

# Quantification of mRNA stability of stress-responsive yeast genes following conditional excision of open reading frames

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**Keywords:** mRNA half-life, stress-responsive genes, Cre recombinase, target of rapamycin complex I (TORC1), type 2 protein phosphatase (PP2A), endosulfine

**Abbreviations:** CEO, conditional excision of open reading frames; TORC1, target of rapamycin complex I; RNA, ribonucleic acid; mRNA, messenger RNA; Tet, tetracycline; 4-tU, 4-thiouracil; 4-sU, 4-thiouridine; DTA, dynamic transcriptome analysis; loxP, locus of X-over P1; Cre, causes recombination; PP2A, protein phosphatase type 2A; YPD, yeast peptone dextrose; SD, synthetic defined; bp, base pair; ORF, open reading frame; PCR, polymerase chain reaction; qPCR, quantitative PCR; qRT-PCR, quantitative reverse transcription PCR; DNA, deoxyribonucleic acid; cDNA, complementary DNA; EBD, estradiol-binding; UTR, untranslated region

Eukaryotic cells rapidly adjust the levels of mRNAs in response to environmental stress primarily by controlling transcription and mRNA turnover. How different stress conditions influence the fate of stress-responsive mRNAs, however, is relatively poorly understood. This is largely due to the fact that mRNA half-life assays are traditionally based on interventions (e.g., temperature-shifts using temperature-sensitive RNA polymerase II alleles or treatment with general transcription inhibitory drugs), which, rather than blocking, specifically induce transcription of stress-responsive genes. To study the half-lives of the latter suite of mRNAs, we developed and describe here a minimally perturbing alternative method, coined CEO, which is based on discontinuance of transcription following the conditional excision of open reading frames. Using CEO, we confirm that the target of rapamycin complex I (TORC1), a nutrient-activated, central stimulator of eukaryotic cell growth, favors the decay of mRNAs that depend on the stress- and/or nutrient-regulated transcription factors Msn2/4 and Gis1 for their transcription. We further demonstrate that TORC1 controls the stability of these mRNAs via the Rim15-Igo1/2-PP2A<sup>Cdc55</sup> effector branch, which reportedly also controls Gis1 promoter recruitment. These data pinpoint PP2A<sup>Cdc55</sup> as a central node in homo-directional coordination of transcription and post-transcriptional mRNA stabilization of a specific array of nutrient-regulated genes.

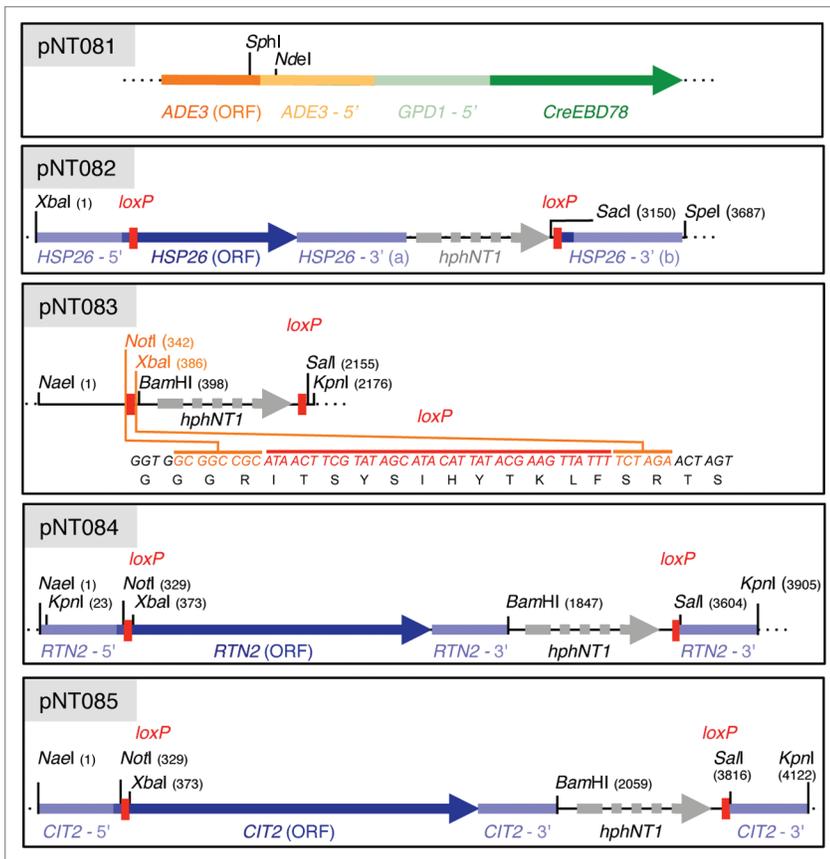
## Introduction

mRNA turnover is a key factor in the regulation of eukaryotic gene expression, which, in parallel to transcriptional activation/repression, allows cells to rapidly adjust their levels of specific transcripts in response to environmental stress conditions. Information on how different stress conditions impact on the post-transcriptional fate of stress-responsive mRNAs, however is still quite limited. Studies in *Saccharomyces cerevisiae* for instance suggest that heat shock favors the stabilization of heat-shock inducible mRNAs, while pre-existing mRNAs may suffer from accelerated degradation via the 5'-3' mRNA decay pathway or be shifted from polysomes toward a repressing mRNA state within P bodies.<sup>1-3</sup> Similarly, nutrient limitation or inactivation of the nutrient-regulated target of rapamycin complex 1 (TORC1)

broadly stimulates 5'-3' mRNA decay,<sup>4</sup> while specifically endorsing the protection of newly expressed mRNAs of genes (e.g., *HSP26*) that are controlled by the stress-responsive and/or nutrient-regulated transcription factors Msn2, Msn4 and Gis1.<sup>5</sup>

The limited amount of information on mRNA half-lives of stress-responsive genes is primarily due to the fact that most of the currently available methods to assess mRNA half-lives suffer from caveats that specifically affect stress-responsive mRNAs. For instance, assays that allow determination of mRNA half-lives are traditionally based on inhibition of general transcription using either a temperature-sensitive allele of the catalytic subunit of RNA polymerase II (RNA Pol II; i.e., *rpb1-1*),<sup>6</sup> or a variety of transcription inhibitors (e.g., thiolutin and 1,10-phenanthroline).<sup>7</sup> However, both interventions per se, namely temperature-shift (when using *rpb1-1* strains) and thiolutin/1,10-phenanthroline

