Set4 is a chromatin-associated protein, promotes survival during oxidative stress, and regulates stress response genes in yeast

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Running title: Set4 protects cells during oxidative stress

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ABSTRACT
The Set4 protein in the yeast Saccharomyces cerevisiae contains both a PHD finger and a SET domain, a common signature of chromatin-associated proteins, and shares sequence homology with the yeast protein Set3, the fly protein UpSET, and the human protein myeloid/lymphoid or mixed-lineage leukemia 5 (MLL5). However, the biological role for Set4 and its potential function in chromatin regulation has not been well defined. Here, we analyzed yeast cell phenotypes associated with loss of Set4 or its overexpression, which revealed that Set4 protects against oxidative stress induced by hydrogen peroxide. Gene expression analysis indicated that Set4 promotes the activation of stress response genes in the presence of oxidative insults. Using ChIP analysis and other biochemical assays, we also found that Set4 interacts with chromatin, and directly localizes to stress response genes upon oxidative stress. However, Set4 did not show detectable methyltransferase activity on histones. Our findings also suggest that Set4 abundance in the cell is balanced under normal and stress conditions to promote survival. Overall, these results suggest a model in which Set4 is a stress-responsive, chromatin-associated protein that activates gene expression programs required for cellular protection against oxidative stress. This work advances our understanding of mechanisms that protect cells during oxidative stress and further defines the role of the Set3–Set4 subfamily of SET domain–containing proteins in controlling gene expression in response to adverse environmental conditions.

INTRODUCTION
Cell survival in the presence of challenging environmental conditions is critically dependent on rapid changes in gene expression. Stress-responsive gene expression programs are controlled by a suite of transcription factors and chromatin proteins that fine-tune expression in response to diverse signals (1–4). These include chromatin-modifying enzymes, such as histone lysine methyltransferases and acetyltransferases, as well as chromatin effector proteins that bind modified histone residues and often stabilize enzymatic activities at chromatin. In Saccharomyces cerevisiae, the roles of numerous transcription factors and chromatin modifiers have been delineated in response to different stresses, including osmotic stress (5,6), nutrient stress (7,8), and oxidative stress (9,10). However, our understanding of the mechanisms controlling stress response gene expression programs is still incomplete, suggesting that the roles of additional chromatin regulators remain to be determined.
A family of methyltransferases that are important for the control of gene expression and linked to stress responses is the SET (Su(var)3-9, Enhancer-of-zeste, Trithorax) domain family, which frequently catalyze methylation of lysine residues. There are 12 SET domain proteins in S. cerevisiae, of which 6 are known or predicted chromatin regulators, and the other 6 are non-histone protein methyltransferases (4,11). The H3K4 methyltransferase Set1, the H3K36 methyltransferase Set2, and the H4K5, K8, and K12 methyltransferase Set5, have each been linked to cell survival in the presence of different environmental stresses (6,8,12,13). Additionally, the protein Set3, which is not known to be an active methyltransferase, inhibits cryptic transcription and represses gene expression in response to changing environmental conditions, such as carbon source shifts (14). Set3 is a component of a histone deacetylase (HDAC) complex and contains a PHD finger which interacts with methylated H3K4 and stabilizes the HDAC complex at chromatin, particularly in the 5’ transcribed regions of genes (15,16).

Set3 shares sequence similarity with the mammalian protein MLL5 (16,17) and the Drosophila protein UpSET (18,19), each of which contain a PHD finger and a SET domain. Yeast Set3, mammalian MLL5, and the fly protein UpSET contain divergent SET domains which are predicted to lack catalytic activity based on amino acid substitutions in SAM binding sites and the lack of a tyrosine in a stereotypical position important for both SAM and target lysine binding (17,20). While mammalian MLL5 had been postulated to catalyze H3K4 methylation, this activity has not been conclusively demonstrated, and the existence of catalytic activity for MLL5 altogether is unlikely based on biochemical and structural analyses (17,21-23). Additionally, catalytic activity has not been detected for the fly protein UpSET (18). However, each of these proteins play critical roles in gene expression and chromatin organization through physical interactions with methylated histones and chromatin modifiers (18,19,24).

The S. cerevisiae genome also contains a paralog to Set3, known as Set4, which possesses a PHD finger and a divergent SET domain that contains similar amino acid substitutions as the SET domains of Set3, fly UpSET and mammalian MLL5 (Fig. 1A). Based on its similarity to this subfamily of SET domain proteins, and the presence of a PHD finger, Set4 is also likely to be a chromatin regulator. Interestingly, genome-wide studies have shown that Set4 is expressed at low levels under normal growth conditions (25), although it appears to be upregulated during stress, such as anoxia (26) and during stationary phase (27). These observations suggest the possibility that Set4 may be a stress-regulated chromatin protein, however its biological function has yet to be well-characterized.

In this study, we identified a protective role for Set4 during oxidative stress and determined that the regulation of genes linked to the response to oxidative stress is dependent on Set4. We find that Set4 is a nuclear protein that associates with chromatin. The localization of Set4 to chromatin appears to be tightly controlled by the cell, which provides for careful calibration of stress defense pathways by Set4. This work therefore identifies Set4 as a regulated chromatin factor required for controlling gene expression in response to stress, and sheds light on potential additional roles for metazoan orthologs such as fly UpSET and mammalian MLL5.

**RESULTS**

*Set4 promotes survival in the presence of oxidative stress*

In a screen for phenotypes associated with overexpression of known and candidate histone lysine (K) methyltransferases (KMTs), we identified that overexpression of Set4 was deleterious to cells. Observation of yeast strains carrying plasmids expressing KMTs under the control of a galactose-inducible promoter showed that ectopic expression of SET4, SET2 and DOT1 limited cell growth (Fig. 1B). Of these, relatively little is known about the biological functions of Set4, therefore we focused on this protein for further analysis. To verify our findings in a system independent of potential confounding effects caused by carbon source shifts, we overexpressed SET4 using the β-estradiol inducible artificial transcription factor Z3EV, which has been shown to limit off-target effects associated with inducible promoters (28). In this system, we also observed inhibited cell growth
when SET4 is highly expressed (Fig. 1C). Our findings are consistent with a previous genome-wide study that reported defective growth upon overexpression of SET4 (29).

Ectopic expression of SET4 had also been linked to increased cell adhesion and haploid invasive growth, a stress response initiated by haploid yeast under nutrient-limiting conditions (30). We transformed the galactose-inducible SET4 overexpression vector, and an empty vector control, into the Σ1278b strain background, which is permissive to adhesion and invasive growth. We performed a standard plate washing assay in which cell adherence to the agar is monitored following vigorous washing of the plate with water (31). In the presence of galactose, cells overexpressing SET4 exhibited increased adherence to the agar after washing, relative to the empty vector control or under glucose conditions (Fig. 1D). We note that cells grown in glucose consistently showed higher background adherence to the agar than those grown in galactose, however no difference was found in the amount of cells adhered to the plate between empty vector or SET4 vector cells in the uninduced, glucose conditions. In addition, we also observed increased adhesion to polystyrene plates using crystal violet staining of Σ1278b cells overexpressing SET4 (Fig. 1E). Together, these data show that ectopic expression of Set4 increases adhesive properties of yeast independent of environmental conditions, suggesting possible inappropriate activation of stress response pathways when Set4 levels are increased.

Our data investigating phenotypes associated with overexpression of SET4 suggest that it may play a role in cellular stress responses. To address this possibility, we subjected cells lacking Set4 to approximately 25 different environmental stress conditions, including multiple carbon sources, temperature variation, nutrient stress, and genotoxic agents, among others. Of the conditions tested, set4Δ cells showed a specific sensitivity to oxidative insults. Two independent set4Δ isolates showed decreased survival following exposure to H2O2 (Fig. 2A) and cadmium chloride (Fig. 2B). Quantitative analysis of colony forming units (CFU) from wildtype and set4Δ cells following treatment with H2O2 also showed a greater than 50% reduction in survival for set4Δ cells compared to wildtype (Fig. 2C). To determine if sensitivity to oxidative stress was specifically due to loss of Set4, we tested survival following H2O2 treatment in wildtype and set4Δ cells containing either an empty vector or a low-copy (ARS/CEN) vector expressing SET4 from its endogenous promoter. While set4Δ cells with the empty vector showed reduced survival following H2O2 treatment, set4Δ cells harboring the SET4-expressing vector survived to a similar extent as wildtype cells with the empty vector (Fig. 2D), indicating the set4Δ phenotype can be rescued by adding back SET4. Interestingly, wildtype cells containing the SET4-expressing plasmid showed a statistically-significant increase in survival relative to those with just the empty vector. This observation suggests that a modest increase in SET4 levels, due to one or two additional copies of the SET4 gene from this ARS/CEN vector, is sufficient to increase cell survival in the presence of oxidative damage.

To further investigate the possibility that increased expression of SET4 promotes survival during oxidative stress, we used the β-estradiol inducible promoter system to overexpress Set4, as described above. We induced SET4 expression using a low amount of β-estradiol, which minimized the toxic effect of SET4 overexpression, as observed in Fig. 1C. Indeed, cells overexpressing SET4 showed increased survival following exposure to H2O2 using both a semi-quantitative plating assay (Fig. 2E), and by quantifying percent survival of CFUs following treatment with H2O2 (Fig. 2F). These data further support our finding that higher protein levels of Set4 in the cell promote survival during oxidative stress.

