Decapping activators Edc3 and Scd6 act redundantly with Dhh1 in post-transcriptional repression of starvation-induced pathways

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ABSTRACT

Degradation of many yeast mRNAs involves decapping by the Dcp1:Dcp2 complex. Previous studies on decapping activators Edc3 and Scd6 suggested their limited roles in mRNA decay. RNA-seq analysis of mutants lacking one or both proteins revealed that Scd6 and Edc3 have largely redundant activities in targeting numerous mRNAs for degradation that are masked in the single mutants. These transcripts are frequently targeted by decapping activators Dhh1 and Pat1, and the collective evidence suggests that Scd6/Edc3 act interchangeably to recruit Dhh1 to Dcp2. Ribosome profiling shows that redundancy between Scd6 and Edc3 and their functional interactions with Dhh1 and Pat1 extend to translational repression of particular transcripts, including a cohort of poorly translated mRNAs displaying interdependent regulation by all four factors. Scd6/Edc3 also participate with Dhh1/Pat1 in post-transcriptional repression of proteins required for respiration and catabolism of alternative carbon sources, which are normally expressed only in limiting glucose. Simultaneously eliminating Scd6/Edc3 increases mitochondrial membrane potential and elevates metabolites of the tricarboxylic acid and glyoxylate cycles typically observed only during growth in low glucose. Thus, Scd6/Edc3 act redundantly, in parallel with Dhh1 and in cooperation with Pat1, to adjust gene expression to nutrient availability by controlling mRNA decapping and decay.

INTRODUCTION

Degradation of mRNA is a key aspect of gene expression that can be regulated in response to nutrient availability, cell stress, and developmental pathways in eukaryotic cells and further serves to eliminate defective mRNAs. A major pathway of cytoplasmic mRNA turnover involves truncating the poly(A) tail by the Ccr4/Not and Pan2/Pan3 complexes, followed by removal of the m^7G cap by the Dcp1/Dcp2 decapping complex and 5' to 3' exonucleolytic degradation by Xrn1. The decapping complex is activated by factors that interact with low-complexity sequence motifs in the C-terminal tail (CTT) of the catalytic subunit Dcp2, including Edc3, Scd6, DEAD-box helicase Dhh1, and Pat1, which also interact with one another extensively. There is evidence that Pat1 is recruited to oligoadenylate tails remaining on mRNAs following partial deadenylation, in association with the Lsm1-Lsm7 complex, and activates decapping via interactions with other decapping activators and with the Dcp2 CTT itself (Parker 2012) (He and Jacobson 2023)

Genome-wide analysis of mRNA abundance (RNA-seq) in yeast mutants lacking Dhh1, Pat1, or both factors revealed functional cooperation by Pat1 and Dhh1 (He et al. 2018), with a large fraction being up-regulated only in the *pat1Δdhh1Δ* double mutant (Vijjamarri et al. 2023a). The majority of mRNAs up-regulated by *dhh1Δ* or *pat1Δ* mutations are likewise up-regulated in *dcp2Δ* cells (He et al. 2018) and exhibit greater than average proportions of decapped mRNAs in WT cells but not in *dhh1Δ* or *pat1Δ* cells (Vijjamarri et al. 2023a), consistent with Dhh1/Pat1 targeting mRNAs for degradation via decapping. While more than half of the mRNAs up-regulated by *dcp2Δ* are up-regulated by *dhh1Δ* and/or *pat1Δ,* a large fraction are targeted

primarily by the Upf factors instead responsible for nonsense-mediated mRNA decay (NMD) (Vijjamarri et al. 2023b) (Celik et al. 2017).

The cumulative contributions of Dhh1 and Pat1 to mRNA decay is consistent with their independent interactions with distinct segments of the Dcp2 CTT (He et al. 2018), which appears to be direct for Pat1 but bridged by Edc3 or Scd6 for Dhh1. There is also evidence for distinct decapping complexes containing either Dhh1 or Pat1 in addition to Xrn1, Edc3 or Scd6 (He et al. 2022). However, Dhh1 occupancy (Miller et al. 2018), tends to be elevated for mRNAs up-regulated by either *dhh1Δ* (23) or *pat1Δ* (Vijjamarri et al. 2023a), consistent with Dhh1 contributing to degradation of mRNAs targeted by Pat1. Moreover, Pat1 binding to the Dcp2 CTT was required for degradation of certain Dhh1-targeted mRNAs when Dhh1 recruitment to the CTT was compromised (He et al. 2022).

There is evidence that Edc3 is a common constituent of decapping complexes containing Xrn1 and one or more of the decapping activators Dhh1, Pat1, Scd6, and Upf1 (He et al. 2022). It is surprising therefore that Edc3 has been implicated in targeting only two transcripts for degradation, *YRA1* and *RPS28B* (Badis et al. 2004; Dong et al. 2007). Edc3 shares sequence similarity with decapping activator Scd6 and both proteins contain an FDF motif shown to interact competitively with the Dhh1 homolog in animal systems (Tritschler et al. 2008; Tritschler et al. 2009). Edc3 and Scd6 also share N-terminal LSm domains that compete for binding to helical-leucine-rich (HLM) motifs in the CTT of fission yeast Dcp2 (Fromm et al. 2012). Analyzing effects of deleting the Edc3 interaction site in the *S. cerevisiae* Dcp2-CTT on levels of several Dhh1-repressed mRNAs suggested that recruitment of Dhh1 to Dcp2 can be mediated interchangeably by Edc3 or Scd6 bound to the same site in the Dcp2 CTT (He et al. 2022). These

findings, plus the fact that deleting *S. cerevisiae SCD6* and *EDC3* simultaneously confers a synthetic growth defect (Decourty et al. 2008), suggest that yeast Scd6 and Edc3 function redundantly in targeting specific mRNAs for decapping and degradation.

Although tethering yeast Dhh1 or Scd6 enhances degradation of reporter mRNAs via Dcp1/Dcp2 (Carroll et al. 2011; Sweet et al. 2012; Zeidan et al. 2018), it is not well understood how these factors are targeted to specific native mRNAs. Dhh1 has been implicated in accelerating degradation associated with non-optimal codons in yeast mRNAs (Presnyak et al. 2015), being required for the rapid turnover conferred by suboptimal codons inserted in reporter mRNAs (Sweet et al. 2012). A queue of slowly elongating ribosomes upstream from non-optimal codons can be recognized by Dhh1, and overexpressing or tethering Dhh1 evokes ribosome stalling at non-optimal codons. Moreover, Dhh1 association and Dhh1-dependent repression of mRNA abundance both correlate with codon non-optimality across the yeast transcriptome (Radhakrishnan et al. 2016). However, the mRNAs most highly up-regulated in *dhh1Δ* and *pat1Δ* cells are not enriched for suboptimal codons, suggesting that other features are responsible for their preferential targeting by Dhh1 or Pat1 for decapping/decay (Vijjamarri et al. 2023a).

In addition to enhancing mRNA decay, there is evidence that Pat1, Dhh1, and Scd6 can repress translation. Tethering Dhh1 or Scd6 represses translation of reporter mRNAs in *dcp2Δ* cells where the tethered transcripts cannot be decapped and degraded (Carroll et al. 2011; Sweet et al. 2012; Zeidan et al. 2018). Deletion of Dhh1 and Pat1 simultaneously eliminated loss of bulk polysomes evoked by nutrient starvation and also increased initiation rates of certain mRNAs (Holmes et al. 2004) (Coller and Parker 2005) (Arribere et al. 2011). Supporting a direct role in repressing translation, overexpressing Dhh1 or Pat1 in nonstarved cells evoked

polysome disassembly and reduced the initiation rate of specific mRNAs; and addition of Dhh1 (Coller and Parker 2005) or N-terminally truncated Pat1 (Nissan et al. 2010) to yeast extracts inhibited bulk translation and 48S preinitiation complex (PIC) assembly in vitro. Ribosome profiling studies of *dhh1Δ, pat1Δ* and *pat1Δdhh1Δ* mutants identified hundreds of genes whose transcripts are translationally down-regulated or activated by Dhh1 or Pat1 in nutrient-replete cells (Jungfleisch et al. 2017) (Radhakrishnan et al. 2016; Zeidan et al. 2018), which frequently involves cooperation between Dhh1 and Pat1 (Vijjamarri et al. 2023a).

Recently, we showed that Pat1 and Dhh1 function with the decapping enzyme in rich medium to repress the abundance or translation of numerous mRNAs encoding proteins required specifically in media containing an alternative carbon or nitrogen source (Vijjamarri et al. 2023a; Vijjamarri et al. 2023b). These include mitochondrial proteins involved in oxidative phosphorylation (Ox. Phos.) and diverse other proteins known to be transcriptionally repressed by carbon or nitrogen catabolite repression in rich medium.

In this study, we used a multi-omics approach to determine whether Edc3 and Scd6 have largely redundant functions in targeting mRNAs for decapping and attendant degradation, and whether they functionally cooperate with Pat1 or Dhh1 in repressing the abundance or translation of specific mRNAs. We identified a large cohort of mRNAs that are up-regulated in an *scd6Δedc3Δ* double mutant but not in either single mutant lacking only Scd6 or Edc3, without a commensurate increase in transcription of the cognate genes. These transcripts display a strikingly similar pattern of up-regulation in the *dhh1Δ* mutant in the manner predicted if Edc3/Scd6 redundantly recruit Dhh1 to Dcp2 for activation of decapping (He et al. 2022). We further observed functional redundancy between Scd6 and Edc3 and extensive cooperation with Dhh1/Pat1 in

repressing translation of particular mRNAs, with evidence for interdependent repression by all four decapping factors. Importantly, Edc3/Scd6 contribute to post-transcriptional repression of proteins required for catabolism of non-preferred carbon or nitrogen sources on rich medium, acting collectively to enhance glucose repression, maintain low-level mitochondrial electron transport and reduce levels of tricarboxylic acid (TCA) and glyoxylate cycle intermediates in glucose-replete cells.

METHODS

Yeast strains and plasmids.

Unless otherwise indicated, the following yeast strains were employed for all experiments: WT strain HFY114 (W303: *MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100*) (He et al. 2003), *scd6Δ* strain SYY2352 (*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 scd6Δ::kanMX6*) (He and Jacobson 2015), *edc3Δ* strain FZY862 (*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 edc3Δ::kanMX4*), and *scd6Δedc3Δ* strain FZY858 (*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 scd6Δ::hphMX4 edc3Δ::kanMX4*).

Strains FZY858 and FZY862 were generated by replacing chromosomal *EDC3* in strains FZY855 and HFY114, respectively, with the *edc3Δ::kanMX4* allele amplified by PCR from the chromosomal DNA of strain 255 (*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 edc3Δ::kanMX4*) obtained from Research Genetics. DNA sequences up to 310 bp upstream and 340 bp downstream of the *EDC3* coding sequence were included in the amplified fragment used for transformation of FZY855 and HFY114 to G418-resistance. FZY855 was derived from SYY2352 by transforming with marker-swap plasmid pAG32 (Goldstein and McCusker 1999) to replace *scd6Δ::kanMX6* with *scd6Δ::hphMX6,* selecting for resistance to hygromycin and screening for

loss of G418-resistance. The presence of all deletion alleles was verified by PCR analysis of chromosomal DNA.

Strains H5695, H5696, H5697, and H5698 strains, employed for co-immunoprecipitation experiments, were generated by PCR-amplification of a *DHH1-TAP-HIS3MX* fragment from strain F2262 using primers AKV224 and AKV225, containing 474 bp upstream and 450 bp downstream of the *DHH1* stop codon, that was used to transform strains HFY114, FZY862, SYY2352, and FZY858, respectively, to His^+. A complete list of yeast strains employed is given in Table S1.

Plasmids pLfz614-7 and pLfz635-5 contain the *EDC3* CDS with 420 bp upstream and 490 bp downstream, on a ~2.6 kb fragment, and plasmids pL615-5 and pLfz636-1 contain the *SCD6* CDS with 500 bp upstream and 180 bp downstream on a ~1.7 kb fragment, amplified by PCR from yeast genomic DNA and inserted between the XhoI and EcoRI sites of YCplac33 or YCplac111, respectively. Plasmid pAK133 containing *DCP2-3HA* was produced by a multi-step PCR amplification scheme. First, the *DCP2* CDS with 920 nucleotides upstream of the start codon and 587 nucleotides downstream of the stop codon was amplified from genomic DNA of WT strain HFY114. Sequences encoding the 3XHA tag were introduced immediately upstream of the *DCP2* stop codon using primer pairs AKV372/AKV373 and AKV374/AKV375 during the first round of PCR amplification; a second round of PCR followed using primers AKV372 and AKV375 to amplify a complete *DCP2-3HA* fragment also containing sequences homologous to the ends of plasmid YCplac33 linearized by digestion with BamHI. The PCR product was fused into BamHI-digested YCplac33 using the Takara In-Fusion cloning kit (#638956) according to the manufacturer's instructions. Primers AKV372 and AKV375 were designed using the Takara on-line primer design tool to ensure optimal homologous recombination during the cloning process. The inserted yeast

DNA fragments were verified by sequencing in their entirety. A complete list of plasmids employed is given in Table S2 and the list of primers in Table S3.

Cell spotting growth assays

Yeast transformants harboring plasmids containing *EDC3*, *SCD6,* or empty vector were grown to mid-logarithmic phase at 30°C in liquid synthetic complete medium (SC) without uracil (SC-U). Cultures were diluted to OD_{600} of 1.0 and 10-fold serial dilutions were spotted on agar medium of the same composition and incubated at 30°C or 37°C for 2 days.

Polysome profiling

Polysome profiling was conducted as described previously (Zeidan et al. 2018). In brief, strains were cultured in YPD medium at 30°C to mid-logarithmic phase (OD_{600} of ~0.5-0.6). Fifteen A_{260} units of WCEs were resolved on a 10–50% sucrose gradient by centrifugation at 35,000 rpm. Gradients were fractionated with continuous scanning at 260 nm. Areas under the A_{260} tracings of polysome and monosome peaks were calculated using ImageJ software and used to calculate polysome to monosome (P/M) ratios in mutants and WT.

Ribosome footprint profiling

Duplicate cultures of yeast strains HFY114 (WT W303), SYY2352 (*scd6Δ*), FZY862 (*edc3Δ*), and FZY858 (*scd6Δedc3Δ*) were cultured in YPD medium at 30˚C to OD_{600} ~0.6-0.7. Yeast cells were quickly filtered, frozen in liquid nitrogen and stored at -80˚C. Cells were lysed in a freezer mill and ribosome protected mRNA fragments (RPF) were isolated and used for cDNA library preparation

as described previously (Vijjamarri et al. 2023b). Single-end 100 bp Illumina sequencing was performed by the National Heart, Lung and Blood Institute (NHLBI) DNA Sequencing and Genomics Core facility (Bethesda, MD).

RNA sequencing with spike-in normalization and CAGE analysis

The same lysates used for RPF library preparation were used to prepare RNA-Seq libraries after adding ERCC RNA Spike-In Control Mix 1 (Thermo Fisher Scientific, Cat. # 4456740). Total RNA was extracted from cell lysates using QIAzol Lysis reagent (Qiagen Cat. # 79306) and miRNeasy Mini Kit (Qiagen, Cat. 217004). Twenty µg of total RNA of each sample was subjected to RNase-free DNase I (Roche, Cat. # 04716728001) treatment and then processed with the RNA Clean and Concentrator Kit (Zymo, Cat. R1018). An aliquot of 2.4 µl of 1:100 diluted ERCC RNA Spike-In Control Mix 1 was added to 1.2 µg of each RNA sample and submitted to the NHLBI DNA Sequencing and Genomics Core facility (Bethesda, MD) for cDNA library preparation and Illumina sequencing. CAGE sequencing and RNA-Seq were conducted in parallel on two biological replicates of total RNA isolated from the same WT and *scd6Δedc3Δ* strains, cultured under the same conditions as employed for ribosomal profiling, exactly as described previously (Vijjamarri et al. 2023a).

Rpb1 ChIP-Seq with spike-in normalization

Triplicates of wild type and *scd6Δedc3Δ* yeast strains were cultured in rich YPD medium at 30˚C to OD600=0.6~0.8. Chromatin extracts were prepared from formaldehyde cross-linked cells as described previously (Qiu et al. 2016). *S. pombe* chromatin was added to each chromatin sample as a spike-in control prior to immunoprecipitation with Rpb1 antibodies, and ChIP-Seq DNA libraries were prepared as described previously (Zheng et al. 2023) subjected to 50 bp paired-end Illumina sequencing by the NHLBI DNA Sequencing and Genomics Core facility (Bethesda, MD) and analyzed as previously described (Zheng et al. 2023).

Western blot analysis

For the results in Fig. 6B-C, WCEs were prepared by trichloroacetic acid (TCA) extraction as previously described (Reid and Schatz 1982) and immunoblot analysis was conducted as described previously (Nanda et al. 2009). After electroblotting to nitrocellulose membranes (Bio-Rad 1620094), membranes were probed with antibodies against Atp20, Cox14, Pet10, Qcr8, Sdh4 (kindly provided by Dr. Nikolaus Pfanner), Cyb2 (kindly provided by Dr. Thomas Fox), Idh1 (Abnova, PAB19472), Cit2 (Antibodies-online.com, ABIN4889057), and Gcd6 (Bushman et al. 1993). Secondary antibodies employed were HRP-conjugated anti-rabbit (Cytiva, NA9340V), anti-mouse IgG (Cytiva, NA931V) and anti-goat IgG (Abnova, PAB29101). Detection was performed using enhanced chemiluminescence (ECL) Western Blotting Detection Reagent (Cytiva, RPN2016) and the Azure 200 gel imaging biosystem. NIH Image J was employed to analyze images for quantification. For analysis of Cox2 levels in Fig. 6D, total proteins were TCA-extracted as described previously (Rashida et al. 2021) and subjected to Western blot analysis as recently

described (Niphadkar et al. 2024) using mouse monoclonal antibody MTCO2 (4B12A5) from Invitrogen.

TMT-MS analysis of global protein abundance

TMT-MS analysis was conducted as described previously (Vijjamarri et al. 2023a) with the following modifications. Replicate cultures of WT, *edc3Δ, scd6Δ* and *scd6Δedc3Δ* strains were cultured in YPD medium for ~3 doublings to OD_{600} of ~0.6, and harvested by centrifugation for 5 min at 3000 x *g.* Cells were resuspended in nuclease-free water, collected by centrifugation, and stored at -80°C. WCEs were prepared in freshly prepared 8M Urea, 25 mM triethylammonium-bicarbonate (TEAB; Thermo Scientific, 90114) by washing the cell pellets once and resuspending again in the extraction buffer, then vortexing with glass beads in the cold room. Lysates were clarified by centrifugation at 13,000 x *g* for 30 min and the quality of extracted proteins was assessed following SDS-PAGE using GelCode™ Blue Stain (Thermo Scientific, 24592) and quantified with the Pierce™ BCA Protein Assay Kit (Thermo Scientific, 23225). Lysates were stored at -80°C. Sample preparation, TMT-MS/MS (Zecha et al. 2019) and data analysis were performed at the IDeA National Resource for Quantitative Proteomics.

Co-immunoprecipitation analysis

Transformants of *DHH1-TAP* strains were cultured in 50 ml YPD at 30°C to OD_{600} ≈ 0.6–0.8, harvested by centrifugation, and washed with 1 ml lysis buffer (LB) containing 0.5 mM PMSF. Cell pellets were resuspended in 500 µl LB supplemented with 0.5 mM PMSF and 1x protease inhibitor cocktail (Roche Cat # 5056489001) and lysed by vortexing in 200 µl glass beads (8 cycles:

30 sec on, 45 sec off) on ice in a cold room. Lysates were clarified by centrifugation (15,000 rpm, 20 min, 4°C), and protein concentrations determined using the Bradford assay. Approximately 1 µg of lysate was incubated with IgG sepharose beads pre-treated with 5% BSA for 2 h at 4°C. Beads were washed five times with LB containing 0.5 mM DTT. Bound complexes were eluted with 500 µl LB + 0.5 mM DTT containing 2 µl TEV protease (1 mg/ml, 10 U/µl; Invitrogen 12575-015) at room temperature for 2 h. Eluates were precipitated with 10% cold TCA on ice for 10 min, pelleted by centrifugation (13,000 rpm, 10 min, 4°C), washed with cold acetone, air-dried, resuspended in 50 µl 2× SDS-PAGE sample buffer, neutralized with 50 µl unadjusted 1 M Tris, and boiled for 5 min. Samples were subjected to immunoblot analysis as described above using rabbit polyclonal TAP antibodies (Thermo Fisher Scientific Cat# CAB1001) and mouse monoclonal antibodies against HA (12CA5) (Roche 10522600) for detecting TAP and HA tags.

Measuring mitochondrial membrane potential

Precultures were grown in SC-Ura (to select for the *URA3* plasmids) to OD_{600} of ~3.0 and used to inoculate YPD medium at OD_{600} of 0.2. Cells were grown to OD_{600} of ~0.6-0.8, incubated with 500 nM TMRM for 1 h and subjected to flow cytometry to measure dye fluorescence in individual cells as described previously (Vijjamarri et al. 2023b). In control samples, 50 µM FCCP was added to dissipate the membrane potential and reveal non-specific background fluorescence. Results are presented in arbitrary fluorescence units normalized to OD_{600} of the cultures.

Analysis of polar metabolites of intermediary metabolism.

Yeast cell culturing. Four replicate 15 mL cultures in YEPD medium were prepared for each strain by inoculating with saturated overnight cultures to OD_{600} of 0.1, culturing with shaking at 30°C, and harvesting at OD_{600} of 0.6 by centrifugation in conical 15mL tubes for 3 min at 3000 x g in an Avanti J-HC centrifuge pre-cooled to -10°C. Cell pellets were resuspended in 1.8 mL of ice-cold PBS and centrifuged in 2 mL screw-cap tubes in a refrigerated microfuge for 30 s. Supernatants were decanted, tube rims blotted on tissue paper, and cell pellets frozen in dry ice/ethanol for 5 min and stored at -80C. Frozen cell pellets were shipped on dry ice to the NYU Metabolomics Core Resource Laboratory, where all subsequent analyses described below were conducted.

Extraction of metabolites. Frozen cell pellets were thawed on wet ice. Extraction buffer, consisting of 80% methanol (Fisher Scientific) and 500 nM metabolomics amino acid mix standard (Cambridge Isotope Laboratories, Inc.), was prepared and placed on dry ice. Samples were extracted by mixing cell pellets with extraction buffer at 10mg/mL (determined by sample OD measurements) in 2.0 mL screw-cap vials containing ~100 µL of disruption beads (Research Products International, Mount Prospect, IL). Each sample was homogenized for 10 cycles on a bead blaster homogenizer (Benchmark Scientific, Edison, NJ), with each cycle consisting of 30 sec homogenization at 6 m/s followed by a 30 sec pause. Samples were centrifuged at 21,000 g for 3 min at 4°C. Aliquots of 450 µL were transferred to 1.5 mL tubes, dried in a Speedvac (Thermo Fisher, Waltham, MA), reconstituted in 50 µL of Optima LC/MS grade water (Fisher Scientific, Waltham, MA), sonicated for 2 min, and centrifuged at 21,000 g for 3 min at 4°C. Aliquots of 20 µL were transferred to LC vials containing glass inserts for analysis, and the remaining samples stored at -80°C.

