

Fig. S1. Concomitant loss of Scd6 and Edc3 blocks P-body assembly and drives nuclear accumulation of Dcp2. (A) Wild-type control strains show no nuclear enrichment of either the decapping complex components Dcp1 and Dcp2, or the exonuclease Xrn1. Logarithmically growing cells expressing genomically tagged Dcp1-, Dcp2- or Xrn1-GFP and the nuclear marker Nup84-mCherry were imaged without additional treatment. Scale bar 5 μ m.

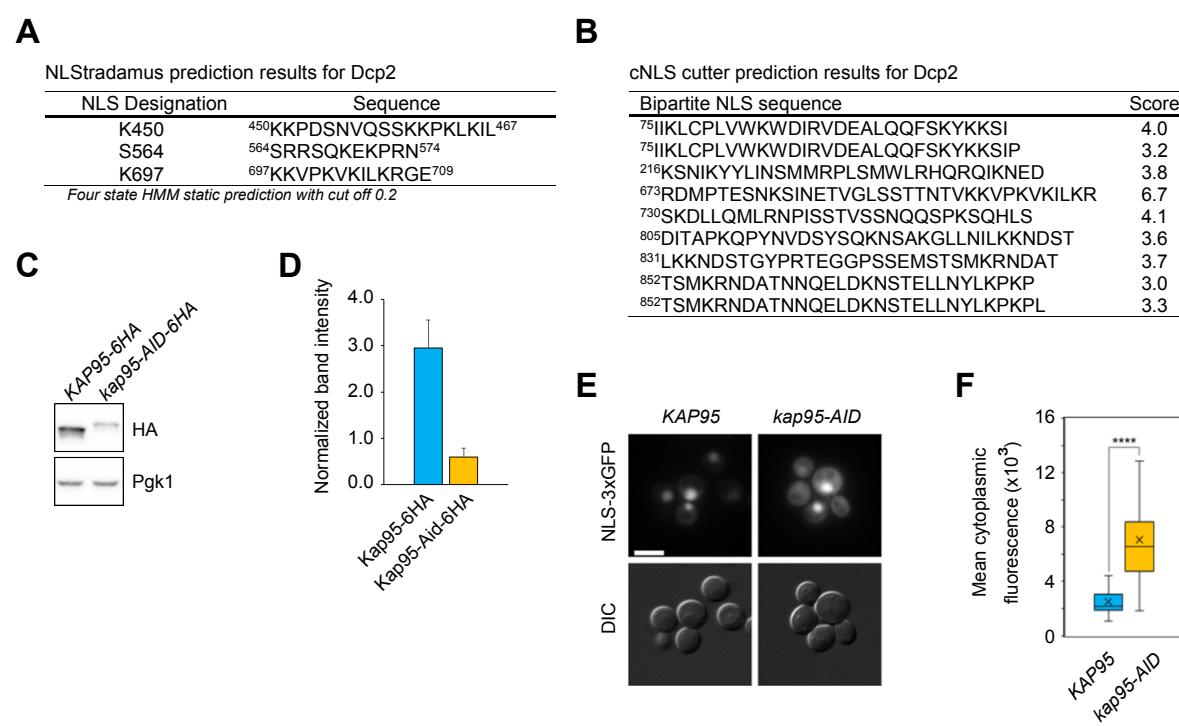


Fig. S2. Dcp2 uses two distinct NLSs and Kap95 for nuclear localization. (A) and (B) Putative NLSs identified in the *Sc* Dcp2 protein sequence using NLStradamus and cNLS cutter web-based tools. (C) and (D) Kap95 C-terminal tagging with an auxin-inducible degron reduces its steady-state levels. Steady-state levels of Kap95 tagged genomically either with 6HA or 6HA-Aid were determined in total protein lysates of logarithmically growing cells by Western blotting using Pgk1 as a reference. (E) and (F) *KAP95* genomic tagging with an auxin-inducible degron results in a defect in the nuclear import of canonical NLSs. (E) Logarithmically growing cells expressing 3xGFP bearing an N-terminal SV40 NLS from a strong promoter (*GPDp*) were imaged without further treatment. Scale bar 5 μ m. (F) Quantification of the mean cytoplasmic fluorescence intensity of the cells in panel E.

