expression, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. *Light* indicates the DIC window. Size bar = 1µm. (D) Localization of Vps10-GFP in wild-type and *ddi1A* cells. WT control (W303), and $ddil\Delta$ cells were transformed with a single-copy plasmid expressing Vps10-GFP. Cells were grown to mid-log phase cells on glucose containing medium at 26°C, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. *Light* indicates the DIC window. Size bar = $1\mu m$. (E) Combined deletions in the ubiquilin paralogs leads to CPY secretion. WT yeast (BY4741) and various deletion mutants (e.g. $ddi1\Delta$, $rad23\Delta$, $ddi1\Delta$ $rad23\Delta$, $dsk2\Delta$, $ddi1\Delta$ $rad23\Delta$ $dsk2\Delta$, and $vps23\Delta$ cells) were patched out and grown on solid medium, replica plated onto nitrocellulose filters and subjected to anti-CPY immunoblot assay, as detailed in below in the detailed in the Materials and Methods. (F) Combined *ddi1* and *cdc48-10* mutations lead to a CPY secretion phenotype. WT control (e.g. W303 and the backgrounds for the cdc48-3, cdc48-10, npl4, and ufd1-1 cells), ddi1/4, cdc48-3, cdc48-10, cdc48-10 $ddi1\Delta$, npl4-1, npl4-2, ufd1-1, $npl4\Delta$, $npl4\Delta$ $ddi1\Delta$, and $vps27\Delta$ cells were grown on glucose-containing medium at 26°C before serial dilution (10-fold each) and plating by drops onto pre-warmed solid medium. Plates were grown for 2-3 days, replica plated onto nitrocellulose filters, and subjected to anti-CPY immunoblot assay, as detailed in the Materials and Methods.



Figure S4. Ddi1 and Rad23 co-label the perivacuolar class E compartment in MVB mutants and Ddi1 labels a perivacuolar compartment in cells bearing mutations in *CDC48*, *NPL4*, and *UFD1*. (A) GFP-Ddi1-labeled puncta in *vps23* Δ cells are non-nuclear. *vps23* Δ cells carrying the genome-integrated copy of *GFP-DD11* under the control of a *GAL* promoter

(GGY13 cells) were grown to mid-log phase on galactose-containing medium and labeled with Hoechst dye (2µg/ml) for 10min prior to visualization by confocal microscopy. Merge indicates merger of the GFP and Hoechst windows. *Light* indicates the DIC window. Size bar = $1\mu m$. (B) GFP-Rad23 and RFP-Ddi1 co-localize in wild-type cells and class E/MVB mutants. Class E mutant cells (e.g. $vps4\Delta$, $vps27\Delta$, $vps23\Delta$, $vps37\Delta$, $vps36\Delta$, $vps25\Delta$, and $vps20\Delta$ cells) were transformed with a multi-copy plasmids expressing GFP-Rad23 and RFP-Ddi1. Cells were grown to mid-log phase cells on glucose-containing medium at 26°C, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and RFP windows. Light indicates the DIC window. Size bar = $1\mu m$. (C) In addition to nuclear and cytoplasmic labeling, Ddi1 localizes to a perivacuolar compartment in cells bearing mutations in CDC48, NPL4, and UFD1. WT control (e.g. BY4741 and the backgrounds for the cdc48-3, cdc48-10, and ufd1-1 strains), cdc48-3, cdc48-10, $npl4\Delta$, and ufd1-1 cells were transformed with a multi-copy plasmid expressing GFP-Ddi1 Mid-log phase cells grown on glucose containing medium at 26°C, pulse-chase labeled with FM4-64, and examined by confocal microscopy. Merge indicates merger of the GFP and FM4-64 windows. Light indicates the DIC window. Size bar = 1 μ m. Only the WT background for *cdc48-10* cells (KFY100) is shown; similar results were obtained with the other backgrounds (data not shown).