LC-MS/MS with the hybrid metabolomics method. Samples were subjected to an LC-MS analysis to detect and quantify known peaks. Extraction of polar metabolites was carried out on each sample based on a previously described method (Jones et al. 2014). LC was conducted using a Millipore™ ZIC-pHILIC (2.1 x150 mm, 5 µm) column coupled to a Dionex Ultimate 3000™ system with gradient elution conducted at 25°C with a flow rate of 100 µL/min using the following buffers A) 10 mM ammonium carbonate in water, pH 9.0, and B) neat acetonitrile. The gradient profile was as follows; 80-20% B (0-30 min), 20-80% B (30-31 min), 80-80% B (31-42 min). Injection volume was set to 2 µL for all analyses with a 42 min total run time per injection.

MS was conducted by coupling the LC system to a Thermo Q Exactive HF™ mass spectrometer operating in heated electrospray ionization mode (HESI). Method duration was 30 min with a polarity switching data-dependent Top 5 method for both positive and negative modes. Spray voltage for both positive and negative modes was 3.5kV and capillary temperature was set to 320 °C with a sheath gas rate of 35, aux gas of 10, and max spray current of 100 µA. The full MS scan for both polarities utilized 120,000 resolution with an AGC target of 3e6 and a maximum IT of 100 ms, and the scan range was from 67-1000 m/z. Tandem MS spectra for both positive and negative mode used a resolution of 15,000, AGC target of 1e5, maximum IT of 50 ms, isolation window of 0.4 m/z, isolation offset of 0.1 m/z, fixed first mass of 50 m/z, and 3-way multiplexed normalized collision energies (nCE) of 10, 35, 80. The minimum AGC target was 1e4 with an intensity threshold of 2e5. All data were acquired in profile mode.

Relative quantification and statistical analyses of polar metabolites. The resulting Thermo™ RAW files were converted to SQLite format using an in-house python script to enable downstream peak detection and quantification. The available MS/MS spectra were first searched against the

NIST17 MS/MS (Simon-Manso et al. 2013), METLIN (Smith et al. 2005) and respective Decoy spectral library databases using an in-house data analysis python script adapted from our previously described approach for metabolite identification false discovery rate control (FDR) (Wang et al. 2018; Wang et al. 2020). Metabolite peaks were extracted based on the theoretical m/z of the expected ion type, e.g., $[M+H]^+$, with a 15 part-per-million (ppm) tolerance and a ± 0.2 min peak apex retention time tolerance within an initial retention time search window of ±0.5 min. For all the group-wise comparisons, t-tests were performed using the Python SciPy (1.5.4) (Virtanen et al. 2020) library to test for differences and generate statistics for the downstream analyses. For the pairwise t-tests, any metabolite with a p-value < 0.01 was considered significantly regulated (up- or down-) for prioritization in the subsequent analyses.

Coverage of a library of polar metabolites of major pathways of intermediary metabolism allowed detection of 130 of the 147 metabolites examined in at least 4 samples, and 91 detected in all 20 samples after background threshold correction. Instrument performance was assessed using the internal standards added to the samples during metabolite extraction and instrument mass accuracy was within tolerance (-2.0 ppm), LC column performance was stable (0.16 min RT range) and internal standard response variability was 13% across the samples. The resulting data were analyzed by principal components analysis (Fig. 7A), by constructing heatmaps with unsupervised hierarchical clustering of the imputed matrix values utilizing the R library pheatmap (1.0.12). GraphPad Prism 9 (9.4.1, GraphPad Software, San Diego, CA), and volcano plots (generated utilizing R library script Manhattanly (0.2.0)), in addition to the statistical comparisons summarized in Supplementary File S7.

$^{13}C_6$-glucose metabolic flux measurements. Three replicate cultures of each strain were grown in YP medium with 2% unlabeled glucose to OD_{600} of 0.6-0.7 and then shifted to YP with 1% unlabeled glucose and cultured for 20 min. $^{13}C_6$-labelled glucose (1%) was then added and growth was continued for 8 min. Cells were collected, and metabolites were extracted, derivatized and subjected to mass spectrometry as described previously, with the addition of additional masses for assessing the label incorporation into the specific labelled intermediates that were analyzed (Walvekar et al. 2018).

ATP Measurements

Cells were cultured in YPD to OD_{600} of 0.6-0.7 and treated or untreated with 5 mM sodium azide for 30 min at 30°C. Five OD_{600} units of cells were harvested and resuspended in 300 µL ice-cold 5% trichloroacetic acid (TCA), incubated on ice for 15 min, and diluted 50-fold in 20 mM Tris-HCl (pH 7.5) to 0.1 % TCA, after which 10 µL was mixed with 90 µL of ATP Determination reaction mixture (Cat. # A22066, Thermo-Fisher Scientific) and incubated at room temperature for 5 min. Units of Firefly Luciferase were measured in a Berthold Centro XS^3 LB 960 Luminometer, and ATP levels were calculated from an ATP standard curve generated using the same assay.

Additional data visualization and statistical analyses

Notched box-plots were constructed using a web-based tool at http://shiny.chemgrid.org/boxplotr/. In all such plots, the upper and lower boxes contain the 2nd and 3rd quartiles and the band gives the median. If the notches in two plots do not overlap, there is roughly 95% confidence that their medians differ. Density scatter plots, Venn diagrams,

significance testing of gene set overlaps in Venn diagrams using the hypergeometric distribution, hierarchical clustering analysis, and gene ontology (GO) analysis all were conducted as described previously (Vijjamarri et al. 2023a).

RESULTS

Evidence that Scd6 and Edc3 functionally cooperate to control the abundance of many individual mRNAs. To determine whether Scd6 and Edc3 function redundantly in post-transcriptional control of gene expression, we constructed a *scd6Δedc3Δ* double mutant isogenic to the *scd6Δ* and *edc3Δ* single mutants we examined previously (Zeidan et al. 2018). Only the double mutant exhibits a marked slow-growth (Slg^-) phenotype on synthetic complete medium (SC), which was largely complemented by introducing either *SCD6* or *EDC3* on a single copy plasmid (Supplemental Fig. S1A). Analysis of polysome assembly revealed a ~40% reduction in ratio of polysomes to monosomes (P/M) in the *scd6Δedc3Δ* double mutant, whereas the single mutants showed little (*scd6Δ*) or no (*edc3Δ*) reduction in bulk translation by this assay (Fig. S1B). These results suggest that Scd6 and Edc3 act redundantly to carry out one or more functions required for WT levels of bulk translation and cell growth in nutrient replete cells.

To examine the effects of the *scd6Δ, edc3Δ,* and *scd6Δedc3Δ* mutations on the abundance and translation of individual mRNAs, we conducted RNA-Seq and ribosome profiling (Ribo-Seq) of the mutant and WT strains following growth in liquid rich medium (YPD) at 30°C (processed data compiled in supplementary File S1). Ribo-Seq entails deep-sequencing of ribosome-protected fragments (RPFs, or ribosome footprints), and cycloheximide was added to the lysates to arrest elongating ribosomes on the mRNA following cell breakage. The ratio of RPF sequencing

reads summed over the coding sequences (CDS) to the total mRNA reads from RNA-Seq for the corresponding transcript provides a measure of translational efficiency (TE) for each mRNA (Ingolia et al. 2009). The ribosome profiling and RNA-Seq results between two biological replicates for each strain were highly reproducible with Pearson correlation coefficients (r) ranging between 0.95-1.0 for different pairwise comparisons of replicates (Fig. S2A-B). We employed DESeq2 (Love et al. 2014) to identify statistically significant differences in relative mRNA abundance, RPF abundance, or TE for all expressed mRNAs between WT and mutant strains (see Methods for details).

Analysis of the RNA-Seq results identified 81 mRNAs that were significantly up-regulated in the *edc3Δ* mutant vs. WT by >1.5-fold at a false discovery rate (FDR) of <0.05 (dubbed mRNA_up_e3 transcripts; Fig. S3A), and 123 mRNAs reduced in abundance by *edc3Δ* by the same criteria (dubbed mRNA_dn_e3, Fig. S3B). Only 14 mRNAs were up-regulated and only 34 down-regulated by the *scd6Δ* single mutation (respectively, mRNA_up_s6 and mRNA_dn_s6, Fig. S3A-B). Importantly, many more mRNAs were dysregulated by the *scd6Δedc3Δ* double mutation: 741 in the mRNA_up_s6,e3 group and 793 in the mRNA_dn_s6,e3 group (Fig. S3A-B), indicating that the two factors have highly redundant functions in controlling mRNA abundance.

Many yeast mutants with Slg$^-$ phenotypes, including *pat1Δ, dhh1Δ,* and *dcp2Δ* deletion mutants, exhibit altered expression of most mRNAs belonging to the Environmental Stress Response (ESR) (O'Duibhir et al. 2014), which includes ~300 induced (iESR) and ~600 down-regulated (rESR) mRNAs dysregulated in WT cells by various stresses (Gasch et al. 2000). In keeping with its Slg$^-$ phenotype, the *scd6Δedc3Δ* mutation conferred a marked reduction in median expression of rESR mRNAs, and increased expression of the iESR mRNAs, which exceeded

in magnitude the changes observed for the slowest growing yeast deletion mutants analyzed previously (O'Duibhir et al. 2014) (Fig. S3C-D). The two single mutations, by contrast, conferred much smaller changes in ESR mRNAs (Fig. S3C-D). (In all box plots, when notches do not overlap between adjacent boxes, their two medians differ with 95% confidence; and when notches do not overlap 0 in $\log_2$ plots, the median differs significantly from that of all mRNAs, which is invariably close to 1.0.) Consistent with these results, the transcripts up-regulated in the double mutant are enriched for iESR mRNAs (Fig. 1A), suggesting that the 187 iESR transcripts up-regulated in this strain are responding indirectly to cell stress. The remaining 75% of mRNAs up-regulated in *scd6Δedc3Δ* cells are not iESR mRNAs however (Fig. 1A), suggesting that their increased abundance arises from eliminating Edc3/Scd6 functions in mRNA decay. Below, we excluded the ESR mRNAs from analyses of mRNA changes in an effort to focus on the transcripts controlled directly by Scd6 and Edc3.

Considering only mRNAs not governed by the ESR, we identified 591 non-iESR mRNAs significantly up-regulated in any of the three mutants (Fig. 1B; eg. Non-iESR mRNA_up_s6,e3 designating the 554 mRNAs up-regulated in the double mutant). Examining the ΔRNA values for the majority fraction of the Non-iESR transcripts up-regulated only in the double mutant reveals little change in median abundance in each single mutant but strong up-regulation in the double mutant (Figs. 1B & 1C, sector (iii)), as expected for redundant repressive functions of Scd6 and Edc3. *MDH2,* encoding an enzyme of the glyoxylate cycle, exemplifies a non-iESR transcript up-regulated in both mRNA and RPF abundance exclusively in the double mutant (Fig. 1D). The small fraction of 27 mRNAs significantly up-regulated in both the *edc3Δ* single mutant and double mutant exhibits only slightly elevated median abundance in the *scd6Δ* single mutant, and only

slightly greater up-regulation in the double mutant vs. *edc3Δ* single mutant (Fig. 1B & 1C, sector (ii)), indicating a minimal repressive contribution by Scd6. Interestingly, the small set of 37 mRNAs significantly up-regulated only in the *edc3Δ* single mutant shows reduced rather than increased abundance in the *scd6Δ* single mutant, and lower up-regulation in the double mutant vs. the *edc3Δ* single mutant (Fig. 1B & C, sector (i)), suggesting that Scd6 enhances rather than represses these mRNAs, especially in *edc3Δ* cells.

Evidence that Dhh1 and Pat1 functionally cooperate with Scd6/Edc3 in repressing mRNA abundance. We recently identified a group of 1018 non-iESR mRNAs up-regulated by either *pat1Δ, dhh1Δ,* or *pat1Δdhh1Δ* mutations (Vijjamarri et al. 2023a). Importantly, this group is highly enriched for the 591 mRNAs up-regulated by *scd6Δ, edc3Δ,* or *scd6Δedc3Δ* mutations (Fig. 2A). Indeed, ~70% of the transcripts up-regulated by *scd6Δ/edc3Δ* are also up-regulated in one of the three *pat1Δ/dhh1Δ* mutants (Fig. 2A, sector (ii)), showing comparable up-regulation in the *scd6Δedc3Δ, pat1Δ,* and *dhh1Δ* mutants, but little change in the *scd6Δ* and *edc3Δ* single mutants (Fig. 2B(ii)). These mRNAs generally exhibit the greatest up-regulation in the *pat1Δdhh1Δ* double mutant, indicating cumulative contributions of Dhh1 and Pat1 to their repression, in contrast to the largely redundant roles played by Scd6 and Edc3 in their repression. As expected, the smaller group of 180 mRNAs significantly up-regulated exclusively by *scd6Δ/edc3Δ* (sector (i) of Fig. 2A) shows strong up-regulation only in the *scd6Δedc3Δ* double mutant; but they are appreciably up-regulated by *dhh1Δ* while being largely unaffected by *pat1Δ* (Fig. 2B, sector (i)). Finally, the majority group of 607 mRNAs significantly up-regulated by only *pat1Δ* or *dhh1Δ* display the largest increases in the two mutants lacking Pat1, but smaller and similar increases in response

to the *scd6Δ/edc3Δ* and *dhh1Δ* mutations (Figs. 2A & 2B, sector (iii)). Overall, these findings suggest that Dhh1 and Pat1 both contribute to repressing the majority of mRNAs repressed redundantly by Scd6 and Edc3, with Dhh1 contributing more extensively than Pat1.

Further evidence for this last point comes from a k-means clustering analysis of mRNA changes in different mutants for the group of 431 non-iESR mRNAs up-regulated by *dhh1Δ,* which revealed a stronger correlation between the changes conferred by *scd6Δ/edc3Δ* and *dhh1Δ* (ρ = 0.90) than between *pat1Δ* with *dhh1Δ* (ρ = 0.74) or *scd6Δ/edc3Δ* (ρ = 0.71) (Fig. 2C). Consistent with this, the *scd6Δ/edc3Δ* mutations up-regulate a considerably larger proportion of the mRNAs significantly up-regulated by *dhh1Δ* (~70%) vs. those up-regulated by *pat1Δ* (~41%) (Fig. 2D). Furthermore, the majority of mRNAs up-regulated by *dhh1Δ* exhibit redundant repression by Scd6 and Edc3, showing marked up-regulation comparable to that given by *dhh1Δ* itself only in the *scd6Δ/edc3Δ* double mutant (Fig. 2E). These findings are consistent with the involvement of Edc3/Scd6 in the degradation of most mRNAs targeted by Dhh1, which are more variably and less extensively repressed by Pat1.

Evidence that Scd6/Edc3 repress mRNA abundance by enhancing decapping/degradation and facilitating Dhh1 association with Dcp2. We next examined whether the mRNAs significantly down-regulated by Edc3/Scd6 are also regulated by the decapping enzyme Dcp1/Dcp2. Supporting this, cluster analysis of mRNA changes revealed that the majority of non-iESR mRNAs up-regulated in the *scd6Δedc3Δ* double mutant are also up-regulated by *dcp2Δ* (Fig. 3A, blue colors in cols. 1 & 3), with a strong correlation between the abundance changes conferred by these mutations relative to WT (ρ=0.74). In addition, *dcp2Δ* increased the median abundance of

this group of mRNAs similarly to that given by *scd6Δedc3Δ* (Fig. 3B, cols. 1 & 4). These findings implicate decapping by Dcp1:Dcp2 as an important driver of the repression of mRNA levels directed by Scd6/Edc3. The cluster analysis in Fig. 3A once again reveals greater similarity between the mRNA changes conferred by *scd6Δedc3Δ* and those given by *dhh1Δ* (ρ = 0.90) versus *pat1Δ* (ρ = 0.69); and *pat1Δ* also confers a smaller median reduction than *dhh1Δ* of the Scd6/Edc3-down-regulated mRNAs (Fig. 3B).

Additional support that Scd6/Edc3 target mRNAs for decapping came from evidence that mRNAs up-regulated in the *scd6Δedc3Δ* mutant tend to accumulate in WT cells as decapped isoforms. Following decapping by Dcp1/Dcp2 mRNAs frequently undergo 5' to 3' decay co-translationally, with Xrn1 following behind the last translating ribosome loaded prior to decapping, and such decapped intermediates account for ~12% of all mRNAs in WT cells (Pelechano et al. 2015). We reasoned that mRNAs preferentially targeted by Scd6/Edc3 for decapping and attendant degradation by Xrn1 should exhibit a greater than average proportion of decapped intermediates in WT cells. To test this, we conducted cap analysis of gene expression (CAGE) to quantify the abundances of all capped mRNA 5' ends and compare them to total mRNA abundances determined by RNA-Seq conducted in parallel on biological replicates prepared from the WT and *scd6Δedc3Δ* strains described above. Transcript numbers per million reads (TPMs) from CAGE (C) and RNA-Seq (T) were determined and C/T ratios calculated as a proxy for the proportion of capped molecules for each transcript (Vijjamarri et al. 2023a) (File S1). (Because the CAGE and RNA-Seq data were normalized separately, the C/T ratios are relative, not absolute, proportions of capped transcripts.) Importantly, the C/T ratios are lower in WT cells for the 498 non-iESR mRNAs up-regulated in the *scd6Δedc3Δ* double

mutant compared to all expressed mRNAs (Fig. 3C, cols. 1 & 5) in the manner expected for mRNAs preferentially targeted for decapping in WT cells. By contrast, the C/T ratios are higher than average for the non-rESR mRNAs that are down-regulated in relative abundance in *scd6Δedc3Δ* cells, as expected for an unusually low degree of decapping in WT (Fig. 3C, cols 3 & 5). Importantly, these C/T ratios were elevated in *scd6Δedc3Δ* cells to nearly the same level for all three groups of mRNAs, which exceeds the ratios found in WT cells, in the manner expected from eliminating Scd6/Edc3-stimulated decapping (Fig. 3C, cf. cols. 2,4,6). Similar results were obtained for these same groups of dysregulated mRNAs by analyzing our previous CAGE data obtained for the *dhh1Δ* mutant (Vijjamarri et al. 2023a) (Fig. S3E). These findings are consistent with the notion that impaired decapping dependent on Scd6/Edc3 and Dhh1 is an important driver of increased mRNA abundance in the *scd6Δedc3Δ* mutant.

Independent evidence for this last conclusion was provided by analyzing the codon protection indices (CPI) of mRNAs up-regulated by *scd6Δedc3Δ*, an indicator of co-translational decay by Xrn1. Decapped degradation intermediates exhibit three-nucleotide periodicity generated by precise Xrn1 cleavage up to the last translating ribosome at the 5' end of mRNA, and the CPI quantifies the prevalence of such intermediates for each mRNA (Pelechano et al. 2015). Importantly, the mRNA_up_s6,e3 transcripts (whether including or excluding ESR mRNAs) exhibit higher than average median CPIs, indicating a greater than average involvement of decapping and co-translational degradation by Xrn1 in their decay, whereas mRNA_dn_s6,e3 transcripts exhibit lower than average CPI values, consistent with an alternative degradation pathway controlling their abundance *scd6Δedc3Δ* (Fig. 3D).

To determine whether increased transcription contributes to increased abundance of mRNAs up-regulated by *scd6Δedc3Δ*, we performed ChIP-Seq analysis of Rpb1 to measure RNA Polymerase II (Pol II) occupancies averaged across the CDS of every gene, obtaining highly reproducible results across replicates (Fig. S2D & S4A). To quantify absolute changes in Pol II occupancies, *S. pombe* chromatin was added to each *S. cerevisiae* chromatin sample prior to immunoprecipitation. To measure absolute changes in mRNA abundance, we re-analyzed the RNA-Seq data taking into account the recovery of External RNA Controls Consortium (ERCC) transcripts that were added to each total RNA sample prior to preparation of cDNA libraries, yielding highly reproducible normalized values among replicates (Fig. S2C). Interrogating the non-ESR mRNAs up- or down-regulated by *scd6Δedc3* revealed a 2.79-fold increase in median normalized mRNA abundance for the non-iESR mRNA_up_s6,e3 group that was associated with only a 1.2-fold increase in normalized Rpb1 occupancies (Fig. 3E, cols. 1 & 4). The down-regulated non-rESR mRNA_dn_s6,e3 transcripts showed 12% and 7% decreases in spike-in normalized median mRNA abundance and Rpb1 occupancies, respectively, (Fig. 3E, cols. 2 & 5). Because the majority of total mRNA is rRNA, the ERCC normalization effectively yields the abundance of each mRNA relative to rRNA, and the ribosome content per cell is expected to be reduced in the *scd6Δedc3Δ* mutant owing to repression of rESR mRNAs encoding ribosomal proteins and biogenesis factors (Fig. S3C). We showed previously that the isogenic *dcp2Δ* mutant displays an ESR response of similar magnitude and a 30% reduction in ribosomal subunits per cell compared to same WT examined here (Vijjamarri et al. 2023b). Assuming a similar reduction in ribosome abundance in *scd6Δedc3Δ* cells, the absolute changes in mRNA per cell conferred by *scd6Δedc3Δ* are expected to be 0.7-fold of the ERCC-normalized values given in Fig. 3E, yielding fold-changes

of 2.0 and 0.62 for the mRNA_up_s6,e3 and mRNA_dn_s6,e3 groups, respectively. Because these predicted changes in mRNA per cell still differ substantially from the corresponding changes in normalized Rpb1 occupancies of 1.2 and 0.93, respectively, there is only a small contribution of altered transcription to the altered abundance of transcripts dysregulated in the double mutant.

Our findings above that the *scd6Δedc3Δ* and *dhh1Δ* mutations up-regulate highly similar sets of mRNAs (Fig. 2C) is consistent with a previous proposal that recruitment of Dhh1 to Dcp2 can be mediated interchangeably by Edc3 or Scd6 bound to the same site in the Dcp2 CTT (He et al. 2022). To test this model we asked whether association of Dhh1 with Dcp2 in cell extracts is impaired only when both Edc3 and Scd6 are eliminated. Indeed, co-immunoprecipitation of HA-tagged Dcp2 with TAP-tagged Dhh1 was reduced in *scd6Δedc3Δ* cells but not in either single mutant in replicate experiments (Fig. 3F, lanes 2-4; Fig. S5(i)-(ii)). The residual association in the double mutant suggests that Dhh1 can interact with Dcp2 either directly or via Pat1 in addition to the interaction mediated by Scd6/Edc3, which might explain why a small fraction of mRNAs are up-regulated by *dhh1Δ* but not by *scd6Δedc3Δ* (Fig. 2C).