An alteration in the cell’s ability to manage intracellular ROS levels may result in differing survival rates in the presence of exogenous oxidative stress. Therefore, we next investigated whether cells lacking or overexpressing SET4 had different levels of reactive oxygen species (ROS) compared to wildtype cells grown under the same conditions. To monitor intracellular ROS, flow cytometry was performed using the ROS indicator dye DCFH-DA (32). Following exposure to H2O2,
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set4Δ cells showed an increase in intracellular ROS relative to wildtype cells (Fig. 3A), indicating that cells lacking Set4 may not efficiently eliminate ROS, potentially causing decreased survival. Furthermore, even in the absence of exogenous H2O2, wildtype yeast overexpressing SET4 showed a clear decrease in the amount of intracellular ROS compared to the control strain carrying an empty vector (Fig. 3B), suggesting that cells with high levels of Set4 maintain low levels of endogenous ROS. Overall, our phenotypic analyses show that higher levels of Set4 correlate with increased survival during oxidative stress, whereas loss of Set4 leads to sensitivity in oxidative stress. Overall, this suggests there is a protective role for Set4 in the presence of oxidative stress, and raises the possibility that the levels of Set4 in the cell are calibrated to promote survival under normal and stress conditions.

Set4 localizes to chromatin and its association is enhanced during oxidative stress

While commonly associated with chromatin, the localization of SET-domain containing proteins is variable, and some members of this protein family show both nuclear and cytoplasmic distribution. The subcellular localization of Set4 has not been characterized, likely because the expression level of Set4 is very low under normal growth conditions (25). To further investigate the protein levels of Set4, we performed immunoprecipitations (IP) of N-terminally 3xFLAG-tagged Set4 expressed from the SET4 locus under control of its endogenous promoter. While FLAG-Set4 was not detectable by immunoblotting of whole cell lysates (data not shown), we were able to detect FLAG-Set4 by IP from the equivalent of 2 L of mid-log phase yeast cells grown in rich medium (Fig. 4A). This shows that Set4 is expressed in cells under normal growth conditions, albeit at low abundance.

The low level of Set4 protein expression precludes the use of common immunological and fluorescence-based assays for determining its localization. Therefore, we analyzed the localization of ectopically-expressed Set4 using two different assays. Live-cell imaging of GFP-Set4 expressed from a galactose-inducible promoter showed GFP-Set4 predominantly localized to the nucleus (Fig. 4B). To determine whether or not ectopically-expressed Set4 is specifically associated with chromatin, we used a subcellular fractionation assay that separates soluble cytoplasmic and nuclear material from insoluble material associated with chromatin (33,34). FLAG-Set4 was expressed from a β-estradiol-inducible promoter (as in Fig. 1C), and was observed predominantly in the chromatin fraction, with a small pool of protein in the soluble fraction (Fig. 4C). To verify that FLAG-Set4 was indeed chromatin associated and not simply insoluble, we used sonication to shear the DNA and solubilize nucleosomes within the pellet containing the chromatin fraction. The pellet was resuspended, sonicated, and subjected to another round of centrifugation. Immunoblot analysis of the supernatant and pellet at this stage showed that the majority of the detectable FLAG-Set4 was released into the supernatant (Fig. 4C), indicating that it is likely to be directly associating with nucleosomes and not simply insoluble. Using this assay, we also tested whether or not the localization of Set4 is altered during oxidative stress. In the presence of H2O2, we observed that all of the FLAG-Set4 is associated with chromatin in the pellet fraction, and there is no FLAG-Set4 in the soluble fraction (Fig. 4D). As further investigated below, this finding suggests the possibility that association of Set4 with chromatin may be regulated during oxidative stress.

Set4 regulates stress response gene expression

Based on the chromatin localization of Set4, we hypothesized that it may act to regulate stress-responsive genes, potentially as a means to promote survival during oxidative stress. A previously-published microarray analysis of set4Δ cells grown under normal conditions identified approximately 120 significantly differentially expressed genes compared to wildtype, with a majority down-regulated in the absence of Set4 (35). Gene ontology (GO) analysis of the 74 down-regulated genes revealed enrichment in oxidation-reduction processes (Fig. 5A), consistent with the phenotypes we have linked to loss of Set4. The 33 up-regulated genes also showed enrichment for the GO categories oxidation-reduction process and iron ion homeostasis. Given the larger quantity of genes down-regulated compared to up-regulated
in set4Δ cells, we focused on down-regulated genes for further targeted analysis.

qRT-PCR was performed to monitor expression of genes that appeared dependent on Set4 in previous work (35) and were linked to the response to oxidative stress. We first analyzed their expression in cells with ectopically-expressed Set4 grown under normal conditions without H2O2 treatment. Expression of these genes (CTT1, PNC1, TFS1, ALD4, CWP1) increased in the presence of excess Set4 (Fig. 5B), suggesting that a higher level of Set4 may be sufficient to promote activation of some stress-response genes. We next investigated the expression of these genes in wildtype and set4Δ cells with or without H2O2 treatment. We observed increased expression of CTT1, PNC1, TFS1, and ALD4, although not CWP1, in the presence of H2O2 in wildtype cells (Fig. 5C). However, their expression was attenuated in set4Δ mutants under stress, suggesting that Set4 is important for full activation of these stress response genes following H2O2 exposure. Additionally, we monitored the expression of SET4 itself in response to H2O2 treatment of wildtype cells. Unexpectedly, we observed a decrease in SET4 mRNA expression in H2O2 (Fig. 5D). This suggests negative regulation of the SET4 transcript in oxidative stress, although we postulate that other types of regulatory mechanisms offset this down-regulation of the transcript during stress, as further outlined in the Discussion.

To determine whether Set4 directly regulates genes induced during oxidative stress, chromatin immunoprecipitation (chIP) of cells expressing FLAG-Set4 from its endogenous promoter, or untagged control cells, was performed either with or without H2O2 treatment. We probed promoters of genes shown to be dependent on Set4 during oxidative stress, including CTT1, PNC1, and TFS1, as well as the promoter of SET4. We were unable to detect substantial association of FLAG-Set4 with any chromatin regions in the absence of H2O2, however specific enrichment of FLAG-Set4 was observed over the CTT1, PNC1 and TFS1 promoters following treatment with H2O2 (Fig. 5E). We did not see any enrichment at the SET4 promoter, which served as a negative control region. This is consistent with the observation that Set4 localization may be regulated during oxidative stress (Fig. 4D) and indicates that these genes may be direct targets of Set4 during stress.

Regulation of ergosterol biosynthetic genes by Set4 is dependent on growth conditions and is not a primary influence during the oxidative stress response

Previous studies have shown that cell survival in the presence of H2O2 is directly linked to the permeability of the plasma membrane (36). Ergosterol biosynthetic genes are largely down-regulated in the presence of oxidative stress (37), likely as a means to protect cells by altering membrane permeability. A recent report showed that Set4 maintains repression of ergosterol biosynthetic (ERG) genes during hypoxia (38). To test whether ERG genes are regulated by Set4 during oxidative stress, potentially as a mechanism to promote cell survival, we analyzed the expression of a subset of ERG genes in wildtype and set4Δ cells following H2O2 treatment. As expected, we observed down-regulation of ERG11, ERG3, ERG2 and ERG6 in wildtype cells treated with H2O2 (Fig. 6A). set4Δ cells, however, showed reduced expression of these genes in rich medium (YPD) alone, without H2O2 treatment, and they were expressed at similar levels in wildtype and set4Δ cells that were treated with H2O2. This indicates that ERG genes depend on Set4 for full activation under normal, aerobic growth conditions in rich medium, although Set4 does not play a role in their repression during oxidative stress. When a similar experiment was performed in synthetic complete (SC) medium, no difference in ERG gene expression was observed in set4Δ cells compared to wildtype (Fig. 6B), suggesting that while regulation of ERG genes by Set4 occurs in unstressed cells, its role in gene expression appears to depend on the composition of the growth medium. As elaborated in the Discussion, this suggests a context-dependent role for Set4 in repression of ergosterol biosynthetic genes (38).

Set4 and Set3 each promote survival during oxidative stress, although have distinct molecular roles

Set4 is a paralog to Set3, although it is unknown whether or not these proteins share
functional redundancy. Notably, overexpression of SET3 does not impair cell growth, while overexpression of SET4 does (Fig. 1B), and gene expression profiles of set3Δ and set4Δ cells grown under the same conditions are distinct (35). We further investigated the extent of genetic redundancy between the two factors by generating double set4Δ set3Δ mutants. These mutants do not show any growth defects in rich medium (Fig. 7A). set3Δ mutants are sensitive to mycophenolic acid (MPA), which interferes with transcription elongation (16), however set4Δ grew similarly to wildtype in the presence of MPA (Fig. 7A). The double mutant grew similar to the set3Δ mutant, suggesting no genetic redundancy for this phenotype. We also analyzed growth of the single and double mutants in the 25 different environmental conditions used to screen set4Δ mutants for phenotypes. We did not observe any difference in growth for the set4Δ set3Δ double mutant compared to the single mutants for any of these conditions (data not shown). However, following treatment with H2O2, we observed that set3Δ cells are sensitive to oxidative stress, and the double set4Δ set3Δ mutant shows enhanced sensitivity (Fig. 7B). These data suggest that there is some functional overlap between the two genes in that they each contribute to cell survival during oxidative stress. However, the lack of a shared phenotype in other contexts, and their distinct biochemical roles (see Discussion), suggest they have primarily independent molecular functions.

Set4 does not show methylation activity towards histones in vitro

Our data suggest that Set4 is a chromatin-associated protein which plays a role in gene expression regulation. While the SET domain of Set4 is similar to other proteins predicted to lack catalytic activity (Fig. 1A), the potential methyltransferase activity of Set4 has not been reported. We therefore investigated the catalytic activity of Set4 using in vitro methylation assays and multiple histone substrates. Recombinant 6xHIS-Set4 was expressed and purified from E. coli, and incubated with individual, recombinant histones, histones purified from calf thymus (which contain pre-existing post-translational modifications), and nucleosomes, in the presence of radiolabeled S-adenosylmethionine (3H-SAM) (Fig. 8A). We did not observe signal on any of these potential substrates, although the positive controls Set2 and Set5 were able to methylate histone substrates (Fig. 8B).