Figure S5. Endogenous Ddi1 binds endogenous Cdc48, while its binding to Npl4 is reduced upon the attenuation of Cdc48 function. A. Endogenous Ddi1 and Cdc48 co-precipitate. WT control and $ddil\Delta$ cells were grown to mid-log phase on glucose-containing YPD medium at 26°C and processed for immunoprecipitation using anti-Ddi1 antibodies, as described in the Materials and Methods. Native endogenously-expressed Cdc48 was detected using polyclonal anti-Cdc48 antibodies (1:500) and native endogenously-expressed Ddi1 was detected using polyclonal anti-Ddi1 antibodies (1:3000). B. Ddi1 binding to Npl4 is reduced upon the attenuation of Cdc48 function. WT control (cdc48-10 background) and cdc48-10 cells were transformed with a multi-copy plasmid expressing HA-Npl4. Cells were grown to mid-log phase cells on glucose-containing synthetic medium at 26°C and either maintained at 26°C or shifted to 37°C for 1hr. Cells were processed for immunoprecipitation using anti-Ddi1 antibodies, as described in the Materials and Methods. Npl4 was detected using monoclonal anti-HA antibodies (1:1000) and native Ddi1 was detected using polyclonal anti-Ddi1 antibodies (1:3000). In this representative experiment, the level of Npl4 bound to Ddi1 declined by 56% in cdc48-10 cells after the temperature shift, while it was unchanged (after normalization for precipitated Ddi1 levels) in the WT background.



Figure S6. Soluble Cps1 declines while insoluble Cps1 increases in cdc48-10, ddi14, cdc48-10 ddi1 Δ , and ddi1 Δ dsk1 Δ rad23 Δ cells. (A) The fraction of detergent-soluble myc-Cps1, but not myc-Pil1, decreases in cdc48-10 ddi14 cells after CHX treatment. Yeast expressing endogenous myc-Cps1 or myc-Pil1 from their genomic loci in WT and cdc48-10 ddi14 cells were subjected to a cycloheximide (CHX)-chase degradation/sedimentation assay to resolve the amount of TX-100 detergent-soluble Cps1 or Pil1 in the pellet fraction, as described under Materials and Methods. Samples of were removed after 0, 15, and 30min of CHX treatment before processing to determine the relative amounts of myc-Cps1 in the total, pellet, and supernatant (see Figure 5A and B for total and pellet) fractions using anti-myc antibodies. The amount of soluble and insoluble Cps1 after 1hr was normalized to the loading control, after which the percentage was calculated relative to the amount at 0hrs. A representative experiment is shown whereby myc-Cps1 levels in the detergent-soluble fraction (*i.e.* supernatant) decline substantially over time, whereas as myc-Pil1 levels remain relatively steady. kDa = kilodaltons (B) The fraction of NP40-insoluble Cps1 increases in cdc48-10 and cdc48-10 ddi11 cells. WT control cells (cdc48-10 background), cdc48-10, and cdc48-10 $ddi1\Delta$ cells transformed with a subjected plasmid expressing HA-Cps1 were to the cycloheximide-chase degradation/sedimentation assay shown in A to resolve the amount of NP-40 detergent-insoluble and -soluble Cps1, as described under Materials and Methods. Samples of the total cell lysate

(TCL: Total), insoluble pellet (Pellet), and soluble (i.e. supernatant; Sup) fraction were resolved by SDS-PAGE and detected in Westerns with anti-HA (1:1000) abs. TCL samples were also probed with anti-Snf7 abs (1:2000) as a loading control (Snf7 is not degraded upon CHX treatment, unlike actin). The amount of soluble and insoluble Cps1 after 1hr was normalized to the loading control, after which the percentage was calculated relative to the amount at 0hrs. A representative experiment is shown, whereby the level of insoluble Cps1 increased by 71% and 76% over that of WT cells in the cdc48-10 and cdc48-10 $ddi1\Delta$ pellet fractions after 1hr. respectively. A histogram showing average±standard deviation of 4 experiments is shown beneath. (C) The fraction of NP-40 detergent-soluble Cps1 decreases in $ddi1\Delta$ and $ddi1\Delta$ $dsk2\Delta$ rad23 Δ cells. WT control cells (W303), $ddi1\Delta$, and $ddi1\Delta$ $dsk2\Delta$ rad23 Δ cells expressing HA-Cps1 were subjected to the same procedure as in A and the percentage of soluble Cps1 in the supernatant fraction after 1hr was calculated after the normalization for gel loading and expression (see Figure 5C for results with total and pellet fractions). A representative experiment is shown. (D) The detergent-insoluble Cps1 fraction decreases in vps27/ cells. WT control cells and $vps27\Delta$ cells transformed with a plasmid expressing HA-Cps1 were subjected to the cycloheximide-chase degradation/sedimentation assay described in A to resolve the amount of NP-40 detergent-insoluble and -soluble Cps1. Samples of the total cell lysate (TCL; Total), insoluble pellet (Pellet), and soluble (i.e. supernatant; Sup) fractions were resolved by SDS-PAGE and detected in Westerns with anti-HA (1:1000) abs. TCL samples were also probed with anti-Snf7 abs (1:2000) as a loading control. The amount of insoluble Cps1 in the pellet was calculated relative to the amount at Ohrs, as described above. A representative experiment is shown.