Slow rates of translation initiation or elongation generally do not dictate preferential decapping/decay by the decapping activators.

Codon non-optimality has been linked with Dhh1-mediated mRNA decay partly by demonstrating that the sTAI values of mRNAs, which quantify their overall codon optimality (Sabi and Tuller 2014), are inversely correlated with the changes in mRNA abundance observed in *dhh1Δ* versus WT cells (Radhakrishnan et al. 2016). Similarly, analyzing the mRNA changes conferred by the *scd6Δedc3Δ* mutation for all non-ESR transcripts reveals a small but statistically

significant negative correlation with sTAI values (Pearson r of -0.085, P = 2 x 10^{-9}) similar to that observed for the *dhh1Δ* mutation (r = -0.071, P = 6 x 10^{-6}) (Fig. S6A, cyan vs. orange), indicating a tendency for mRNAs with lower codon optimality/sTAI scores to show greater increases in relative abundance in response to *scd6Δedc3Δ* or *dhh1Δ*. However, the 591 non-iESR mRNAs up-regulated by the *scd6Δ/edc3Δ* mutations (from Fig. 1B) have a median sTAI value (0.35) nearly identical to that of all nonESR mRNAs, which is also the case for the group of 1018 mRNAs up-regulated by the *pat1Δ* or *dhh1* mutations (Vijjamarri et al. 2023a) (Fig. S6B). Similar results were obtained for other metrics of codon optimality, tAI and average CSC (Fig. S6B), suggesting that poor codon optimality is not a key property defining the mRNAs repressed most extensively by these decapping activators. It has also been proposed that competition between translation initiation and mRNA decay, rather than codon optimality and elongation, is a major determinant of mRNA stability in yeast (Muhlrad et al. 1995; LaGrandeur and Parker 1999; Schwartz and Parker 1999; Chan et al. 2018). However, the mRNAs up-regulated in the *scd6Δ/edc3Δ* or *pat1Δ/dhh1* mutants have slightly greater than average median translational efficiencies (TEs) in WT cells (Fig. S6C), as determined by ribosome profiling experiments described below. Thus, neither slow rates of translation initiation nor pausing during elongation at non-optimal codons appears to dictate preferential targeting of the mRNAs most strongly repressed by these four decapping activators.

Scd6 and Edc3 act redundantly and cooperate more extensively with Dhh1 than Pat1 in controlling translation of individual mRNAs.

The changes in mRNA abundance were highly correlated with changes in RPF abundance for the *scd6Δedc3Δ* mutant compared to WT for all expressed transcripts, with an r value of 0.81 (Fig. S2F), providing strong mutual validation of the RNA-Seq and Ribo-Seq data for these strains. Nevertheless, the fact that this correlation is weaker than that observed between biological replicates of RNA-Seq or Ribo-Seq data (r values >0.95, Fig. S2A-B), suggests that certain mRNAs exhibit altered translational efficiencies in the double mutant. Indeed, DESeq2 analysis of the Ribo-Seq data identified 184 mRNAs showing TE increases of >1.41-fold at FDR < 0.10 in the *scd6Δedc3Δ* strain (dubbed TE_up_s6,e3) but only 42 and one such mRNA in the *scd6Δ* and *edc3Δ* single mutants, respectively (Fig. 4A), suggesting that Scd6 and Edc3 have overlapping functions in repressing the translation of particular mRNAs. Supporting this, a group of 169 mRNAs translationally up-regulated exclusively in the *scd6Δedc3Δ* double mutant exhibit only modest TE increases in the two single mutants (Fig. 4A-B, sector (iii)). *SPI1,* encoding a cell wall protein, is a representative transcript displaying increased mRNA abundance coupled with an even greater increase in RPF abundance to confer a TE increase of ~3-fold only in the double mutant (Fig. 4C). As expected, the 28 mRNAs showing substantial TE increases only in *scd6Δ* cells show no increase in median TE in the *edc3Δ* strain (Fig. 4A-B, sector (i)), and thus appear to be translationally repressed by Scd6 alone.

We explored next whether the increased ribosome occupancies observed in the *scd6Δedc3Δ* mutant are associated with increased protein synthesis by conducting TMT mass spectrometry (TMT-MS) of total cell proteins to obtain ratios of peptide abundance in the *scd6Δedc3Δ* strain vs. WT for >4000 different proteins (Fig. S2E). Importantly, significant correlations exist between changes in protein abundance and RPFs across the translatome (Fig.

4D). Moreover, mRNAs showing increased or decreased RPFs in *scd6Δedc3Δ* vs. WT cells (>1.5-fold, FDR<0.05, Ribo_up and Ribo_dn) likewise exhibit increased or decreased median protein abundances determined by TMT-MS (Fig. 4E). These results suggest that increased ribosome occupancies measured by Ribo-Seq, which could occur by increases in mRNA, TE, or both, are generally associated with increased synthesis of the encoded proteins in *scd6Δedc3Δ* cells.

It was possible that translational repression by Edc3/Scd6 generally occurs by slowing elongation, leading to increased ribosome densities (RPF/mRNA ratios, ie. calculated TEs) in WT cells and decreased TE values in *scd6Δedc3Δ* cells that would be associated with increased protein expression. In this scenario, changes in TEs would be inversely associated with changes in protein expression. Instead, mRNAs showing increased or decreased TEs in the double mutant (TE_up_s6,e3 and TE_dn_s6,e3 transcripts defined above) also exhibit increased or decreased protein expression in *scd6Δedc3Δ* vs. WT cells (Fig. 4F), implying that Scd6/Edc3 generally influence translation at the initiation step.

We previously identified 274 mRNAs whose TEs are up-regulated in the *pat1Δ, dhh1Δ,* or *pat1Δdhh1Δ* mutants by the same criteria employed here (>1.41-fold at FDR < 0.10) (Vijjamarri et al. 2023a). Interestingly, these mRNAs overlap significantly with those translationally up-regulated in the single or double *scd6Δ/edc3Δ* mutants (Fig. 5A). The 76 mRNAs common to both groups show larger TE increases in the *scd6Δedc3Δ* mutant compared to the 136 transcripts up-regulated exclusively in the *scd6Δ/edc3Δ* mutants (Figs. 5A-B, sector (ii) vs. sector (i)). These 76 mRNAs also show marked TE increases in the *dhh1Δ, pat1Δ*, and *pat1Δdhh1Δ* mutants (Fig. 5B(ii)), indicating that all four decapping activators are required for efficient translational repression of these mRNAs in WT cells. The 136 mRNAs significantly up-regulated only in the *scd6Δ/edc3Δ*

mutants show a moderate increase in median TE in *dhh1Δ* cells, but little response to *pat1Δ* (Fig. 5B(i)). The 198 mRNAs up-regulated only in the *pat1Δ/dhh1Δ* mutants show only a small TE increase in the *scd6Δedc3Δ* strain and cumulative TE increases in the *pat1Δdhh1Δ* double mutant (Fig. 5B(iii)). In summary, similar to our findings for repression of mRNA abundance, efficient translational repression of certain mRNAs requires the combined functions of Pat1, Dhh1, and either Scd6 or Edc3, whereas other mRNAs are translationally repressed by either Edc3/Scd6 or Pat1 with appreciable contributions from Dhh1.

Greater cooperation of Scd6/Edc3 with Dhh1 vs. Pat1 in controlling translation is also revealed by clustering analysis of TE changes in different mutants for the mRNAs exhibiting altered TEs in the *scd6Δ/edc3Δ* mutants, with greater similarity between TE changes conferred by *scd6Δedc3Δ* vs. *dhh1Δ* ($\rho = 0.82$) compared to *scd6Δedc3Δ* vs. *pat1Δ* ($\rho = 0.68$) or *scd6Δedc3Δ* vs. *pat1Δdhh1Δ* ($\rho = 0.69$) cells (Fig. 5C). However, as noted above, the group showing the strongest up-regulation of TEs in the *scd6Δedc3Δ* double mutant tends to be highly up-regulated in all three of the other mutants lacking Dhh1 or Pat1 (bracketed mRNAs at the top of Fig. 5C), as in Fig. 5D for a group of 54 mRNAs whose TEs are up-regulated by 2.0-fold or more in both the *scd6Δedc3Δ* and *pat1Δdhh1Δ* double mutants. Thus, although Scd6/Edc3 appear to cooperate more extensively with Dhh1 than Pat1 in translational control, the subset of 50-60 mRNAs exhibiting the strongest repression by Scd6/Edc3 or Pat1/Dhh1 require the concerted functions of Pat1, Dhh1, and either Scd6 or Edc3 to achieve their strong translational repression in WT cells.

To assess whether mRNAs translationally repressed by the decapping activators are also targeted for degradation by these factors, we examined mRNA changes for the groups of mRNAs exhibiting TE up-regulation in the *scd6Δ/edc3Δ* or *pat1Δ/dhh1Δ* mutants (sectors (i) to (iii) of Fig.

5A). The mRNAs showing increased TEs only in the *pat1Δ/dhh1Δ* strains show little change in mRNA abundance in these mutants (Fig. S7A(iii)), indicating selective repression of translation vs degradation. Similarly, mRNAs translationally up-regulated only in the *scd6Δ/edc3Δ* mutants show little change in mRNA abundance in the *scd6Δedc3Δ* strain and only modest up-regulation in the *pat1Δ/dhh1Δ* mutants (Fig. S6A(i)). In contrast, the transcripts showing increased TEs in all of the mutants also show markedly increased abundance in the same mutants (Fig. S6A(ii)). Thus, coupled repression of translation and abundance by the decapping factors occurs only for the subset of transcripts exhibiting concerted translational repression by all four factors. In contrast, the much larger groups of transcripts defined above showing increased mRNA abundance in the mutants (described in Fig. 2A) exhibit little change in median TE in all four mutants (Fig. S6B), suggesting that most mRNAs targeted for enhanced turnover do not exhibit translational repression of the fraction of undegraded transcripts remaining in WT cells.

We next examined the translational efficiencies of mRNAs translationally repressed by Scd6/Edc3 by interrogating the Ribo-Seq data for WT cells on rich medium. The mRNAs translationally repressed by Scd6/Edc3 in concert with Pat1/Dhh1 tend to be poorly translated in WT, having a substantially lower median relative TE compared to all mRNAs (0.24 vs. 0.95) (Fig. S6C, col. 2), thus resembling the mRNAs translationally repressed exclusively by Dhh1/Pat1 (col. 3). In contrast, the transcripts translationally repressed exclusively by Edc3/Scd6 are generally well translated, exhibiting a ~2.5-fold greater than average median TE in WT cells (Fig. S6C, col. 1). Consistent with this distinction, gene ontology (GO) analysis revealed that products of the 136 mRNAs translationally repressed exclusively by Scd6/Edc3 are enriched for cytoplasmic or mitochondrial ribosomal proteins ($P = 1 \times 10^{-7}$), whereas products of the 76 transcripts repressed

by Scd6/Edc3/Pat1/Dhh1 are enriched for factors involved in fermentation ($P = 2 \times 10^{-7}$), carbohydrate metabolism ($P = 1 \times 10^{-6}$) or metabolism of non-protein amino acids ($P = 3 \times 10^{-6}$). Thus, Scd6/Edc3 translationally repress distinct groups of mRNAs depending on whether Dhh1/Pat1 participate in the repression.

We showed previously (Zeidan et al. 2018) that mRNAs up-regulated by *dhh1Δ* are enriched for Dhh1 protein association in vivo as judged by RIP-Seq analysis of yeast mRNAs using antibodies against Dhh1 (Miller et al. 2018), thus providing evidence for a direct role of Dhh1 decapping/degradation of these transcripts. The same observation was made for the mRNAs up-regulated by *pat1Δ,* consistent with widespread cooperation between Dhh1 and Pat1 in repressing mRNA abundance (Vijjamarri et al. 2023a). Interestingly, here we observed greater than average Dhh1 occupancies for all four mRNA groups defined above (in Figs. 2A or 5A) that are up-regulated in transcript abundance or TE by the *scd6Δ/edc3Δ* or *dhh1Δ/pat1Δ* mutations (Fig. 5E). This finding is consistent with the fact that Dhh1 contributes to repressing the abundance or TE of the majority of transcripts in these groups (Figs. 2B & 5B). It is possible that Dhh1 is recruited to most of these mRNAs in a complex with Dcp1:Dcp2 and other decapping activators (He et al. 2022), but contributes differentially to their degradation or translational repression.

Scd6/Edc3 post-transcriptionally repress mRNAs encoding enzymes for respiration and catabolism of non-glucose carbon sources in rich medium.

Recently, we reported that mRNAs up-regulated in abundance or TE in the *dcp2Δ, pat1Δ* and *dhh1Δ* mutants are enriched for mitochondrial proteins that function in Ox. Phos. (Vijjamarri et

al. 2023a; Vijjamarri et al. 2023b). GO analysis led to the same finding here for the non-iESR mRNAs up-regulated in abundance by the *scd6Δ/edc3Δ* mutations, including many of the same categories of mitochondrial functions enriched among the mRNAs up-regulated by *dhh1Δ/pat1Δ* mutations (Fig. S8A-B, green type). GO analysis of genes showing increased ribosome occupancies (RPFs), indicating either increased mRNA abundance or TE, confirms that the *scd6Δ/edc3Δ* mutations derepress the translation of Ox. Phos. gene transcripts (Fig. S8C-D). Examining a collection of Ox. Phos. genes functioning in electron transport, the TCA cycle or mitochondrial ATP synthase reveals that the *scd6Δedc3Δ* and *pat1Δdhh1Δ* double mutations up-regulate expression of these genes primarily at the level of mRNA abundance, with small additional increases in TE (Fig. 6A). Western blot analysis revealed increased expression of four Ox. Phos. proteins (Qcr8, Atp20, Idh1, and Sdh4), two proteins (Cox14 and Cox20) involved in cytochrome c oxidase assembly, and mitochondrial cytochrome b2 (Cyb2) required for lactate utilization in *scd6Δedc3Δ* cells, relative to Gcd6 examined as loading control (Fig. 6B-C). Results similar to these were obtained for the same mitochondrial proteins in the *dhh1Δ* and *pat1Δ* mutants (Vijjamarri et al. 2023a) and for a subset in *dcp2Δ* cells (Vijjamarri et al. 2023b). Importantly, we also observed increased expression of Cox2, a mitochondrially encoded subunit of cytochrome *c* oxidase, terminal enzyme of the mitochondrial ETC, whose expression correlates with mitochondrial activity (Vengayil et al. 2024). Except for *dcp2Δ*, all the decapping mutants had significantly increased Cox2 protein (Fig 6D), suggesting an increase in ETC activity in these mutants. Up-regulation of mRNA and RPF abundance in *scd6Δedc3Δ* and *pat1Δdhh1Δ* double mutants also occurred for enzymes of the glyoxylate cycle (Fig. 6E), which catalyze certain reactions of the TCA cycle in the cytoplasm to support gluconeogenesis during respiratory growth

on two-carbon compounds; and the increased expression of one such enzyme, Cit2, was confirmed by Western analysis (Figs. 6B-C). Both Ox. Phos. and the glyoxylate cycle normally operate at low levels in yeast growing with abundant glucose, as in our experiments, suggesting that Scd6/Edc3 cooperate with Dhh1/Pat1 to help suppress these pathways in glucose-replete cells.

Consistent with post-transcriptional control of Ox. Phos. genes, the median relative RPF levels were up-regulated in the *scd6Δedc3Δ* mutant substantially more than the increases in relative Pol II occupancies observed at the cognate genes by ChIP-Seq analysis of Rpb1 (Fig. S9B, cols. 1-2). Moreover, the transcription factors responsible for induction of Ox. Phos. genes, the Hap2/Hap3/Hap4/Hap5 complex, were not activated in *scd6Δedc3Δ* cells: expression of a *CYC1-lacZ* reporter activated by this complex (Forsburg and Guarente 1989) was not elevated in the *scd6Δ/edc3Δ* mutants in glucose-containing medium (Fig. 6F(ii)) but showed the expected induction in WT cells grown with glycerol/ethanol versus glucose (6F(i)) (Broach 2012). These findings support the notion that reduced decapping stabilizes Ox. Phos. gene transcripts in *scd6Δedc3Δ* cells.

In addition to Ox. Phos., GO analysis of genes up-regulated in mRNA or RPF abundance in the *scd6Δ/edc3Δ* mutants revealed enrichment for utilization of alternative carbon sources (Fig. S8A-D), as observed recently for *dhh1Δ,pat1Δ* mutants (Vijjamarri et al. 2023a). Consistent with this, 83 carbon catabolite down-regulated (CCR) genes, known to be glucose-repressed or activated by transcription factors Adr1 or Cat8 (Young et al. 2003; Tachibana et al. 2005), exhibit increased translation (RPFs) largely through increased mRNA abundance in both *scd6Δedc3Δ* and *pat1Δdhh1Δ* double mutants (Fig. S9A). These genes encode enzymes for β-

oxidation of fatty acids in addition to the glyoxylate cycle, which allow cells to synthesize precursors that feed into gluconeogenesis or amino acid biosynthesis, or produce acetyl-CoA and generate NADH by respiration on non-fermentable carbon sources (Young et al. 2003). The CCR genes exhibit larger increases in RPFs compared to Pol II occupancies at the cognate genes in *scd6Δedc3Δ* vs. WT cells (Fig. S9B, cols. 3-4), consistent with post-transcriptional repression by Scd6/Edc3. Supporting this, an *ADH2-lacZ* reporter transcriptionally induced by activated Adr1 (Sloan et al. 1999) displayed the expected large induction in our WT strain cultured with glycerol/ethanol versus glucose as carbon source (Fig. S9C(i)), but was down-regulated by *scd6Δedc3Δ* in glucose-grown cells (Fig. S8C(ii)).

Functional evidence that Scd6/Edc3 repress oxidative phosphorylation.

We examined the effects of eliminating Scd6/Edc3 on mitochondrial electron transport by measuring mitochondrial membrane potential ($\Delta\Psi_m$) generated by the ETC using the probe tetramethylrhodamine (TMRM)—a cationic fluorescent dye that accumulates in mitochondria as a function of $\Delta\Psi_m$. Quantifying dye fluorescence by flow cytometry revealed increased TMRM fluorescence in the *scd6Δedc3Δ* mutant containing an empty vector compared to both the isogenic WT strain and the mutant complemented by WT *EDC3* (Fig. 6G). These results are consistent with increased mitochondrial ETC activity in glucose-grown *scd6Δedc3Δ* cells.

To determine whether up-regulation of Ox. Phos. and other glucose-repressed genes in the decapping activator mutants alters cellular metabolites, we used targeted, quantitative LC-MS/MS based approaches (see Methods) to quantify levels of 147 polar metabolites in the isogenic *scd6Δedc3Δ*, *dhh1Δ, pat1Δ, dcp2Δ* and WT strains described above, cultured in YPD

medium. Principle component analysis revealed clustering of results from biological replicates in the manner expected for reproducible differences in metabolite levels among different strains, with results for the *scd6Δedc3Δ* mutant most closely resembling those for *dhh1Δ,* which in turn were more similar to the results for *pat1Δ* vs. the *dcp2Δ* mutant or WT strains (Fig. 7A). This conclusion was borne out by cluster and correlation analyses of changes in metabolites between each mutant compared to WT, with the strongest correlation observed for *scd6Δedc3Δ* vs. *dhh1Δ*, followed by *dhh1Δ* vs. *pat1Δ* (Fig. 7B). Considering the subset of 46 metabolites up-regulated in any two of the four mutants again showed greatest similarity between changes conferred by *scd6Δedc3Δ* vs. *dhh1Δ* followed by *dhh1Δ* vs. *pat1Δ* (Fig. 7C). These findings mirror the results from RNA-seq and ribosome profiling in which the up-regulation of mRNA levels or translation was most similar between the *scd6Δedc3Δ* and *dhh1Δ* mutants. Pathway analysis of the 46 up-regulated metabolites (at https://www.metaboanalyst.ca/MetaboAnalyst/Secure/pathway) revealed a significant enrichment for metabolites of both the TCA and glyoxylate cycles (Fig. 7D), with five of the six TCA cycle intermediates detected (fumarate, malate, α-ketoglutarate, cis-aconitate and citrate) being elevated in the decapping mutants (Fig. 7E). These results are consistent with the possibility that up-regulation of Ox. Phos. proteins (Fig. 6A-D) and ETC function (Fig. 6F) in the decapping mutants leads to increased flux from glucose towards the TCA cycle.

To confirm increased flux through the TCA cycle coming from glucose breakdown, WT and mutant cells were grown in high glucose, pulsed with $^{13}C_6$ glucose, and relative ^{13}C label incorporation into TCA cycle intermediates was estimated for each carbon molecule derived from glucose (as indicated schematically in Fig. 8A) eight min following the pulse. In all mutants,

^{13}C label incorporation in all TCA cycle intermediates was significantly higher than in WT cells (Fig. 8A), demonstrating increased carbon flux from glucose into the TCA cycle. These results, along with increased ETC activity (Fig. 6G), indicate that mitochondrial function is up-regulated in these mutants on glucose. If so, we might expect them to show increased ATP production from respiration versus glycolysis. Measuring total ATP levels in glucose-grown cells revealed that, while all decapping mutants except *pat1Δ* showed reduced ATP per cell (Fig. 8B), the proportion of ATP produced from respiration, and thus eliminated by sodium azide treatment (by inhibiting the ETC), was elevated in all of the mutants (Fig. 8C).

Interestingly, amino acids are also up-regulated in the decapping mutants (Fig. 7D), particularly in *pat1Δ* cells (Fig. 7F), as well as intermediates in amino acid biosynthesis and amino acid derivatives (Fig. 7D). The expression of amino acid biosynthetic enzymes is unaffected or reduced in the mutants however (Fig. S9D), suggesting that increased amino acid abundance results from metabolic reprogramming rather than increased biosynthetic capacity. One possibility is that accumulation of the TCA cycle intermediate α-ketoglutarate leads to increased production of glutamate and glutamine, precursors in all amino acid biosynthetic pathways (Ljungdahl and Daignan-Fornier 2012). The two 3-phosphotrioses generated in glycolysis (glyceraldehyde 3-phosphate and dihydroxyacetone phosphate) are also elevated in the mutants, possibly owing to increased glyoxylate shunt function, which might stimulate synthesis of amino acids serine and glycine (Ljungdahl and Daignan-Fornier 2012) (Fig. 7D, Methane metabolism category). The increases in fructose 1,6-bisphosphate, fructose 6-phosphate, glucose 6-phosphate, and UDP-glucose in all four mutants (Fig. 7D, Starch/Sucrose metabolism category) all suggest substantial metabolic rewiring indicative of glucose up-

regulation and usage of alternative carbon sources. In addition to amino acids, pyrimidine nucleotides are up-regulated in the mutants (Fig. 7D, Pyrimidine metab.), which might be driven by the elevated glutamine levels or increased glycolytic flux towards the pentose phosphate pathway (Ljungdahl and Daignan-Fornier 2012).