We also performed genetic tests to investigate the requirement for the SET domain in Set4 function. We found that complete deletion of the SET domain partially destabilized the protein, precluding use of this mutation in genetic assays (data not shown). We therefore generated point mutations within the SET domain, as indicated in the sequence in Fig. 1A. These mutations include a tyrosine conserved with Set3 (Y424), a conserved glutamic acid within a region implicated in SAM binding in other SET domains (E468), and a tryptophan that replaces a tyrosine found in other SET domains implicated in SAM and target lysine binding or catalysis (W473). In addition, we also mutated a tyrosine conserved with other SET domains which has been shown to act as a base for catalysis in some enzymes (Y375; not shown in sequence in Fig. 1A, (20)). Using the galactose-induced overexpression system, expression of the Y424A, E468A and W473A mutants conferred similar growth defects to cells overexpressing wildtype SET4 (Fig. 8C). Cells overexpressing the Y375A mutant using the β-estradiol-inducible promoter also showed very similar growth to cells with wildtype SET4 overexpression (Fig. 8D), indicating that Set4 function is largely intact in the presence of this mutation. While there may be additional residues required for a function associated with the SET domain, these data indicate that some of the conserved residues, and those substituted compared to canonical SET domains, are not required for Set4 function.

**DISCUSSION**

In this study, we investigated the biological functions of the uncharacterized SET-domain containing protein Set4 in budding yeast. Although its yeast paralog, Set3, is well-characterized as a regulator of gene expression (14,16), little has been uncovered about the function of Set4. We identified an important role for Set4 in protecting cells when challenged with oxidative insults, primarily H2O2. Interestingly,
high levels of Set4 expression were deleterious to cells under normal growth conditions, however increased expression of Set4 appeared to promote survival during oxidative stress. Our results also indicated that Set4 promotes proper expression of stress response genes, likely through direct binding to chromatin. The association of Set4 to chromatin also appears regulated, with increased association when cells are treated with H$_2$O$_2$. Overall, our results support a model in which Set4 localization to chromatin is regulated by the cell in order to fine-tune stress response gene expression, which promotes cell survival following oxidative insults.

Our phenotypic analysis of SET4-overexpressing and set4Δ cells uncovered a protective role for Set4 in the presence of oxidative stress. Based on its domain structure, nuclear localization and association with chromatin, we hypothesized that Set4 may protect cells by contributing to the cascade of gene expression changes that underlie the response to oxidative stress. Analysis of previously-published genome-wide data (35) indicated that Set4 might regulate genes associated with defending against oxidative damage, and that it appeared to promote activation of a higher number of genes than it repressed. Additional investigation of Set4-dependent changes in gene expression showed that overexpression of Set4 resulted in increased expression of stress response genes, and the loss of Set4 attenuated induction of these genes following H$_2$O$_2$ treatment, suggesting a role for Set4 in gene activation. We note that we did not see down-regulation of these genes in unstressed conditions, as observed by Kemmeren et al. (35). However, we suspect this difference is due to our low-throughput growth conditions which have maximum shaking and culture aeration, whereas standard high-throughput growth conditions may induce mild stress on cells. Moreover, we saw a clear defect in induction of these genes in set4Δ cells once the cells were stressed by H$_2$O$_2$.

Interestingly, we observed increased ROS in set4Δ cells upon H$_2$O$_2$ treatment compared to wildtype, and also observed substantially decreased ROS under normal conditions when Set4 is overexpressed (Fig. 3). One possibility is that the Set4-dependent changes in intracellular ROS are due to gene expression differences that contribute to ROS-scavenging activities, most likely cytosolic catalase, encoded by CTT1. In SET4-overexpressing cells, CTT1 is highly expressed, whereas it is not fully induced in set4Δ mutants treated with H$_2$O$_2$. These changes in CTT1 expression correlate with the respective ROS levels in the tested genotypes, and are also likely linked to the ability of cells to survive challenges by exogenous H$_2$O$_2$. While there may be gene expression-independent functions of Set4 that contribute to its role in ROS regulation and cell defense pathways in oxidative stress, further experiments are required to address these possibilities. It is also possible that alterations in ROS levels are due to indirect effects associated with SET4 overexpression or loss. Of note, previous work has shown that mouse hematopoietic stem and progenitor cells (HSPCs) lacking MLL5 have increased ROS, which has been linked to defective HSPC function (39). This highlights potential functional similarity between yeast Set4 and mammalian MLL5, and a possible conserved role of this SET domain subfamily in ROS regulation.

Given that increased membrane permeability sensitizes cells to exogenous H$_2$O$_2$ (36), another plausible mechanism for Set4-mediated protection in the presence of H$_2$O$_2$ could be the regulation of ergosterol biosynthetic genes, which control the levels of the plasma membrane sterol, ergosterol, in yeast. A recent report found that Set4 represses ERG genes during hypoxia, in a manner dependent on the transcription factor Hap1 (38). Our data suggest that proper expression of ERG genes is dependent on Set4 in cells grown in rich medium even under unstressed conditions, although their expression is Set4-independent either with H$_2$O$_2$ treatment or in a more depleted medium, such as synthetic complete medium (Fig. 6). This finding suggests that changes to ERG gene expression in set4Δ cells are not likely to be the primary mechanism driving their sensitivity to H$_2$O$_2$, given our result that set4Δ cells are sensitive to H$_2$O$_2$ in both rich and synthetic medium (Fig. 2). In addition, these data indicate that the regulation of ERG gene expression by Set4 is not limited to hypoxia (38) and, ERG genes show differential expression in
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set4Δ even in aerobic conditions prior to hypoxic treatment when cells are grown in rich medium.

While our observation that Set4 promotes full activation of ERG genes in aerobic conditions in rich medium appears contradictory to the finding that Set4 promotes repression of ERG genes during chronic hypoxia in rich medium (38), this discrepancy may be explained by condition-specific functions of Set4, and may underscore potentially different roles in acute stress (short H2O2 treatment) versus chronic stress. Set4 may be able to both activate and repress genes, particularly in a condition-specific manner. Similar behavior has been characterized for a number of stress-responsive transcription factors, including Hap1, Mot3, and Rox1 (40,41).

Unlike the most well-studied SET-domain chromatin regulators in yeast, including Set1, Set2, and Set3, Set4 has been reported to be expressed at very low levels under normal growth conditions (29). Based on our observations that Set4 was required for full ERG gene expression under normal conditions, as well as survival and gene expression regulation following relatively short treatments with H2O2, we predicted that Set4 is present and functioning at low abundance in cells without stress. Indeed, endogenous levels of FLAG-Set4 are detectable by IP from a high quantity of cells grown in normal conditions (Fig. 4A), indicating that Set4 may function in specific pathways in unstressed cells, even at low abundance. Based on the deleterious effect of Set4 overexpression (Fig. 1), it appears important to maintain low protein levels of Set4 to promote survival in the absence of stress.

In the presence of H2O2, we also observed increased association of Set4 with chromatin. ChIP experiments showed a specific increase in Set4 binding at promoters of genes dependent on Set4 for expression in H2O2 (Fig. 5E), which is also supported by our finding that when Set4 is overexpressed in cells treated with H2O2, it is all associated with chromatin (Fig. 4D). These data indicate the existence of post-translational regulatory mechanisms that promote Set4 binding to chromatin during oxidative stress, and suggest that Set4 is highly responsive to environmental conditions. Although increased transcription of SET4 has been reported when cells are grown under anaerobic (26) or hypoxic (38) conditions, our data suggest that acute stress with H2O2 results in lower steady-state levels of the SET4 transcript (Fig. 5D). This raises the possibility that SET4 expression may be subject to negative feedback regulation, at least during acute oxidative stress, which appears to differ from the positive transcriptional regulation of its expression during longer-term exposure to low or no oxygen (38). It is plausible that the negative regulation of SET4 transcript levels during oxidative stress is counteracted by the increased association of Set4 with chromatin, and potentially other means of translational or post-translational control. Although the mechanisms which regulate Set4 function are not yet clear, these observations suggest that there are likely multiple modes of regulation acting on Set4, including at the level of its expression and localization. This implies a specialized, regulated role for Set4 activity at chromatin.

Based on the sequence of its SET domain, Set4 belongs to a sub-family of SET domain containing proteins which includes the yeast paralog Set3, as well as the fly protein UpSET and mammalian MLL5. Biochemical and structural analysis of the SET domains within these proteins have indicated they lack intrinsic methyltransferase activity (17,20), although a biochemical test of Set4 activity had not been previously reported. Based on its localization to chromatin and its role in gene expression, we postulated that the most likely substrates for Set4 are histones. However, our in vitro methylation assays with recombinant Set4 and multiple histone substrates did not detect any methylation activity (Fig. 8A). While it remains formally possible that Set4 requires interacting partners or post-translational modifications for its activity, or that it targets non-histone substrates, this finding is consistent with previous reports regarding Set3, UpSET and MLL5 (15,17,18,23). Additionally, we generated a number of mutations within the SET domain which did not appear to alter Set4 function (Fig. 8C,D). It remains possible that there are functional roles for the SET domain independent of histone methylation, or that the domain may catalyze methylation through an alternate mechanism, however there is not yet clear evidence that it is a primary contributor to the biological function of Set4.
The yeast protein Set3 is also thought to lack catalytic activity, although it has clear roles in gene expression regulation by forming a complex with HDACs and other associated proteins (14-16). The full extent of Set4's physical interactions in the cell remain to be determined, but it may be that, similar to Set3, a primary function for Set4 is to regulate the activity of other chromatin modifiers or transcriptional machinery.