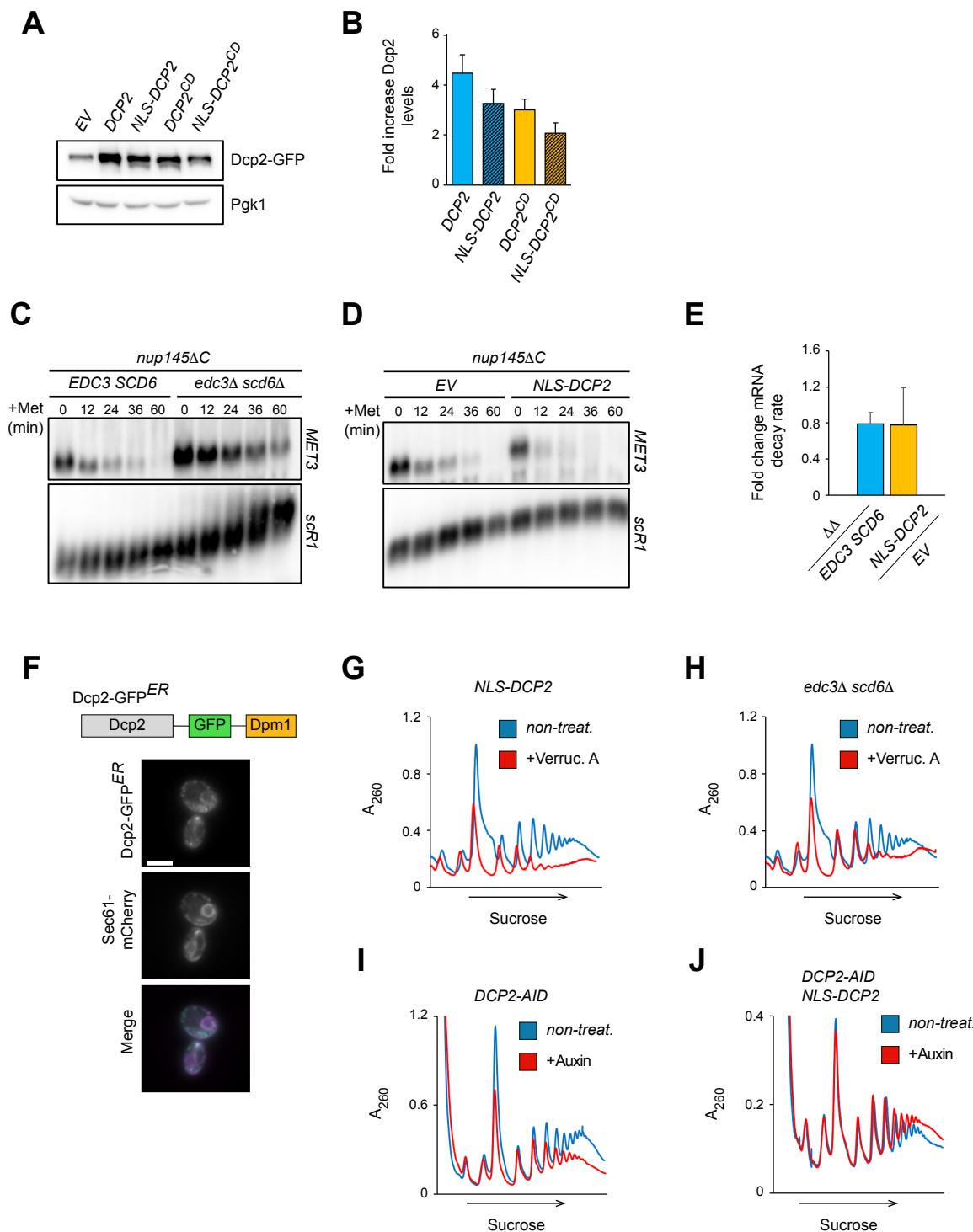


Fig. S3. The decapping complex is stored in the nucleus as a readily releasable pool. (A) and (B) Overexpression of NLS-appended and catalytically dead (CD) variants of Dcp2. Cells expressing Dcp2-GFP from a genomic locus were transformed with a low-copy plasmid expressing different versions of Dcp2-GFP from the strong *GPD* promoter. The GFP expression of logarithmically growing cells was analyzed by Western blotting and quantified using Pgk1 as reference. (C)-(E) Northern blot analysis of *MET3* mRNA nuclear degradation. *nup145ΔC* strain background was either deleted for *EDC3* and *SCD6* or transformed with low-copy plasmids expressing the indicated Dcp2 constructs. Logarithmically growing cultures were starved for methionine to induce the expression of *MET3* and then shifted to 37°C to inhibit mRNA nuclear export. *MET3* transcription was then blocked by addition of methionine and aliquots for Northern blotting analysis were taken at the indicated time points. The *scR1* mRNA served as a loading control. (F) ER-localization of the Dcp2-GFP-Dpm1 construct. Cells expressing the ER-marker Sec61-mCherry were transformed with the low-copy construct expressing Dcp2-GFP-Dpm1 from the *DCP2* promoter. Logarithmically growing cultures were imaged without treatment. Scale bar 5 μm. (G) and (H) Translation attenuation upon treatment with verrucarin A. The global translation in wild-type cells expressing NLS-Dcp2-GFP from a strong promoter or *edc3Δ scd6Δ* expressing genetically tagged Dcp2-GFP was analyzed by polysome profiling upon verrucarin A treatment as in Figure 3-I. (I) and (J) NLS-Dcp2 rescues translation upon depletion of the endogenous Dcp2. Cells with *DCP2* tagged genetically with an auxin-inducible degron were transformed with a low-copy plasmid expressing NLS-Dcp2 from a *GPD* promoter. The global translation of logarithmically growing cultures was analyzed by polysome profiling upon depletion of the endogenous Dcp2 with auxin.