DISCUSSION

RNA-seq analysis of single and double *scd6Δ* and *edc3Δ* mutants has revealed that Scd6 and Edc3 have largely overlapping functions in repressing mRNA abundance, as the presence of either protein alone is sufficient for nearly WT levels of most mRNAs found up-regulated in the double mutant (Fig. S3A & Fig. 1B-C(ii)-(iii)). Although the mRNAs dysregulated in the *scd6Δedc3Δ* mutant are enriched for ESR mRNAs; the majority are not ESR transcripts (Fig. 1A-B) and are most likely repressed more directly by Scd6/Edc3. Functional redundancy of Scd6/Edc3 is consistent with their similarities in sequence and domain structure, including shared FDF motifs that interact competitively with Dhh1 in animals(Tritschler et al. 2008; Tritschler et al. 2009) and N-terminal LSm domains that compete for binding motifs in the Dcp2 CTT of *S. pombe* (Fromm et al. 2012), as well as the synthetic growth defect produced by deleting both genes simultaneously (Decourty et al. 2008) (Fig. S1A). Interestingly, a set of 37 mRNAs appears to be repressed by Edc3 exclusively (Fig. 1B-C(i)), including the canonical Edc3 targets identified previously, *YRA1* and *RPS28B* (He et al. 2022), and is enriched for genes belonging to the GO category “mitochondrion” (22/37 genes) and the Ox. Phos. categories of electron transport and mitochondrial ATP synthesis (11/37 genes: *ATP3 ATP16 ATP5 TIM11 ATP17 COX4 QCR9 CYC1 COX12 ATP18 COX5A*). The fact that deleting *SCD6* in the double mutant frequently diminishes the up-regulation of these

transcripts conferred by deleting *EDC3* alone (Fig. 1C(i)) might indicate that eliminating both Scd6 and Edc3 together enables a distinct degradation pathway that compensates for loss of Edc3-stimulated decapping/decay.

Several lines of evidence support the conclusion that most of the changes in mRNA abundance in the *scd6Δedc3Δ* double mutant result from impaired decapping and attendant 5'-3' degradation by Xrn1. ChIP-seq analysis of Rpb1 shows that Pol II occupancies in the coding sequences increase by much smaller amounts compared to the increased transcript levels for non-iESR mRNAs up-regulated in *scd6Δ/edc3Δ* cells (Fig. 3E), indicating a minor contribution of increased transcription to their up-regulation. The transcriptional activators of Ox-Phos. and CCR genes, many of whose transcripts are up-regulated by *scd6Δ/edc3Δ*, remain largely inert in this mutant, ruling out inappropriate transcriptional induction of their target genes in glucose-replete *scd6Δ/edc3Δ* cells. Consistent with mRNA turnover via decapping, most of these transcripts are up-regulated similarly by *scd6Δedc3Δ* and deletion of *DCP2* (Fig. 3A-B), exhibit a heightened proportion of decapped isoforms in WT cells that is diminished by deleting *SCD6/EDC3* or *DHH1* (Fig. 3C & Fig. S3E), and show evidence of co-translational 5'-3' decay of decapped intermediates by Xrn1 (Fig. 3D); none of which was observed for the mRNAs down-regulated in *scd6Δ/edc3Δ* cells. Similar findings were reported previously for sets of mRNAs up-regulated by *dhh1Δ* or *pat1Δ* (Vijjamarri et al. 2023a), consistent with the widespread involvement of Dhh1 and Pat1 in controlling the levels of mRNAs preferentially targeted by Scd6/Edc3.

Supporting this last assertion, most (~70%) of the mRNAs repressed in abundance by Edc3/Scd6 are also repressed by Dhh1 and Pat1, and their efficient repression in WT cells involves independent contributions of similar magnitude by Pat1, Dhh1 and either Edc3 or Scd6 (Fig. 2A-

B(ii)). Another large set of mRNAs is repressed predominantly by Pat1 with lesser contributions by Dhh1 and Scd6/Edc3 (Fig. 2A-B(iii)). Our finding of extensive cooperation among these four decapping factors is consistent with our recent finding that ~55% of the mRNAs up-regulated in the *dcp2Δ* mutant, and thus targeted by Dcp2 for enhanced degradation, tend to be up-regulated in the *pat1Δdhh1Δ* and *scd6Δedc3Δ* mutants, whereas the remaining 45% are generally up-regulated by *upf1Δ* instead. This finding suggested a major bifurcation of Dcp2-activation by either Pat1/Dhh1/Scd6/Edc3 or the Upf factors responsible for NMD (Vijjamarri et al. 2023b).

Closer examination of the effects of individual mutations on mRNA levels revealed a greater overlap between the mRNAs dysregulated by *dhh1Δ* and *scd6Δ/edc3Δ* versus those altered by *pat1Δ* (Fig. 2C-E), consistent with the aforementioned FDF motifs in Scd6 and Edc3 that interact with Dhh1 in animal systems, and with evidence for distinct complexes of the decapping enzyme containing Dhh1 and Edc3 or Scd6 but lacking Pat1. It also supports the recent suggestion that Edc3 and Scd6 act interchangeably to recruit Dhh1 to the Edc3-interaction site in the Dcp2 CTT to stimulate turnover of several Dhh1 target mRNAs (He et al. 2022). Our RNA-seq results support this last proposal in showing that all four Dhh1 target mRNAs examined in that study (*EDC1, SDS23, HXT6,* and *HSP12*) are up-regulated in the *scd6Δedc3Δ* double mutant while changing little in the single mutants (Fig. S10), two of which (*SDS23* and *HXT6*) were shown previously to have longer half-lifes in *dhh1Δ* vs. WT cells (He et al. 2018). Finding that selective up-regulation in the *scd6Δedc3Δ* double mutant applies to most mRNAs up-regulated in *dhh1Δ* cells (Fig. 2E), we propose that redundant Scd6/Edc3 targeting is a widespread mechanism of Dhh1-enhanced mRNA degradation in the yeast transcriptome (Fig. S11). Supporting this, our co-

immunoprecipitation analysis revealed diminished Dhh1-Dcp2 association in cell extracts of the *scd6Δedc3Δ* double mutant but for either single mutant (Fig. 3F).

Examining our Ribo-Seq and TMT-MS data suggests that Dhh1 translation and steady-state abundance are increased ~2-fold in the *scd6Δedc3Δ* strain, indicating that up-regulation of many of the same mRNAs by *scd6Δedc3Δ* and *dhh1Δ* does not result indirectly from reduced levels of Dhh1 in the *scd6Δedc3Δ* mutant. The increased Dhh1 expression might signify a compensatory response to the absence of Scd6/Edc3. We also observed an ~40% reduction in Dcp2 translation and abundance in the *scd6Δedc3Δ* strain, which might contribute to the up-regulation of mRNAs dysregulated in this mutant. However, our immunoblot analyses revealed no significant reduction in steady-state Dcp2 levels in *scd6Δedc3Δ* cells (Input lanes in Figs. 3F and S4C(i)-(ii)). Moreover, our previous finding that the majority of mRNAs subject to NMD, up-regulated by both *upf1Δ* and *dcp2Δ,* are not up-regulated by *scd6Δedc3Δ* (Vijjamarri et al. 2023b) implies that Dcp2 abundance in *scd6Δedc3Δ* cells is adequate for normal levels of NMD. Accordingly, we favor a direct role for Scd6/Edc3 in accelerating degradation of most transcripts up-regulated in the *scd6Δedc3Δ* mutant.

Despite strong evidence for the involvement of decapping in mRNA turnover directed by either Scd6/Edc3 or Pat1/Dhh1, it appears that neither enrichment for non-optimal codons nor low translational efficiencies are principal determinants of preferential targeting of mRNAs by these proteins (Fig. S6A-C). There are probably exceptions to these generalizations among the hundreds of transcripts repressed by these factors; nor can we rule out the involvement of clusters of non-optimal codons in transcripts of average overall codon optimality that generate a queue of slowly elongating ribosomes that triggers decapping. Nevertheless, it seems likely that

other sequences or properties of the transcripts most strongly repressed by Scd6/Edc3 or Dhh1/Pat1 frequently underlie their preferential targeting by these factors for decapping/decay. Sequence-specific RNA-binding proteins that actively recruit these decapping activators is an attractive potential mechanism (Fig. S11). For example, there is evidence that Dhh1 is recruited to mRNAs in association with the Ccr4-NOT deadenylase via RNA-binding protein Puf5 (Goldstrohm et al. 2006). Involvement of RNA-binding proteins would also be consistent with the observed specific targeting of mRNAs whose expression is repressed in response to nutrient abundance.

Ribosome profiling of the single and double *scd6Δ* and *edc3Δ* mutants provided evidence that Scd6 and Edc3 also have highly overlapping functions in repressing the translation of ~200 mRNAs, whose TE values are up-regulated substantially only in the double mutant (Fig. 4A-B(iii)). The observation that changes in TE (RPF density) generally correlate with changes in protein abundance conferred by *scd6Δedc3Δ* (Fig. 4E) implies that Scd6/Edc3 generally repress translation at the stage of initiation rather than elongation. Many mRNAs translationally repressed by Scd6/Edc3 additionally require Dhh1, and the subset most strongly repressed also requires Pat1 for efficient translational repression (Fig. 5B(ii) and 5D). This last group of mRNAs is translated at very low levels in WT cells on rich medium (Fig. S7C), which might reflect the concerted action of all four decapping activators in suppressing translation. The transcript abundance of these mRNAs is also up-regulated in each of the mutants (Fig. S7A(ii)), indicating enhanced degradation coupled with translational repression by the four decapping activators. One possibility is that a complex of Dcp1:Dcp2 containing Scd6/Edc3, Pat1/Dhh1, or different combinations of these factors (He et al. 2022), is recruited to these mRNAs and impedes

recruitment of PICs to diminish translation in parallel with stimulating decapping and 5'-3' degradation by Xrn1 (Fig. S11(i) & (ii)-(iv)).

The additional sets of mRNAs identified here that are translationally repressed exclusively by Scd6/Edc3 or Pat1/Dhh1 (Fig. 5A(i) & (iii)) show much less evidence of transcript degradation promoted by these factors (Fig. S7A(i) & (iii)), suggesting that inhibition of translation initiation occurs without decapping, or involves decapping uncoupled from degradation by Xrn1 (Fig. S10 (ii)-(iii)). In the latter scenario, the decapped mRNAs would be unable to recruit the cap-binding initiation factors necessary for PIC recruitment and hence persist in WT cells as translationally-inert degradation intermediates. Eliminating the decapping activators would diminish decapping and eliminate these fractions of poorly translated uncapped isoforms to confer the increased TE values we observed for the cognate genes in the decapping mutants. This hypothetical mechanism of translational repression via decapping is consistent with the lower than average capped to total mRNA (C/T) ratios found in WT cells for the mRNAs translationally repressed by all four decapping activators or by Pat1/Dhh1 (Fig. S6D (ii)-(iii)), indicating accumulation of decapped isoforms in WT cells, as observed previously for a subset of mRNAs translationally repressed by Dhh1 (Vijjamarri et al. 2023b). In contrast, the mRNAs that are translationally repressed exclusively by Scd6/Edc3 display higher than average C/T ratios in WT (Fig. S7D(i)), which is more compatible with an inhibition of PIC recruitment independently of decapping (Fig. S11(iii)). Translational repression without decapping could also occur if transcripts bound by decapping complexes are sequestered from the translation initiation machinery in RNA granules where mRNA decapping occurs inefficiently (Fig S11(iv)). Finally, it is important to note that mRNA decay occurs apparently without translational control for the much larger groups of ~600

and ~1000 transcripts showing up-regulated mRNA abundance but little evidence of TE changes in the *scd6Δedc3Δ* and *pat1Δdhh1Δ* mutants, respectively (Fig. S7B). It is unclear whether these mRNAs escape translational repression and are targeted exclusively for decapping/degradation (Fig. S11(i)) or are simply degraded too fast to allow translational repression to be detected by ribosomal profiling of steady-state mRNAs.

Recently, we reported that Pat1 and Dhh1 functionally collaborate with the decapping enzyme to repress genes and cellular pathways normally repressed in rich medium (Vijjamarri et al. 2023a; Vijjamarri et al. 2023b). Here we found evidence that Scd6 and Edc3 broadly cooperate with Pat1/Dhh1 in this control, acting redundantly to repress the abundance, translation, or both, of mRNAs encoding numerous proteins involved in respiration or utilization of alternative carbon sources (Figs. 6A-C, S8A-D), without affecting transcription of the cognate genes Fig. 6F, S9A-C). Evidence that up-regulation of Ox. Phos. mRNAs/proteins in the *scd6Δedc3Δ* mutant is sufficient to increase respiration in glucose-replete cells came from our findings of increased mitochondrially-encoded subunit II of ETC component cytochrome *c* oxidase (Fig. 6D) and elevated mitochondrial membrane potential (Fig. 6G) in the *scd6Δedc3Δ* mutant, extending similar findings we made previously for *dcp2Δ, dhh1Δ* and *pat1Δ* mutants (Vijjamarri et al. 2023a; Vijjamarri et al. 2023b). Consistent with this, our metabolomics analysis revealed elevated steady-state levels of TCA cycle intermediates in all four decapping mutants (Fig. 7D), and increased ^{13}C carbon incorporation from $^{13}C_6$-glucose breakdown into TCA cycle intermediates in the same mutant strains (Fig. 8A). Analysis of ATP levels further revealed increased proportions of ATP derived from Ox. Phos. in the decapping mutants (Fig. 8B), which together provide strong evidence that mitochondrial respiration is inappropriately elevated in glucose-replete cells of

decapping activator mutants. It is well established that the enzymes involved in respiration and catabolism of non-glucose carbon sources are repressed at the transcriptional level in glucose-replete yeast (Zaman et al. 2008). Our findings demonstrate that Scd6/Edc3 collaborate with Dhh1/Pat1 to provide an additional layer of post-transcriptional control of these enzymes through enhanced decapping/decay or translational repression to help ensure their complete suppression when glucose is abundant.

DATA AVAILABILITY

Ribosome profiling, RNA-Seq, ChIP-Seq and CAGE-Seq data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession numbers GSE270789 and GSE270790. TMT-MS/MS proteomics raw data have been deposited in ProteomeXchange with accession number PXD053307. Previously published datasets used in this study can be found in (Vijjamarri et al. 2023a; Vijjamarri et al. 2023b).

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FIGURES & LEGENDS

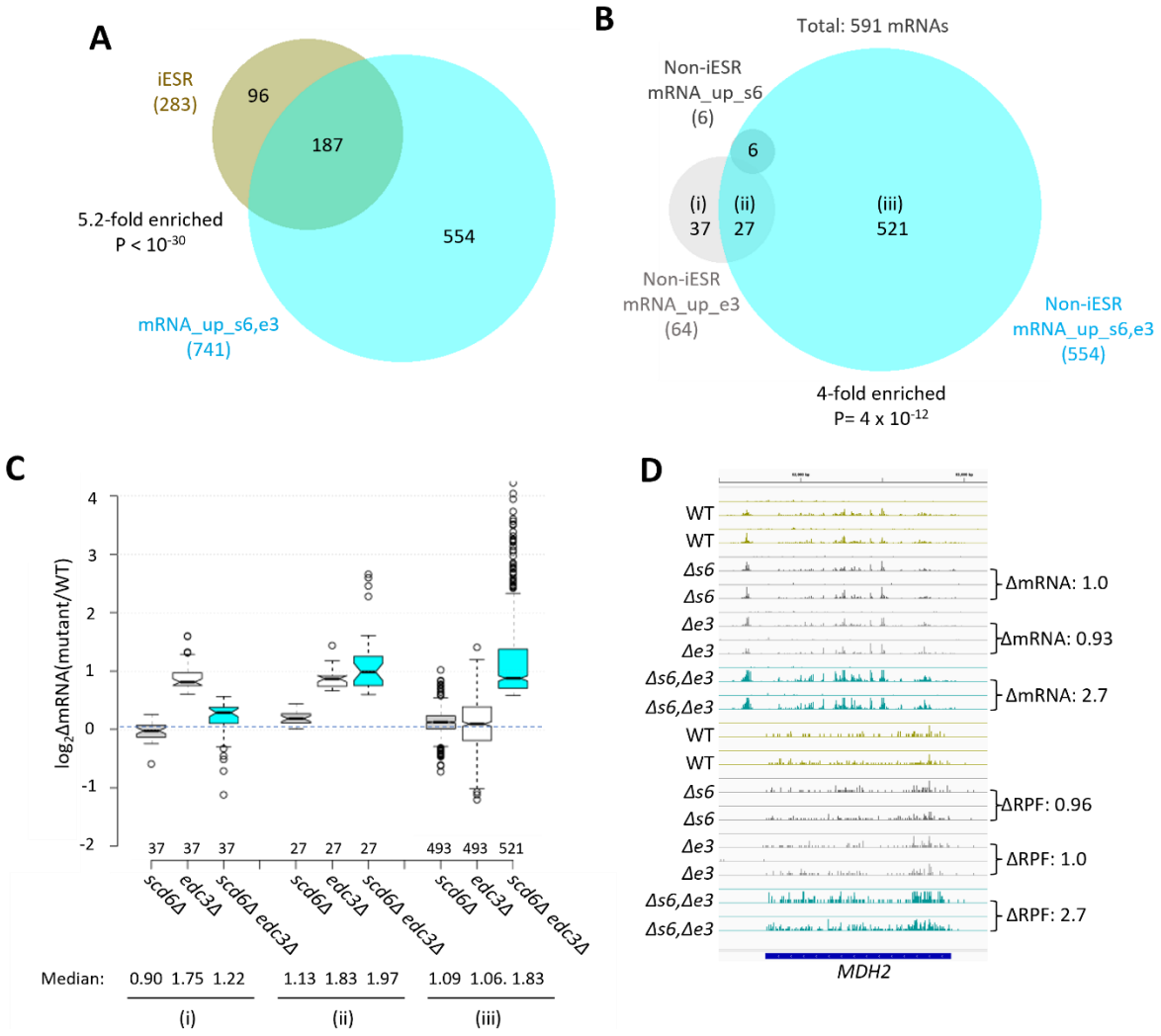

Fig. 1. Most mRNAs up-regulated in the *scd6Δedc3Δ* mutant are not iESR transcripts and exhibit Scd6/Edc3 functional redundancy in repression of transcript abundance. (A) Venn diagram of overlap between the 741 mRNAs up-regulated in the *scd6Δedc3Δ* mutant vs. WT (mRNA_up_s6,e3) and the 283 induced ESR (iESR) mRNAs, indicating fold-enrichment and P value of overlap determined by the hypergeometric distribution. **(B)** Venn diagram of overlaps involving all 591 non-iESR mRNAs up-regulated in abundance by *scd6Δ* (6 Non-iESR mRNA_up_s6

transcripts), *edc3Δ* (64 mRNA_up_e3 transcripts) or *scd6Δedc3Δ* mutations (554 Non-iESR mRNA_up_s6,e3 transcripts). **(C)** Notched box-plot analyses of $\log_2$ changes in mRNA abundance ($\log_2$ΔmRNA) determined by DESeq2 analysis between the indicated mutants vs. WT for mRNAs belonging to the specified sectors of the Venn diagram in (B). The numbers of mRNAs in each group for which data were obtained are indicated immediately above the x-axis; un-logged median values are indicated for each column at the bottom. **(D)** Gene browser image for *MDH2* showing the mRNA (top 16 tracks) and RPF (bottom 16 tracks) reads measured by parallel RNA-Seq and ribosome profiling analyses for two biological replicates of WT and the indicated mutants with fold-changes in mRNA or RPFs between mutant and WT indicated to the right of each track. In panels A-D, results for the *scd6Δ, edc3Δ,* and *scd6Δedc3Δ* mutations, abbreviated as *Δs6, Δe3,* and *Δs6,Δe3,* are shown in grey, white or light grey, and cyan, respectively.