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**Figure 1.** Schematic representation of the relevant features of the various plasmids used in this study. The *NdeI-SphI* 10.4-kb fragment from plasmid pNT081 can be integrated at the *ADE3* locus via homologous recombination and mediates constitutive expression of Cre-EBD78. Plasmids pNT082, pNT084, and pNT085 contain the *HSP26*, *RTN2*, and *CIT2* reporter constructs that, following excision from the plasmids with *XbaI/SpeI*, *KpnI* or *NaeI/KpnI* as indicated, can be integrated at the respective endogenous loci via homologous recombination. The plasmid pNT083 serves as a backbone to facilitate construction of any reporter construct of choice. Please note that the *loxP* site codes for 12 additional amino acids and cloning of any ORF should be designed to be in-frame with the 5' and 3' ends of the indicated *loxP*-derived reading frame. For a more detailed description of plasmid constructions, please see the section Materials and Methods.

treatment, can alter mRNA stability and, rather than blocking, in fact strongly induce transcription of heat-shock and/or stress-responsive genes.<sup>8-12</sup> In addition, since stress-responsive genes depend on their native promoters for normal induction under stress conditions, alternative methods that make use of conditionally repressible promoters to downregulate transcription (such as the Tet<sub>off</sub> system)<sup>7</sup> cannot be applied to assess the half-life of the respective mRNAs. Most recent mRNA half-life assays are based on metabolic labeling of newly transcribed mRNAs with 4-thiouracil (4-tU) or 4-thiouridine (4-sU), which requires the heterologous expression of a human nucleoside transporter (hENT1) to enable 4-sU uptake by yeast cells.<sup>13,14</sup> Potential concerns regarding the applicability of 4-tU-pulse/uracil-chase experiments to assess the half-lives of newly expressed mRNAs under dynamic stress conditions, however, include the required long pulse/labeling period (i.e. > 4 h) and the possibility of uncontrolled 4-tU recycling within cells.<sup>15</sup> Finally, dynamic

transcriptome analysis (DTA), which combines metabolic mRNA labeling with dynamic kinetic modeling, is applicable on a genome-wide level and may currently be best suited to estimate mRNA half-lives under stress conditions.<sup>13,16</sup> A theoretical concern of this method, which is technically challenging,<sup>15</sup> may be the fact that it is built on the assumption that mRNA synthesis and decay rates remain constant during the labeling time.

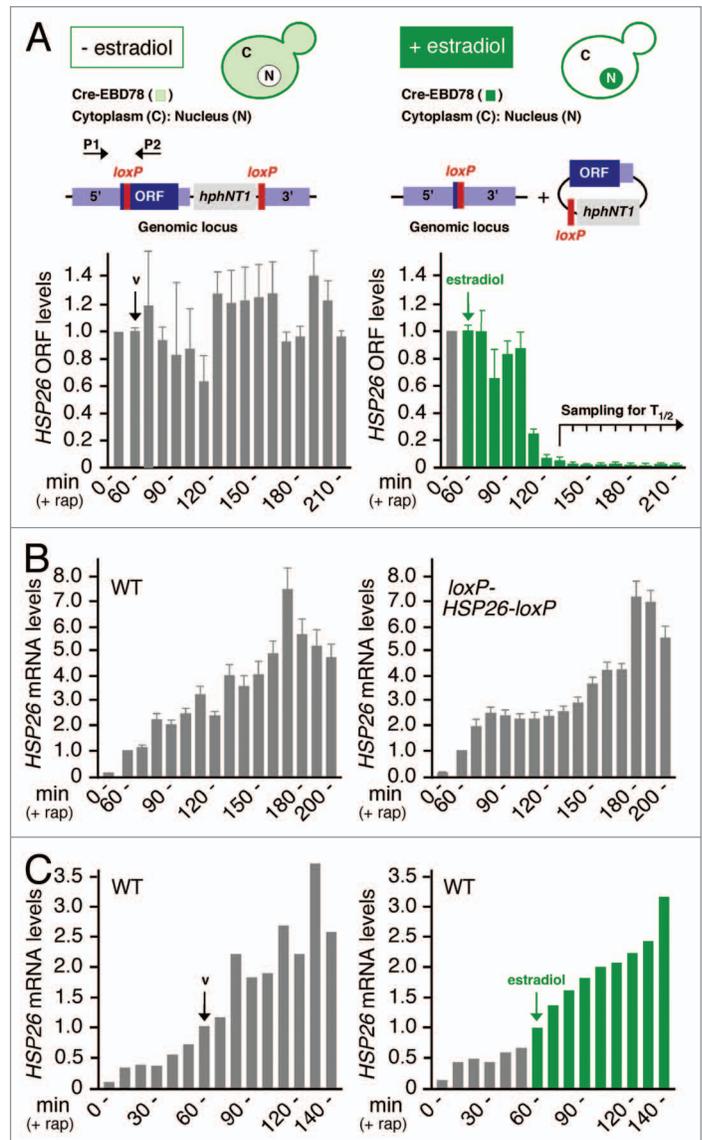
To specifically study the mRNA half-life of individual stress-responsive mRNAs, we developed a minimally perturbing method, which is not susceptible to any of the caveats of the classical mRNA half-life studies outlined above. Our method is based on the excision from the genome of a given *loxP*-flanked open reading frame, and hence discontinuance of transcription, following conditional nuclear targeting of the Cre recombinase. Using this assay, which we coin CEO (for conditional excision of the open reading frame [ORF]), we confirm our previous data, which indicated that inactivation of TORC1 results in stabilization of newly expressed mRNAs of Msn2-, Msn4-, and Gis1-controlled genes.<sup>5,17-19</sup> Using CEO, we extend our earlier studies and demonstrate that TORC1 controls mRNA stability via the Cdc55-protein phosphatase 2A (PP2A<sup>Cdc55</sup>), which we recently found to be also implicated in direct regulation of the transcription factor Gis1.<sup>18</sup> Thus, our data indicate the existence of a mechanism that allows cells to tightly coordinate transcription with the post-transcriptional fate of specific mRNAs under nutrient stress conditions.