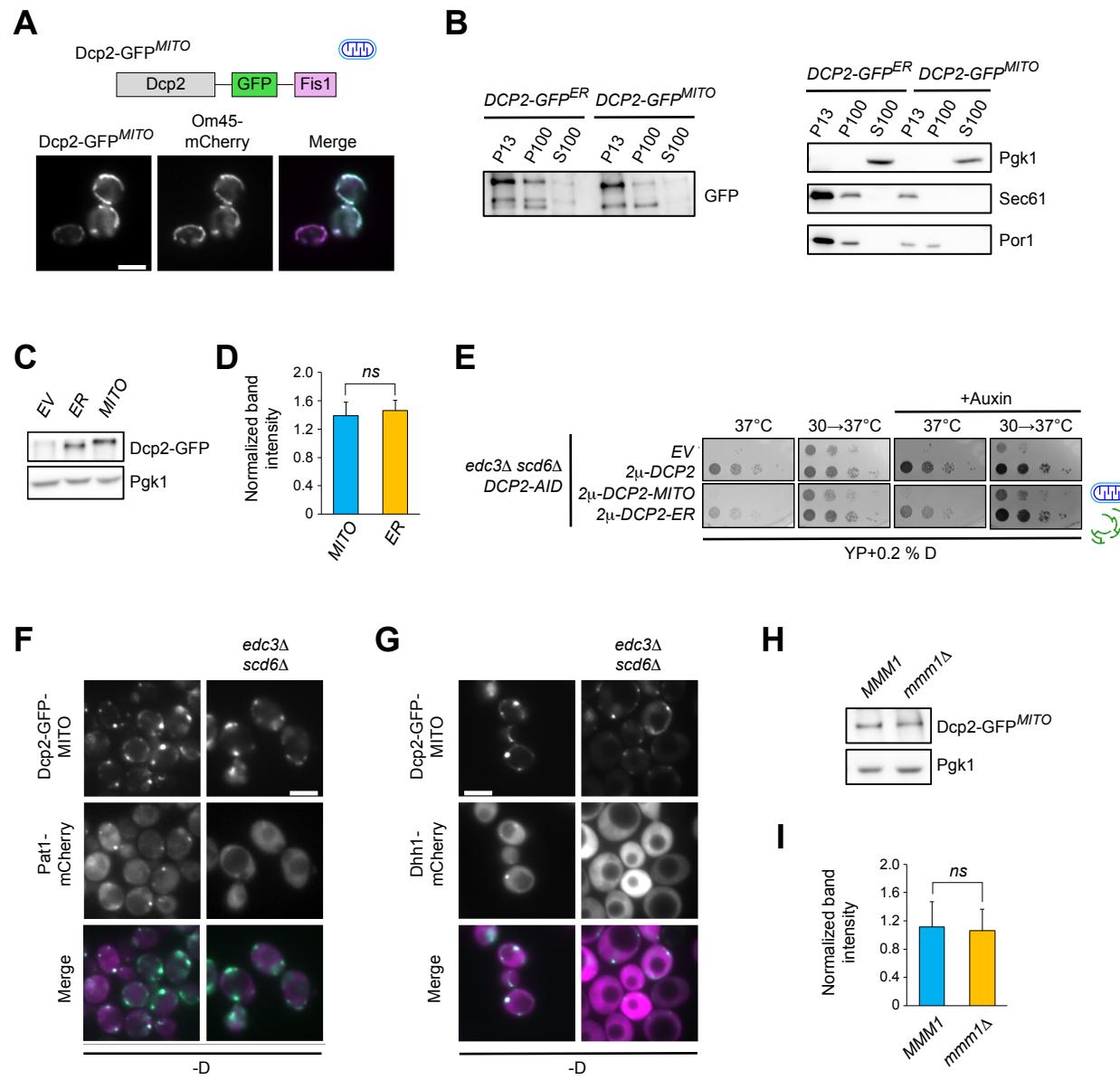


Fig. S4. Dcp1/Dcp2 performs essential functions on the cytoplasmic face of the ER. (A) and (B) Subcellular localization of the Dcp2-GFP^{MITO} and Dcp2-GFP^{ER}. *edc3Δ scd6Δ* with genomically tagged Om45-mCherry were transformed with a low-copy plasmid expressing Dcp2-GFP-Fis1 (Dcp2-GFP^{MITO}) from a *DCP2* promoter. Logarithmically growing cultures were imaged directly, scale bar 5 μm (A). (B) Subcellular localization of Dcp2-GFP^{ER} and Dcp2-GFP^{MITO}. *edc3Δ scd6Δ* with *DCP2* tagged genomically with an auxin-inducible degron were transformed with low-copy plasmids expressing the Dcp2-GFP-Dpm1 (Dcp2-GFP^{ER}) or Dcp2-GFP-Fis1 (Dcp2-GFP^{MITO}) from the endogenous *DCP2* promoter. Spheroplast lysates were subjected to differential centrifugation and the P13, P100 and S100 fractions analyzed by Western blotting. (C) and (D) Dcp2-GFP^{ER} and Dcp2-GFP^{MITO} are expressed at similar levels. The Dcp2-GFP levels in logarithmically growing cells from the strains in panel B and an empty vector control were analyzed by Western blotting. (E) Dcp2 at the ER is required for growth under stress. *edc3Δ scd6Δ* with *DCP2* tagged genomically with an auxin-inducible degron were transformed with high-copy plasmids expressing the indicated Dcp2-constructs from the endogenous *DCP2* promoter. Serial dilutions of the respective logarithmically growing cultures were spotted on YP-agar with 0.2 % glucose, supplemented with 0.2 M auxin as indicated. Agar plates were incubated for 2 days at 37°C, and followed by 3 days at 30°C. (F) and (G) Dcp2-GFP^{MITO} is able to recruit other PB components. Strains with *DCP2* tagged genomically with an auxin-inducible degron were transformed with low-copy plasmids expressing Pat1-mCherry, resp. Dhh1-mCherry from its own promoter. Logarithmically growing cells were treated with 2 mM auxin for 2 h, then subjected to 30 min glucose deprivation and imaged. Scale bar 5 μm. (H) and (I) Dcp2-GFP^{MITO} levels do not change upon deletion of *MMM1*. *edc3Δ scd6Δ DCP2-AID* was deleted for *MMM1* and the Dcp2-GFP^{MITO} levels expressed from a low-copy plasmid on the *DCP2* promoter were determined by Western blotting and compared with isogenic background strain.