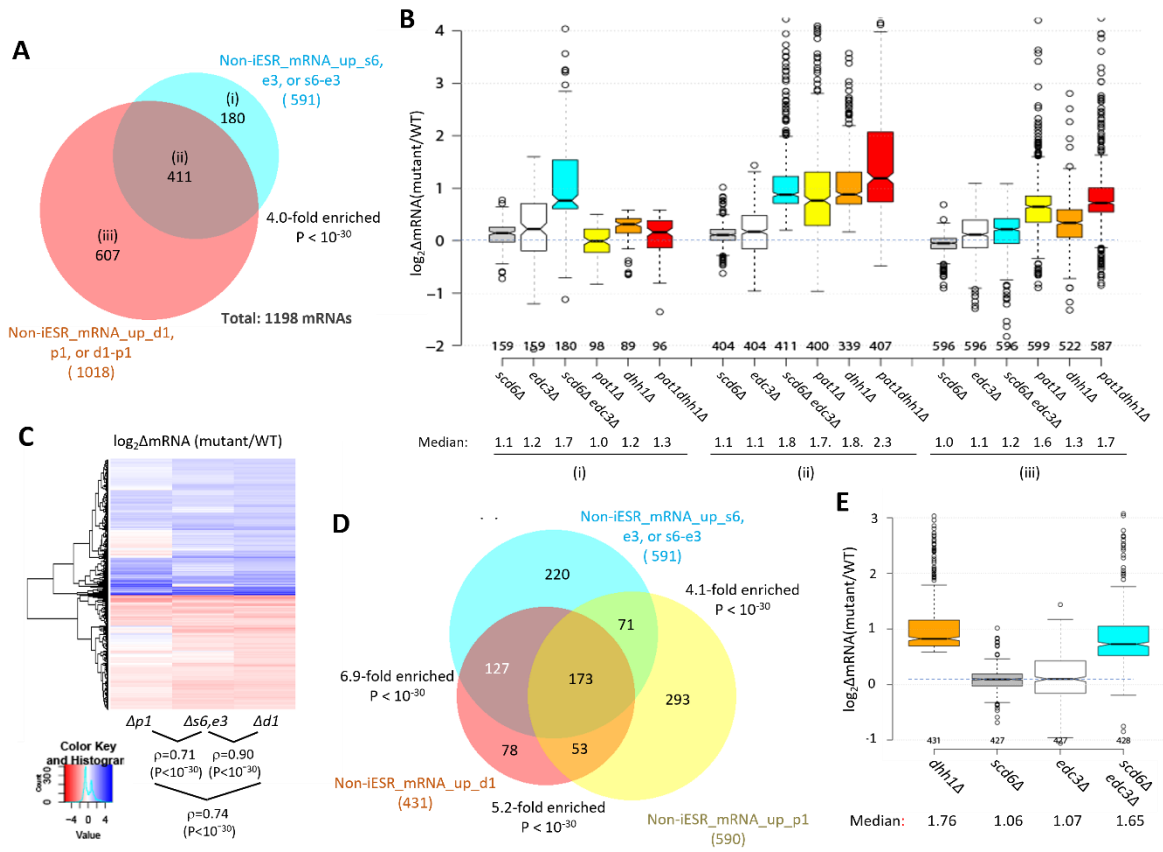

Fig. 2. Most mRNAs up-regulated in the *scd6Δedc3Δ* mutant are also up-regulated by *dhh1Δ* and *pat1Δ*. (A) Venn diagram of overlap between all 591 non-iESR mRNAs up-regulated in abundance by the *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutations (from Fig. 1B) and 1018 non-iESR mRNAs up-regulated by the *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* mutations identified previously (Vijjamarri et al. 2023a). **(B)** Notched box-plots of $\log_2$ΔmRNA between the indicated mutants vs. WT for mRNAs in the three sectors specified in (A). **(C)** Hierarchical clustering analysis of $\log_2$ΔmRNA values conferred by the indicated mutations vs. WT for 784 of the 794 mRNAs up- or down-regulated in *dhh1Δ* vs. WT cells for which RNA-Seq data was obtained in all four strains and with $\log_2$ΔmRNA values >-5 and <5, conducted with R heatmap.2 function from R 'gplots' library, using default hclust hierarchical clustering algorithm. Spearman coefficients (ρ) and associated P

values are given for the indicated correlation analyses. **(D)** Venn diagram of overlaps between the 591 non-iESR mRNAs up-regulated by the *scd6Δ/edc3Δ* mutations vs. WT (from Fig. 1B) and the indicated 431 and 590 non-iESR mRNAs up-regulated by *dhh1Δ* or *pat1Δ* vs. WT, respectively, identified previously (Vijjamarri et al. 2023a). The 220, 78, and 293 mRNAs found exclusively in only one of the three sets are indicated in the cyan, red-orange, and yellow sectors, respectively while the 127, 71 and 53 mRNAs shared by two of the three sets and the 173 mRNAs shared by all three sets, are indicated in the corresponding regions of overlap. **(E)** Notched box-plots of $\log_2$ΔmRNA between the indicated mutants vs. WT for the 431 non-iESR mRNAs up-regulated by *dhh1Δ* vs. WT shown in panel (D). In panels A, B, D & E, results for mRNAs up-regulated by the *scd6Δ, edc3Δ,* and *scd6Δedc3Δ* mutations are shown in grey, white, and cyan, respectively, while those for mRNAs up-regulated by the *pat1Δ, dhh1Δ,* and *pat1Δdhh1Δ* mutations are shown in yellow, orange, and red, respectively.

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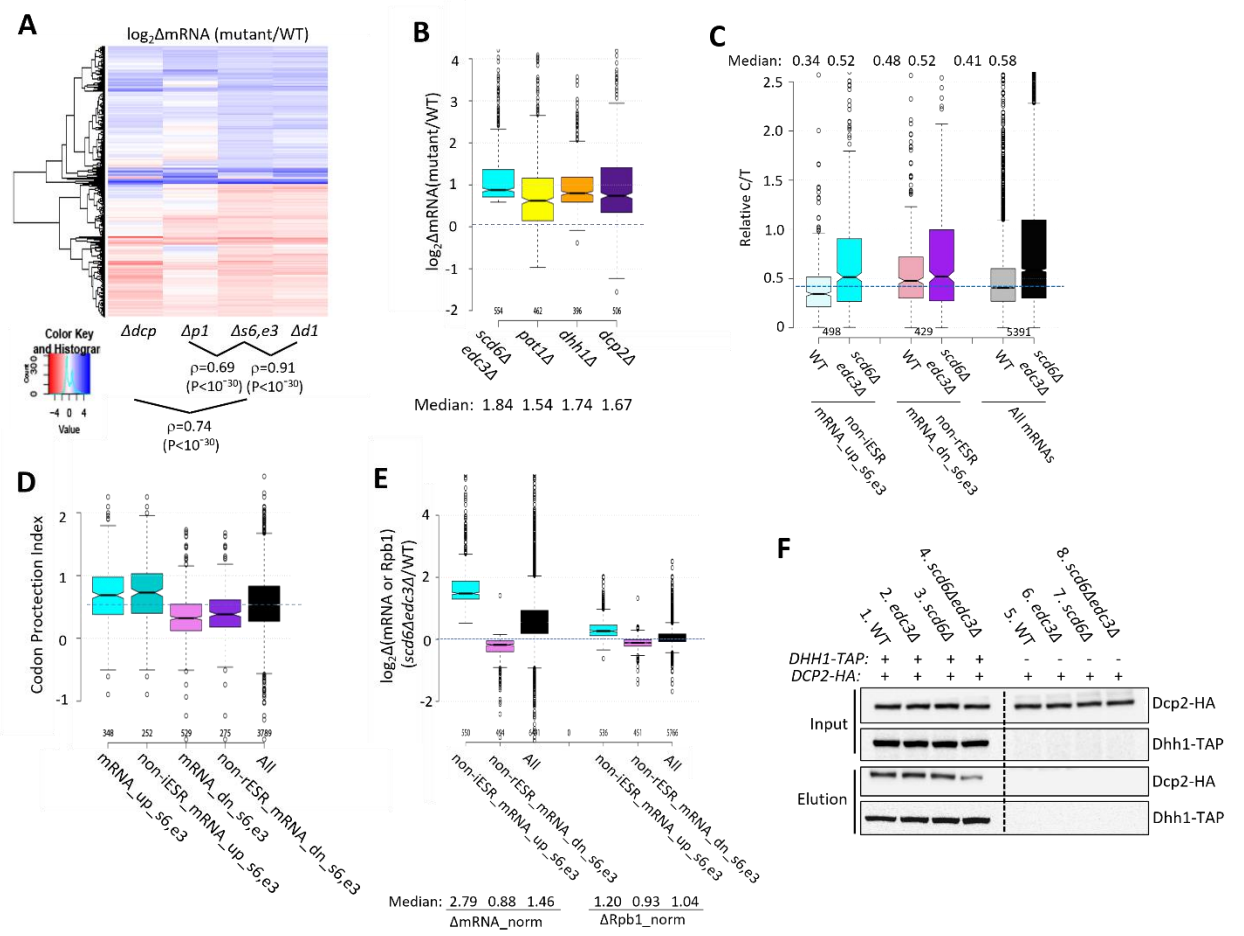

Fig. 3. Evidence that impaired decapping not increased transcription drives changes in mRNA abundance in *scd6Δedc3Δ* cells and that Edc3/Scd6 redundantly promote Dhh1 association with Dcp2. (A) Hierarchical clustering analysis of $\log_2$ΔmRNA values conferred by the indicated mutations vs. WT for 741 of the 1052 mRNAs up- or down-regulated in *scd6Δedc3Δ* vs. WT cells for which RNA-Seq data was obtained in all five strains and with $\log_2$ΔmRNA values >-5 and <5, conducted as in Fig. 2C, showing Spearman coefficients and P values for indicated correlations. **(B)** Notched box-plots of $\log_2$ΔmRNA between the indicated mutants vs. WT for the 554 non-iESR mRNAs up-regulated by *scd6Δedc3Δ* vs. WT (shown in Fig. 1B). **(C)** Ratios of capped to total mRNA abundance in TPMs (Relative C/T) in WT or *scd6Δedc3Δ* cells plotted for all 5391 mRNAs, the 498

non-iESR mRNA_ up_s6,e3, or 429 non-rESR mRNA_down_s6,e3 transcripts dysregulated by *scd6Δedc3Δ* vs. WT. **(D)** Notched box-plots of the codon-protection index (CPI) for all mRNAs or for the sets of mRNAs up- or down-regulated by *scd6Δedc3Δ* vs. WT, including or excluding ESR transcripts, as indicated. **(E)** Notched box-plots showing $\log_2$ changes in absolute mRNA abundance from ERCC spike-in normalized RNA-Seq (left) or absolute Rpb1 occupancies averaged over the CDSs from *S. pombe* chromatin spike-in normalized Rpb1 ChIP-Seq (right) in *scd6Δedc3Δ* vs. WT cells for all mRNAs or the 554 or 526 non-ESR mRNAs up- or down-regulated, respectively, by *scd6Δedc3Δ* vs. WT. **(F)** Co-immunoprecipitation analysis of Dhh1-Dcp2 association in yeast cell extracts. Transformants of *DHH1-TAP* strains H5695 (WT), H5696 (*edc3Δ*), H5697 (*scd6Δ*), and H5698 (*edc3Δ scd6Δ*) and the parental untagged strains all harboring single-copy plasmid pAK133 expressing HA-tagged Dcp2 were cultured in SC-Ura at 30°C and whole cell extracts were incubated with IgG sepharose beads to purify Dhh1-TAP and associated proteins. Washed beads were eluted by boiling in SDS loading buffer and eluates and input extracts were resolved in parallel by SDS-PAGE and subjected to immunoblot analysis to detect the tagged proteins. Immune complexes were visualized with enhanced chemiluminescence.

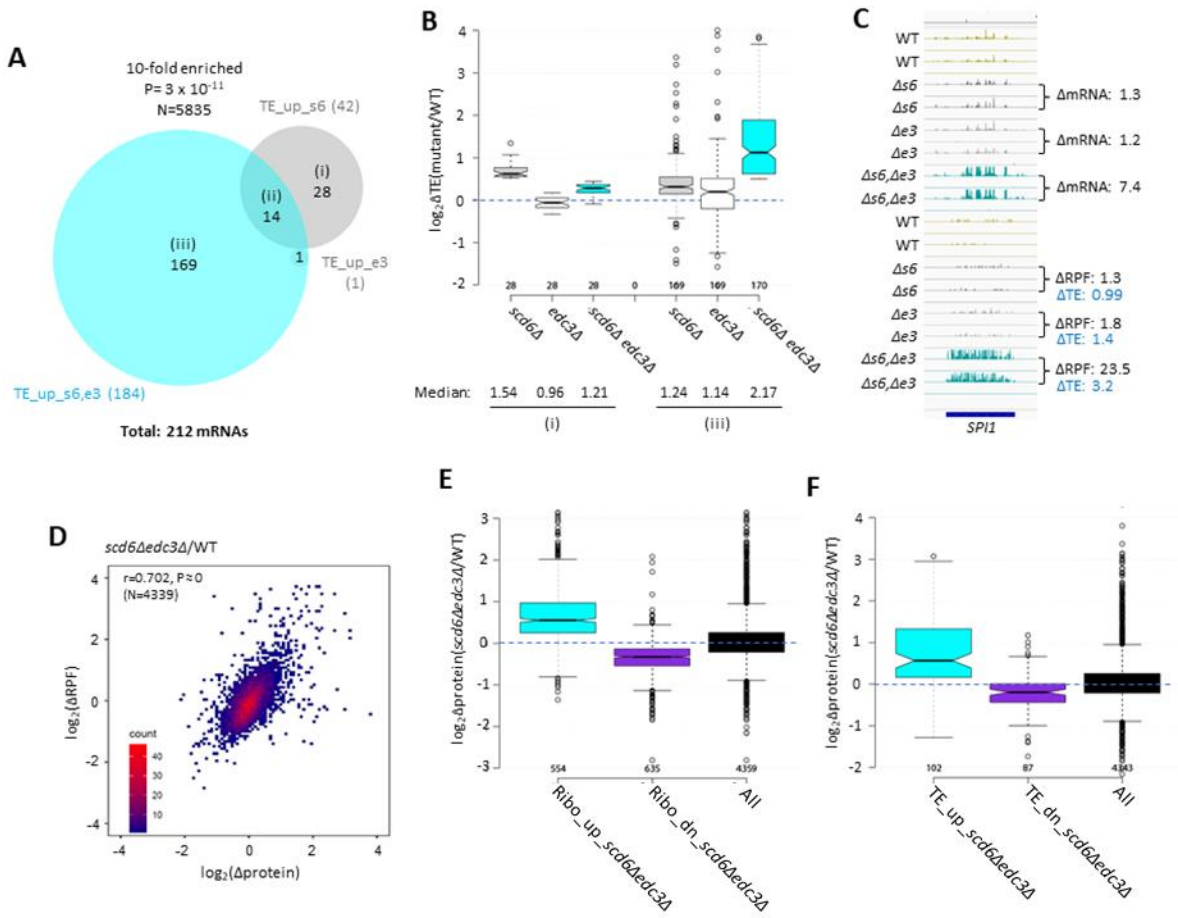

Fig. 4. Most mRNAs translationally up-regulated in *scd6Δedc3Δ* cells exhibit Scd6/Edc3 functional redundancy for repressing TE and show correlated changes in TE and protein abundance. (A) Venn diagram of overlap between the 184 and 42 mRNAs in the TE_up groups identified in the *scd6Δedc3Δ* vs. WT or *scd6Δ* vs. WT comparisons, respectively. **(B)** Notched box-plots of $\log_2\Delta$TE values between the indicated mutants vs. WT for the mRNAs belonging to sectors (i) or (iii) of the diagram in (A). **(C)** Gene browser image for *SPI1* presented as in Fig. 1D, except also giving the TE changes for each mutant vs. WT on the lower right. **(D)** Density scatterplot of $\log_2\Delta$RPF values measured by ribosome profiling vs. $\log_2\Delta$protein values measured by TMT-MS for 4339 mRNAs for which data were obtained in both analyses, indicating the Pearson

correlation coefficient (r) and P-value of the correlation. **(E-F)** Notched box-plots of log_2Δprotein values from TMT-MS analysis between the *scd6Δedc3Δ* mutant vs. WT for the 843 and 839 mRNAs belonging to the Ribo_up or Ribo_down groups, respectively (D), or the 184 and 152 TE_up or TE_down mRNA groups (E) determined for the *scd6Δedc3Δ* mutant vs. WT, or for all mRNAs, for which TMT-MS data was obtained.

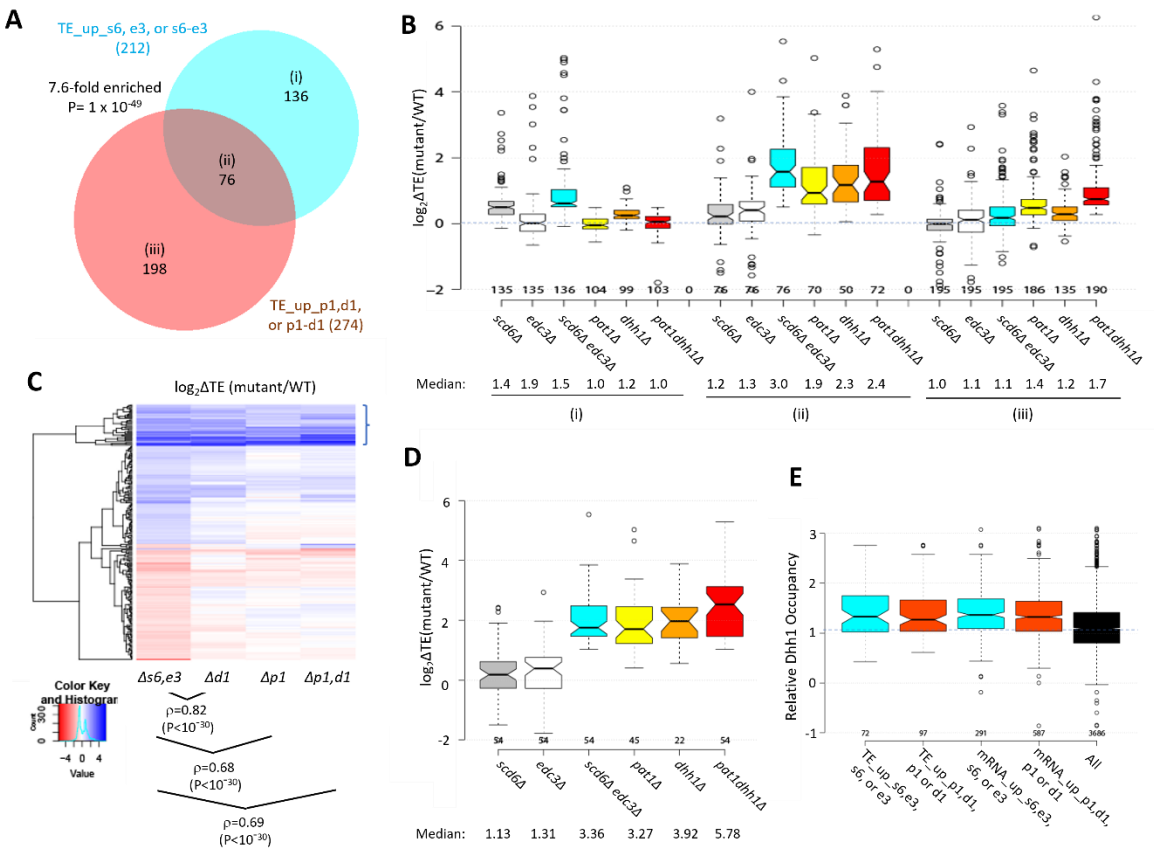

Fig. 5. Most mRNAs translationally up-regulated in the *scd6Δedc3Δ* mutant are also translationally up-regulated by *dhh1Δ* or *pat1Δ*. (A) Venn diagram of overlap between all 212 mRNAs translationally up-regulated by *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* (defined in Fig. 4A) or all 274 mRNAs translationally up-regulated by *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* vs. WT identified previously (Vijjamarri et al. 2023a). **(B)** Notched box-plots of $\log_2\Delta$TE values between the indicated mutants vs. WT for the mRNAs belonging to the specified sectors of the diagram in (A). **(C)** Hierarchical clustering analysis of $\log_2\Delta$TE values conferred by the indicated mutations vs. WT for 222 of the 336 mRNAs translationally up- or down-regulated in *scd6Δedc3Δ* vs. WT cells for which RNA-Seq and Ribo-Seq data were obtained in all five strains and with $\log_2\Delta$TE values >-5 and <5 conducted as in Fig. 2C, including the Spearman coefficients (ρ) and P values

for the indicated correlations. **(D)** Notched box-plots of $\log_2\Delta$TE values between the indicated mutants vs. WT for the 54 mRNAs showing >2-fold TE increases conferred by both *scd6Δedc3Δ* and *pat1Δdhh1Δ* mutations vs. WT. **(E)** Relative Dhh1 occupancies from the Dhh1 RIP-seq experiments of Miller et al (2018) for the 212 and 274 mRNAs identified as TE_up in the *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutants, or the *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* mutants, vs. WT, respectively (cols 1-2), or for the 591 and 1018 mRNAs identified as mRNA_up in either the *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutants, or the *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* mutants, vs. WT, respectively (cols. 3-4).

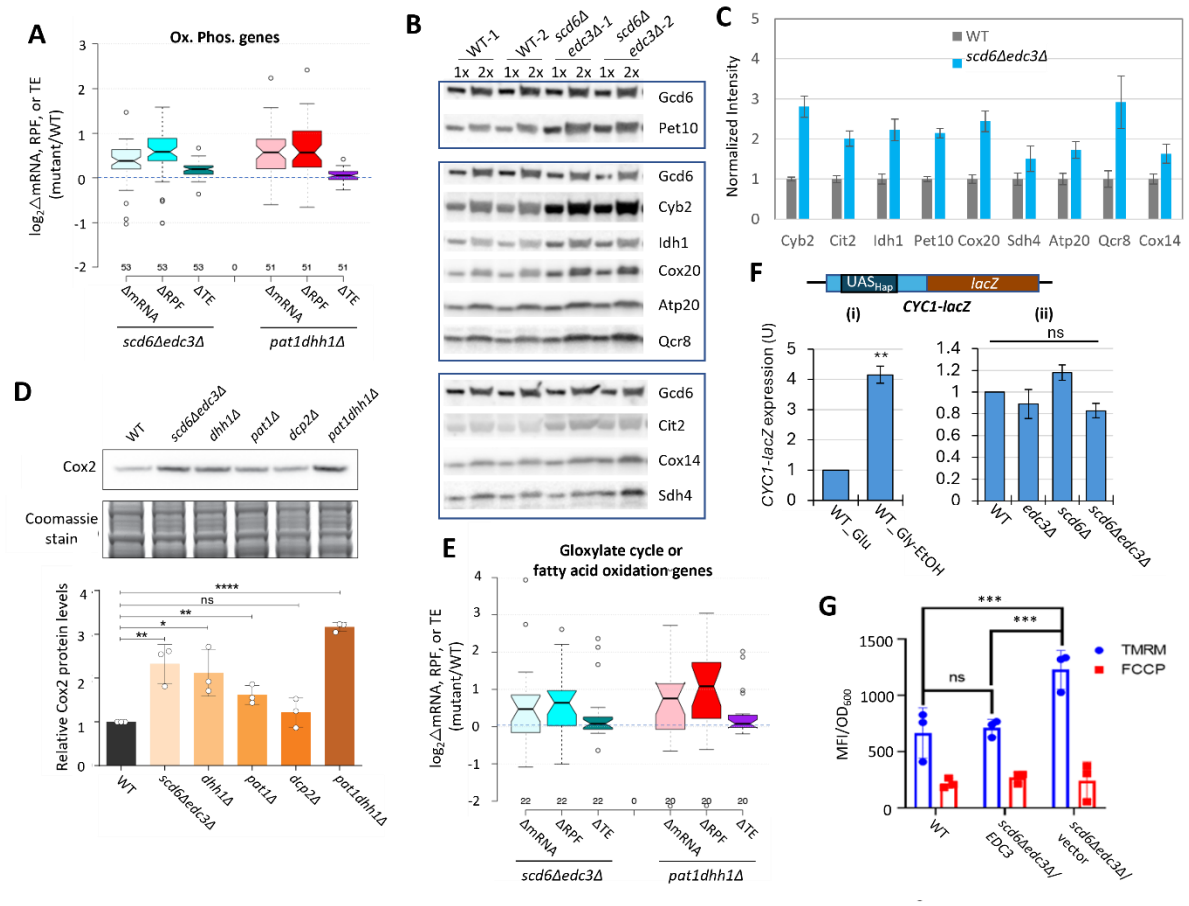

Fig. 6. Scd6/Edc3 post-transcriptionally repress proteins involved in respiration and suppress mitochondrial membrane potential in rich medium. (A) Log_2 changes in mRNA, RPFs, or TE conferred by the indicated double mutations vs. WT for 53 nuclear genes encoding mitochondrial proteins involved directly in oxidative phosphorylation. **(B-C)** Western blot analysis of 9 mitochondrial proteins and Gcd6 (examined as loading control) in WT and *scd6Δedc3Δ* strains, cultured in duplicate in YPD medium to OD_{600} of ~0.6-0.8. WCEs were extracted under denaturing conditions and aliquots corresponding to 1X or 2X amounts of WCE were loaded in successive lanes for the two replicate cultures. Immune complexes were visualized with enhanced chemiluminescence (B). Signals for each protein were quantified, normalized to the

corresponding signals for Gcd6 in the same extract and expressed relative to the resulting values for WT cells. Mean values and standard errors are plotted (C). **(D)** Western blot analysis of Cox2 in strains of the indicated genotypes in cells cultured as in (B). Cox2 signal intensity was normalized to total Coomassie-stained protein and the resulting relative Cox2 protein levels from three biological replicates were averaged and plotted. **(E)** Log_2 changes in mRNA, RPFs, or TE conferred by the indicated double mutations vs. WT for 22 genes encoding enzymes of the glyoxylate cycle or fatty acid metabolism. **(F)** Expression of the *CYC1-lacZ* reporter on plasmid pLG265, lacking UAS1 and containing the optimized version of UAS2, UAS2UP1, in the WT strain grown on SC-Ura medium containing either 2% glucose or 3% glycerol/2% ethanol as carbon sources (i), or in WT and the indicated mutant strains on SC-Ura with 2% glucose (ii). β-galactosidase activity (nmoles of o-nitrophenyl-β-D-galactopyranoside (ONPG) cleaved per min per mg of total protein) was measured in whole cell extracts for 3 biological replicates of each strain and the mean values were normalized to the mean activity measured in WT grown with glucose as carbon source. **, P-value <0.01 from student's t-test; ns, not significant. **(G)** Measurements of mitochondrial membrane potential. WT cells or transformants of the *scd6Δedc3Δ* mutant containing the *EDC3* plasmid pLfz614-7 or empty vector were cultured in SC-Ura to mid-log phase. TMRM (500 nM) was added and incubated for 30 min before samples were collected and washed once with deionized water. $\Delta\Psi_m$ was determined by measuring TMRM fluorescence intensity using flow cytometry. Data are presented in arbitrary fluorescence intensity units per OD_{600}. 2-way ANOVA was used for statistical analysis and data are given as mean values ± SD (n=3) (****p<0.0001).