Figure S7. Ubiquitin over-expression does not rescue Cps1 mistrafficking in $ddi1\Delta$, cdc48-10, and cdc48-10 $ddi1\Delta$ cells. WT control (e.g. W303 and the backgrounds for the cdc48-10, strains), $ddi1\Delta$, cdc48-10, and cdc48-10 $ddi1\Delta$ cells were transformed with multicopy plasmids expressing GFP-Cps1 and ubiquitin (Ub; *UBL4*). Cells grown to mid-log phase on glucose containing medium at 26°C were examined by confocal microscopy. *Merge* indicates merger of the GFP and light windows. *Light* indicates the DIC window. Size bar = 1µm. Only one WT cell background (e.g. W303) is shown, the others were identical with respect to Cps1 localization.

Table S1. Yeast strains used in this study

Name	Genotype	Source
W303-1b	MATa can1-100 his3-2,15 leu2-3,112 lys2-1 trp1-1 ura3-1 ade2-1	J. Gerst
BY4741	$MATa\ his 3\Delta I\ leu 2\Delta 0\ met 15\Delta 0\ ura 3\Delta 0$	Euroscarf
yPC1507 (<i>cdc48-3</i> WT background)	MATa ura3-52 his3 Δ 200 leu2 Δ 1 trp1 Δ 63	P. Carvalho
yPC1614 (<i>cdc48-3</i>)	$MATa\ ura3-52\ his3\Delta200\ leu2\Delta1\ trp1\Delta63\ cdc48-3^{ts}$	P. Carvalho
RK8 (<i>cdc48-3 ddi1</i> ∆)	MATa ura3-52 his3 Δ 200 leu2 Δ 1 trp1 Δ 63 cdc48-3 ^{ts} ddi1 Δ ::NAT1	This study
KFY100 (<i>cdc48-10</i> WT background)	MATa his4-619 leu2-3,112 ura3-52	S. Bar-Nun
KFY194 (cdc48-10)	MATa his4-619 leu2-3,112 ura3-52 cdc48-10 ^{ts}	S. Bar-Nun
SBN 100 (<i>cdc48-10</i> WT background)	MATa his4-619 leu2-3,112 ura3-52 trp1::LEU2	S. Bar-Nun
SBN194 (cdc48-10)	MATa his4-619 leu2-3,112 ura3-52 cdc48-10 ^{ts} trp1::LEU2	S. Bar-Nun
RK10 (<i>cdc48-10 ddi1</i> ∆)	MATa his4-619 leu2-3,112 ura3-52 cdc48-10 ^{ts} ddi1∆::NAT1	This study
$cps1\Delta$	MATa his3Δ1 leu2Δ met15Δ0 ura3Δ0 cps1Δ::kan MX	Euroscarf
VL2 (<i>ddi1∆</i> ; W303-1a background)	MATa his3-11,15 leu2-3,112 trp1-1 ade2-1 ddi1∆::URA3	J. Gerst
<i>ddi1</i> ∆ (W303-1b background)	MATα can1-100 his3-11,15 leu2-3,112 lys2-1 trp1-1 ura3-1 ade2-1 ddi1Δ::NAT1	This study
<i>ddi1∆</i> (BY4741 background)	MATa his3Δ1 leu2Δ met15Δ0 ura3Δ0 ddi1Δ::kanMX	Euroscarf
GGY21 (<i>ddi1∆ rad23∆</i>)	MATa his3Δ1 leu2Δ met15Δ0 ura3Δ0 rad23Δ::kanMX ddi1Δ::URA3	This study