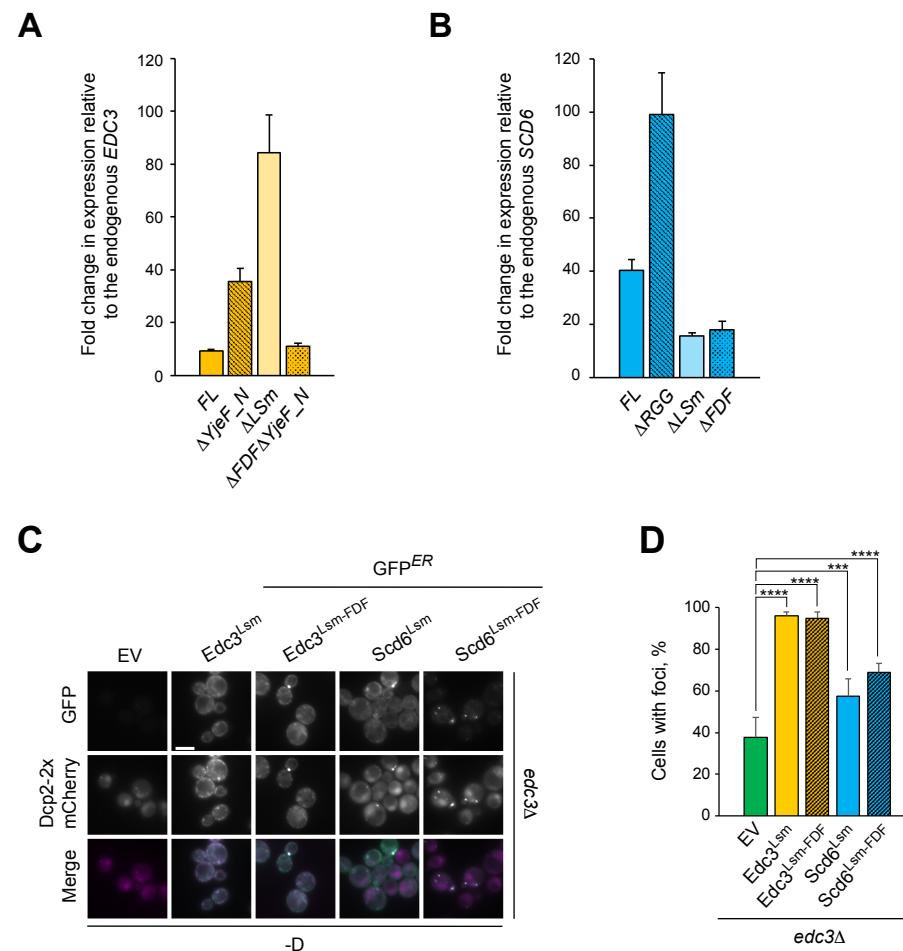


Fig. S5. Scd6 and Edc3 bridge the interaction of Dcp2 with Dhh1 during P-body assembly. (A) and (B) Expression of the *EDC3* and *SCD6* domain constructs. Wild-type or *edc3Δ* *scd6Δ* with genomically tagged Dcp2-GFP were transformed with low-copy plasmids expressing the indicated *SCD6* or *EDC3* constructs from the strong *GPD* promoter. Logarithmically growing cells were harvested and levels of the respective construct mRNAs relative to PGK1 were determined by qRT-PCR. (C) Bridging Dcp2 to Dhh1 at the ER rescues PB-formation in *edc3Δ*. *edc3Δ* cells with *DCP2* genomically tagged with 2×mCherry were transformed with low-copy constructs expressing GFP-ER-anchored (as fusions with Dpm1) Edc3 and Scd6 truncations from the respective own promoters. Logarithmically growing cultures were starved for glucose for 30 min and imaged. (D) Quantification of the number of Dcp2-2×mCherry foci in the strains from panel C upon 30 min –D.

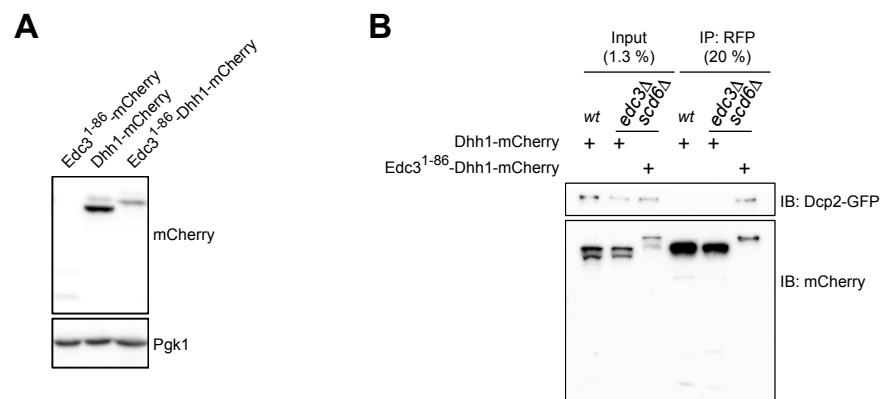


Fig. S6. Linking Dcp2 and Dhh1 drives P-body formation and functional stress response. (A) The Edc3¹⁻⁸⁶-Dhh1 fusion is expressed at lower levels than Dhh1. The expression of the mCherry constructs from Figure 6-A in an *edc3Δ scd6Δ* background was analyzed by Western blotting. (B) The Edc3 LSm-domain (Edc3¹⁻⁸⁶) efficiently links Dhh1 to Dcp2. Logarithmically growing wild-type or *edc3Δ scd6Δ* cells expressing the indicated constructs from a low-copy vector and the *DHH1* promoter were immunoprecipitated with RFP_Trap and the immunoprecipitates were analyzed by Western blotting.

Table S1. *S. cerevisiae* strains used in the study

Strain	Genotype	Reference
YPH499	MAT _a ade2-101 his3-200 leu2-1 lys2-801 trp-63 ura3-52	(Sikorski and Hieter, 1989)
YAS1031A	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4	(Kilchert et al., 2010)
YAS1097	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 scd6Δ::LEU2 (<i>K.lactis</i>)	(Kilchert et al., 2010)
YAS2300	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 edc3Δ::URA3 (<i>K.lactis</i>)	(Kilchert, 2010)
YAS5243	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::natMX4	This study
YAS5716	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP1::DCP1-yEGFP-hphNT1 NUP84::NUP84-mCherry-natNT1	This study
YAS5281	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP84::NUP84-mCherry-natNT1	This study
YAS5718	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 XRN1::XRN1-yEGFP-TRP1 (<i>K.lactis</i>) NUP84::NUP84-mCherry-natNT1	This study
YAS5278	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP1::DCP1-yEGFP-kanMX4 NUP84::NUP84-mCherry-natNT1 edc3::URA3 (<i>K.lactis</i>) scd6::LEU2 (<i>K.lactis</i>)	This study
YAS5311	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP84::NUP84-mCherry-natNT1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>)	This study
YAS5313	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 XRN1::XRN1-yEGFP-TRP1 (<i>K.lactis</i>) NUP84::NUP84-mCherry-natNT1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>)	This study
YAS2355	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 lsm1Δ::URA3 (<i>K.lactis</i>)	(Kilchert, 2010)
YAS5314	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::natMX4 dcp1Δ::LEU2 (<i>K.lactis</i>)	This study
YAS5871	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 NUP84::NUP84-mCherry-natNT1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::hphMX4	This study
YAS2298	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 edc3Δ::URA3 (<i>K.lactis</i>)	(Kilchert, 2010)
YAS5890	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 KAP95::kap95-aid-6HA-hph edc3Δ::URA3 (<i>K.lactis</i>)	This study
YAS5996	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP84::NUP84-mCherry-natNT1 KAP95::kap95-aid-6HA-hph edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>)	This study
YAS5788	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP84::NUP84-mCherry-natNT1 KAP95::KAP95-6HA-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>)	This study
YAS5391	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP145::nup145ΔC-3MYC-TRP1	This study
YAS5392	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-yEGFP-kanMX4 NUP145::nup145ΔC-3MYC-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::natMX4	This study
YAS5905	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 SEC61::SEC61-mCherry-kanMX4	This study
YAS4163	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-2xmCherry-hphNT1	(Wang et al., 2018)
YAS5888	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-2xmCherry-hphNT1 edc3Δ::natMX4	This study
YAS5449	MAT _a ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT trp1::ADH _p -AFB2-TRP1	This study