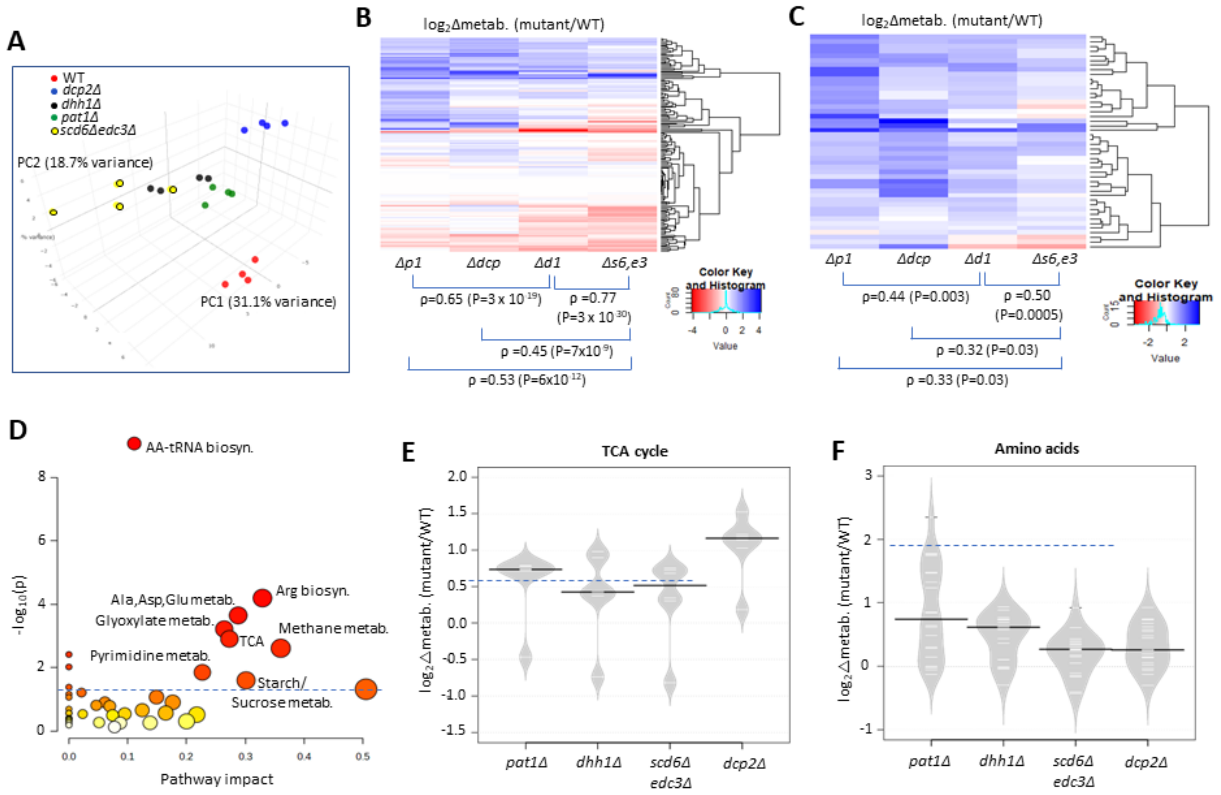

Fig. 7. Eliminating decapping activators or decapping enzyme confers similar changes in polar metabolites. (A) Principal component analysis of the levels of 147 metabolites in biological replicates of each strain. **(B-C)** Hierarchical clustering analysis of $\log_2$ changes in all 147 metabolites analyzed (B) or the 46 metabolites up-regulated in any two of the four mutants (C) conferred by the indicated mutations vs. WT, including the Spearman coefficients (ρ) and P values for the indicated correlations. **(D)** Results of pathway analysis of the 46 up-regulated metabolites described in (C) conducted at https://www.metaboanalyst.ca/MetaboAnalyst/Secure/pathway. Red ovals depict groups of metabolites significantly enriched among the set of 46 compounds,

with P-value <0.05. **(E-F)** Log_2 changes in levels of TCA cycle intermediates (E) or amino acids (F) conferred by the indicated mutations vs. WT.

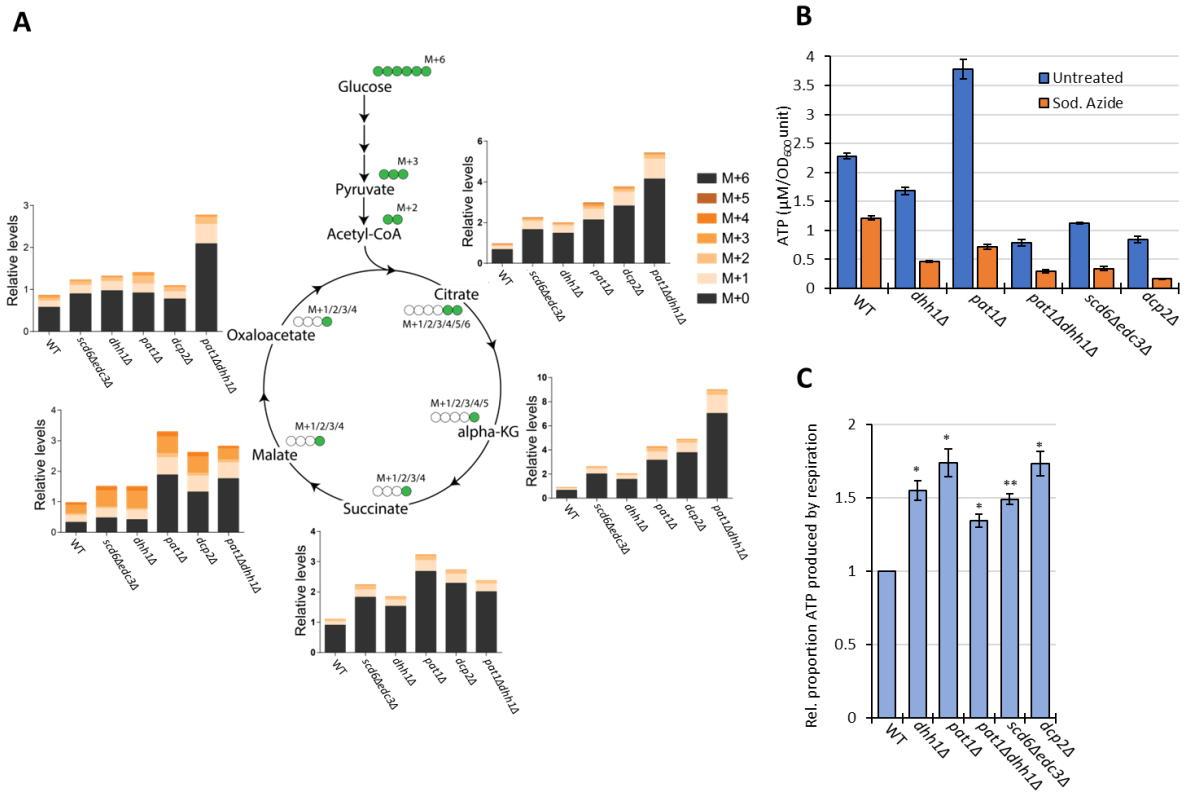

Fig. 8. Elimination of decapping activators or decapping enzyme up-regulates respiration, increasing flux from glucose into TCA cycle intermediates and proportion of ATP produced by Ox. Phos. (A) Three biological replicates of cells of each indicated genotype were cultured in YP with 2% unlabeled glucose, shifted to YP with 1% unlabeled glucose for 20 min, and pulsed with $^{13}C_6$ labelled glucose (at final concentration of 1%) for 8 min, followed by extraction of metabolites and quantification of the indicated TCA cycle intermediates by mass spectrometry. In the diagrams, green circles signify the labelled carbon atom and the notation M+1, M+2, etc. indicate the mass increase in the molecules due to the labelled carbon. The depicted labelling pattern of metabolites reflects on cycle of the TCA cycle, resulting in mass additions of M+1 and

M+2; however, across multiple cycles, a broader range of metabolite species with different mass additions will emerge. The metabolite signal intensities in all samples are expressed relative to that determined for the first replicate of the WT strain. **(B-C)** Measurements of ATP levels and proportions of total ATP impaired by azide inhibition of ETC activity. Cells cultured in YPD were treated or untreated with sodium azide for 30 min prior to harvesting. ATP levels were determined in extracts and normalized to OD_{600} units of cells for three biological replicates each of treated and untreated cell aliquots. Mean values for each strain are plotted in (B) and relative fractions of ATP in untreated samples retained following azide treatment (ATP_untreated)-(ATP_Azide)/ATP_untreated), normalized to the values determined for WT are plotted in (C) with results from a student's t-test indicated with asterisks: **, $P<0.005$; *, $P<0.05$.

SUPPLEMENTARY MATERIAL FOR:

Decapping activators Edc3 and Scd6 act redundantly with Dhh1 in post-transcriptional repression of starvation-induced pathways

Rakesh Kumar[1#], Fan Zhang[1#], Shreyas Niphadkar[3], Chisom Onu[2], Anil Kumar Vijjamarri[1], Miriam L. Greenberg[2], Sunil Laxman[3], and Alan G. Hinnebusch[1]

SUPPLEMENTARY TABLES

Table S1. Yeast strains employed.

Strain	Genotype	Source
255	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 edc3Δ::kanMX4*	Research Genetics
HFY114 (W303)	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3, 112 can1-100*	(1)
SYY2352	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3, 112 can1-100 scd6Δ::kanMX6*	(2)
FZY855	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3, 112 can1-100 scd6Δ::hphMX4*	This study
FZY858	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3, 112 can1-100 scd6Δ::hphMX4 edc3Δ::kanMX4*	This study
FZY862	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3, 112 can1-100 edc3Δ::kanMX4*	This study
H5217/QZY126	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 dhh1Δ::kanMX*)	(3)
F2181/ BSY3037	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 pat1Δ::HIS3*)	(4)
F2182/ YFW168	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 pat1Δ::HIS3 dhh1Δ::kanMX*	(4)
CFY1016	*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 dcp2::HIS3*	(1)
F2262	*MATa his3-Δ1 leu2-Δ0 met15-Δ0 ura3-Δ0 DHH1::TAP::HIS3MX*	GE Healthcare Dharmacon
H5695	*MATa ade2-1 ura3-1 his3-11,15 leu2-3,112 can1-100 DHH1-TAP::HIS3MX*	This study
H5696	*MATa ade2-1 ura3-1 his3-11,15 leu2-3,112 can1-100 edc3Δ::kanMX4 DHH1-TAP::HIS3MX*	This study
H5697	*MATa ade2-1 ura3-1 his3-11,15 leu2-3,112 can1-100 scd6Δ::kanMX4 DHH1-TAP::HIS3MX*	This study
H5698	*MATa ade2-1 ura3-1 his3-11,15 leu2-3,112 can1-100 scd6Δ::hphMX4 edc3Δ::kanMX4 DHH1-TAP::HIS3MX*	This study

Table S2. Plasmids employed.

Plasmid	Description	Source
YCplac33	s.c. *URA3* vector	(5)
YCplac111	s.c. *LEU2* vector	(5)
pLfz614-7	*EDC3* in YCplac33	This study
pLfz615-5	*SCD6* in YCplac33	This study
pLfz635-5	*EDC3* in YCplac111	This study (in case used)
pLfz636-1	*SCD6* in YCplac111	This study (in case used)
pLGADH2	*ADH2* 5' non-coding region fused to *lacZ*	(6)
pLG265	*CYC1-lacZ* reporter lacking UAS1 and containing the optimized version of UAS2, UAS2UP1	(7)
pRK4	UAS_{GATA}-*CYC1-lacZ* reporter containing the UAS from *MEP2* modified to contain additional GATA sequences	(8)
pAK133	*DCP2-3XHA* cloned in YCplac33 under its native promoter.	This study

Table S3. Primers employed.

Primer	Sequence (5' to 3')
AKV224	CAAGCCGTTAATGTCGTTATCAATTTCGAT
AKV225	TTCATCTTGTCAGTTGAAATGAATAGTTTA
AKV372	CGACTCTAGAGGATCAAAGAACAATGAACTCTAGAGCATC
AKV373	TCCTGCATAGTCCGGGACGTCATAGGGATAGCCCGCATAGTCAGGAACATCGTATGGGTAAACGG CCGCCTTCCTATGCAAAATGCTTAATAATT
AKV374	TATCCCTATGACGTCCCGGACTATGCAGGATCCTATCCATATGACGTTCCAGATTACGCTCCGGCCG CCTGAAAGAATAAGTGTTATACGTTTTA
AKV375	CGGTACCCGGGGATCAATATCGACAGTTTTAAGAACCGC

SUPPLEMENTARY FIGURES

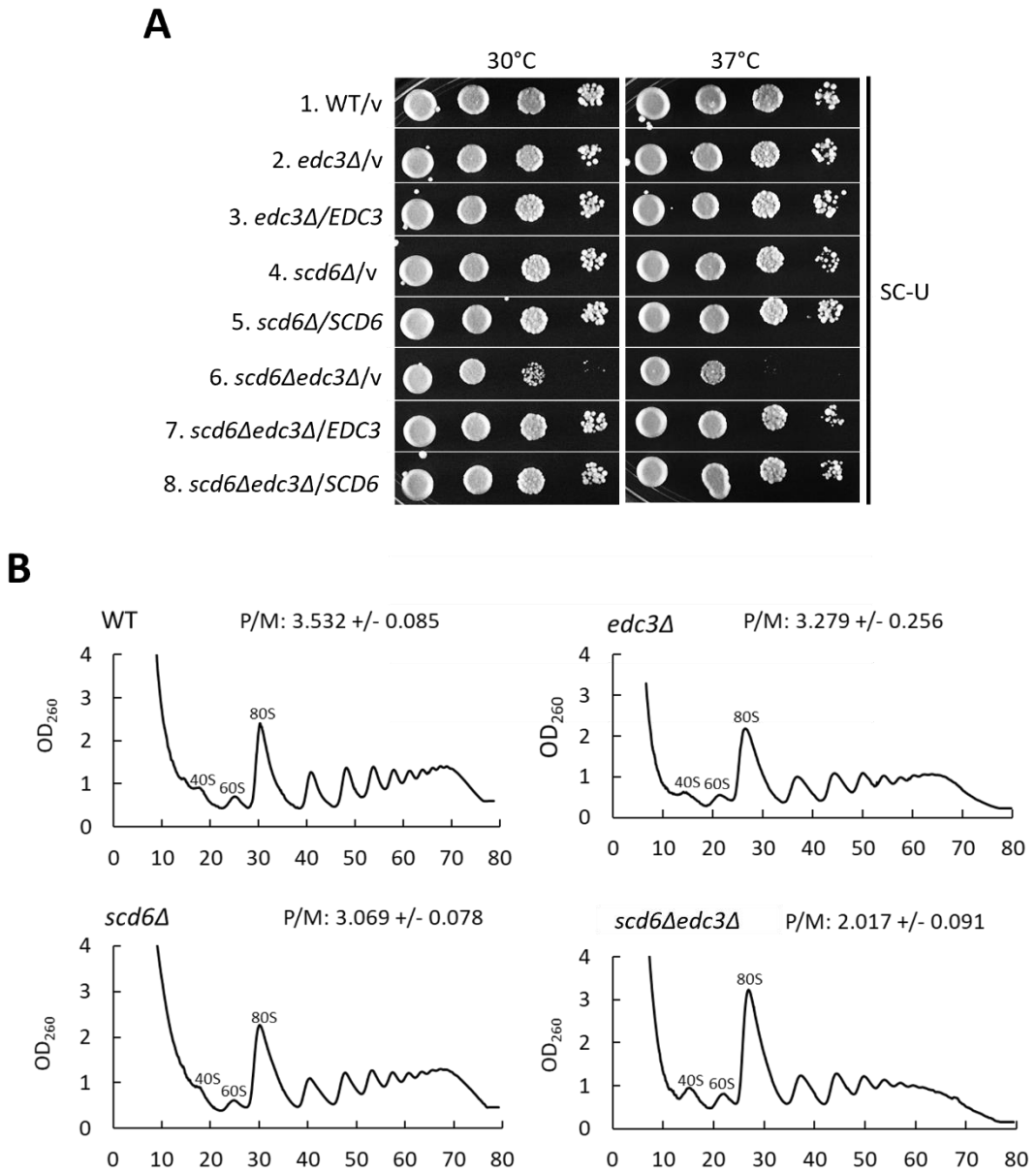

Figure S1. Combining *scd6Δ* and *edc3Δ* mutations confers synthetic reductions in cell growth and polysome assembly. (A) Serial dilutions of WT strain HFY114, *edc3Δ* strain FZY862, *scd6Δ* strain SYY2352, and *scd6Δedc3Δ* strain FZY858 transformed with empty *URA3 CEN* vector YCplac33 or derivatives of this vector containing *EDC3* (pLfz614-7) or *SCD6* (pLfz615-5) were spotted on synthetic complete plates minus uracil (SC-Ura) and incubated at the indicated

temperatures. **(B)** Polysome profiles of the strains in (A) but lacking plasmids cultured in YPD medium at 30°C to log-phase growth and treated with cycloheximide prior to harvesting to block run-off of elongating ribosomes during cell lysis. Cell extracts were resolved by sedimentation through 10-50% sucrose gradients, and gradients were scanned at 260 nm to yield the indicated tracings. Average polysome/monosome ratios (P/M) from 2 biological replicates are shown, with means +/- SEMs.

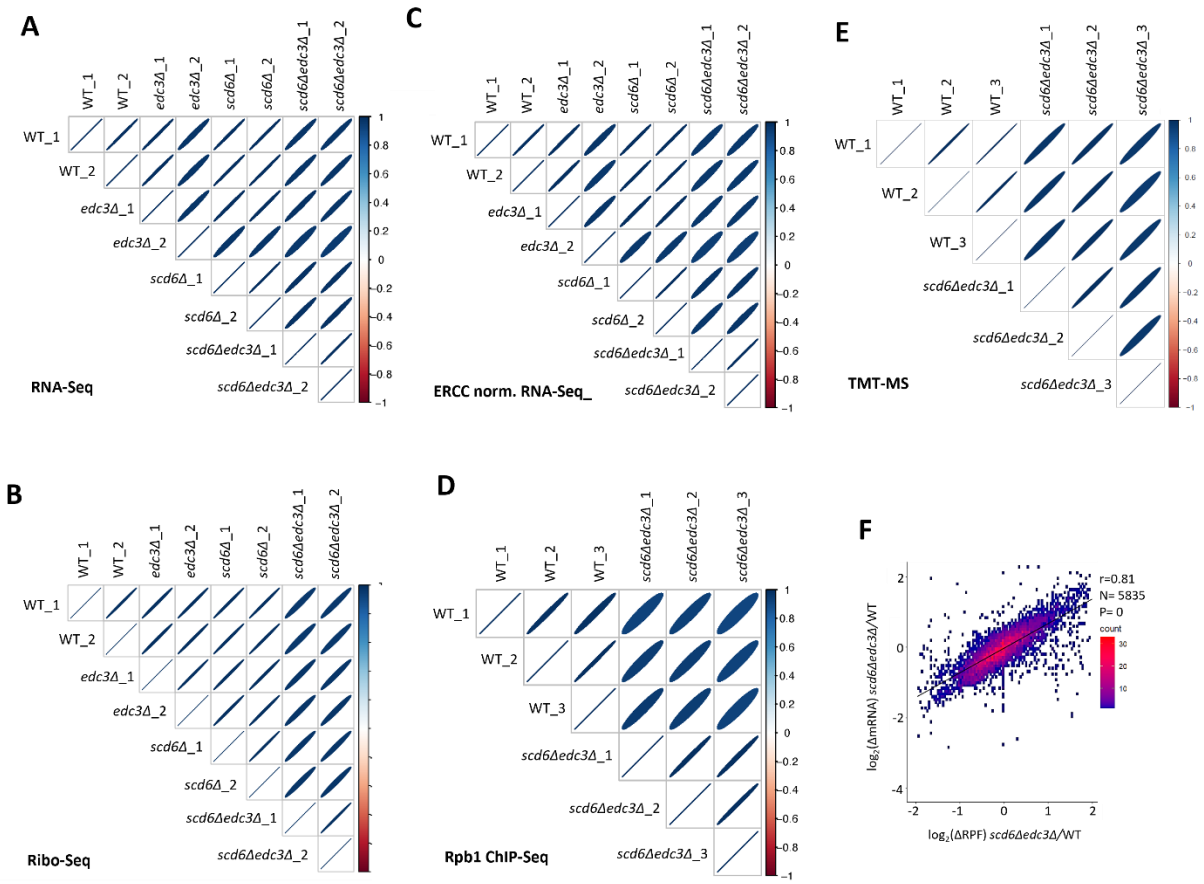

Figure S2. Reproducibility among biological replicates of RNA-Seq, Ribo-Seq, ERCC-normalized RNA-Seq, Rpb1 ChIP-seq, and TMT-MS data. (A) Correlation matrix showing Spearman correlation coefficients calculated for pair-wise comparisons of numbers of RPKM-normalized RNA-Seq reads for all expressed genes among all 8 RNA-Seq libraries generated for 2 biological replicates (_1,_2) of the indicated genotypes. The correlation coefficients between replicates are ≥0.98 and for all comparisons >0.95 with P-values of ≈0. For this and all similar plots below, the eccentricity of the ellipses are scaled parametrically to the correlation value between the two samples. **(B)** Same as (A) but for Ribo-Seq data, with correlation coefficients between replicates >0.995 and for all comparisons >0.96 with P-values of ≈0. **(C)** Same as (A) but for ERCC-normalized RNA-Seq data, with correlation coefficients between replicates >0.97 and for all comparisons

>0.94 with P-values of ≈0. **(D)** Same as (A) but for Rpb1 ChIP-Seq data comparing 3 normalized occupancies averaged across the CDS of all 5770 expressed genes, with correlation coefficients between replicates >0.98 and for all comparisons >0.91 with P-values of ≈0. **(E)** Same as (A) but for TMT-MS data, comparing $\log_2$ cyclic Loess-normalized exclusive MS1 intensities for all expressed proteins with correlation coefficients between replicates >0.96 and for all comparisons >0.95 with P-values of ≈0. **(F)** Correlation between changes in abundance of RNA vs. RPFs for 5835 expressed transcripts in the *scd6Δedc3Δ* double mutant compared to WT, calculated from RPKM-normalized RNA-Seq and Ribo-Seq reads obtained after combining data from biological replicates, with the Pearson correlation coefficient (r) and P-value of the correlation indicated.