## Results

**The experimental system.** To design our method, we used a Cre recombinase that is fused to the estradiol-binding domain (EBD) of the murine estrogen receptor (Cre-EBD78),<sup>20,21</sup> which mediates the cytoplasmic to nuclear translocation of the fusion protein following its association with estradiol. This construct can therefore be used to conditionally grant the Cre recombinase access to *loxP* sites in the genome.<sup>22</sup> Stable and constitutive expression (from the *GPD1* promoter) of the Cre-EBD78 fusion protein was achieved by integration of the corresponding fusion gene at the *ADE3* locus in the genome (Fig. 1; of note, expression of this fusion protein as such did not measurably alter the expression profile of *HSP26* [or of *RTN2* or *CIT2*; see below] in exponentially growing and rapamycin-treated wild-type cells; data not shown). In parallel, *loxP* sites were introduced just downstream of and in-frame with the ATG as well as downstream of the 3' untranslated region (UTR) of the *HSP26* gene using the single-step PCR-based gene replacement technique (Material and Methods; Fig. 1).<sup>23</sup> Addition of

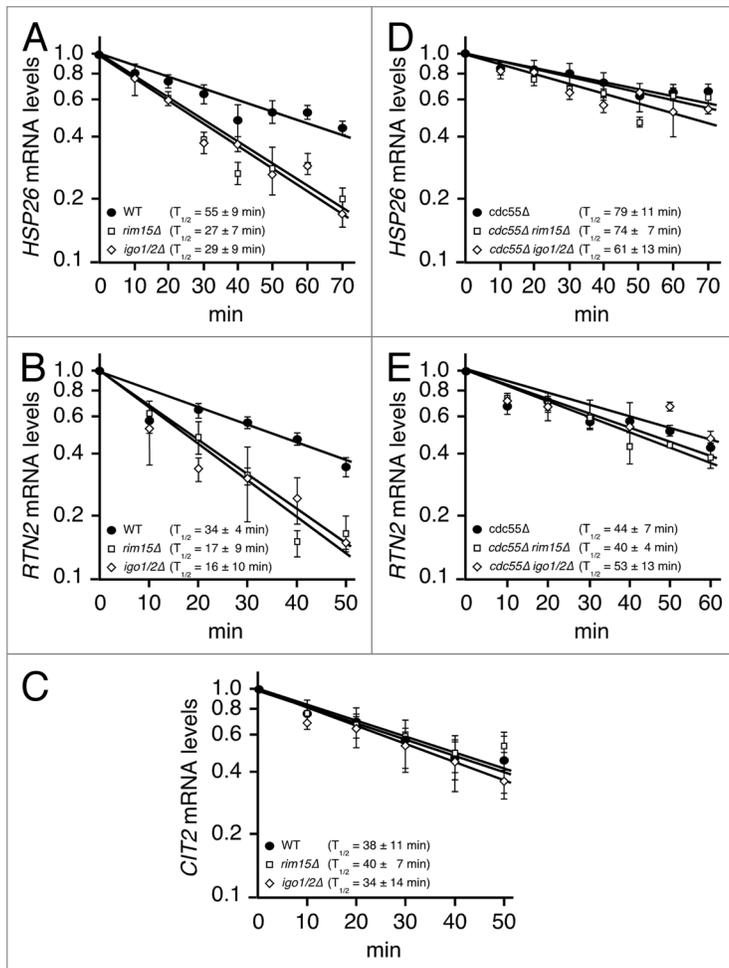
**Figure 2.** Description of the CEO method. **(A)** The Cre-EBD78 fusion protein (expressed under the control of the *GPD1* promoter) is predominantly localized in the cytoplasm in the absence of estradiol, but shuttles into the nucleus following estradiol (1  $\mu$ M) addition to reporter cells. Nuclear Cre-EBD78 mediates recombination between *loxP* sites that are introduced (in tandem orientation) in the genome just downstream of and in-frame with the ATG as well as downstream of the 3' UTR of target genes using the single-step PCR-based gene replacement technique (and the hygromycin-resistance gene (*hphNT1*) as selectable marker). As a proof of principle, exponentially growing wild-type cells harboring the Cre-EBD78 and *loxP*-*HSP26*-*loxP* reporter constructs (NT393-6D) were treated with rapamycin (200 ng ml<sup>-1</sup>) to induce the expression of *HSP26*, followed by addition of estradiol (at time 60 min) to trigger excision of the *HSP26* ORF and the *hphNT1* cassette from the genome (as illustrated). The efficacy of *HSP26* excision was assessed by qPCR using the indicated primers (P1 and P2) and genomic DNA as template. Bar graphs show the mean levels of three independent experiments ( $\pm$  S.D.) of PCR-amplified *HSP26* (normalized to 1.0 for exponentially growing, untreated cells) in cells treated with either vehicle alone (v; on the left) or with estradiol (on the right) for the times indicated. Samples to determine the half-life of *HSP26* mRNA were collected (at 10 min intervals) 70 min following vehicle or estradiol treatment and the respective data are presented in **Figure 3A**. **(B)** qRT-PCR analysis of *HSP26* mRNA induction in wild-type (WT) and *loxP*-*HSP26*-*loxP* reporter cells (same as in **(A)**) treated for the times indicated with 200 ng ml<sup>-1</sup> rapamycin. Mean *HSP26* mRNA levels of three independent experiments ( $\pm$  S.D.), normalized to the values at 60 min, are shown. Notably, in terms of absolute levels, the rapamycin-induced accumulation of *HSP26* mRNA (and of *HSP26* protein) did not significantly differ in *loxP*-*HSP26*-*loxP* reporter cells when compared with wild-type cells (data not shown). **(C)** Estradiol per se (added at time 60 min), like vehicle alone, does not interfere with rapamycin-induced *HSP26* expression (quantified by qRT-PCR as in **(B)**) in wild-type cells.

estradiol to yeast cells containing both reporter constructs should therefore trigger nuclear transfer of the Cre-EBD78 fusion protein and consequent excision of the *HSP26* ORF (including the *HSP26* - 3'(a) region; Fig. 2A). To verify this assumption, exponentially growing wild-type cells harboring the two reporter constructs (referred to as “reporter cells/strain” hereafter) were treated with rapamycin for 60 min to induce the expression of *HSP26* (which was normal when compared with wild-type cells bearing no reporter constructs; Fig. 2B). The culture was then equally split and the two sub-cultures were either treated with vehicle alone or with estradiol, which per se did not significantly alter the *HSP26* expression levels in rapamycin-treated wild-type cells carrying no reporter genes (Fig. 2C). As expected, estradiol treatment, but not treatment with the vehicle alone, triggered the excision of the ORF at the *HSP26* locus in reporter cells (Fig. 2A). Notably, most of the *HSP26* loci (i.e. > 96%) were excised within 20 min following a 50 min lag period (Fig. 2A) and the remaining fraction of *HSP26* loci contributed only marginally (i.e. < 3%) to the existing pool of *HSP26* mRNAs (as assessed in separate experiments in which *HSP26* mRNA expression was quantified during a 1 h rapamycin treatment in reporter cells that had been first exposed to estradiol for 70 min; data not shown). To determine the half-life of *HSP26* mRNAs, we have therefore started to collect samples (in 10 min intervals) 70 min following estradiol treatment, at which point in time *HSP26* mRNA levels were maximally



high in this experiment. Using this method, we determined a half-life of 55 min for *HSP26* mRNA in rapamycin treated (130 min) cells (Fig. 3A).