While Set3 and Set4 are paralogs, previous work suggests they are not likely to have overlapping molecular functions. Set3 binds methylated H3K4 via its PHD finger (16,42), although the PHD finger of Set4 is not able to bind H3K4me (or H3K36me) in vitro (42,43). The abundance of Set3 is much higher than Set4 under normal growth conditions, and gene expression profiles of cells lacking either Set3 or Set4 are quite distinct under normal growth conditions (35). Analysis of set4Δ set3Δ mutants suggests that they share partial genetic redundancy in promoting survival during oxidative stress (Fig. 7B). We did not observe any redundancy in the response of the mutants to MPA (Fig. 7A) or other stresses, nor do SET3 and SET4 show similar phenotypes when overexpressed (Fig. 1B). Combined with previous observations regarding molecular functions of these proteins, we postulate that they are likely to each contribute to cell defense during oxidative stress through distinct molecular mechanisms. Further investigation will be required to reveal the molecular details underlying the role of Set3 in oxidative stress and mechanisms driving the stress-responsive regulation of gene expression by Set4.

This study provides insight into the biological functions of Set4, and uncovers a key role for Set4 in protecting cells during oxidative stress, likely through the direct control of gene expression. Set4 localization to chromatin appears to be regulated by the cell, indicating that it is very responsive to changes in environmental conditions. Our results suggest that Set4 functions in a stress defense pathway that allows the cell to carefully calibrate gene expression in response to environmental stress, and we expect further study will shed light on the mechanisms by which Set4 is regulated and acts at chromatin.

EXPERIMENTAL PROCEDURES
Yeast strains, plasmids and growth conditions
Yeast were grown in standard media, including YPD (1% yeast extract, 2% peptone, 2% dextrose) and synthetic complete (SC) or dropout media (US Biological). Agar plates were prepared with the same media conditions and, where necessary, the carbon source was substituted with 2% galactose or additional reagents were added to the medium following autoclaving, including β-estradiol (Sigma-Aldrich), cadmium chloride or mycophenolic acid (MPA; MP Biomedicals).

All yeast strains used in this study are listed in Table 1. Yeast gene deletions were constructed using insertion of targeted PCR cassettes amplified from the pFA6a vector series (44). The N-terminal 3xFLAG-tagged SET4 was generated using PCR amplification from plasmid pZM467 (kindly provided by K. Struhl) and loopout of the URA3 marker from transformed cells by selection on plates containing 5-fluoroorotic acid (45). Double set4Δ set3Δ strains were generated by crossing parental strains yEG325 and yEG330 and performing tetrad dissection. All newly constructed strains were confirmed by growth on selective media and colony PCR using primers targeting individual gene deletions or epitope tag insertions.

All plasmids used in this study are listed in Table 2. Plasmids for GAL1 promoter-driven overexpression were constructed by insertion of open reading frames for each gene into the pRS315-GAL1p vector using ApaI and SalI restriction sites. Similarly, GFP-SET4 was amplified from a yeast strain containing an integrated N-terminal GFP tag and cloned into the pRS315-GAL1p vector to generate pRS315-GAL1p-GFP-SET4. The pRS316-SET4 expression vector was generated by cloning a PCR fragment that amplified the SET4 locus, including its promoter and 3’UTR, into pRS316. SET4 and FLAG-SET4 were amplified from yeast strains yEG001 and yEG513, respectively, and cloned into the pMN3 vector (kindly provided by Scott McIsaac, Botstein Lab) downstream of the modified GAL1 promoter recognized by the artificial transcription factor Z3EV (28). Mutations in the SET domain were generated in
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either pRS315-GAL1p-SET4 or pMN3-modGAL1p-SET4 using a Quickchange site-directed mutagenesis protocol. Full-length Set4 was cloned into pRSET-B using the SacI and NcoI restriction sites for expression of 6xHis-Set4 in E.coli.

Adhesion assays
To monitor adhesion to agar, the Σ1278b strain (kindly provided by P. Farabaugh) carrying either pRS316-GAL1p or pRS316GAL1p-SET4 was grown to mid-log phase in SC-URA with 2% glucose. 50 µL of each culture was spotted on SC-URA containing either 2% glucose or 2% galactose and incubated at 30°C for 10 days. The plates were washed with sterile water using a shaking platform, as described (31), and imaged. To monitor adhesion to polystyrene, the strains were grown in SC-URA with 2% glucose or 2% galactose for 7 days at 30°C. Cell densities were adjusted to an OD$_{600}$ = 2.0, and 100 µL of each culture was added to a well in a 96-well plate. The cells were allowed to settle and stained with crystal violet, as described (46).

Hydrogen peroxide survival assays
Wildtype (wt; yEG001) and set4Δ (yEG322) cultures were diluted 1:10000 in YPD and grown to mid-log phase (OD$_{600}$ = 0.6 – 0.7). The cultures were normalized such that all strains had the same OD$_{600}$ and then divided in half. One culture received 4mM H$_2$O$_2$ and both treated and untreated cells were incubated an additional 30 min, shaking at 30°C. The cells were serially-diluted ten-fold and spotted on to YPD plates. To count colony forming units (CFUs), equivalent volumes of cultures prior to H$_2$O$_2$ treatment were serially-diluted and plated on YPD to determine total CFU per culture. Following H$_2$O$_2$ treatment, equivalent volumes of cultures were plated directly on YPD to determine surviving CFU. Percent survival was determined based on surviving CFU after H$_2$O$_2$ treatment compared to total CFU prior to treatment. For experiments in which the pRS316-SET4 rescue plasmid was used, cells were grown in or plated on SC-URA medium and 20 mM H$_2$O$_2$ treatment was used. The higher concentration of H$_2$O$_2$ was used to account for the increased inherent resistance to H$_2$O$_2$ of yeast grown in synthetic medium. To test the role of SET4 overexpression, yeast strain yEG375, carrying the pMN3-SET4 vector, and yEG372, carrying the empty vector control, were grown overnight in SC-URA with shaking at 30°C. The following day, two cultures diluted back to an OD$_{600}$ ~ 0.2 were prepared, and one culture was treated with either 1 µM (plate assay) or 50 nM (CFU assay) β-estradiol. The cells were grown to mid-log phase, and the culture volumes were normalized based on OD$_{600}$. One set of cultures was treated with 20 mM H$_2$O$_2$ for 30 min, and survival was monitored by spotting serial dilutions or counting CFU as described above.

Intracellular ROS detection
Detection of intracellular ROS was performed using 2, 7-dichlorodihydrofluorescein diacetate (DCFH-DA; Sigma) as previously described (32). Briefly, 10 mL of mid-log phase yeast cells (strains yEG001 and yEG322) grown in YPD at 30°C were treated with 4 mM H$_2$O$_2$ for 30 minutes. 10 µM DCFH-DA was added to the culture media for 1 hour. For experiments with ectopic Set4 expression, yeast strains yEG372 and yEG375 were grown to early log phase in SC-URA at 30°C and treated with 25 µM β-estradiol. DCFH-DA (10 µM) was added to the culture for 1 hour with shaking. After treatment with DCFH-DA, cells were washed twice in PBS (phosphate buffered saline), resuspended in PBS and analyzed using a Beckman Coulter CyAn ADP flow cytometer. Data were further analyzed using Summit software. Wildtype cells not treated with DCFH-DA were used as a negative control, and cells treated with 6 mM H$_2$O$_2$ and DCFH-DA served as a positive control for dye staining. Gating was performed to calculate percent stained cells per culture by excluding all cells overlapping with the unstained control.

Immunoprecipitation of FLAG-Set4
Wildtype (yEG001) and SET4::FLAG-SET4 (yEG513) strains were grown in 4 L YPD to mid-log phase. Cells were harvested, resuspended in lysis buffer (100 mM HEPES pH 8.0, 20 mM MgOAc, 10% glycerol, 10 mM EGTA, 0.1 mM EDTA, 1 mM PMSF, yeast protease inhibitor cocktail (Sigma)) and frozen drop-wise in liquid nitrogen. Cell pellets were ground in a coffee grinder with dry ice, the dry ice was allowed to evaporate, and lysates were clarified by centrifugation at 7K rpm for 15 min. IPs were set
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up with equal protein concentrations of lysate and anti-FLAG M2 magnetic beads (Sigma-Aldrich) and rotated for 3 hours at 4°C. Proteins were eluted with SDS loading buffer and 50% of the protein eluted from IPs was run on SDS-PAGE and subjected to immunoblotting with mouse anti-FLAG (Sigma-Aldrich; catalog no. F1804). 0.2% of input protein was also run as a loading control and probed with anti-hexokinase (Hxk2)-HRP (Novus Biologicals; catalog no. NB120-20547).

**GFP-Set4 live cell microscopy**

A set4Δ strain carrying pRS15-GAL1-GFP-SET4 (yEG735) was grown overnight at 30°C in SC-LEU plus 2% glucose, transferred to SC-LEU plus 2% raffinose and induced with 2% galactose until mid-log phase. The cells were washed with phosphate buffered saline (PBS), stained with Hoechst (2μg/ml; Life Technologies), harvested and mounted on a glass slide in 5% low temperature melting agarose dissolved in SC-LEU plus 2% galactose medium. Images were obtained using a Leica SP5 confocal microscope and image processing was performed using Image J.

**Chromatin fractionation**

Yeast strains yEG372 and yEG626, carrying an empty vector or pMN3-FLAG-SET4 were grown to mid-log phase in 25 mL SC-URA with shaking at 30°C. FLAG-Set4 expression was induced by treating cells with 10 μM β-estradiol for 3 hours, and then treated with 20 mM H2O2 for one hour, harvested and frozen in liquid nitrogen. Cell pellets were processed for chromatin fractionation as previously described (33,34,47). For experiments in which the pellet fraction was subjected to sonication to shear chromatin, the fractions were sonicated for 8 cycles of 20 sec each at 15% output in a Branson sonifier. Collected fractions were boiled in SDS loading buffer and equivalent volumes were subjected to SDS-PAGE. Immunoblots were probed with mouse anti-FLAG, mouse anti-H4 (Abcam; catalog no. ab31830) and anti-Hxk2-HRP. Blot imaging was performed on a Licor C-Digit Chemiluminescent Western Blot Scanner.