$GGY22 (ddi1\Delta rad23\Delta \\ dsk2\Delta)$	$MATa\ leu\Delta 0\ met15\Delta 0\ rad23\Delta$::HIS3 ddi1 Δ ::URA3 dsk2 Δ ::kanMX	This study
$GGY10 (ddil\Delta vps23\Delta)$	$MATa\ his3\Delta 1\ leu2\Delta\ met15\Delta 0\ ura3\Delta 0\ vps23\Delta::kanMX$ $ddi1\Lambda::URA3$	This study
GGY13 (GAL-GFP-DD11 vps234)	$MATa leu\Delta 0 met15\Delta 0 ura3\Delta 0 GAL1-GFP-DD11::HIS3 vps23A::kanMX$	This study
doal	$MATa\ his3\Delta I\ leu2\Delta\ met15\Delta 0\ ura3\Delta 0\ doa1\Delta::kanMX$	Euroscarf
RK11 <i>dsk2</i> Δ (W303-1b background)	MATα can1-100 his3-11,15 leu2-3,112 lys2-1 trp1-1 ura3-1 ade2-1 dsk2Δ::NAT1	This study
YYH46 (<i>NPL4</i>)	<i>MATa ura3-52 leu2Δl trp1$\Delta 63$</i> (originally PSY580)	P. Carvalho
YYH1 (<i>npl4-1</i>)	<i>MAT</i> a <i>ura3-52 leu2</i> Δ <i>1 trp1</i> Δ <i>63 np14-1</i> ^{ts} (originally PSY2340)	P. Carvalho
YYH2 (npl4-2)	<i>MATa ura3-52 leu2D1 trp1Δ63 npl4-2^{ts}</i> (originally PSY2341)	P. Carvalho
$npl4\Delta$	MATa his3Δl leu2Δ met15Δ0 ura3Δ0 npl4 Δ ::kanMX	Euroscarf
RK9 ($npl4\Delta ddil\Delta$)	$MATa\ his3\Delta 1\ leu2\Delta\ met15\Delta 0\ ura3\Delta 0\ npl4\Delta::kanMX$ $ddi1\Delta::NAT1$	This study
JBY120 (SNF7-RFP)	MAT his $3\Delta 1$ leu $2\Delta 0$ lys $2\Delta 0$ ura $3\Delta 0$ SNF7-RFP:: KanMX4	W. Huh
RK12 <i>rad23∆</i> (W303-1b background)	MATα can1-100 his3-11,15 leu2-3,112 lys2-1 trp1-1 ura3-1 ade2-1 rad23∆::NAT1	This study
TCY6210 WT	MATα leu2-3, 112 ura3-52 his3-Δ200 trp1-Δ901 lys2-801 suc2Δ9	S. Emr
SSY22 (<i>rsp5^{ts}</i>)	МАТа leu2-3, 112 ura3-52 his3-Δ200 trp1-Δ901 ade2-101 suc2-Δ9 rsp5-326	S. Emr
YYH3 (UFD1)	<i>MATa his4-519 ura3-52 ade1-100 leu2-3,112</i> (originally BWG1-7a)	P. Carvalho
YYH4 (<i>ufd1-1</i>)	MATa ufd1-1 (derivative of BWG1-7a; originally PM373)	P. Carvalho
$vps4\Delta$	$MATa\ his 3\Delta I\ leu 2\Delta\ met 15\Delta 0\ ura 3\Delta 0\ vps 23\Delta$::kan MX	Euroscarf
$vps23\Delta$	$MATa\ his 3\Delta I\ leu 2\Delta\ met 15\Delta 0\ ura 3\Delta 0\ vps 4\Delta::kanMX$	Euroscarf
vps27Δ	$MATa\ his 3\Delta I\ leu 2\Delta\ met 15\Delta 0\ ura 3\Delta 0\ vps 27\Delta$::kan MX	Euroscarf
vps37 Δ	$MATa\ his3\Delta 1\ leu2\Delta\ met15\Delta 0\ ura3\Delta 0\ vps37\Delta$::kan MX	Euroscarf