YAS5639	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT trp1::ADH_p-AFB2-TRP1 trp1Δ::kanMX4</i>	This study
YAS5483	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT trp1::ADH_p-AFB2-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>)</i>	This study
YAS5641	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT trp1::ADH_p-AFB2-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::hphMX4 trp1Δ::kanMX4</i>	This study
YAS5644	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT MDM34::MDM34-mCherry-kanMX4 trp1::ADH_p-AFB2-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>) trp1Δ::hphMX4</i>	This study
YAS5721	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT OM45::OM45-mCherry-kanMX4 trp1::ADH_p-AFB2-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) scd6Δ::LEU2 (<i>K.lactis</i>) trp1Δ::hphMX4</i>	This study
YAS5713	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT trp1::ADH_p-AFB2-TRP1 edc3Δ::URA3 (<i>K.lactis</i>) mmm1Δ::LEU2 (<i>K.lactis</i>) scd6Δ::hphMX4 trp1Δ::kanMX4</i>	This study
YAS5705	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT XRN1::XRN1-mCherry-kanMX4 trp1::ADH_p-AFB2-TRP1</i>	This study
YAS5707	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT EDC3::EDC3-yEGFP-hphNT1 XRN1::XRN1-mCherry-kanMX4 trp1::ADH_p-AFB2-TRP1</i>	This study
YAS5709	<i>MATa ade2::ARF1::ADE2 arf1::HIS3 arf2::HIS3 ura3 lys2 trp1 his3 leu2 DCP2::DCP2-AID-9MYC-natNT SCD6::SCD6-yEGFP-hphNT1 trp1::ADH_p-AFB2-TRP1</i>	This study

Table S2. Yeast plasmids used in the study

Construct	Primers and templates for PCR generation of the assembly fragments				Vector	Vector cut with		
	Fragment	Primer	Primer sequence	PCR template				
<i>pRS414-PAT1p-PAT1-mCherry</i>	<i>PAT1p-PAT1</i>	kt2026	AGGGAAACAAAAGCTGGAGCTGAGGGTTCAAGGAAATCC	gDNA YPH499	<i>pRS414-ADH_p</i>	SacI/Sall		
		kt2101	GTCGACCTGCAGCGTACG CTTTAGTTCTGATATTTCACC					
	<i>mCherry</i>	kt2103	CGT ACG CTG CAG GTC GAC	<i>pYM-mCherry-kanMX</i>				
		kt2070a	TACCGGGCCCCCCTCGAGGTCGAC ATGGGGATGTATGGGCTAAA					
<i>pRS415-PAT1p-PAT1-mCherry</i>	<i>PAT1p-PAT1</i>	kt2026	AGGGAAACAAAAGCTGGAGCTGAGGGTTCAAGGAAATCC	gDNA YPH499	<i>pRS415-GPD_p</i>	SacI/Sall		
		kt2101	GTCGACCTGCAGCGTACG CTTTAGTTCTGATATTTCACC					
	<i>mCherry</i>	kt2103	CGT ACG CTG CAG GTC GAC	<i>pYM-mCherry-kanMX</i>				
		kt2070a	TACCGGGCCCCCCTCGAGGTCGAC ATGGGGATGTATGGGCTAAA					
<i>pRS415-GPD_p-DCP2-GFP</i>	<i>DCP2</i>	kt2066	CGGCCGCTCTAGAACACTAGTGGATCCATGTCACTGCCGCTACGACAC	gDNA YPH499	<i>pRS415-GPD_p</i>	BamHI/Xhol		
		kt2068	GTCGACCTGCAGCGTACGCTTCCATGCAAATGCTTAA					
	<i>GFP</i>	kt2069	TTAAGCATTTCGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2070	GGTACCGGGCCCCCCTCGAG ATGGGGATGTATGGGCTAAA					
<i>pRS415-GPD_p-NLS-DCP2-GFP</i>	<i>NLS-DCP2</i>	kt2076	CGGCCGCTCTAGAACACTAGTGGATCCATGTCACTGCCGCTACGACAC	gDNA YPH499	<i>pRS415-GPD_p</i>	BamHI/Xhol		
		kt2068	GTCGACCTGCAGCGTACGCTTCCATGCAAATGCTTAA					
	<i>GFP</i>	kt2069	TTAAGCATTTCGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2070	GGTACCGGGCCCCCCTCGAG ATGGGGATGTATGGGCTAAA					
<i>pRS415-GPD_p-DCP2(cat. dead)-GFP</i>	<i>DCP2p-DCP2-mut-1</i>	kt2066	CGGCCGCTCTAGAACACTAGTGGATCCATGTCACTGCCGCTACGACAC	gDNA YPH499	<i>pRS415-GPD_p</i>	BamHI/Xhol		
		kt2077	ACCAAT TGCAGCTTTAACTGCAGC AATGCAACAATCTATGTCATT					
	<i>DCP2-mut-2</i>	kt2078	TGCATT GCT GCA GTT AAA GCT GCA ATTGGTTTCGATTTGACGGAC	gDNA YPH499				
		kt2068	GTCGACCTGCAGCGTACGCTTCCATGCAAATGCTTAA					
<i>pRS415-GPD_p-NLS-DCP2(cat. dead)-GFP</i>	<i>GFP</i>	kt2069	TTAAGCATTTCGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2070	GGTACCGGGCCCCCCTCGAG ATGGGGATGTATGGGCTAAA					
	<i>NLS-DCP2-mut-1</i>	kt2076	CGGCCGCTCTAGAACACTAGTGGATCCATGTCACTGCCGCTACGACAC	gDNA YPH499	<i>pRS415-GPD_p</i>	BamHI/Xhol		
		kt2077	ACCAAT TGCAGCTTTAACTGCAGC AATGCAACAATCTATGTCATT					
	<i>DCP2-mut-2</i>	kt2078	TGCATT GCT GCA GTT AAA GCT GCA ATTGGTTTCGATTTGACGGAC	gDNA YPH499				
		kt2068	GTCGACCTGCAGCGTACGCTTCCATGCAAATGCTTAA					
	<i>GFP</i>	kt2069	TTAAGCATTTCGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2070	GGTACCGGGCCCCCCTCGAG ATGGGGATGTATGGGCTAAA					
<i>pRS414-DCP2p-DCP2-GFP-FIS1</i>	<i>DCP2p-DCP2</i>	kt2072	AGGGAAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	gDNA YPH499	<i>pRS414-ADH_p</i>	SacI/Sall		
		kt2068	GTCGACCTGCAGCGTACGCTTCCATGCAAATGCTTAA					
	<i>GFP</i>	kt2069	TTAAGCATTTCGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2073	TTCGCCCCTGCCCGCGCAGCGCGGGCAGC TTTGTACAATTCCAT					
	<i>FIS1</i>	kt2074	TTGTACAAA GCTGCCCGCGCTGCCGCAGCGCGAA ATGACCAAAGTAGATT	gDNA YPH499				
		kt2075	TACCGGGCCCCCCTCGAGGTCGAC AGAAGGCAAATAGCAGTG					