**Gene expression analysis by quantitative RT-PCR**

To test gene expression changes in the presence of SET4 overexpression, strains yEG372 and yEG375 were grown in SC-URA overnight at 30°C, diluted back to an OD600 ~ 0.2, and treated with 1μM β-estradiol until cells reached mid-log phase (approximately 6 hr). Cells were harvested and frozen in liquid nitrogen prior to RNA isolation. To test expression in wildtype (yEG001) and set4Δ (yEG322), cultures were prepared as described for the H2O2 survival assays, except that 0.4 mM H2O2 treatment for 30 min was performed to provide acute stress but not dramatically decrease survival, as previously performed for measurement of gene expression changes following H2O2 treatment in yeast (9,48,49). RNA isolation, removal of genomic DNA contamination, cDNA synthesis and quantitative RT-PCR (qRT-PCR) was performed as previously described (50,51). Gene specific primers for the qPCR are listed in Table 3. Gene expression was normalized to SCR1, which was observed to have stable expression under the growth conditions tested.

**Chromatin immunoprecipitation**

Wildtype (yEG001) and SET4::FLAG-SET4 (yEG513) were grown as described for gene expression analysis, including treatment with 0.4 mM H2O2 for 30 min in 100 mL YPD. Cells were fixed with 1% formaldehyde for 45 min and chIP procedures were performed as previously described (51,52). Mouse anti-FLAG (Sigma; catalog no. F1804) was prebound to protein A/G magnetic beads (Pierce) and then incubated with chIP lysates for 3 hours at 4°C. qPCR was performed on eluted DNA, as described (51,52), with primers listed in Table 3. Percent input was calculated relative to 10% input, and the signal for FLAG-Set4 was determined relative to wildtype (untagged) either with or without H2O2 treatment.

**Recombinant protein purification**

6xHIS-Set4 was expressed and purified from plasmid p325 using E. coli BL21 (DE3). Protein expression was induced using 0.1 mM IPTG at 37°C for 4 hours and cell lysates were prepared in 20 mM sodium phosphate pH 7.4, 150 mM NaCl, 10 mM imidazole, 0.5% NP-40, 1 mM PMSF and protease inhibitors (ThermoScientific Pierce protease inhibitor tablet). 6xHIS-Set4 was bound
to Ni-NTA resin for 1 hr at 4°C. The resin was washed with lysis buffer including 300 mM NaCl and 25 mM imidazole. 6xHIS-Set4 was eluted with 250 mM imidazole, and subsequently dialyzed into 20 mM Tris-HCl pH 8.0, 20 mM KCl, 5 mM MgCl₂, 5% glycerol prior to performing methylation assays. Purification of GST-Set5 and GST-Set2 was performed as previously described (13).

In vitro methylation assays
Methylation assays were performed as previously described (13). Briefly, 30 µg of 6xHIS-Set4 was incubated with 1 µg of substrate in 50 mM Tris-HCl (pH 8.0), 10% glycerol, 20 mM KCl, 5 mM MgCl₂ plus 2 µCi ³H-S-adenosyl methionine (Perkin Elmer). Reactions were incubated at 30°C overnight and proteins were resolved by SDS-PAGE, followed by autoradiography. For reactions with GST-Set5 and GST-Set2, 5 µg of enzyme was used. Substrates include recombinant histones (NEB), histones purified from calf thymus (Worthington Biochemical) and mono-nucleosomes purified from HeLa cells (Epicypher).

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CONFLICT OF INTEREST
The authors declare that they have no conflicts of interest with the contents of this article.

REFERENCES
1. Feil, R., and Fraga, M. F. (2011) Epigenetics and the environment: emerging patterns and implications. Nat Rev Genet 13, 97-109
2. Badeaux, A. I., and Shi, Y. (2013) Emerging roles for chromatin as a signal integration and storage platform. Nat Rev Mol Cell Biol 14, 211-224
3. Suganuma, T., and Workman, J. L. (2011) Signals and combinatorial functions of histone modifications. Annu Rev Biochem 80, 473-499
4. Jaiswal, D., Turniansky, R., and Green, E. M. (2017) Choose Your Own Adventure: The Role of Histone Modifications in Yeast Cell Fate. J Mol Biol 429, 1946-1957
5. De Nadal, E., Zapater, M., Alepuz, P. M., Sumoy, L., Mas, G., and Posas, F. (2004) The MAPK Hog1 recruits Rpd3 histone deacetylase to activate osmoreponsive genes. Nature 427, 370-374
6. Nadal-Ribelles, M., Mas, G., Millán-Zambrano, G., Solé, C., Ammerer, G., Chávez, S., Posas, F., and de Nadal, E. (2015) H3K4 monomethylation dictates nucleosome dynamics and chromatin remodeling at stress-responsive genes. Nucleic Acids Res 43, 4937-4949
7. Law, M. J., and Ciccaglione, K. (2015) Fine-tuning of histone H3 Lys4 methylation during pseudohyphal differentiation by the CDK submodule of RNA polymerase II. Genetics 199, 435-453
8. McDaniel, S. L., Hepperla, A. J., Huang, J., Dronamraju, R., Adams, A. T., Kulkarni, V. G., Davis, I. J., and Strahl, B. D. (2017) H3K36 Methylation Regulates Nutrient Stress Response in Saccharomyces cerevisiae by Enforcing Transcriptional Fidelity. Cell Rep 19, 2371-2382
9. Baker, L. A., Ueberheide, B. M., Dewell, S., Chait, B. T., Zheng, D., and Allis, C. D. (2013) The yeast Snt2 protein coordinates the transcriptional response to hydrogen peroxide-mediated oxidative stress. Mol Cell Biol 33, 3735-3748

10. Morano, K. A., Grant, C. M., and Moyle-Rowley, W. S. (2012) The response to heat shock and oxidative stress in Saccharomyces cerevisiae. Genetics 190, 1157-1195

11. Clarke, S. G. (2013) Protein methylation at the surface and buried deep: thinking outside the histone box. Trends Biochem Sci 38, 243-252

12. Weiner, A., Chen, H. V., Liu, C. L., Rahat, A., Klien, A., Soares, L., Gudipati, M., Pfeffer, J., Regev, A., Buratowski, S., Pleiss, J. A., Friedman, N., and Rando, O. J. (2012) Systematic dissection of roles for chromatin regulators in a yeast stress response. PLoS Biol 10, e1001369

13. Green, E. M., Mas, G., Young, N. L., Garcia, B. A., and Groudine, M. (2012) Methylation of H4 lysines 5, 8 and 12 by yeast Set5 calibrates chromatin stress responses. Nat Struct Mol Biol 19, 361-363

14. Kim, T., Xu, Z., Claude-Münster, S., Steinmetz, L. M., and Buratowski, S. (2012) Set3 HDAC mediates effects of overlapping noncoding transcription on gene induction kinetics. Cell 150, 1158-1169

15. Pijnappel, W. W., Schaft, D., Roguev, A., Shevchenko, A., Tekotte, H., Wilm, M., Rigaut, G., Séraphin, B., Aasland, R., and Stewart, A. F. (2001) The S. cerevisiae SET3 complex includes two histone deacetylases, Hos2 and Hst1, and is a meiotic-specific repressor of the sporulation gene program. Genes Dev 15, 2991-3004

16. Kim, T., and Buratowski, S. (2009) Dimethylation of H3K4 by Set1 recruits the Set3 histone deacetylase complex to 5' transcribed regions. Cell 137, 259-272

17. Madan, V., Madan, B., Brykczynska, U., Zilbermann, F., Hogeveen, K., Döhner, K., Döhner, H., Weber, O., Blum, C., Rodewald, H. R., Sassone-Corsi, P., Peters, A. H., and Fehling, H. J. (2009) Impaired function of primitive hematopoietic cells in mice lacking the Mixed-Lineage-Leukemia homolog MLL5. Blood 113, 1444-1454

18. Rincon-Arano, H., Halow, J., Delrow, J. J., Parkhurst, S. M., and Groudine, M. (2012) UpSET recruits HDAC complexes and restricts chromatin accessibility and acetylation at promoter regions. Cell 151, 1214-1228

19. McElroy, K. A., Jung, Y. L., Zee, B. M., Wang, C. I., Park, P. J., and Kuroda, M. I. (2017) upSET, the Drosophila homologue of SET3, Is Required for Viability and the Proper Balance of Active and Repressive Chromatin Marks. G3 (Bethesda) 7, 625-635

20. Dillon, S. C., Zhang, X., Trievel, R. C., and Cheng, X. (2005) The SET-domain protein superfamily: protein lysine methyltransferases. Genome Biol 6, 227

21. Nin, D. S., Yew, C. W., Tay, S. K., and Deng, L. W. (2014) Targeted silencing of MLL5 inhibits tumor growth and promotes gamma-irradiation sensitization in HPV16/18-associated cervical cancers. Mol Cancer Ther 13, 2572-2582

22. Sebastian, S., Sreenivas, P., Sambasivan, R., Cheedipudi, S., Kandalla, P., Pavlath, G. K., and Dhawan, J. (2009) MLL5, a trithorax homolog, indirectly regulates H3K4 methylation, represses cyclin A2 expression, and promotes myogenic differentiation. Proc Natl Acad Sci USA 106, 4719-4724

23. Mas-Y-Mas, S., Barbon, M., Teyssier, C., Déméné, H., Carvalho, J. E., Bird, L. E., Lebedev, A., Fattori, J., Schubert, M., Dumas, C., Bourguet, W., and le Maire, A. (2016) The Human Mixed Lineage Leukemia 5 (MLL5), a Sequentially and Structurally Divergent SET Domain-Containing Protein with No Intrinsic Catalytic Activity. PLoS One 11, e0165139