To demonstrate that CEO is more broadly applicable, we also studied two additional genes (i.e., *RTN2* and *CIT2*) and their respective mRNAs, which we previously found to be strongly induced following rapamycin treatment.<sup>5</sup> To this end, we constructed an additional hygromycin-selectable plasmid (pNT083) containing the two *loxP* sites and several restriction sites that facilitate construction of the DNA fragments that allow introduction of the *loxP*-reporter genes by single-step gene replacement in yeast (Materials and Methods; Fig. 1). Like the *HSP26* reporter gene described above, Cre-EBD78-excisable *RTN2* and *CIT2* reporter genes were efficiently (and with similar kinetics) removed from the genomes of the respective reporter strains following addition of estradiol, which on its own had no detectable effect on *RTN2* or *CIT2* expression (not shown). Using the same conditions as above for determination of the *HSP26* mRNA half-life, we found that *RTN2* and *CIT2* mRNAs exhibited



**Figure 3.** TORC1 controls mRNA stability via the PP2A<sup>Cdc55</sup>-inhibitory endosulfines. (A–E) qRT-PCR analysis of *HSP26* (A and D), *RTN2* (B and E) and *CIT2* (C) mRNA levels in rapamycin-treated cells. mRNA samples were harvested from cells, which harbored the Cre-EBD78 and an appropriate *loxP*-ORF-*loxP* reporter construct (see Table 1) and that were treated with rapamycin and estradiol following the protocol outlined in Figure 2A. The values for the reference samples at time point 0 (corresponding to the time point 130 min of the rapamycin treatment) were normalized to 1.0 for each strain. Notably, the Rim15-Igo1/2-PP2A<sup>Cdc55</sup> signaling branch also regulates transcription (in part via Gis1) of *HSP26* and *RTN2*, but not of *CIT2* (see also the model in Fig. 4).<sup>5,18,31</sup> Before their normalization to 1.0, the relative levels of *HSP26* and *RTN2* mRNAs, but not the ones of *CIT2*, therefore differed significantly between the various mutant strains. Accordingly, the *HSP26* mRNA levels in *rim15Δ*, *igo1/2Δ*, *cdc55Δ*, *cdc55Δ rim15Δ*, and *cdc55Δ igo1/2Δ* cells were 23%, 13%, 225%, 170%, and 196%, respectively, when compared with those in wild-type cells (in [A and D]). Similarly, *RTN2* mRNA levels in *rim15Δ*, *igo1/2Δ*, *cdc55Δ*, *cdc55Δ rim15Δ*, and *cdc55Δ igo1/2Δ* cells were 17%, 25%, 155%, 150% and 132%, respectively, when compared with those in wild-type cells (in [B and E]). Estradiol-induced excision of the *loxP*-ORF-*loxP* loci was verified independently and found to be at least 85% complete for each strain at time point 0 (i.e. 70 min following estradiol addition). Data points represent means ± S.D. of three independent experiments.

half-lives of 34 and 38 min, respectively, in rapamycin-treated cells (Fig. 3B and C).

**Validation of CEO.** We have previously reported that inactivation of TORC1 results in stabilization of newly expressed mRNAs of Msn2-, Msn4- and Gis1-controlled genes via a

process that depends on the greatwall protein kinase ortholog Rim15 and its targets Igo1/2.<sup>5</sup> In this study, the experimental caveats of mRNA half-life assays (outlined above) were circumvented by rendering *HSP26* transcription doxycycline-repressible due to the insertion of a series of doxycycline-responsive *tetO* elements in the *HSP26* promoter. Notably, identification of sites in the *HSP26* promoter that tolerated the respective *tetO* insertions without interfering with normal transcriptional regulation of *HSP26* was challenging and time-consuming. Using the much easier applicable CEO assay, we confirm here our earlier results that loss of Rim15 or of Igo1/2 reduced the *HSP26* mRNA half-life in rapamycin-treated cells about 2-fold (Fig. 3A). To further extend these data, we also studied the half-lives of two additional mRNAs, which were encoded by genes that either depended (i.e., *RTN2*), or did not depend (i.e., *CIT2*), on the presence of Rim15 and Igo1/2 for normal expression following TORC1 inactivation.<sup>5</sup> In line with our expectations, we found that the half-life of the *RTN2* mRNA, but not the one of *CIT2* mRNA, was reduced 2-fold in rapamycin treated *rim15Δ* and *igo1Δ igo2Δ* cells when compared with wild-type cells (Fig. 3B and C). These data not only demonstrate the validity of CEO for mRNA half-life studies, but also corroborate our earlier conclusion that TORC1 controls the stability of a specific set of mRNAs via Rim15-Igo1/2.<sup>5,17,24,25</sup>