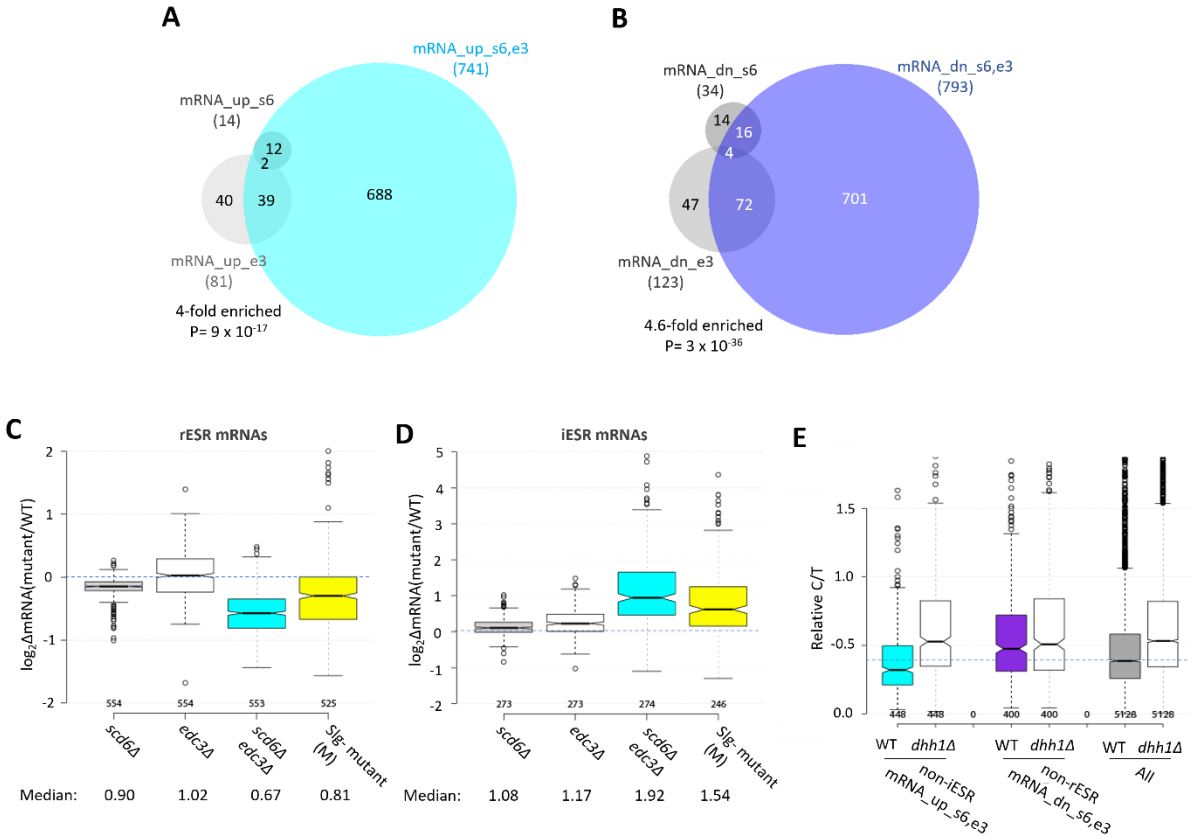

Figure S3. Functional redundancy between Scd6 and Edc3 in controlling mRNA abundance and mobilizing the ESR. (A-B) Venn diagrams of overlaps between all mRNA_up (A) and all mRNA_dn (B) groups identified in *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutants vs. WT, with fold-enrichments and P values from the hypergeometric distribution indicated for overlapping sets. **(C-D)** Notched box-plot analyses of $\log_2$ changes in mRNA abundance in mutant vs. WT for 585 rESR (C) and 283 iESR (D) mRNAs conferred by *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutations and those observed for the slowest-growing yeast deletion mutants (M) analyzed previously (9). Each box depicts the interquartile range containing 50% of the data, intersected by the median; the notch indicates a 95% confidence interval (CI) around the median. Median changes (un-logged) are shown at the bottom. **(E)** Ratios of capped to total mRNA abundance in TPMs (Relative C/T) in WT or *dhh1Δ*

cells plotted for all mRNAs, the 554 non-iESR mRNA_ up_s6,e3, or 526 non-rESR mRNA_down_s6,e3 transcripts dysregulated in *scd6Δedc3Δ* vs. WT cells.

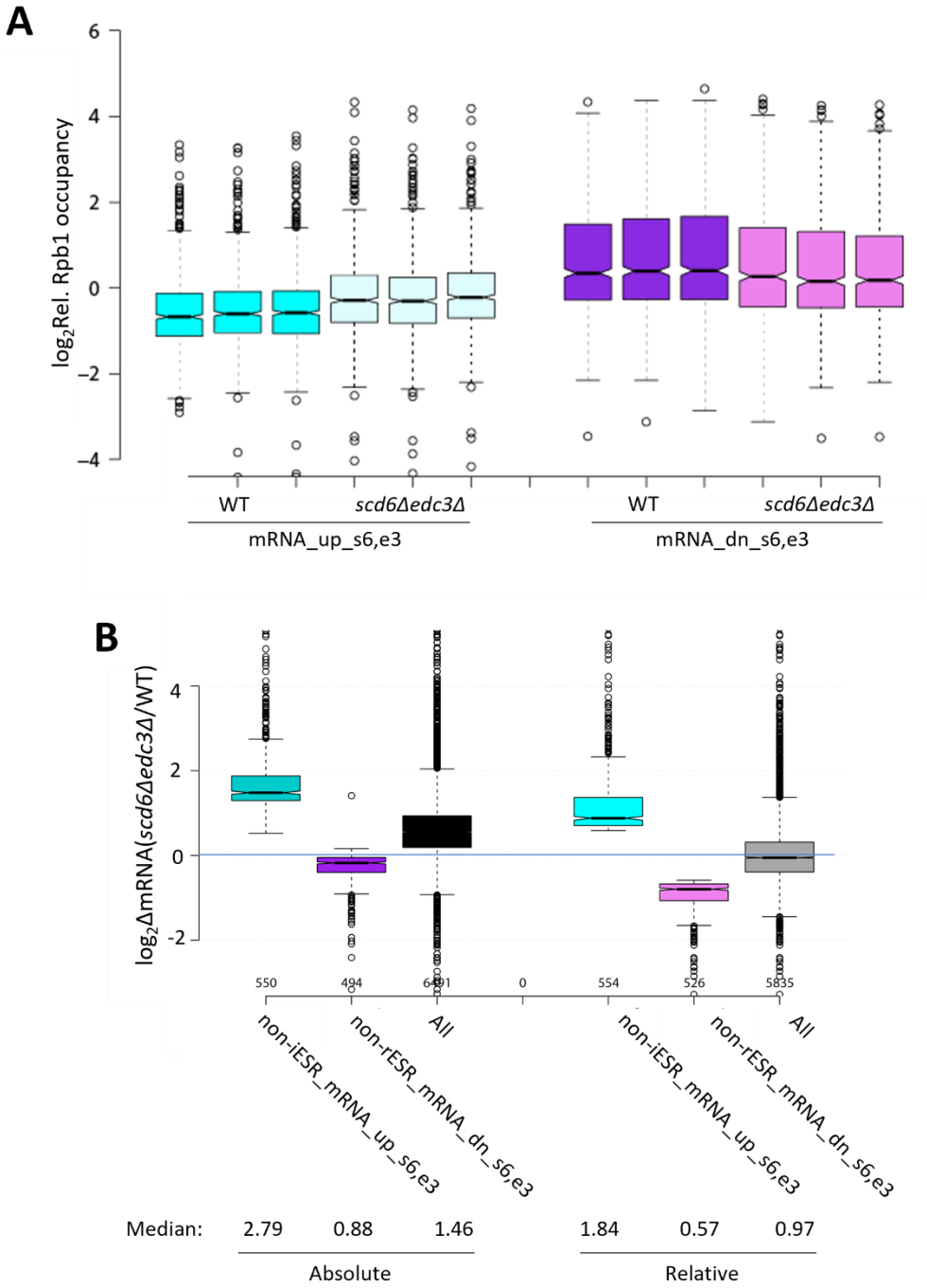

Figure S4. Supporting information for measurements of transcription and abundance of transcripts dysregulated in the *scd6Δedc3Δ* double mutant. (A) Reproducibility among biological replicates of Rpb1 ChIP-seq data. Log_2 values of relative Rpb1 occupancies averaged over the CDSs for three replicates of WT or *scd6Δedc3Δ* cells for the mRNAs up- or down-

regulated by *scd6Δedc3Δ* vs. WT, without excluding ESR transcripts. **(B)** Notched box-plots showing $\log_2$ changes in absolute mRNA abundance from ERCC spike-in normalized RNA-Seq (left) or relative mRNA abundance determined by DESeq2 analysis of RNA-Seq results (right) in *scd6Δedc3Δ* vs. WT cells for all mRNAs or the 554 or 526 non-ESR mRNAs up- or down-regulated, respectively, by *scd6Δedc3Δ* vs. WT.

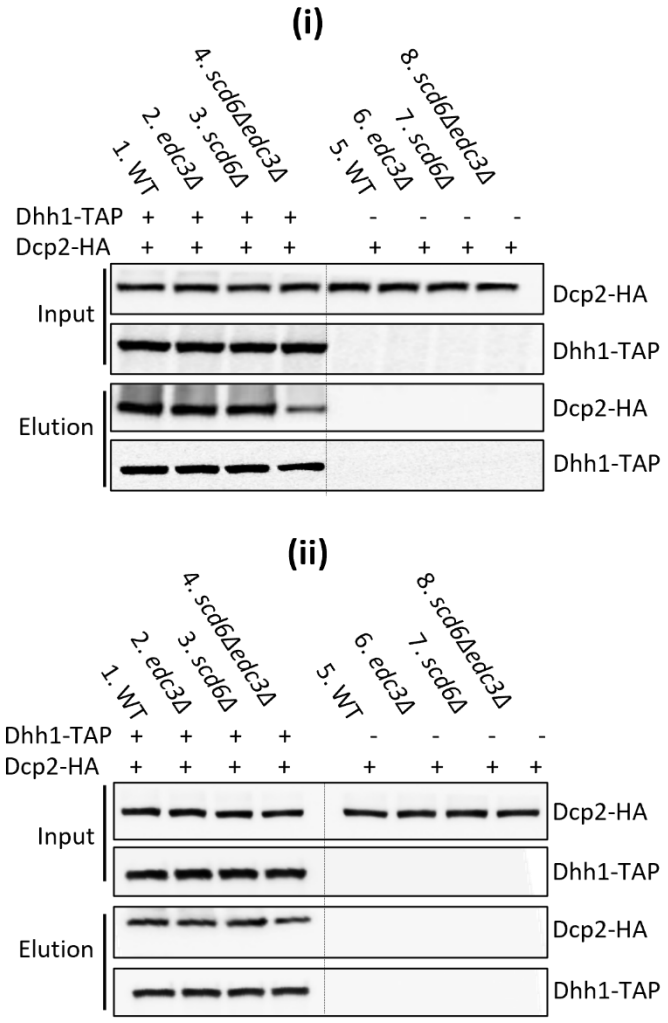

Figure S5. Co-immunoprecipitation analysis of Dhh1-Dcp2 association in yeast cell extracts. (i)-(ii) Results for two of three biological replicates of the experiment described in Fig. 3F.

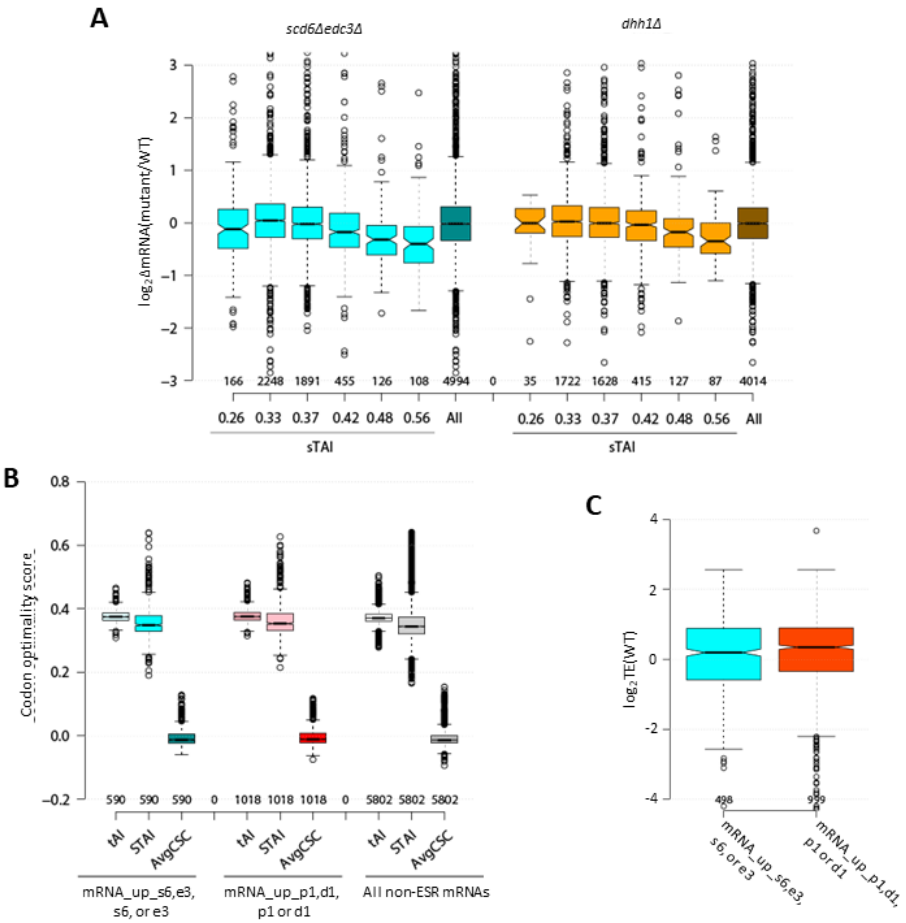

Figure S6. Average median codon optimality scores and average median TE values in WT cells for mRNAs repressed in abundance by Scd6/Edc3 or Dhh1/Pat1. (A) Notched box-plots of $\log_2\Delta$mRNA between *scd6Δedc3Δ* (left, cyan) or *dhh1Δ* (right, orange) vs. WT for 6 bins of all non-ESR mRNAs sorted according to stAI values, designated by the median stAI value for each bin, or for all non-ESR mRNAs (All). **(B)** tAI, stAI, and average CSC values for the 591 non-iESR mRNAs derepressed in abundance by the *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutations, the 1018 non-ESR mRNAs up-regulated by the *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* mutations, or all 5802 non-ESR mRNAs. **(C)** Log_2 values of TE determined in WT cells for the same groups of non-iESR mRNAs derepressed by the *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* mutations or by the *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* mutations analyzed in (A).

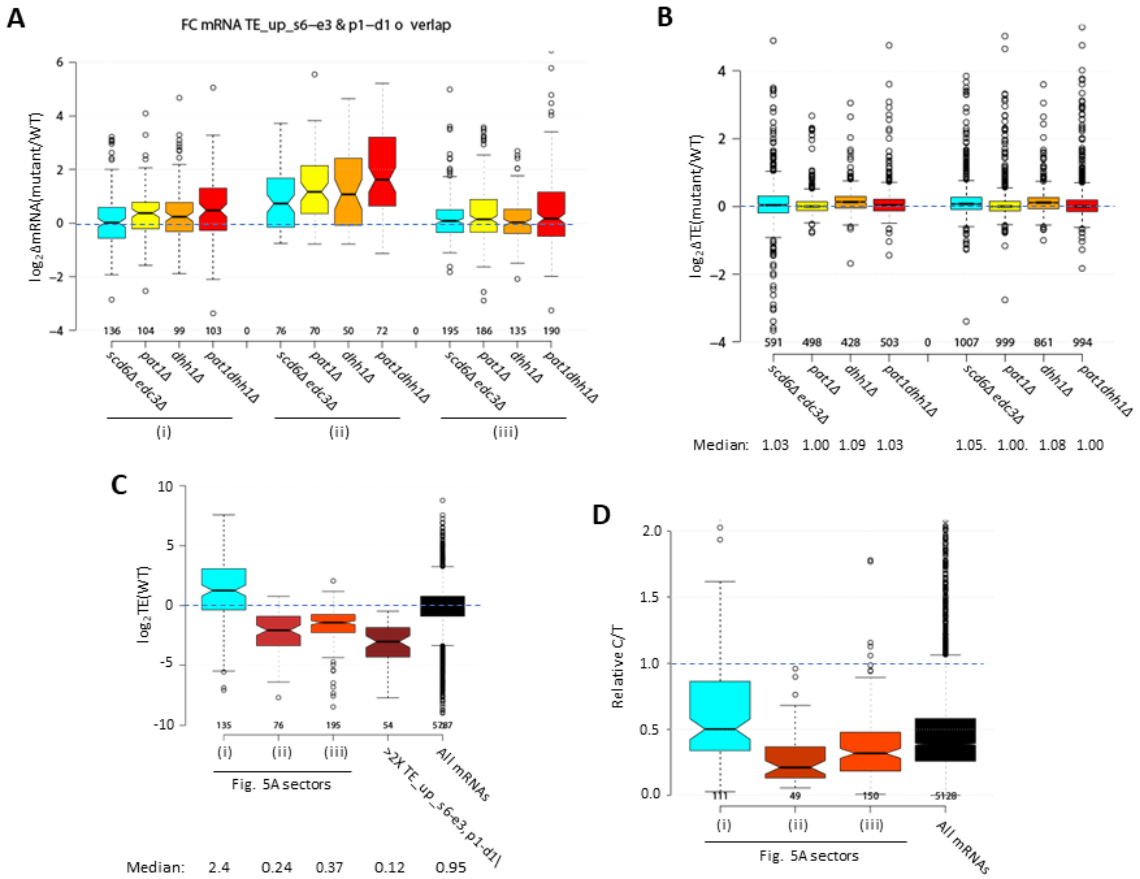

Figure S7. Properties of mRNAs translationally repressed by Scd6/Edc3 or Dhh1/Pat1. (A) Notched box-plots of $\log_2\Delta$mRNA values between the indicated mutants vs. WT for the translationally up-regulated mRNAs belonging to the specified sectors of the diagram in Fig. 5A. **(B)** Notched box-plots of $\log_2\Delta$TE values between the indicated mutants vs. WT for the mRNAs belonging to the 591 non-iESR mRNAs derepressed in abundance by *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* vs. WT or the 1018 non-ESR mRNAs up-regulated by *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* vs. WT. **(C)** Box-plot of $\log_2$ values of TE determined in WT cells for the translationally up-regulated mRNAs belonging to the specified sectors of the diagram in Fig. 5A, the 54 mRNAs showing >2-fold TE increases conferred by both *scd6Δedc3Δ* and *pat1Δdhh1Δ* mutations vs. WT, or for all mRNAs. **(D)** Box-plot of ratios of capped to total mRNA abundance in TPMs (Relative C/T) in WT cells for

the translationally up-regulated mRNAs belonging to the specified sectors of the diagram in Fig. 5A, or for all mRNAs.