Table S2 (continued)

<i>PRS414-DCP2p-DCP2-GFP-DPM1</i>	<i>DCP2p-DCP2</i>	kt2072	AGGGAAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	gDNA YPH499	<i>pRS414-ADHp</i>	SacI/SalI		
		kt2068	GTCGACCTGCAGCGTACGCTTCTATGCAAATGCTTAA					
	<i>GFP</i>	kt2069	TTAAGCATTTCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2073	TTCGCCCTGCCCGCGCAGCGCAGGGCAGC TTTGTACAATTCCAT					
	<i>DPM1</i>	kt2081	TTGTACAAA GCTGCCCGCGCTGCCCGGGCAGCGCGAA ATGAGCATCGAATACTCTGT	gDNA YPH499				
		kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCAAAAGCA					
	<i>PRS424-DCP2p-DCP2-GFP-FIS1</i>	kt2072	AGGGAAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	gDNA YPH499	<i>pRS424-ADHp</i>	SacI/SalI		
		kt2068	GTCGACCTGCAGCGTACGCTTCTATGCAAATGCTTAA					
		kt2069	TTAAGCATTTCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2073	TTCGCCCTGCCCGCGCAGCGCAGGGCAGC TTTGTACAATTCCAT					
		kt2074	TTGTACAAA GCTGCCCGCGCTGCCCGGGCAGCGCGAA ATGACCAAAGTAGATT	gDNA YPH499				
	<i>PRS424-DCP2p-DCP2-GFP-DPM1</i>	kt2075	TACCGGGCCCCCTCGAGGTCGAC AGAAGGCAAATAGCAGTG					
		kt2072	AGGGAAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	gDNA YPH499	<i>pRS424-ADHp</i>	SacI/SalI		
		kt2068	GTCGACCTGCAGCGTACGCTTCTATGCAAATGCTTAA					
		kt2069	TTAAGCATTTCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2073	TTCGCCCTGCCCGCGCAGCGCAGGGCAGC TTTGTACAATTCCAT					
	<i>DPM1</i>	kt2081	TTGTACAAA GCTGCCCGCGCTGCCCGGGCAGCGCGAA ATGAGCATCGAATACTCTGT	gDNA YPH499				
		kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCAAAAGCA					
<i>PRS415-GPDp-SCD6 FL</i>	<i>SCD6</i>	kt2042	CGGCCGCTCTAGAACTAGTGGATCCATGTCGCACTCGTAAAC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>		
		kt2043C	ATTGGGTACCGGGCCCCCTCGAGTTAAATTCAACGTTGGAAGGAGG					
<i>PRS415-GPDp-SCD6 ΔRGG</i>	<i>SCD6 ΔRGG</i>	kt2042	CGGCCGCTCTAGAACTAGTGGATCCATGTCGCACTCGTAAAC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>		
		kt2043A	ATTGGGTACCGGGCCCCCTCGAGTTAAAGGTAAACGTTGGAAGGAGG					
<i>PRS415-GPDp-SCD6 DLSm</i>	<i>SCD6 ΔLSm</i>	kt2043B	CGGCCGCTCTAGAACTAGTGGATCCATGAATGACATACAGCGGGTTTT	gDNA YPH499	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>		
		kt2043C	ATTGGGTACCGGGCCCCCTCGAGTTAAATTCAACGTTGGAAGGAGG					
<i>PRS415-GPDp-SCD6 ΔFDF</i>	<i>SCD6 LSm</i>	kt2042	CGGCCGCTCTAGAACTAGTGGATCCATGTCGCACTCGTAAAC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>		
		kt2043E1	AGAGTCAAATCTGGTCTGGCGATGTTAGCATCTAAATGCT					
		kt2043E2	AGCATTAGATGCTAACATC GCCAGACCAAGATTCACTCT	gDNA YPH499				
		kt2043C	ATTGGGTACCGGGCCCCCTCGAGTTAAATTCAACGTTGGAAGGAGG					
<i>PRS415-GPDp-EDC3 FL</i>	<i>EDC3 FL</i>	kt2055N	CGGCCGCTCTAGAACTAGT ATGTCACAATTGTTGGTTTC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>Spel/Xhol</i>		
		kt2056	TACCGGGCCCCCTCGAG TTACAAATCTAATAGCAGGG					
<i>PRS415-GPDp-EDC3 ΔYjeF_N</i>	<i>EDC3 ΔYjeF_N</i>	kt2055N	CGGCCGCTCTAGAACTAGT ATGTCACAATTGTTGGTTTC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>Spel/Xhol</i>		
		kt2057	TACCGGGCCCCCTCGAG TTACAAATCTAATAGCAGGG					
<i>PRS415-GPDp-EDC3 ΔLSm</i>	<i>EDC3 ΔLSm</i>	kt2097c	CGGCCGCTCTAGAACTAGTGGATCC ATG GAACATATTGATTGGCAA	gDNA YPH499	<i>pRS415-GPDp</i>	<i>Spel/Xhol</i>		
		kt2056	TACCGGGCCCCCTCGAG TTACAAATCTAATAGCAGGG					