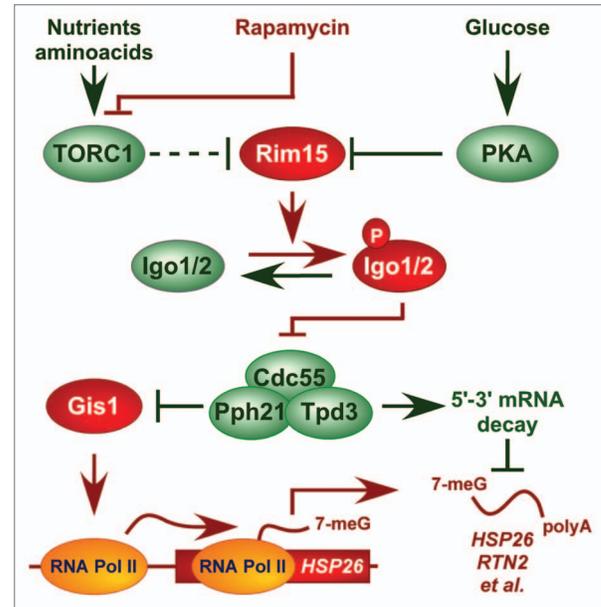
**TORC1 controls mRNA stability via the PP2A<sup>Cdc55</sup>-inhibitory endosulfines.** We recently discovered that Rim15, analogous to the greatwall kinase in *Xenopus*, phosphorylates endosulfines (i.e. Igo1/2) to directly inhibit the Cdc55-protein phosphatase 2A (PP2A<sup>Cdc55</sup>).<sup>18</sup> Accordingly, when phosphorylated by Rim15 on Ser<sup>64</sup>, Igo1 directly binds to and prevents PP2A<sup>Cdc55</sup> from dephosphorylating various target proteins among which we identified the transcription factor Gis1. Inhibition of PP2A<sup>Cdc55</sup> preserves Gis1 in a phosphorylated state and consequently promotes its recruitment to and activation of transcription from promoters of specific nutrient-regulated genes such as *RTN2*. Together with our earlier studies, these recent data suggest that Igo1/2, following their activation by Rim15, stimulate both transcriptional activation of Gis1-dependent genes and post-transcriptional stability of the respective mRNAs by inhibiting PP2A<sup>Cdc55</sup>. To address this assumption further, using the CEO method, we studied whether loss of Cdc55 may suppress the defect in *HSP26* and *RTN2* mRNA stability that we observed in rapamycin-treated *rim15Δ* and *igo1Δ igo2Δ* cells (Fig. 3A and B). Mutant *cdc55Δ* cells exhibited slightly enhanced (i.e. 1.3–1.4-fold) *HSP26* and *RTN2* mRNA half-lives when compared with wild-type cells treated with rapamycin (Fig. 3D and E). Interestingly, in contrast to the situation in wild-type cells, loss of Rim15 or of Igo1/2 had no significant impact on the observed *HSP26* and *RTN2* mRNA half-lives in *cdc55Δ* cells under the same conditions (Fig. 3D and E). Thus, the enhanced turnover of *HSP26* and *RTN2* mRNAs in rapamycin-treated *rim15Δ* and *igo1/2Δ* cells can be suppressed by loss of Cdc55.

These data extend our previous model and suggest that TORC1 controls in fact both transcriptional activation of Gis1-dependent genes and post-transcriptional stability of the respective mRNAs via the Rim15-Igo1/2-PP2A<sup>Cdc55</sup> effector branch (Fig. 4).

## Discussion

Here we describe an alternative method to study the mRNA half-life of stress-responsive genes in yeast that is based on the conditional excision of ORFs (CEO). CEO offers a distinct advantage over conventional mRNA half-life assays that build on the inactivation of transcription using either the temperature-sensitive *rpb1-1* allele or a variety of specific transcription inhibitors (see Introduction). Accordingly, CEO relies on estradiol treatment (to induce cytoplasmic to nuclear transfer of the Cre-EBD78 fusion protein), which, unlike heat-shock (when using *rpb1-1* mutants) or various treatments with transcription inhibitory drugs, per se does neither induce the expression nor interfere with the normal (rapamycin-mediated) regulation of stress-responsive genes such as *HSP26*, *RTN2*, and *CIT2* (Fig. 2C and data not shown). Based on our observation that estradiol-induced excision of various target ORFs was exerted to a large extent within a time frame of 10–20 min (following a lag period of 50 min), we infer that CEO represents a valid method to determine the stability of those mRNA species that exhibit half-lives of at least 10–20 min. An additional advantage of CEO is that it preserves the endogenous structures of the 5'/3' UTRs and the promoters of the genes under study, which makes CEO less likely to alter the fate of mRNAs than traditional methods that are based on the use heterologous repressible promoters.<sup>26–30</sup> Although it remains theoretically possible that the insertion of a *loxP* site within the ORF of a given target gene may affect its expression, our control experiments, in which we compared the level of *HSP26* mRNAs between rapamycin-treated wild-type and *loxP-HSP26-loxP* cells, indicated that the introduction of a *loxP* site within the *HSP26* ORF per se is minimally invasive with no significant effect on the expression and/or stability of *HSP26* mRNAs. Taken together, despite a few limitations (regarding the resolution of half-lives of very short-lived mRNAs and the unsuitability for genome-wide analyses), CEO offers a valid alternative to sample the mRNA half-life of stress-responsive genes, which, together with the toolbox offered here, only requires relatively easily applicable standard yeast genetic methods. Finally, although not specifically studied here, we would like to point out that CEO may in principle also be applied to the analysis of gene function as it allows conditional inactivation of specific genes. Provided that the respective gene products have a relatively limited half-life, CEO could be particularly useful to replace and/or complement analyses of essential genes that have hitherto relied on the use of temperature-sensitive alleles.

The use of CEO allowed us to confirm our previous finding that the protein kinase Rim15, which is indirectly and negatively controlled by TORC1,<sup>24,25,31,32</sup> plays a key role in stabilizing mRNAs of Msn2/4- and Gis1-controlled genes via its direct targets Igo1/2. More recently, we discovered that, following their phosphorylation by Rim15, Igo1/2 serve to inhibit PP2A<sup>Cdc55</sup>,



**Figure 4.** Model for the role of Igo1/2-PP2A<sup>Cdc55</sup> in controlling expression of nutrient-regulated genes. Arrows and bars denote positive and negative interactions, respectively. TORC1 regulates Rim15 indirectly via Sch9.<sup>25</sup> For details, see text.

thereby favoring promoter recruitment of and transcription by the transcription factor Gis1.<sup>18</sup> These new data raised the question whether Igo1/2-mediated inhibition of PP2A<sup>Cdc55</sup> may, in addition to its role in transcription, also be implicated in post-transcriptional control of mRNA stability. Our data presented here indicate that this is the case. Thus, Igo1/2-dependent regulation of PP2A<sup>Cdc55</sup> appears to represent a key node in nutrient-sensitive, homo-directional coordination of transcription and post-transcriptional mRNA stabilization of a specific array of genes (Fig. 4). Interestingly, loss of components of the 5'-3' mRNA decay pathway, like loss of Cdc55, suppresses the defect in *HSP26* expression in rapamycin-treated *igo1/2Δ* cells.<sup>5,17,18</sup> It is therefore possible that PP2A<sup>Cdc55</sup> regulates, in addition to Gis1, a specific protein(s) within the 5'-3' mRNA decay pathway. In this context, our previously published phosphoproteome studies pinpointed, among others, Vts1 as a potential PP2A<sup>Cdc55</sup> target.<sup>18</sup> Vts1 is a member of the Smaug family of proteins, which directly binds a defined RNA motif in target mRNAs of nutrient-regulated genes and controls their stability by interfering with the 5'-3' mRNA decay pathway.<sup>33,34</sup> It will therefore be interesting to explore in future studies whether parallel, temporally coordinated regulation by the Igo1/2-PP2A<sup>Cdc55</sup> module of both Gis1 and Vts1 (or of other candidate proteins) may allow cells to coordinate transcription and posttranscriptional mRNA stability.