A

591 Non-iESR mRNAs w/ abundance repressed by Edc3/Scd6#			
Category	**p-value**	**k**	**f**
GO Biological process			
ATP synthesis coupled proton transport [GO:0015986]	3.23E-07	10	17
mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]	1.37E-06	8	12
cristae formation [GO:0042407]	5.56E-06	5	5
ATP biosynthetic process [GO:0006754]	6.56E-06	12	31
cellular cell wall organization [GO:0007047]	7.22E-06	22	89
GO Cellular Component			
mitochondrial inner membrane [GO:0005743]	5.86E-09	45	204
mitochondrion [GO:0005739]	2.60E-08	145	1072
mitochondrial respiratory chain complex IV [GO:0005751]	5.81E-08	9	12
fungal-type cell wall [GO:0009277]	3.19E-06	22	85
MIPS Functional Classification			
electron transport and membrane-associated energy conservation [02.11]	<1e-14	34	58
electron transport [20.01.15]	2.02E-10	28	83
aerobic respiration [02.13.03]	4.75E-09	25	77
energy generation (e.g. ATP synthase) [02.45.15]	3.16E-08	12	21
respiration [02.13]	8.95E-06	17	59
(ii) ***212 mRNAs translationaly repressed by Edc3/Scd6#***			
GO Biological process			
asparagine catabolic process [GO:0006530]	5.04E-06	4	5
cellular aldehyde metabolic process [GO:0006081]	1.28E-05	5	11
GO Cellular Component			
cell wall [GO:0005618]	8.85E-06	11	68
extracellular region [GO:0005576]	9.09E-06	13	95
ribosome [GO:0005840]	1.70E-05	25	310
MIPS Functional Classification			
degradation of asparagine [01.01.06.02.02]	5.04E-06	4	5
fermentation [02.16]	6.92E-06	7	24

B

1018 Non-iESR mRNAs w/ abundance repressed by Pat1/Dhh1#			
Category	**p-value**	**k**	**f**
GO Biological process			
tricarboxylic acid cycle [GO:0006099]	2.87E-08	18	30
mitochondrial respiratory chain complex IV assembly [GO:0033617]	4.03E-06	10	14
GO Cellular Component			
fungal-type cell wall [GO:0009277]	3.12E-08	34	85
cell wall [GO:0005618]	9.82E-07	27	68
extracellular region [GO:0005576]	2.29E-06	33	95
mitochondrion [GO:0005739]	4.81E-06	215	1072
mitochondrial inner membrane [GO:0005743]	1.20E-05	55	204
plasma membrane [GO:0005886]	1.93E-05	83	350
MIPS Functional Classification			
tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle) [02.10]	5.86E-08	18	31
electron transport and membrane-associated energy conservation [02.11]	3.90E-07	25	58
aerobic respiration [02.13.03]	1.43E-06	29	77
(ii) ***274 mRNAs translationaly repressed by Pat1/Dhh1#***			
GO Molecular Function			
sequence-specific DNA binding [GO:0043565]	3.85E-06	21	165
GO Biological process			
cellular aldehyde metabolic process [GO:0006081]	1.88E-06	6	11
allantoin catabolic process [GO:0000256]	2.33E-06	5	7
transmembrane transport [GO:0055085]	6.78E-06	30	303
flocculation [GO:0000128]	1.40E-05	4	5
GO Cellular Component			
cell wall [GO:0005618]	3.29E-06	13	68
extracellular region [GO:0005576]	7.03E-06	15	95
plasma membrane [GO:0005886]	4.41E-05	31	350
MIPS Functional Classification			
C-compound and carbohydrate metabolism [01.05]	4.18E-07	27	223
fermentation [02.16]	3.27E-06	8	24
catabolism of nitrogenous compounds [01.02.02.09]	1.40E-05	4	5
metabolism of nonprotein amino acids [01.20.17.01]	2.52E-05	5	10
osmosensing and response [34.11.03.13]	7.03E-05	8	35
proton driven symporter [20.03.02.02.01]	7.07E-05	3	3

C

853 mRNAs with ribosome occupancy repressed by Edc3/Scd6#			
GO Biological process			
response to stress [GO:0006950]	2.57E-11	51	152
thiamine biosynthetic process [GO:0009228]	9.28E-07	11	17
mitochondrial respiratory chain complex IV assembly [GO:0033617]	1.05E-05	9	14
glycogen biosynthetic process [GO:0005978]	2.30E-05	8	12
mitochondrial electron transport, cytochrome c to oxygen [GO:0006123]	2.30E-05	8	12
GO Cellular Component			
mitochondrion [GO:0005739]	2.81E-13	227	1072
mitochondrial inner membrane [GO:0005743]	1.39E-08	56	204
extracellular region [GO:0005576]	1.45E-05	28	95
mitochondrial intermembrane space [GO:0005758]	1.60E-05	16	40
plasma membrane enriched fraction [GO:0001950]	1.78E-05	26	86
mitochondrial respiratory chain complex IV [GO:0005751]	2.30E-05	8	12
cell wall [GO:0005618]	2.43E-05	22	68
fungal-type cell wall [GO:0009277]	4.31E-05	25	85
MIPS Functional Classification			
electron transport and membrane-associated energy conservation [02.11]	1.24E-13	31	58
metabolism of energy reserves (e.g. glycogen, trehalose) [02.19]	1.81E-11	28	56
sugar, glucoside, polyol and carboxylate catabolism [01.05.02.07]	5.92E-11	34	81
stress response [32.01]	1.15E-09	50	162
aerobic respiration [02.13.03]	2.98E-08	29	77
electron transport [20.01.15]	2.01E-07	29	83
C-compound and carbohydrate metabolism [01.05]	3.82E-07	56	223
oxidative stress response [32.01.01]	4.14E-07	22	55
sugar, glucoside, polyol and carboxylate anabolism [01.05.02.04]	1.94E-06	16	35
oxidation of fatty acids [02.25]	1.67E-05	7	9
glutathione conjugation reaction [32.07.07.03]	3.56E-05	5	5
detoxification by modification [32.07.03]	0.0001015	6	8

D

1350 mRNAs with ribosome occupancy repressed by Pat1/Dhh1#			
GO Biological process			
tricarboxylic acid cycle [GO:0006099]	6.14E-09	21	30
response to stress [GO:0006950]	4.06E-06	55	152
glycogen biosynthetic process [GO:0005978]	5.45E-06	10	12
cellular response to oxidative stress [GO:0034599]	1.77E-05	29	67
GO Cellular Component			
mitochondrion [GO:0005739]	3.75E-12	305	1072
fungal-type cell wall [GO:0009277]	5.62E-12	46	85
extracellular region [GO:0005576]	1.06E-08	44	95
cell wall [GO:0005618]	1.15E-08	35	68
plasma membrane [GO:0005886]	7.34E-05	101	350
MIPS Functional Classification			
metabolism of energy reserves (e.g. glycogen, trehalose) [02.19]	8.14E-09	31	56
C-compound and carbohydrate metabolism [01.05]	1.75E-08	81	223
oxidative stress response [32.01.01]	1.05E-07	29	55
tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle) [02.10]	7.92E-07	19	31
stress response [32.01]	1.42E-06	59	162
electron transport and membrane-associated energy conservation [02.11]	1.82E-06	28	58
aerobic respiration [02.13.03]	6.14E-06	33	77
metabolism of vitamins, cofactors, and prosthetic groups [01.07]	7.04E-06	22	43
sugar, glucoside, polyol and carboxylate catabolism [01.05.02.07]	7.75E-06	34	81
osmotic and salt stress response [32.01.03]	3.27E-05	26	

Figure S8. mRNAs repressed in abundance or translation by Scd6/Edc3 or Dhh1/Pat1 are enriched for common functional categories, including Ox. Phos. proteins and cell wall

components. (A-B) Functional categories showing enrichment for genes encoding the 591 non-iESR mRNAs derepressed in abundance by *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* vs. WT or the 1018 non-ESR mRNAs up-regulated by *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* vs. WT, using color-coding to indicate related functions or cellular components. **(C-D)** Functional categories showing enrichment for genes encoding the 853 mRNAs with RPFs up-regulated by *scd6Δ, edc3Δ*, or *scd6Δedc3Δ* vs. WT or the 1350 mRNAs with RPFs up-regulated by *dhh1Δ, pat1Δ*, or *pat1Δdhh1Δ* vs. WT, conducted using the Web-based tool FunSpec and applying the Bonferroni correction and $P<0.05$ cutoff.

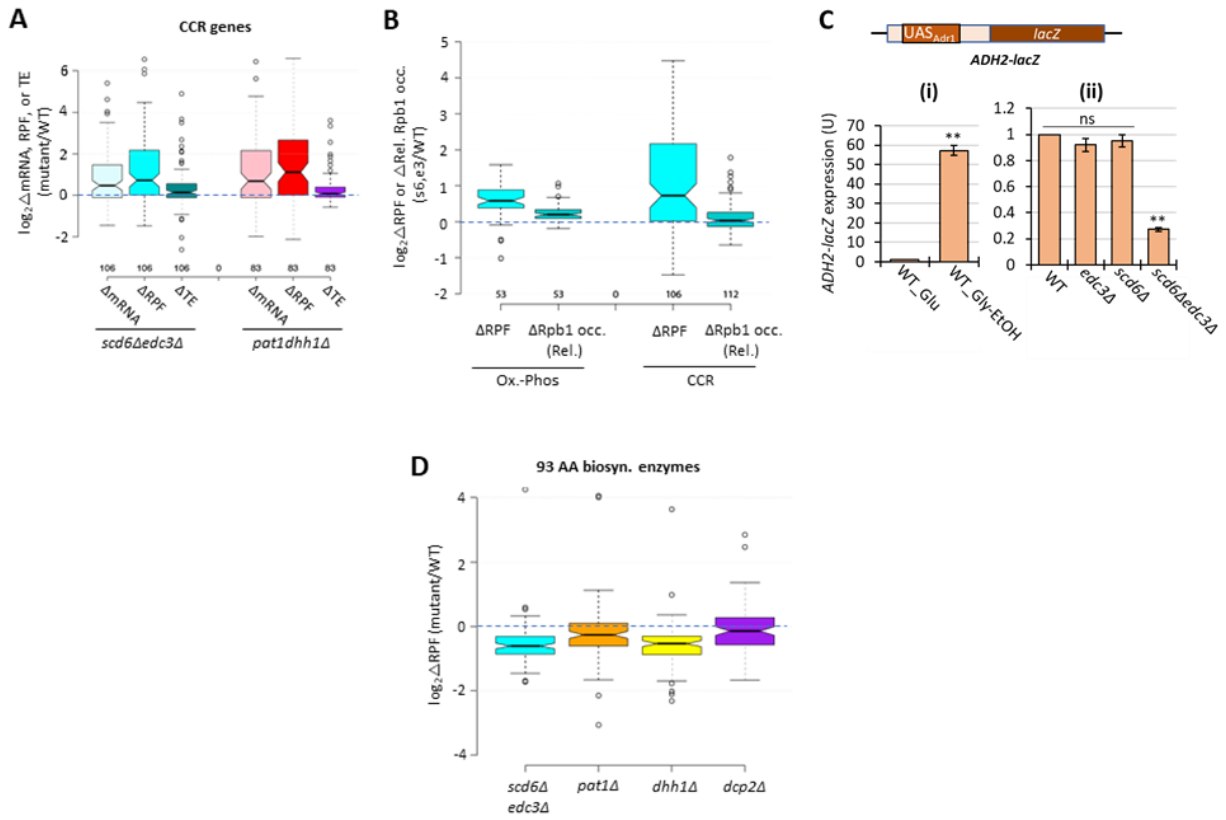

Figure S9. Scd6/Edc3 post-transcriptionally repress carbon-catabolite-repressed (CCR) genes in rich medium. (A) Log_2 changes in mRNA, RPFs, or TE conferred by the indicated double mutations vs. WT for 106 genes subject to carbon catabolite repression or activated by transcription factors Adr1 or Cat8. **(B)** Notched box-plots showing log_2ΔRPFs or log_2ΔRpb1 relative occupancies averaged over the CDSs in *scd6Δedc3Δ* vs. WT cells for the same Ox-Phos. (left) or CCR genes (right) analyzed in Figures 6A and S7A, respectively. **(C)** Expression of the *ADH2-lacZ* reporter on plasmid pLGADH2, containing the entire *ADH2* 5' non-coding region, in the WT strain grown on SC-Ura medium containing either 2% glucose or 3% glycerol/2% ethanol as carbon sources (i), or in WT and the indicated mutant strains on SC-Ura cultured with 2% glucose (ii). For (ii), mean values of β-galactosidase activity measured for 3 biological replicates of each strain were

normalized to the mean value measured for WT cells. **, P-value <0.01 from student's t-test; ns, not significant. **(D)** Log_2 changes in RPFs for 93 genes encoding amino acid biosynthetic enzymes in the indicated mutants vs. WT.

Gene id	Gene	log_2ΔmRNA (*scd6Δ*/WT)	FDR	log_2ΔmRNA (*edc3Δ*/WT)	FDR	log_2ΔmRNA (*scd6Δedc3Δ*/WT)	FDR	Targeted by
YGL222C	*EDC1*	0.415787885	4.48E-05	0.316768752	0.257140053	1.98410287	1.86E-155	Dhh1
YGL056C	*SDS23*	0.05093765	0.764889364	-0.201352497	0.530102611	0.472035691	8.08E-10	Dhh1
YDR343C	*HXT6*	0.328862276	0.422677908	0.683203554	0.035918099	2.593164006	4.20E-28	Dhh1/Pat1
YFL014W	*HSP12*	0.731412062	0.033263692	0.885066918	0.115640255	6.847403632	0	Dhh1/Pat1

Figure S10. Synthetic genetic up-regulation of four Dhh1 target mRNAs on combining *scd6Δ* and *edc3Δ* mutations. RNA-seq results obtained here for the four Dhh1 target mRNAs, two of which were designated as Pat1 targets as well, identified by He et al. (2022), in the *scd6Δ, edc3Δ,* and *scd6Δedc3Δ* mutants versus WT. The log_2ΔmRNA values for each of the three mutants vs. WT are listed together with the FDR values and color-coded according to derepression ratios.

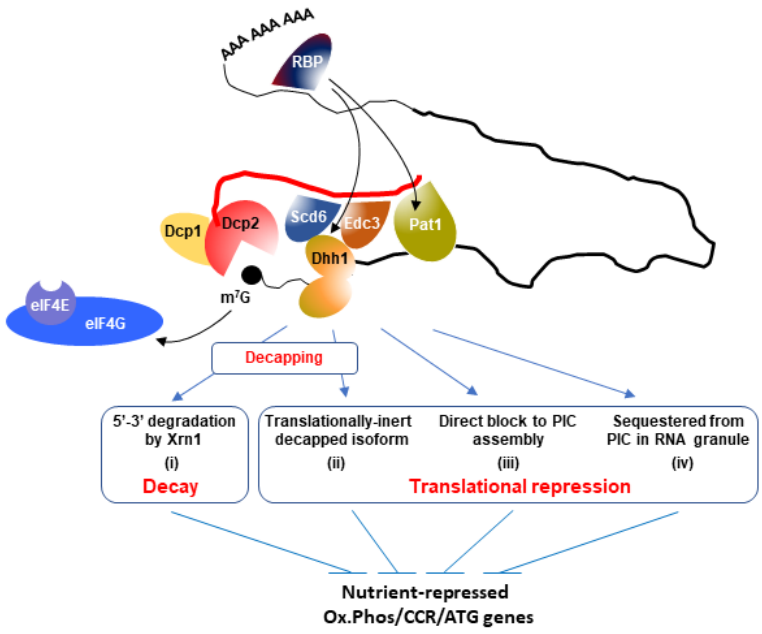

Figure S11. Hypothetical model to explain concerted repression of mRNA abundance or translation of particular mRNAs by decapping activators Scd6, Edc3, Dhh1, and Pat1. A complex of Dcp1:Dcp2 containing Scd6/Edc3, Pat1/Dhh1, or different combinations of these factors, is recruited to target mRNAs, possibly by a sequence-specific RNA-binding protein (RBP) binding to the 3'UTR. In agreement with a recent proposal (10), the recruitment of Dhh1 is enhanced by its redundant interactions with Scd6 or Edc3, which interact with the same segment of the Dcp2 CTT, whereas Pat1 is recruited independently to a distinct region of the CTT. One outcome of association of the decapping complex with an mRNA is activation of decapping with attendant 5'-3' degradation by Xrn1 occurring without detectable repression of translation (i). A different outcome is translational repression by decapping wherein degradation by Xrn1 is inefficient and decapped intermediates accumulate that cannot bind the cap-binding initiation factors eIF4E and eIF4G (depicted as subunits of eIF4F excluded from the

m^7G mRNA cap) and thus persist as translationally inert isoforms (ii). Alternatively, decapping may not occur and the decapping complex competes with the cap-binding initiation factors to selectively inhibit translation initiation (iii), a fate that could be favored by sequestration of the transcript in RNA granules in a manner facilitated by the decapping activator proteins (iv).

SUPPLEMENTARY FILES

File S1: Parallel RNA-Seq and Ribo-Seq analysis of decapping mutants, gene groups dysregulated in decapping mutants or belonging to specific functional categories, and capped/total mRNA ratios, codon optimality scores, codon protection indices, and Dhh1 occupancy values for all mRNAs. Sheets 1-7 labeled "mutant vs WT all comp" contain the processed data from Ribo-seq and RNA-seq analysis of 2 or 3 biological replicates of each strain listing the fold-changes in mRNA, RPFs, or TE between the relevant mutant vs. WT with the P-values and adjusted P-values (FDRs) assigned by DESeq2 analysis. The data for *dhh1Δ, dcp2Δ* (3)*, pat1Δ,* and *pat1Δdhh1Δ* mutants (8) were reported previously. Sheet "Gene groups_mRNA analysis" contains the lists of mRNAs (identified by systematic gene name) that are up-regulated or down-regulated in abundance by ≥1.5-fold at FDR < 0.05 in the *scd6Δ, edc3Δ,* or *scd6Δedc3Δ* mutants vs. WT, either including or excluding iESR mRNAs for up-regulated transcripts or rESR mRNAs for down-regulated transcripts, as indicated. It also lists the transcripts belonging to the three sectors of Figs. 1B-C, the iESR and rESR transcripts defined previously (11), and all of the non-iESR mRNAs up-regulated by ≥1.5-fold at FDR < 0.05 in *dhh1Δ, pat1Δ,* or *pat1Δdhh1Δ* mutants, as well as those equally up-regulated by the *dcp2Δ* mutation. Sheet "Gene groups_TE analysis" contains the lists of mRNAs that are up-regulated or down-regulated in TE by ≥1.41-fold at FDR < 0.10 in the different mutants vs. WT. Sheet "Gene groups_RPF analysis" contains the lists of mRNAs that are up-regulated or down-regulated in RPFs by ≥1.5-fold at FDR < 0.05 in the different mutants vs. WT. Sheet "Pathway gene groups" lists the genes involved in specific pathways (eg. Ox. Phos.) analyzed for changes in expression

or translation. Sheet “Codon Opt Scores nonESR mRNAs” lists the tRNA adaptation index (tAI), species-specific tRNA adaptation index (stAI), and the average codon stabilization coefficient (AvgCSC) for all non-ESR yeast genes (12,13). Sheet “Codon Protection Indices” lists the CPI values for all genes determined previously (14). Sheet “Capped to Total RNA ratios” lists the ratios of TPMs determined by CAGE sequencing of capped mRNAs (C) to TPMs determined by parallel RNA-seq of the same total RNA samples for 5129 genes, determined previously for *dhh1Δ* and WT cells (8). Sheet “Dhh1 occ enrich scores” lists the relative Dhh1 occupancies (enrichment scores) determined globally for yeast mRNAs by RIP-seq analysis (15) for the 3686 transcripts for which both Dhh1 enrichment score and Ribo-seq and RNA-seq data from the *dhh1Δ* vs. WT comparison (3) are available. Sheet “IGV tracks” lists the results of ribosome profiling of the *scd6Δ, edc3Δ,* and *scd6Δedc3Δ* mutants vs. WT for the genes selected for gene-browser depictions.

File S2: Relative and spike-in normalized Rpb1 occupancies from ChIP-seq analysis. Sheets 1-2 labeled "Relative occs._replicates” and “Relative occs._ Reps._averaged” contain the processed data from ChIP-Seq analysis of Rpb1 in three biological replicates of WT and *scd6Δedc3Δ* strains and the averaged data from combining the replicates, respectively, listing the relative occupancies averaged over the coding sequences for each expressed gene normalized to the average occupancy on each chromosome. Sheet “*S. pombe* norm. factor calcs,” lists the calculations of normalization factors obtained from total numbers of reads aligned to the *S. pombe* genome for each chromatin sample spiked-in with equal aliquots of *S. pombe* chromatin prior to immunoprecipitation with Rpb1 antibodies. Factors are calculated for each individual

replicate (col. E) or for the combined replicates for each strain (col. G). Sheets "Normalized occs._replicates" and "Normalized occs._reps._avged" lists the spike-in normalized Rpb1 occupancies calculated for each replicate or the combined replicates for each strain, respectively, calculated using the respective normalization factors for individual or combined replicates determined in the previous two sheets.

File S3: ERCC spike-in normalized RNA-Seq data. Sheet 1 lists the numbers of reads for each ERCC molecule identified in each RNA sample and calculations of the normalization factors for each sample. Sheet 2 lists the un-normalized reads for each yeast gene in each RNA sample, the ERCC-normalized reads for each sample, and the density of normalized reads for each gene calculated by normalizing for CDS lengths. Sheets 2-4 lists processed data from DESeq2, including $\log_2\Delta$ mRNA, P-value and adj. P-value determined for each gene in the indicated mutant vs. WT strain, obtained by setting the size factor to unity.

File S4: TMT-MS data. Processed data from TMT-MS analysis of *scd6Δedc3Δ* vs. WT strains. Sheet **"All proteins data" lists the normalized MS intensities of peptides for each expressed gene in three replicates each of WT (L-N) and** *scd6Δedc3Δ* (M-Q) strains and the calculated $\log_2$ fold-changes in protein expression and statistics in the *scd6Δedc3Δ* vs. WT comparison for all expressed proteins. Sheet "log2FC_protein (s6,e3 v WT)" extracts the data from columns B, Q, W, and X from the previous sheet.

File S5: Source data for Western blot analysis. Sheet "Fig. 6B-C Western analysis" lists averages of band intensities normalized to the loading control (Gcd6) on the same blots and the corresponding S.E.M. values calculated from the replicates for each protein analyzed in Fig. 6B-C. Sheet "Fig. 6D Western analysis" lists the Cox2 band intensities normalized to total stained proteins and the ratios of normalized Cox2 for each mutant vs. WT.

File S6: Source data for *lacZ* reporter assays. Lists the specific activities of β-galactosidase determined from three biological replicates of each strain harboring the *CYC1-lacZ* or *ADH2-lacZ* reporters analyzed in Figs. 6F and S7C, respectively.

File S7: Source data for metabolomics of polar compounds of intermediary metabolism. Sheets 1-4 list the statistical analyses of changes in metabolite concentrations in four biological replicates of the indicated four mutants vs. the WT determined in parallel for all 20 samples of metabolite extracts. Sheet 5 summarizes the $\log_2$ fold-changes in metabolite levels and corresponding P-values for all 147 metabolites detected in for each of the four mutants. Sheet 6 lists the 46 metabolites up-regulated in any two of the four mutants (analyzed in Fig. 7C), TCA cycle intermediates, and amino acids. Sheet 7 lists 93 amino acid biosynthetic genes interrogated in Fig. S8D.

File S8. Source data for glucose flux analysis. In Sheet 2 "raw intensity", the numbers indicate the signal intensities (areas under the peaks from mass spectrometry) of the metabolite listed in column A in the three biological replicates of the indicated mutant or WT strains. In the

subsequent sheets, raw data from Sheet 2 is collated for the different labeled isoforms of the indicated metabolite in the upper eight rows, and the proportion of the metabolite comprised of each isoform is given in the lower rows for the different samples. The "_N" labelling indicates the label addition in the metabolite, ie. _1 indicates mass addition of 1 labelled carbon, _2 indicates mass addition of 2 labelled carbons). Please let me know if you have any doubts regarding this.

File S9. Source data for measurements of cellular ATP content. Sheets 2-3 provide source data for measurements of ATP content in three biological replicates of the indicated five mutants vs. WT and the fraction of total ATP content that is eliminated by inhibiting respiration by sodium azide treatment. Sheet 4 shows the standard curve produced using pure ATP employed to determine the ATP content in cell extracts.

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