Table S2 (continued)								
<i>pRS415-GPDp-EDC3</i> Δ <i>DFD-YjeF_N</i>	<i>EDC3 LSm</i>	kt2087	CGGCCGCTAGAACTAGTGGATCC ATGTACAATTGTTGGTTTCG TACCGGGCCCCCTCGAGGTCGAC TTA ACCCGGATTTGATTATAATC	gDNA YPH499	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>		
<i>pRS415-DHH1p-</i> <i>EDC3(aa 1-86)-mCherry</i>	<i>DHH1p</i>	kt2094	AGGGAACAAAAGCTGGAGCTC TGGTGTGCAATTGGACAA	gDNA YPH499	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2095	GAAACCAACAAATTGTGACATTACTACTATTTCTTCTTG	gDNA YPH499				
	<i>EDC3(aa 1-86)</i>	kt2096	ACAAGAAAGAAAATAGTAGTA ATGTCACAATTGTTGGTTTC	gDNA YPH499				
		kt2097b	GTCGACCTGCAGCGTAGC ACCCGGATTTGATTATAATC	gDNA YPH499				
	<i>mCherry</i>	kt2103	CGT ACG CTG CAG GTC GAC	<i>pYM-mCherry-kanMX</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGAC ATGGGGATGTATGGGCTAAA	<i>pYM-mCherry-kanMX</i>				
<i>pRS415-DHH1p-DHH1-</i> <i>mCherry</i>	<i>DHH1p-DHH1</i>	kt2079	AGGGAACAAAAGCTGGAGCTC TTTTCTTATCATTAGTGTGCG	gDNA YPH499	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2100	GTCGACCTGCAGCGTAGC ATACTGGGGTTGTGACTGACC	gDNA YPH499				
	<i>mCherry</i>	kt2103	CGT ACG CTG CAG GTC GAC	<i>pYM-mCherry-kanMX</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGAC ATGGGGATGTATGGGCTAAA	<i>pYM-mCherry-kanMX</i>				
<i>pRS415-DHH1p-</i> <i>EDC3(1-86)-DHH1-</i> <i>mCherry</i>	<i>DHH1p</i>	kt2094	AGGGAACAAAAGCTGGAGCTC TGGTGTGCAATTGGACAA	gDNA YPH499	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2095	GAAACCAACAAATTGTGACATTACTACTATTTCTTCTTG	gDNA YPH499				
	<i>EDC3(aa 1-86)</i>	kt2096	ACAAGAAAGAAAATAGTAGTA ATGTCACAATTGTTGGTTTC	gDNA YPH499				
		kt2097	TTCGCCGCTGCCGCCGGCAGCGCGGGCAGC ACCCGGATTTGATTATAATC	gDNA YPH499				
	<i>DHH1</i>	kt2098	GCTGCCGCCCTGCCGGGGCAGCGGGCAA ATGGGTTCCATCAATAAACTTC	gDNA YPH499				
		kt2100	GTCGACCTGCAGCGTAGC ATACTGGGGTTGTGACTGACC	gDNA YPH499				
	<i>mCherry</i>	kt2103	CGT ACG CTG CAG GTC GAC	<i>pYM-mCherry-kanMX</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGAC ATGGGGATGTATGGGCTAAA	<i>pYM-mCherry-kanMX</i>				
<i>pRS415-DCP2p-DCP2-</i> <i>GFP</i>	<i>DCP2p-DCP2</i>	kt2072	AGGGAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	gDNA YPH499	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2068	GTCGACCTGCAGCGTAGCCTCATGCAAATGCTAA	gDNA YPH499				
	<i>GFP</i>	kt2069	TTAACGCATTTGCATAGGAAG CGT ACG CTG CAG GTC GAC	<i>pYM44</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGACATGGGGATGTATGGGCTAAA	<i>pYM44</i>				
<i>pRS415-DCP2p-DCP2-</i> <i>GFP</i> <i>NLS R229</i>	<i>DCP2p-DCP2-</i> <i>mut. 1</i>	kt2072	AGGGAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2142	CGTTAACACATTGATAAGGGTGTATGAAATTAAATCG	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
	<i>DCP2-mut. 2-GFP</i>	kt2143	TTA TCA ATG TGG TTA ACG CAT CAG ACT CAA ATA AAA AAT GAA GAT	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGACATGGGGATGTATGGGCTAAA	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
<i>pRS415-DCP2p-DCP2-</i> <i>GFP</i> <i>NLS K450</i>	<i>DCP2p-DCP2-</i> <i>mut. 1</i>	kt2072	AGGGAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2138	TGTAAGCGTTGGCGTTGTGCTTGATTGCACGTTGCTGTC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
	<i>DCP2-mut. 2-GFP</i>	kt2139	ACA ACG CCA ACG CTT ACA ATC TTA CAG AGA GGA ACG GAC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
		kt2070a	TACCGGGCCCCCTCGAGGTCGACATGGGGATGTATGGGCTAAA	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
<i>pRS415-DCP2p-DCP2-</i> <i>GFP</i> <i>NLS S564+K697</i>	<i>DCP2p-DCP2-</i> <i>mut. 1</i>	kt2072	AGGGAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>	<i>pRS415-TEFp</i>	<i>SacI/Sall</i>		
		kt2136	TGGTGTTCGTTTGACTTGTGCTGTCTTTCTGCTTGGCAT	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
	<i>DCP2-mut. 2-GFP</i>	kt2137	ACA AGT CAA ACG GAA ACA CCA ACG AAC GAC GCA AGC AAA ACA AAC	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
		kt2134	TAGTATTGTAACTGTGGGTACCGTTACAGTATTGTTGATGA	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				
	<i>DCP2-mut. 3-GFP</i>	kt2135	GTA CCC ACA GTT ACA ATA CTA ACA ACA GGT GAA ACC TTT GCC AGT CTG	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>		<i>SacI/Sall</i>		
		kt2070a	TACCGGGCCCCCTCGAGGTCGACATGGGGATGTATGGGCTAAA	<i>pRS415-DCP2p-</i> <i>DCP2-GFP</i>				