RK12 [myc(x9)-Cps1]	MATα can1-100 his3-2,15 leu2-3,112 lys2-1 trp1-1 ura3-1 ade2-1 CPS1::myc(x9)-CPS1	This study
RK13 [<i>cdc48-10 ddi1</i> ∆	MATa his4-519 leu2-3,112 ura3-52 cdc48-10 ^{ts} ddi1∆∷NAT1	This Study
myc(x9)-Cps1]	CPS1::myc(x9)-CPS1	
RK14 [<i>cdc48-10 ddi1</i> ∆	MATa his4-519 leu2-3,112 ura3-52 cdc48-10 ^{ts} ddi1∆::NAT1	This Study
myc(x9)-Pil]	PIL1::myc(x9)-PIL1	

Table S2. Plasmids used in this study

Plasmid name	Gene expressed	Vector	Sites of	Сору	Selectable	Source
nAD54	HA		cioning	2µ	marкer LEU2	J Gerst
pADH-HA-GFP	HA-GFP	nAD54	Sall/SacI	2//	LEU2	I Gerst
pADH-HA-DDI1	HA-DDII	nAD54	Sall/Sacl	2µ 2µ	LEU2	J. Gerst
pADH-DDI1 ¹⁻¹⁶³	$H4-DD11^{1-163}$	nAD54	Sall/Sacl	2µ 2µ		J. Gerst
pADH-DDI1 ¹⁻³²⁶	$H_{4-}DDH^{1-326}$	p/1051	Sall/Sacl	2µ 2µ		J. Gerst
pADH DDI1 ¹⁻³⁸⁹	$H_{4} DDH^{1-389}$	pAD54	Sall/Sacl	2µ 2µ		J. Gerst
pADH DDI1 ^{D220A}	$HA DDU^{D220A}$	pAD54	Sall/Sacl	2μ 2μ		J. Gerst
pADH DD11 ⁷⁸⁻⁴²⁸	$HA DDH^{78-428}$	pAD54	Sull/Sucl	2μ 2		J. Gerst
r A DLL DD11 ⁴²⁰²⁻²⁹⁹	11A-DD11	pAD54	Sull/Sucl	2μ 2		J. Gerst
pADH- DDH /323-344	$HA-DD11^{2202-296}$	pAD34		2μ 2		J. Gerst
pADH- DDI1 ⁷⁸⁻³²⁶	$HA-DDH^{78-326}$	pAD54	Sall/Sacl	2μ 2	LEU2	J. Gerst
pADH-DD11 A D11 - DD11 - 4323-390	HA-DDI1	pAD54		2μ	LEU2	J. Gerst
pADH- DDII	HA-DDII	pAD54	Sall/Sacl	2μ	LEU2	J. Gerst
pADH-GFP- DDI1	HA-GFP-DDII	pAD54	Sall/Sacl	2μ	LEU2	J. Gerst
pADH- GFP-DDI1 ^{14/3}	HA-GFP-DDI1 ¹⁻⁷⁵	pAD54	Sall/Sacl	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ¹⁻¹⁰⁵	HA-GFP-DDI1 ¹⁻¹⁰⁵	pAD54	Sall/Sacl	2μ	LEU2	J. Gerst
pADH-GFP-DDI1	HA-GFP-DDI1 ¹⁻³²⁰	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ¹⁻³⁸⁹	HA-GFP-DDI1 ¹⁻³⁸⁹	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ^{D220A}	HA-GFP-DDI1 ^{D220A}	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ⁷⁸⁻⁴²⁸	HA-GFP-DDI1 ⁷⁸⁻⁴²⁸	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ⁴²⁰²⁻²⁹⁹	HA -GFP-DDI1 ^{$\Delta 202-298$}	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ⁴³²³⁻³⁴⁴	HA - GFP - $DDI1^{\Delta 323-344}$	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-GFP-DDI1 ⁷⁸⁻³²⁶	HA-GFP-DDI1 ⁷⁸⁻³²⁶	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pADH-RFP-DDI1	HA-RFP-DDI1	pAD54	SalI/SacI	2μ	LEU2	This study
pADH-GFP-RAD23	HA-GFP-RAD23	pAD54	SalI/SacI	2μ	LEU2	This study
pGOGFP-CPS1	GFP-CPS1	pRS426	-	2μ	URA3	C. Stefan
pMB118	GFP-CPS1		-	2μ	LEU2	M. Babst
pADH-CPS1	HA-CPS1	pAD54	SmaI-SacI	2μ	LEU2	This study
pGO-GFP-VPS27	GFP-VPS27	pRS426	BamHI	2μ	URA3	S. Emr
pADH-RFP-VPS27	HA-RFP-VPS27	pAD54	SalI/SacI	2μ	LEU2	J. Gerst
pRS315-STE2-GFP	STE2-GFP	pRS315	-	CEN	LEU2	R. Piper
pUG45-CDC48-GFP	CDC48-GFP	pUG45		CEN	URA3	This study
pADH-GFP-SNX4	HA-GFP-SNX4	pAD54	SalI	2μ	LEU2	J. Gerst
pRS313-VPS10-GFP	HA-VPS10-RFP	pRS313	BamHI	CEN	HIS3	J. Gerst
pRS313-VPS10-RFP	HA-VPS10-RFP	pRS313	BamHI	CEN	HIS3	This study
pAD54-GFP-NPL4	HA-GFP-NPL4	pAD54	SmaI-SacI	2μ	LEU2	This study
pRS316-FUR4-GFP	HA-FUR4-GFP	pAD54	BamHI	CEN	LEU2	This Study
pRS316-GFP-YIF1	HA-GFP-YIF1	pRS316	BamHI	CEN	URA3	J. Gerst
pGAL∆BglII-CPY(1-50)- GFP	CPY ¹⁻⁵⁰ -GFP	pGALΔ BglII		CEN	URA3	D. Deloche
pRS425-UBL4	UBL4	pRS425		2μ	HIS3	M. Babst