24. Ali, M., Rincón-Arano, H., Zhao, W., Rothbart, S. B., Tong, Q., Parkhurst, S. M., Strahl, B. D., Deng, L. W., Groudine, M., and Kutateladze, T. G. (2013) Molecular basis for chromatin binding and regulation of MLL5. Proc Natl Acad Sci USA 110, 11296-11301

25. Ghaemmaghami, S., Huh, W. K., Bower, K., Howson, R. W., Belle, A., Dephoure, N., O'Shea, E. K., and Weissman, J. S. (2003) Global analysis of protein expression in yeast. Nature 425, 737-741
Set4 protects cells during oxidative stress

26. Lai, L. C., Kosorukoff, A. L., Burke, P. V., and Kwast, K. E. (2006) Metabolic-state-dependent remodeling of the transcriptome in response to anoxia and subsequent reoxygenation in Saccharomyces cerevisiae. *Eukaryot Cell* 5, 1468-1489

27. Aragon, A. D., Rodriguez, A. L., Meirelles, O., Roy, S., Davidson, G. S., Tapia, P. H., Allen, C., Joe, R., Benn, D., and Werner-Washburne, M. (2008) Characterization of differentiated quiescent and nonquiescent cells in yeast stationary-phase cultures. *Mol Biol Cell* 19, 1271-1280

28. McIsaac, R. S., Gibney, P. A., Chandran, S. S., Benjamin, K. R., and Botstein, D. (2014) Synthetic biology tools for programming gene expression without nutritional perturbations in Saccharomyces cerevisiae. *Nucleic Acids Res* 42, e48

29. Sopko, R., Huang, D., Preston, N., Chua, G., Papp, B., Kafadar, K., Snyder, M., Oliver, S. G., Cyert, M., Hughes, T. R., Boone, C., and Andrews, B. (2006) Mapping pathways and phenotypes by systematic gene overexpression. *Mol Cell* 21, 319-330

30. Cullen, P. J., and Sprague, G. F., Jr. (2012) The regulation of filamentous growth in yeast. *Genetics* 190, 23-49

31. Shively, C. A., Eckwahl, M. J., Dobry, C. J., Mellacheruvu, D., Nesvizhskii, A., and Kumar, A. (2013) Genetic networks inducing invasive growth in Saccharomyces cerevisiae identified through systematic genome-wide overexpression. *Genetics* 193, 1297-1310

32. Azad, G. K., Singh, V., Mandal, P., Singh, P., Golla, U., Baranwal, S., Chauhan, S., and Tomar, R. S. (2014) Ebselen induces reactive oxygen species (ROS)-mediated cytotoxicity in Saccharomyces cerevisiae with inhibition of glutamate dehydrogenase being a target. *FEBS Open Bio* 4, 77-89

33. Liang, C., and Stillman, B. (1997) Persistent initiation of DNA replication and chromatin-bound MCM proteins during the cell cycle in cdc6 mutants. *Genes Dev* 11, 3375-3386

34. Donovan, S., Harwood, J., Drury, L. S., and Diffley, J. F. (1997) Cdc6p-dependent loading of Mcm proteins onto pre-replicative chromatin in budding yeast. *Proc Natl Acad Sci U S A* 94, 5611-5616

35. Kemmeren, P., Sameth, K., van de Pasch, L. A., Benschop, J. J., Lenstra, T. L., Margaritis, T., O'Duibhtr, E., Apweiler, E., van Wageningen, S., Ko, C. W., van Heesch, S., Kashani, M. M., Ampatziadis-Michailidis, G., Brok, M. O., Brabers, N. A., Miles, A. J., Bouwmeester, D., van Hooft, S. R., van Bakel, H., Sluiers, E., Bakker, L. V., Snel, B., Lijnzaad, P., Van Leenen, D., Groen Koerkamp, M. J., and Holstege, F. C. (2014) Large-scale genetic perturbations reveal regulatory networks and an abundance of gene-specific repressors. *Cell* 157, 740-752

36. Branco, M. R., Marinho, H. S., Cyrme, L., and Antunes, F. (2004) Decrease of H2O2 plasma membrane permeability during adaptation to H2O2 in Saccharomyces cerevisiae. *J Biol Chem* 279, 6501-6506

37. Kelley, R., and Ideker, T. (2009) Genome-wide fitness and expression profiling implicate Mga2 in adaptation to hydrogen peroxide. *PLoS Genet* 5, e1000488

38. Serratore, N. D., Baker, K. M., Macadlo, L. A., Gress, A. R., Powers, B. L., Atallah, N., Westerhouse, K. M., Hall, M. C., Weake, V. M., and Briggs, S. D. (2018) A Novel Sterol-Signaling Pathway Governs Azole Antifungal Drug Resistance and Hypoxic Gene Repression in. *Genetics* 208, 1037-1055

39. Tasdogan, A., Kumar, S., Allies, G., Bausinger, J., Beckel, F., Hofemeister, H., Mulaw, M., Madan, V., Scharfetter-Kochanek, K., Feuring-Buske, M., Doehner, K., Speit, G., Stewart, A. F., and Fehling, H. J. (2016) DNA Damage-Induced HSPC Malfunction Depends on ROS Accumulation Downstream of IFN-1 Signaling and Bid Mobilization. *Cell Stem Cell* 19, 752-767

40. Hickman, M. J., and Winston, F. (2007) Heme levels switch the function of Hap1 of Saccharomyces cerevisiae from transcriptional activator and transcriptional repressor. *Mol Cell Biol* 27, 7414-7424

41. Martinez-Montañés, F., Rienzo, A., Poveda-Huertes, D., Pascual-Ahuir, A., and Proft, M. (2013) Activator and repressor functions of the Mot3 transcription factor in the osmmostress response of Saccharomyces cerevisiae. *Eukaryot Cell* 12, 636-647

42. Gatchalian, J., Ali, M., Andrews, F. H., Zhang, Y., Barrett, A. S., and Kutateladze, T. G. (2016) Structural Insight into Recognition of Methylated Histone H3K4 by Set3. *J Mol Biol*
Set4 protects cells during oxidative stress

43. Shi, X., Kachirskaia, I., Walter, K. L., Kuo, J. H., Lake, A., Davrazou, F., Chan, S. M., Martin, D. G., Fingerman, I. M., Briggs, S. D., Howe, L., Utz, P. J., Kutateladze, T. G., Lugovskoy, A. A., Bedford, M. T., and Gozani, O. (2007) Proteome-wide analysis in Saccharomyces cerevisiae identifies several PHD fingers as novel direct and selective binding modules of histone H3 methylated at either lysine 4 or lysine 36. *J Biol Chem* **282**, 2450-2455

44. Longtine, M. S., McKenzie, A., Demarini, D. J., Shah, N. G., Wach, A., Brachat, A., Philippsen, P., and Pringle, J. R. (1998) Additional modules for versatile and economical PCR-based gene deletion and modification in Saccharomyces cerevisiae. *Yeast* **14**, 953-961

45. Moqtaderi, Z., and Struhl, K. (2008) Expanding the repertoire of plasmids for PCR-mediated epitope tagging in yeast. *Yeast* **25**, 287-292

46. Cullen, P. J. (2015) Biofilm/Mat assays for budding yeast. *Cold Spring Harb Protoc* 2015, 172-175

47. Lopes da Rosa, J., Holik, J., Green, E. M., Rando, O. J., and Kaufman, P. D. (2011) Overlapping regulation of CenH3 localization and histone H3 turnover by CAF-1 and HIR proteins in *Saccharomyces cerevisiae*. *Genetics* **187**, 9-19

48. Gasch, A. P., Spellman, P. T., Kao, C. M., Carmel-Harel, O., Eisen, M. B., Storz, G., Botstein, D., and Brown, P. O. (2000) Genomic expression programs in the response of yeast cells to environmental changes. *Mol Biol Cell* **11**, 4241-4257

49. Tsang, C. K., Liu, Y., Thomas, J., Zhang, Y., and Zheng, X. F. (2014) Superoxide dismutase 1 acts as a nuclear transcription factor to regulate oxidative stress resistance. *Nat Commun* **5**, 3446

50. Jezek, M., Gast, A., Choi, G., Kulkarni, R., Quijote, J., Graham-Yooll, A., Park, D., and Green, E. M. (2017) The histone methyltransferases Set5 and Set1 have overlapping functions in gene silencing and telomere maintenance. *Epigenetics* **12**, 93-104

51. Jaiswal, D., Jezek, M., Quijote, J., Lum, J., Choi, G., Kulkarni, R., Park, D., and Green, E. M. (2017) Repression of Middle Sporulation Genes in *G3* (Bethesda) **7**, 3971-3982

52. Jezek, M., Jacques, A., Jaiswal, D., and Green, E. M. (2017) Chromatin Immunoprecipitation (ChIP) of Histone Modifications from *Saccharomyces cerevisiae*. *J Vis Exp* 130, e57080

**TABLES**

Table 1. Yeast strains used in this study.