## Materials and Methods

**Strains and growth conditions.** *S. cerevisiae* strains (Table 1) were grown at 30°C in standard rich medium (YPD) with 2% glucose or in synthetic defined (SD) medium (0.17% yeast nitrogen base, 0.5% ammonium sulfate, and 2% glucose) complemented with

**Table 1.** Strains used in this study

| Strain    | Genotype   | Source     | Figure |
|-----------|--|------------|--------|
| BY4741    | <i>MATa; ura3Δ0, leu2Δ0, his3Δ1, met15Δ0</i>   | Euroscarf  | 2B, C  |
| BY4742    | <i>MATα; ura3Δ0, leu2Δ0, his3Δ1, lys2Δ0</i>  | Euroscarf  |        |
| NT393–1D  | <i>MATa; HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3'</i> [BY4741/2]   | this study | 2B     |
| NT393–6D  | <i>MATa; HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]  | this study | 2A, 3A |
| NT394–1C  | <i>MATa; rim15Δ::kanMX, HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                             | this study | 3A     |
| NT395–8A  | <i>MATα; igo1Δ::kanMX, igo2Δ::kanMX, HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                | this study | 3A     |
| NT401–10C | <i>MATa; cdc55Δ::kanMX, HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                             | this study | 3D     |
| NT402–13C | <i>MATa; cdc55Δ::kanMX, rim15Δ::kanMX, HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]              | this study | 3D     |
| NT404–14D | <i>MATα; cdc55Δ::kanMX, igo1Δ::kanMX, igo2Δ::kanMX, HSP26-5'-loxP-HSP26-HphNT1-loxP-HSP26-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2] | this study | 3D     |
| NT418–10B | <i>MATα; RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]   | this study | 3B     |
| NT417–2B  | <i>MATα; rim15Δ::kanMX, RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                                | this study | 3B     |
| NT416–17C | <i>MATα; igo1Δ::kanMX, igo2Δ::kanMX, RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                   | this study | 3B     |
| NT417–4C  | <i>MATα; cdc55Δ::kanMX, RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                                | this study | 3E     |
| NT417–17C | <i>MATα; cdc55Δ::kanMX, rim15Δ::kanMX, RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                 | this study | 3E     |
| NT425–3D  | <i>MATα; cdc55Δ::kanMX, igo1Δ::kanMX, igo2Δ::kanMX, RTN2-5'-loxP-RTN2-HphNT1-loxP-RTN2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]    | this study | 3E     |
| NT422–1C  | <i>MATa; CIT2-5'-loxP-CIT2-HphNT1-loxP-CIT2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]   | this study | 3C     |
| NT424–17D | <i>MATa; rim15Δ::kanMX, CIT2-5'-loxP-CIT2-HphNT1-loxP-CIT2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                                | this study | 3C     |
| NT423–1B  | <i>MATa; igo1Δ::kanMX, igo2Δ::kanMX, CIT2-5'-loxP-CIT2-HphNT1-loxP-CIT2-3', ADE3::GPD1:Cre-EBD78-LEU2</i> [BY4741/2]                   | this study | 3C     |

the appropriate nutrients for plasmid maintenance. Rapamycin and estradiol were used at a concentration of 200 ng ml<sup>-1</sup> and 1 μM, respectively.

**Plasmid constructions.** The plasmids used in this study are depicted in **Figure 1**. pNT081, containing part of the *ADE3* gene (i.e. 600 bp upstream and 400 bp downstream of the ATG), is derived from p*GPD1:Cre-EBD78*.<sup>20,21</sup> Digestion of pNT081 with *NdeI* and *SphI* generates a 10.4 kb fragment that drives integration of the *GPD1:Cre-EBD78* cassette into the genomic *ADE3* locus in yeast. Positive clones can be selected using the *LEU2* marker that is also present on this fragment. pNT082 was constructed by inserting, via homologous recombination, elements of the *HSP26* gene into the pFA6a-*CEN4-ASK1-loxP-HphNT1* plasmid (kind gift of Yves Barral). Digestion of pNT082 with *XbaI* and *SpeI* generates two fragments (3686 and 3240 bp) of which the 3686 bp fragment can be inserted at the *HSP26* locus by homologous recombination. As illustrated in **Figure 1**, this fragment contains sequentially the 347 bp upstream of and including the ATG plus the first 18 bp of the *HSP26* ORF (*HSP26-5'*), a first *loxP* site that preserves the reading frame with respect to the preceding ATG and the following *HSP26* ORF (encoding amino acids 2–214), the 428 bp downstream of and including the stop codon of *HSP26* (*HSP26-3'* [a]), the *hphNT1* cassette, a second *loxP* site (in tandem orientation with the first *loxP* site) and the last 42 bp of the *HSP26* ORF, including the stop codon followed by 343 bp of the 3' region (*HSP26-3'* [b]). The *hphNT1* cassette allows expression of the hygromycin B resistance gene under the

control of the *TEF1* promoter. pNT083 is based on pRS316 and was designed to facilitate construction of reporter cassettes for use in CEO assays. To this end, a fragment containing the 300 bp upstream of and including the ATG plus the first 15 bp of the ORF of a given gene can be cloned at the *NaeI* and *NotI* sites (or only at *NotI*) in pNT083 (in-frame with the subsequent *loxP*-encoded sequence indicated in **Fig. 1**). A second fragment coding for the entire ORF (except the ATG) plus at least 300 bp downstream of and including the stop codon can be cloned at the *XbaI* and *BamHI* sites (or only at *XbaI*; in frame with the preceding *loxP*-encoded sequence). Finally, a third fragment including at least the first 300 bp of the 3' region following the stop codon can be cloned at the *SalI* and/or *KpnI* sites. For homologous recombination in yeast, the entire cassette can then be removed from the plasmid by digestion with *NaeI* and *KpnI*. Both plasmids pNT084 and pNT085 were constructed using this approach and pNT083 as template. Accordingly, pNT084 contains sequentially the 300 bp upstream of and including the ATG plus the first 18 bp of *RTN2* (*RTN2-5'*), a first *loxP* site that preserves the reading frame with respect to the preceding ATG and the following *RTN2* ORF (encoding amino acids 4–393), the 295 bp downstream of and including the *RTN2* stop codon (*RTN2-3'*), the *hphNT1* cassette, a second *loxP* site (in tandem orientation with the first *loxP* site), and the 295 bp downstream of the *RTN2* stop codon (*RTN2-3'*). Digestion of pNT084 with *KpnI* generates two fragments (3882 and 4482 bp) of which the 3882 bp fragment can be inserted at the *RTN2* locus by homologous

recombination. Similarly, the pNT085 contains sequentially the 295 bp upstream of and including the ATG plus the first 18 bp of *CIT2* (*CIT2-5'*), a first *loxP* site that preserves the reading frame with respect to the preceding ATG and the following *CIT2* ORF (encoding amino acids 2–460), the 300 bp downstream of and including the *CIT2* stop codon (*CIT2-3'*), the *hphNT1* cassette, a second *loxP* site (in tandem orientation with the first *loxP* site) and the 300 bp downstream of the *CIT2* stop codon (*CIT2-3'*). Digestion of pNT085 with *NaeI* and *KpnI* generates two fragments (4121 and 4460 bp) of which the 4121 bp fragment can be inserted at the *CIT2* locus by homologous recombination.