Table S2 (continued)							
<i>pRS415-DCP2p-DCP2-GFP NLS R229+K450</i>	<i>DCP2p-DCP2-mut.1</i>	kt2072	AGGGAAACAAAAGCTGGAGCTC ATAATAAGGGTCATCGATCC	<i>pRS415-DCP2p-DCP2-GFP NLS K450</i>	<i>pRS415-TEFp</i>		SacI/SalI
		kt2142	CGTTAACCAATTGATAAGGGTGTATCATGGAAATTACAG				
	<i>DCP2-mut. 2-GFP</i>	kt2143	TTA TCA ATG TGG TTA ACG CAT CAG ACT CAA ATA AAA AAT GAA GAT				
		kt2070a	TACCGGGCCCCCCCCTCGAGGTCGACATGGGATGTATGGGCTAAA				
<i>pRS415-NLS-3xGFP</i>	<i>5'-NLS-GFP</i>	kt2144	TCTAGAACTAGTGGATCC ATG CCA AAG AAG AAA AGA AAG GTT CGT ACG CTG CAG GTC GAC	<i>pYM44</i>	<i>pRS415-GPDp</i>	<i>BamHI/Xhol</i>	
		kt2073	TTCGCCGCTGCCGCAGCGCGGGCAGCGCGGGCAGC TTTGTACAATTCCAT				
	<i>middle GFP</i>	kt2147	GCTGCCCGCGCTGCCGCAGCGGGCAGCGGGCGAA CGT ACG CTG CAG GTC GAC				
		kt2148	CTCTCCAGATCCAGCTCGGGCCCGCGCGC TTTGTACAATTCCAT				
	<i>GFP-3'</i>	kt2149	GCCGCGGGCCGCAGCTGGATCTGGAGAG CGT ACG CTG CAG GTC GAC				
		kt2070	GGTACGGGGCCCCCTCGAG ATGGGATGTATGGGCTAAA				
	<i>EDC3p-EDC3^{LSm}-GFP-DPM1</i>	kt2086	AGGGAAACAAAAGCTGGAGCTC TAAAAAAATGTCGTGATATTGC	<i>gDNA YPH499</i>	<i>pRS415-TEFp</i>		SacI/SalI
		2097b	GTCGACCTGCAGCGTAGC ACCCGGATTTGATTATAATC				
	<i>GFP-DPM1</i>	kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCTAAAGCA	<i>pRS414-DCP2p-DCP2-GFP-DPM1</i>			
		kt2103	CGT ACG CTG CAG GTC GAC				
<i>pRS415-EDC3p-EDC3^{LSm-FDF}-GFP-DPM1</i>	<i>EDC3p-EDC3^{LSm-FDF}</i>	kt2086	AGGGAAACAAAAGCTGGAGCTC TAAAAAAATGTCGTGATATTGC	<i>gDNA YPH499</i>	<i>pRS415-TEFp</i>		SacI/SalI
		kt2146	GTCGACCTGCAGCGTAGC TAGTAGTTGTACTGGTGT				
	<i>GFP-DPM1</i>	kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCTAAAGCA	<i>pRS414-DCP2p-DCP2-GFP-DPM1</i>			
		kt2103	CGT ACG CTG CAG GTC GAC				
<i>pRS415-SCD6p-SCD6^{LSm}-GFP-DPM1</i>	<i>SCD6p-SCD6^{LSm}</i>	kt2127	AGGGAAACAAAAGCTGGAGCTC AGACTCTAGAGTTAACATTGA	<i>gDNA YPH499</i>	<i>pRS415-TEFp</i>		SacI/SalI
		kt2130	GTCGACCTGCAGCGTAGC GATGTTAGCATCTAAAGCA				
	<i>GFP-DPM1</i>	kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCTAAAGCA	<i>pRS414-DCP2p-DCP2-GFP-DPM1</i>			
		kt2103	CGT ACG CTG CAG GTC GAC				
<i>pRS415-SCD6p-SCD6^{LSm-FDF}-GFP-DPM1</i>	<i>SCD6p-SCD6^{LSm-FDF}</i>	kt2127	AGGGAAACAAAAGCTGGAGCTC AGACTCTAGAGTTAACATTGA	<i>gDNA YPH499</i>	<i>pRS415-TEFp</i>		SacI/SalI
		kt2145	GTCGACCTGCAGCGTAGC AGAGTCAAATCTGGTCTGG				
	<i>GFP-DPM1</i>	kt2082	TACCGGGCCCCCTCGAGGTCGAC TAATGATCTATTCTAAAGCA	<i>pRS414-DCP2p-DCP2-GFP-DPM1</i>			
		kt2103	CGT ACG CTG CAG GTC GAC				

Table S3. qPCR Primers used in the study

Target	Primer name	Primer sequence	Reference
<i>ACT1</i>	CW961	AGGTTGCTGCTTGTTATTG	Wang <i>et al.</i> (2018)
	CW962	CCGACGATAGATGGGAAGAC	
<i>BSC1</i>	CW562	TCTGACGGTTGCACAGTTG	
	CW729	TGCCAAGTTGCCAGTACTG	
<i>EDC3</i> ^{LSm}	ktq037	ATGGGAAGCTCATTCAAGGGG	This study
	ktq038	CACCATCGCCGAATTGAACG	
<i>EDC3</i> ^{FDF-YjeF_N}	ktq039	AACTCGGCAGGGCTACTAGA	
	ktq040	CGGCCACCTAGTTCTGCTT	
<i>ILM1</i>	CW969	CAATTGGGTCTTCGCTCT	Wang <i>et al.</i> (2018)
	CW970	CTGGCACAAACAGATTGGAAG	
<i>PGK1</i>	CW963	TTGATTGACAACTTGTTGGA	
	CW964	CAGTGACAGTCTTGGTGTG	
<i>SCD6</i> ^{LSm}	ktq033	AGAAGGTCGCAAGAACTGGG	This study
	ktq034	TCCTTGACTCACTGCCGTT	
<i>SCD6</i> ^{RGG}	ktq035	CTCAAGCACACGTGCAAACA	
	ktq036	ACACCATATCCAGCGACAGC	

Supplementary References

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