| Strain       | Background | Genotype                                      | Source     |
|--------------|------------|-----------------------------------------------|------------|
| yEG001       | BY4741     | MATα his3Δ1 leu2Δ0 met15Δ0 ura3Δ0             | YKO        |
| yEG322       | BY4741     | MATα set4Δ::HIS3MX                            | This study |
| yEG325       | BY4741     | MATα set4Δ::HIS3MX                            | This study |
| yEG638       | BY4741     | MATα yEG001 + p045 (pRS316)                   | This study |
| yEG639       | BY4741     | MATα yEG322 + p045 (pRS316)                   | This study |
| yEG640       | BY4741     | MATα yEG001 + p188 (pRS316-SET4)              | This study |
| yEG641       | BY4741     | MATα yEG322 + p188 (pRS316-SET4)              | This study |
| yEG513       | BY4741     | MATα SET4::FLAG-SET4                          | This study |
| yEG735       | BY4741     | MATα set4Δ::HIS3MX + p171 (pRS315-GAL1p-GFP-SET4) | This study |
| yEG330       | BY4741     | MATα set4Δ::HATMX                             | This study |
| yEG347       | BY4741     | MATα set4Δ::HIS3MX set3Δ::HATMX               | This study |
| yEG315       | DBY12394   | MATα ura3Δ leu2Δ0::ACT1pr-Z::EV-NATMX         | Ref. 28    |
| yEG372       | DBY12394   | MATα yEG315 + p183 (pMN3)                     | This study |
| yEG375       | DBY12394   | MATα yEG315 + p180 (pMN3-SET4)                | This study |
| yEG626       | DBY12394   | MATα ura3Δ leu2Δ0::ACT1pr-Z::EV-NATMX set4Δ::HIS3MX + p302 (pMN3-FLAG-SET4) | This study |
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| yEG282 | Sigma1278b | MATa ura3-52 | from P. Farabaugh |
| yEG443 | Sigma1278b | MATa yEG282 + p041 (pRS316-GAL1p) | This study |
| yEG444 | Sigma1278b | MATa yEG282 + p175 (pRS316-GAL1p-SET4) | This study |

Table 2. Plasmids used in this study.

| Number | Description |
|--------|-------------|
| p040   | pRS315-GAL1p |
| p185   | pRS315-GAL1p-SET1 |
| p186   | pRS315-GAL1p-SET2 |
| p157   | pRS315-GAL1p-SET3 |
| p132   | pRS315-GAL1p-SET4 |
| p133   | pRS315-GAL1p-SET5 |
| p134   | pRS315-GAL1p-SET6 |
| p187   | pRS315-GAL1p-DOT1 |
| p041   | pRS316-GAL1p |
| p175   | pRS316-GAL1p-SET4 |
| p171   | pRS315-GAL1p-GFP-SET4 |
| p183   | pMN3-modGAL1p (from ref. 30) |
| p180   | pMN3-modGAL1p-SET4 |
| p302   | pMN3-modGAL1p-FLAG-SET4 |
| p045   | pRS316 |
| p188   | pRS316-SET4 |
| p325   | pRESET-6xHIS-SET4 |
| p008   | pGEX-GST-SET5 |
| p018   | pGEX-GST-SET2 |
| p154   | pRS315-GAL1p-SET4Y42A |
| p155   | pRS315-GAL1p-SET4E468A |
| p156   | pRS315-GAL1p-SET4W473A |
| p161   | pRS315-GAL1p-SET4E468A,W473A |
| p286   | pMN3-modGAL1p-SET4Y375A |

Table 3. Primers used in this study.

| Gene | Analysis | Sequence |
|------|----------|----------|
| CTT1 | RT-qPCR  | 5'AGACCAGACGCGCCCTATCTT3' |
|      |          | 5'TACACGCTCGGAACCTTCTT3' |
| TFS1 | RT-qPCR  | 5'CACACCTCCAGTCTACTT3' |
|      |          | 5'TGAAACAATCGTCTCCTG3' |
| ALD4 | RT-qPCR  | 5'GACAACGACACCTTACCA3' |
|      |          | 5'TTGGAAGCTGCTGGTGAATTCA3' |
| PNC1 | RT-qPCR  | 5'GACCACGTCTGCTGGATAT3' |
|      |          | 5'TCTGGAACCTTTCACAATCTT3' |
| CWP1 | RT-qPCR  | 5'GAAGGTTCTTGAAGCGATCG3' |
|      |          | 5'GACCCGCTCCTGTAAGATGTA3' |
| SET4 | RT-qPCR  | 5'CTTATACCCGCCCACAC3' |
|      |          | 5'TTAAATGGTACGTCTG3' |
| SCR1 | RT-qPCR  | 5'GGAGGTCTTTATCCAGGGTCA3' |
|      |          | 5'GAAGCGATCAAATTCGTTGAA3' |
Set4 protects cells during oxidative stress

| Gene  | Method   | Primers                        |
|-------|----------|--------------------------------|
| ERG11 | RT-qPCR  | 5'CCTCTTTATTCGTCGGTGAA3' 5'TGTTGTCTACCACCACCGAA3' |
| ERG3  | RT-qPCR  | 5'GTCGATTTCTCAACCATCCTCGT3' 5'TCGACATCCATGGATAGAC3' |
| ERG2  | RT-qPCR  | 5'AGACGCACCTGGCTCTCATT3' 5'GGATACGGAAAGTGTAAGGA3' |
| ERG6  | RT-qPCR  | 5'GTCTAGCCCCAGAAGGTTCC3' 5'TTCCTAGCGAGAAAGCAT3' |
| CTT1 promoter | chIP | 5'ATTCGACGTCAGCTCGAGAC3' 5'TGGAATAGAGGTAAGCAACGA3' |
| PNC1 promoter | chIP | 5'TTCAAGGGGACGGGTTT3' 5'TATTAGCAGACATCAAATCGTATCTGGA3' |
| TFS1 promoter | chIP | 5'AAGGAGTAGAGGCGTGTTC3' 5'AGGAGCAGTCATCGATTCTT3' |
| SET4 promoter | chIP | 5'TGAAAAGGAAAGGAGGAAA3' 5'GCGTTCCACGCTGAAATTAT3' |
FIGURES AND FIGURE LEGENDS

Figure 1. Overexpression of SET4 is deleterious and promotes cell adhesion. A, The domain structure of Set4 (left) indicating the position of the PHD finger (orange), the SET domain (blue) and the post-SET domain (purple). A percent identity matrix (right) comparing the SET domains of S. cerevisiae Set4 (ScSet4), Set3 (ScSet3), D. melanogaster UpSET (DmUpSET) and H. sapiens MLL5 (HsMLL5). Percent identity was determined using Clustal Omega. Sequence alignment of the most conserved region of the SET domain among ScSet4, ScSet3, DmUpSET and HsMLL5. Amino acids highlighted in blue represent differences to canonical SET domains in regions required for SAM and lysine binding (20). Amino acids predominantly found in other SET domains are indicated in bold at the top of the alignment. Underlined amino acids within the Set4 sequence indicates mutations used in Fig 8C. B, Wildtype yeast (yEG001) carrying plasmids expressing known and putative histone methyltransferases under the control of the GAL1 promoter. Ten-fold serial dilutions were spotted on either SC-LEU with 2% glucose (GLU) or 2% galactose (GAL) and grown at 30°C for 3 days. C, Strains harboring a β-estradiol inducible artificial transcription factor and either the empty pMN3 vector or pMN3-SET4 were grown in SC-URA and ten-fold serial dilutions were spotted on SC-URA or SC-URA with 100 μM β-estradiol and grown at 30°C for 3 days. D, The Σ1278b strain with pRS316-GAL1p-SET4 or an empty vector was grown on SC-URA with either 2% glucose or 2% galactose for 10 days to promote adhesion to the agar and invasion. Images were obtained before washing (pre-wash) and after gentle washing with water to remove non-adherent cells (post-wash). E, Crystal violet staining of Σ1278b cells containing an empty vector or pRS316-GAL1p-SET4 grown in either 2% glucose (GLU) or 2% galactose (GAL) and adhered to 96-well polystyrene plates, as described (46).

Figure 2. Set4 promotes survival during oxidative stress. A, Ten-fold serial dilutions of wildtype (wt; yEG001) and set4Δ (yEG325) strains grown to mid-log phase in YPD, or YPD with 4 mM H₂O₂ for 30 min. B, Ten-fold serial dilutions of wt (yEG001) and set4Δ (yEG325) strains spotted on YPD, YPD with 100 μM CdCl₂ or with 150 μM CdCl₂. C, Percent survival calculated from CFU of wt (yEG001) and set4Δ (yEG325) strains following treatment with 4 mM H₂O₂ for 30 min. Scatter plot shows the mean and standard deviation from three biological replicates. An unpaired t test was used to determine statistical significance. D, Percent survival of wt and set4Δ cells (yEG638, yEG639, yEG640, yEG641) carrying either the empty pRS316 vector or pRS316-SET4, with SET4 under the control of its endogenous promoter, calculated from CFU on SC-URA following treatment with 20 mM H₂O₂ for 30 min. One-way ANOVA was performed, followed by Turkey’s post-hoc test to determine statistical significance. E, Ten-fold serial dilutions of strains carrying either pMN3 (empty) or pMN3-SET4 (yEG372 and yEG375, respectively) that were pre-treated with 1 μM β-estradiol for 4-5 hours, followed by exposure to 20 mM H₂O₂ for 30 min. F, Percent survival calculated from CFU of cells grown as in E, except that 50 nM β-estradiol was used to induce SET4, and plated on SC-URA. An unpaired t test was used to determine statistical significance. For all panels, asterisks represent p-values as follows: * ≤ 0.05, ** ≤ 0.01, *** ≤ 0.001, not significant is shown as ns.

Figure 3. Intracellular ROS levels are altered in set4Δ and SET4-overexpressing cells. Representative flow cytometric histograms of intracellular ROS levels detected using DCFH-DA (left) and percent fluorescent cells for each strain (right). A, wt (yEG001) and set4Δ (yEG325) strains were grown to mid-log phase in YPD, or YPD with 4 mM H₂O₂ for 30 min. B, Yeast carrying either pMN3 (empty) or pMN3-SET4 (yEG372 and yEG375) were grown to early-log phase with SC-URA and treated with 25 μM β-estradiol for 3 hours. Error bars represent SEM from three biological replicates. Asterisks represent p-values from unpaired t tests (* ≤ 0.05, *** ≤ 0.001).