**Real-time qPCR and qRT-PCR.** High-quality yeast genomic DNA preparation was mainly performed as described previously with minor modifications.<sup>35</sup> At each step, one-tenth of the indicated values was used. Total RNA was extracted using the hot acidic phenol method. DNA was removed with the DNA-free Kit (Ambion) and first-strand cDNA was synthesized with the PrimeScript RT Reagent Kit (TaKaRa). Quantitative RT-PCR (qRT-PCR) was performed on a Rotor-Gene 6000 machine (Corbett Life Science), with the 5 x EvaGreen QPCR Mix II no Rox (Bio&SELL) or with the QuantiTect SYBR Green PCR Kit (Qiagen). *HSP26*, *RTN2* and *CIT2* DNA and mRNA levels were normalized with respect to *NSR1* DNA or mRNA. Oligonucleotides used for qPCR and qRT-PCR were as follows:

AAGGCCGTCT CTCCTCTTC (NSR1qF2);  
GTTTTCAGC TTCACTTTCG C (NSR1qR2);  
TGTTTTTAAT CCATTCACCT TTCAT (HSP26  
gF2; P1); CCTTCACCCA GCAATCTGTT (HSP26  
gR2; P2); AGTTAGCAAA CACACCCGCA AAGG  
(HSP26qF1); TGCTCTCCTT GACCTTGACC  
(HSP26qR1); TCTGGTGAGT TTGCTGATCC  
(RTN2qF1); GCGGTTCGATA TGAGGCTTTA AG  
(RTN2qR1); ATCACCTTAT CTGTCCCTTG C  
(CIT2qF1); ACAGCATGAC CATAACGGG (CIT2qR1).

#### Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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#### Author's Contribution

NT designed and performed the experiments. All authors contributed to the data analysis and creation of figures and commented on the manuscript, which was written by CDV.

#### References

- Wang Y, Liu CL, Storey JD, Tibshirani RJ, Herschlag D, Brown PO. Precision and functional specificity in mRNA decay. *Proc Natl Acad Sci USA* 2002; 99:5860-5; PMID:11972065; <http://dx.doi.org/10.1073/pnas.092538799>
- Bond U. Stressed out! Effects of environmental stress on mRNA metabolism. *FEMS Yeast Res* 2006; 6:160-70; PMID:16487339; <http://dx.doi.org/10.1111/j.1567-1364.2006.00032.x>
- Gasch A. The environmental stress response: a common yeast response to environmental stresses. In: Hohmann S, Mager P, (eds). *Yeast stress responses*. Springer, Berlin Heidelberg, New York. 2002
- Albig AR, Decker CJ. The target of rapamycin signaling pathway regulates mRNA turnover in the yeast *Saccharomyces cerevisiae*. *Mol Biol Cell* 2001; 12:3428-38; PMID:11694578
- Talarek N, Cameroni E, Jaquenoud M, Luo X, Bontron S, Lippman S, et al. Initiation of the TORC1-regulated G<sub>0</sub> program requires Igo1/2, which license specific mRNAs to evade degradation via the 5'-3' mRNA decay pathway. *Mol Cell* 2010; 38:345-55; PMID:20471941; <http://dx.doi.org/10.1016/j.molcel.2010.02.039>
- Nonet M, Scafe C, Sexton J, Young R. Eucaryotic RNA polymerase conditional mutant that rapidly ceases mRNA synthesis. *Mol Cell Biol* 1987; 7:1602-11; PMID:3299050; <http://dx.doi.org/10.1128/MCB.7.5.1602>
- Coller J. Methods to determine mRNA half-life in *Saccharomyces cerevisiae*. *Methods Enzymol* 2008; 448:267-84; PMID:19111181; [http://dx.doi.org/10.1016/S0076-6879\(08\)02614-1](http://dx.doi.org/10.1016/S0076-6879(08)02614-1)
- Adams CC, Gross DS. The yeast heat shock response is induced by conversion of cells to spheroplasts and by potent transcriptional inhibitors. *J Bacteriol* 1991; 173:7429-35; PMID:1938939
- Holstege FC, Jennings EG, Wyrick JJ, Lee TI, Hengartner CJ, Green MR, et al. Dissecting the regulatory circuitry of a eukaryotic genome. *Cell* 1998; 95:717-28; PMID:9845373; [http://dx.doi.org/10.1016/S0092-8674\(00\)81641-4](http://dx.doi.org/10.1016/S0092-8674(00)81641-4)
- Li B, Nierras CR, Warner JR. Transcriptional elements involved in the repression of ribosomal protein synthesis. *Mol Cell Biol* 1999; 19:5393-404; PMID:10409730; <http://dx.doi.org/10.1152/ajpgi.00315.2009>
- Herruer MH, Mager WH, Raué HA, Vreken P, Wilms E, Planta RJ. Mild temperature shock affects transcription of yeast ribosomal protein genes as well as the stability of their mRNAs. *Nucleic Acids Res* 1988; 16:7917-29; PMID:3047675; <http://dx.doi.org/10.1093/nar/16.16.7917>
- Pelechano V, Pérez-Ortín JE. The transcriptional inhibitor thiolutin blocks mRNA degradation in yeast. *Yeast* 2008; 25:85-92; PMID:17914747; <http://dx.doi.org/10.1002/yea.1548>
- Miller C, Schwab B, Maier K, Schulz D, Dümcke S, Zacher B, et al. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. *Mol Syst Biol* 2011; 7:458; PMID:21206491; <http://dx.doi.org/10.1038/msb.2010.112>
- Munchel SE, Shultzaberger RK, Takizawa N, Weis K. Dynamic profiling of mRNA turnover reveals gene-specific and system-wide regulation of mRNA decay. *Mol Biol Cell* 2011; 22:2787-95; PMID:21680716; <http://dx.doi.org/10.1091/mbc.E11-01-0028>
- Pérez-Ortín JE, Alepuz P, Chávez S, Choder M. Eukaryotic mRNA Decay: Methodologies, Pathways, and Links to Other Stages of Gene Expression. *J Mol Biol* 2013; In press; PMID:23467123; <http://dx.doi.org/10.1016/j.jmb.2013.02.029>
- Sun M, Schwab B, Schulz D, Pirkel N, Etzold S, Larivière L, et al. Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. *Genome Res* 2012; 22:1350-9; PMID:22466169; <http://dx.doi.org/10.1101/gr.130161.111>
- Luo X, Talarek N, De Virgilio C. Initiation of the yeast G<sub>0</sub> program requires Igo1 and Igo2, which antagonize activation of decapping of specific nutrient-regulated mRNAs. *RNA Biol* 2011; 8:14-7; PMID:21289492; <http://dx.doi.org/10.4161/rna.8.1.13483>
- Bontron S, Jaquenoud M, Vaga S, Talarek N, Bodenmiller B, Abersold R, et al. Yeast endosulfines control entry into quiescence and chronological life span by inhibiting protein phosphatase 2A. *Cell Rep* 2013; 3:16-22; PMID:23273919; <http://dx.doi.org/10.1016/j.celrep.2012.11.025>
- Cameroni E, Hulo N, Roosen J, Winderickx J, De Virgilio C. The novel yeast PAS kinase Rim 15 orchestrates G<sub>0</sub>-associated antioxidant defense mechanisms. *Cell Cycle* 2004; 3:462-8; PMID:15300954; <http://dx.doi.org/10.4161/cc.3.4.791>
- Lindstrom DL, Gottschling DE. The mother enrichment program: a genetic system for facile replicative life span analysis in *Saccharomyces cerevisiae*. *Genetics* 2009; 183:413-22; PMID:19652178; <http://dx.doi.org/10.1534/genetics.109.106229>
- Hotz M, Leisner C, Chen D, Manatschal C, Wegleiter T, Ouellet J, et al. Spindle pole bodies exploit the mitotic exit network in metaphase to drive their age-dependent segregation. *Cell* 2012; 148:958-72; PMID:22385961; <http://dx.doi.org/10.1016/j.cell.2012.01.041>
- Cheng TH, Chang CR, Joy P, Yablok S, Gartenberg MR. Controlling gene expression in yeast by inducible site-specific recombination. *Nucleic Acids Res* 2000; 28:E108; PMID:11121495; <http://dx.doi.org/10.1093/nar/28.24.e108>
- Wach A, Brachar A, Pöhlmann R, Philippsen P. New heterologous modules for classical or PCR-based gene disruptions in *Saccharomyces cerevisiae*. *Yeast* 1994; 10:1793-808; PMID:7747518; <http://dx.doi.org/10.1002/yea.320101310>
- Urban J, Souillard A, Huber A, Lippman S, Mukhopadhyay D, Deloche O, et al. Sch9 is a major target of TORC1 in *Saccharomyces cerevisiae*. *Mol Cell* 2007; 26:663-74; PMID:17560372; <http://dx.doi.org/10.1016/j.molcel.2007.04.020>
- Wanke V, Cameroni E, Uotila A, Piccolis M, Urban J, Loewith R, et al. Caffeine extends yeast lifespan by targeting TORC1. *Mol Microbiol* 2008; 69:277-85; PMID:18513215; <http://dx.doi.org/10.1111/j.1365-2958.2008.06292.x>

26. Trcek T, Larson DR, Moldón A, Query CC, Singer RH. Single-molecule mRNA decay measurements reveal promoter-regulated mRNA stability in yeast. *Cell* 2011; 147:1484-97; PMID:22196726; <http://dx.doi.org/10.1016/j.cell.2011.11.051>
27. Bregman A, Avraham-Kelbert M, Barkai O, Duek L, Guterman A, Choder M. Promoter elements regulate cytoplasmic mRNA decay. *Cell* 2011; 147:1473-83; PMID:22196725; <http://dx.doi.org/10.1016/j.cell.2011.12.005>
28. Shalgi R, Lapidot M, Shamir R, Pilpel Y. A catalog of stability-associated sequence elements in 3' UTRs of yeast mRNAs. *Genome Biol* 2005; 6:R86; PMID:16207357; <http://dx.doi.org/10.1186/gb-2005-6-10-r86>
29. Tuller T, Ruppin E, Kupiec M. Properties of untranslated regions of the *S. cerevisiae* genome. *BMC Genomics* 2009; 10:391; PMID:19698117; <http://dx.doi.org/10.1186/1471-2164-10-391>
30. Beilharz TH, Preiss T. Widespread use of poly(A) tail length control to accentuate expression of the yeast transcriptome. *RNA* 2007; 13:982-97; PMID:17586758; <http://dx.doi.org/10.1261/rna.569407>
31. Pedruzzi I, Dubouloz F, Cameroni E, Wanke V, Roosen J, Winderickx J, et al. TOR and PKA signaling pathways converge on the protein kinase Rim15 to control entry into G<sub>0</sub>. *Mol Cell* 2003; 12:1607-13; PMID:14690612; [http://dx.doi.org/10.1016/S1097-2765\(03\)00485-4](http://dx.doi.org/10.1016/S1097-2765(03)00485-4)
32. Wanke V, Pedruzzi I, Cameroni E, Dubouloz F, De Virgilio C. Regulation of G<sub>0</sub> entry by the Pho80-Pho85 cyclin-CDK complex. *EMBO J* 2005; 24:4271-8; PMID:16308562; <http://dx.doi.org/10.1038/sj.emboj.7600889>
33. Riordan DP, Herschlag D, Brown PO. Identification of RNA recognition elements in the *Saccharomyces cerevisiae* transcriptome. *Nucleic Acids Res* 2011; 39:1501-9; PMID:20959291; <http://dx.doi.org/10.1093/nar/gkq920>
34. Rendl LM, Bieman MA, Smibert CA. *S. cerevisiae* Vts1p induces deadenylation-dependent transcript degradation and interacts with the Ccr4p-Pop2p-Not deadenylase complex. *RNA* 2008; 14:1328-36; PMID:18469165; <http://dx.doi.org/10.1261/rna.955508>
35. Philippsen P, Stotz A, Scherf C. DNA of *Saccharomyces cerevisiae*. *Methods Enzymol* 1991; 194:169-82; PMID:2005785; [http://dx.doi.org/10.1016/0076-6879\(91\)94014-4](http://dx.doi.org/10.1016/0076-6879(91)94014-4)