Figure 4. Set4 localizes to the nucleus and associates with chromatin. A, Immunoblot of anti-FLAG IP from either wt (yEG001) cells or cells expressing FLAG-Set4 from its endogenous locus (yEG513) grown

Set4 protects cells during oxidative stress
Set4 protects cells during oxidative stress
to mid-log phase in YPD. Anti-FLAG blot is shown for the IP eluates, and anti-Hxk2 (hexokinase) is shown for the input as a protein loading control (FLAG-Set4 is not detectable in the input samples). Arrowhead indicates FLAG-Set4; * indicates a non-specific protein that binds to the anti-FLAG beads. B, Fluorescence microscopy of cells carrying pGAL1-GFP-SET4 (yEG735), induced in 2% galactose. DNA is stained with Hoechst. Scale bar represents 5 µm. C, Anti-FLAG immunoblots from chromatin fractionation of extracts from wt cells or cells with FLAG-Set4 (yEG626) induced with 10 µM β-estradiol for 3 hr. The soluble supernatant (Sup) and insoluble, chromatin pellet (Pel) fractions are shown. Pellet + sonication indicates samples which come from sonication of the resuspended chromatin pellet and subsequent centrifugation to separate soluble (Sup) and insoluble (Pel) material. Anti-H4 and anti-Hxk2 blots are shown as controls for chromatin and soluble proteins, respectively. D, Immunoblots from chromatin fractionation performed as in C except that cells induced to express FLAG-Set4 were treated with 20 mM H2O2 for 60 min.

Figure 5. Set4 promotes activation of stress response genes. A, Gene ontology (GO) analysis of significantly differentially expressed genes identified by microarray analysis of set4Δ cells from Kemmeren et al. (35). The $-\log_{10} P$ value of the enriched GO biological process categories are shown for both down-regulated and up-regulated genes. B, RT-qPCR of stress response genes identified in Kemmeren et al. (35) from yeast with empty pMN3 or pMN3-SET4 in the presence or absence of β-estradiol. Expression levels were normalized to SIR1. Fold change relative to empty vector strain either with or without H2O2 treatment is shown. Error bars represent SEM from at least three biological replicates. C, RT-qPCR of stress response genes from wt (yEG001) and set4Δ (yEG322) strains grown in YPD and treated with 0.4 mM H2O2 for 30 min. Expression levels were normalized to SIR1. Fold change relative to the wt strain without H2O2 treatment is shown. Error bars represent SEM from at least three biological replicates. PNC1 consistently showed lower expression in set4Δ cells treated with H2O2 although this did not reach the threshold for statistical significance due to variability in its expression levels in H2O2. D, Fold change, as in C, of SET4 mRNA in wt cells without or with 0.4 mM H2O2 for 30 min. E, chIP of FLAG-Set4 (expressed from its endogenous promoter; yEG513) from cells grown to mid-log phase in YPD or YPD with 0.4 mM H2O2 for 30 min. Percent input was calculated for each IP and primer set and enrichment is shown for FLAG-Set4 relative to the wt (untagged) strain either with or without H2O2 treatment. The primers detect the promoter sequences for each of the indicated genes. Error bars represent SEM from three biological replicates. For all panels, asterisks represent p-values from unpaired t-tests (* P ≤ 0.05, ** P ≤ 0.01, *** P ≤ 0.001; not significant is shown as ns), except panel E, in which a paired t-test was used.

Figure 6. Set4-dependent regulation of ERG gene expression. A, RT-qPCR of ERG genes from wt (yEG001) and set4Δ (yEG322) strains grown in YPD and treated with 0.4 mM H2O2 for 30 min. Expression levels were normalized to SIR1. Fold change relative to the wt strain without H2O2 treatment is shown. Error bars represent SEM from three biological replicates. B, RT-qPCR as in A except that cells were grown in synthetic complete (SC) medium, and H2O2 treatment was not performed. Asterisks represent p-values from unpaired t-tests (** P ≤ 0.01, *** P ≤ 0.001).

Figure 7. Partial functional overlap between SET3 and SET4. A, Ten-fold serial dilutions of wt (yEG001), set3Δ (yEG330), set4Δ (yEG325), and set4Δ set3Δ (yEG347) strains spotted on YPD or YPD with 15 µg/mL MPA. B, Percent survival of the same strains as in A following growth in YPD and treatment with 4 mM H2O2 for 30 min. Scatter plot shows the mean and standard deviation from four biological replicates. One-way ANOVA was performed, followed by Turkey’s post-hoc test to determine statistical significance. Asterisks represent p-values as follows: * ≤ 0.05, ** ≤ 0.01.

Figure 8. Recombinant Set4 does not methylate histones in vitro. A, Autoradiograph and Coomassie blue staining of SDS-PAGE with in vitro methylation assays using purified 6xHis-Set4 and histone substrates, including recombinant H3 (rH3), rH4, rH2A, rH2B, calf thymus histones (CTH), and nucleosomes purified from Hela cells (Nuc). A reaction with GST-Set5 and CTH as substrate was run on the same gel as a positive
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control. Coomassie blue of KMTs shows both 6xHIS-Set4 and GST-Set5 used in the reactions. B, Autoradiograph and Coomassie blue staining of SDS-PAGE with in vitro methylation assays using purified GST-Set2 and GST-Set5 on multiple substrates. C, Ten-fold serial dilutions of wildtype yeast (yEG001) carrying wildtype and mutant SET4 under the control of the GAL1 promoter spotted on either SC-LEU with 2% glucose (GLU) or 2% galactose (GAL) and grown at 30°C for 2-3 days. D, Serial dilutions of wildtype strains (yEG315) with either wildtype or Y375A mutant pMN3-SET4 spotted on SC-URA or SC-URA with 100 µM β-estradiol and grown at 30°C for 3 days.
Figure 1

A

|    | 1  | 162 | 208 | 346 | 481 | 560 |
|----|----|-----|-----|-----|-----|-----|
|    | PHD| SET |

**SET domain percent identity matrix**

|          | ScSet4 | ScSet3 | DmUpSET | HsMLL5 |
|----------|--------|--------|---------|--------|
| ScSet4   | -      | 54%    | 25%     | 27%    |
| ScSet3   | 54%    | -      | 24%     | 24%    |
| DmUpSET  | 25%    | 24%    | -       | 48%    |
| HsMLL5   | 27%    | 24%    | 48%     | -      |

NH

ScSet4: DSR78G6LTRY1RESCFPVEVLVTVPDRE-----KPRGDNDCRVRKVFLRAIRDHRKGEISVEVDLDNLNP
ScSet3: DARL8SNTRY1RESSQPVEVLVTIKLQDTNDGKSSGRKSGRIRKVFLRALLHIDSEDDELYIKKQWD5KIP
DmUpSET: DTRTYGNDAFVRDSCPRAELQHYFEK----------GTHLYIVALTHRAQTEITRIERPHDHTLA
HsMLL5: DARTFGNARFRRSCPNAERHRIQ0----------GTHYIYSIHSIPKGEITIALD-----

B

empty

SET1

SET2

SET3

SET4

SET5

SET6

DOT1

SC-LEU +2% GLU

SC-LEU +2% GAL

C

empty

SET4

SC-URA

empty

SET4

SC-URA + 100μM β-estradiol

D

empty

SET4

pre-wash

post-wash

SC-URA +2% GLU

SC-URA +2% GAL

E

empty

SET4

GLU

GAL

GLU

GAL
Figure 2

A

B

C

D

E

F

Percent survival

Percent survival

Percent survival

Percent survival
Figure 3

(A) Fluorescence intensity counts for different conditions:
- No dye
- wt + H$_2$O$_2$
- set4$\Delta$ + H$_2$O$_2$

(B) Fluorescence intensity counts for different conditions:
- No dye
- Empty
- SET4

Graphs show percent fluorescent at different conditions:
- -H$_2$O$_2$
- +H$_2$O$_2$

Significance indicated by asterisks:
- * ns
- **
- ***
Figure 5

A

| oxidation-reduction process | Down-regulated genes |
|-----------------------------|----------------------|
| iron ion homeostasis        | 74 genes             |

| Up-regulated genes          |
|-----------------------------|

B

![Bar graph showing fold change for various genes](#)

C

![Bar graph showing fold change for various genes](#)

D

![Bar graph showing fold change for SET4](#)

E

![Bar graph showing relative enrichment](#)
Figure 6

A

YPD

\[ \frac{\text{wt}_{\text{set4}}}{\text{∆wt}_{\text{set4}}} \]

Fold Change

0

0.5

1.0

1.5

ERG11  ERG3  ERG2  ERG6

***  ***  ***  **

B

Synthetic Complete

\[ \frac{\text{wt}_{\text{set4}}}{\text{∆wt}_{\text{set4}}} \]

Fold Change

0

0.5

1.0

1.5

2.0

ERG11  ERG3  ERG2  ERG6

wt

set4Δ

-\( \text{H}_2\text{O}_2 \)

+\( \text{H}_2\text{O}_2 \)
Figure 7

A

YPD

wt
set3Δ
set4Δ
set4Δ set3Δ

YPD + 15μg/mL MPA

B

Percent survival

wt set3Δ set4Δ set4Δ set3Δ

**

*
Figure 8

A

| 6xHis-Set4 | GST-Set5 |
|------------|----------|
| rH3        | CTH      |
| rH4        | Nuc      |
| rH2A       | CTH      |
| rH2B      | 15kD     |

- $^3$H-SAM
- KMTs
- substrates (Coomassie blue)

B

| GST-Set2 | GST-Set5 |
|----------|----------|
| rH3      | CTH      |
| rH4      | CTH      |

- $^3$H-SAM
- substrates (Coomassie blue)

C

- empty
- SET4<sub>WT</sub>
- SET4<sub>Y475A</sub>
- SET4<sub>E468A</sub>
- SET4<sub>E468A,W473A</sub>

SC-LEU + 2% GLU

SC-LEU + 2% GAL

D

- empty
- SET4<sub>WT</sub>
- SET4<sub>Y475A</sub>

SC-URA

SC-URA + 100µM β-estradiol
Set4 is a chromatin-associated protein, promotes survival during oxidative stress, and regulates stress response genes in yeast

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