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New Clox Systems for Rapid and Efficient Gene Disruption in *Candida albicans*

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New Clox Systems for Rapid and Efficient Gene Disruption in Candida albicans


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**Abstract**

Precise genome modification is essential for the molecular dissection of Candida albicans, and is yielding invaluable information about the roles of specific gene functions in this major fungal pathogen of humans. C. albicans is naturally diploid, unable to undergo meiosis, and utilizes a non-canonical genetic code. Hence, specialized tools have had to be developed for gene disruption in C. albicans that permit the deletion of both target alleles, and in some cases, the recycling of the Candida-specific selectable markers. Previously, we developed a tool based on the Cre recombinase, which recycles markers in C. albicans with 90–100% efficiency via site-specific recombination between loxp sites. Ironically, the utility of this system was hampered by the extreme efficiency of Cre, which prevented the construction in Escherichia coli of stable disruption cassettes carrying a methionine-regulatable CanMET3p-cre gene flanked by loxP sites. Therefore, we have significantly enhanced this system by engineering new Clox cassettes that carry a synthetic, intron-containing cre gene. The Clox kit facilitates efficient transformation and marker recycling, thereby simplifying and accelerating the process of gene disruption in C. albicans. Indeed, homozygous mutants can be generated and their markers resolved within two weeks. The Clox kit facilitates strategies involving single marker recycling or multi-marker gene disruption. Furthermore, it includes the dominant NAT1 marker, as well as URA3, HIS1 and ARG4 cassettes, thereby permitting the manipulation of clinical isolates as well as genetically marked strains of C. albicans. The accelerated gene disruption strategies afforded by this new Clox system are likely to have a profound impact on the speed with which C. albicans pathobiology can be dissected.

**Introduction**

Candida albicans is a major opportunistic pathogen of humans. Most healthy individuals carry C. albicans as a relatively harmless commensal in the microflora of their oral cavity, gastrointestinal and urogenital tracts. However, the fungus is a frequent cause of mucosal infections (thrush) in otherwise healthy individuals, and in severely immunocompromized patients C. albicans is able to disseminate throughout the body, causing potentially fatal systemic infections [1,2]. Therefore, major goals in the field include the dissection of C. albicans pathobiology as well as the development of more sensitive diagnostic tools and more effective antifungal therapies [3].

The precise mechanistic dissection of C. albicans pathobiology and drug resistance has depended upon the development of molecular tools that permit the accurate disruption of target genes in this fungus. Several aspects of C. albicans biology have slowed progress and demanded the development of Candida-specific tools. Specifically, C. albicans exists primarily as a diploid, and although haploid forms can now be generated via concerted chromosome loss [4], this fungus does not seem to undergo meiosis to complete a standard sexual cycle [5–7]. Therefore, both alleles of a target locus must be disrupted to generate homozygous deletion mutants in C. albicans, and ideally, the genetic markers used to select transformants must be recycled to permit the sequential deletion of more than one locus [8–11]. As a result, gene disruption in C. albicans is a relatively time-consuming process. Furthermore, C. albicans exploits a non-canonical genetic code [12–14]. Consequently, specific selectable markers that circumvent the issues associated with usage of the CTG codon have had to be developed for this fungus [8,13,15–19].

Existing strategies for gene disruption include the exploitation and recycling of the URA3 marker [8,10,11]. These approaches involve the deletion of the first allele in a C. albicans ura3/ura3 host
by targeted integration of a *URA3*-based disruption cassette at the desired locus, and the selection of transformants via uridine prototrophy. Positive selection using 5-fluoroorotic acid (5-FOA) is then required to recycle the *URA3* marker, because the generation of *ura3*-segregants, via homologous recombination between the flanking repeats in these disruption cassettes, is relatively rare [0,10]. 5-FOA selection for *ura3*-cells is commonly used in model yeasts [20]. However, 5-FOA has been shown to cause chromosomal damage in *C. albicans* [21]. Alternative auxotrophic transformation markers have been developed, such as HIS4, *ARG6* and *LEU2* genes [15,16,18], but in most cases these cassettes are not recyclable.

Morschhauser and colleagues [22] addressed the paucity of recyclable marker systems by generating a FLP recombinase-mediated *C. albicans* gene disruption system. In this cassette, FLP expression is regulated by the inducible *SAP2* promoter to mediate site-specific recombination between the FRT sites that flank this *URA3* disruption cassette. The serial use of this system allows the sequential disruption of both target alleles using the *URA3* marker [22]. This system was improved by the addition of a dominant selection marker, *SAT1*, which confers nourseothricin resistance upon *C. albicans* (the *SAT1* flipper) [23]. Shen and co-workers [19] then adapted this FLP-based system by replacing the *SAT1* marker with *MAT1*, which is a codon-optimized *Streptomyces noursei* NAT1 gene that also confers nourseothricin resistance. More recently, Morschhauser’s group has described a modified *SAT1* flipper, which was designed to minimize basal FLP expression levels [24]. These recyclable FLP cassettes have proven invaluable tools for the study of genes involved in *C. albicans* pathogenicity. The efficiency of FLP-mediated recombination and marker recycling varies, with reports of 8–40% resolution for the *URA3*-FLP system [22], about 20% for *SAT1*-FLP [23], and more recently, resolution frequencies of up to 100% for *SAT1*-FLP cassettes (Joachim Morschhauser, personal communication).

Recently, we constructed a Cre-loxP system for gene disruption and marker recycling in *C. albicans* [25]. Cre catalyses site-specific recombination between *lox* elements in P1 bacteriophage [26,27]. This molecular specificity has been exploited through the development of Cre-locP-based recombination tools developed for *Saccharomyces cerevisiae* and mammalian cells [28,29]. Our *C. albicans* system is analogous to these tools, involving the use of Cre to recycle transformation markers via recombination between flanking *loxP* sites [25]. We constructed a methionine-regulatable *MET3*-cre cassette (CAD) and three disruption cassettes with different selectable markers: *loxP*-ARG4-loxP (LAL), *loxP*-HIS1-loxP (LHL) and *loxP*-URA3-loxP (LUL). We were unable to clone *MET3*-cre into these *loxP* disruption cassettes because the Cre recombinase encoded by the synthetic, codon-optimized cre gene was exceedingly efficient, catalysing self-resolution of *loxP*-MET3*-cre-loxP* cassettes in *E. coli*. Therefore, this Cre-loxP system suffers the disadvantage that, in comparison with other gene disruption systems [19,23], it requires an additional transformation step to introduce the *MET3*-cre sequences into *C. albicans* after the two target alleles have been disrupted [25]. However, this Cre-loxP system enjoys the advantage of high recombination efficiencies in *C. albicans* (>90% marker resolution), thereby circumventing the need to select for resolved segregants [25] and providing the potential to significantly accelerate the gene disruption process.

Here we describe the development of an enhanced Cre-locP toolkit (Clox) that exploits the advantages of the old tools while overcoming their disadvantages. The new Clox kit facilitates rapid, efficient and flexible gene disruption and marker recycling in *C. albicans*, both for auxotrophic laboratory strains and prototrophic clinical isolates. The construction of a new synthetic, codon-optimized, intron-containing cre gene has allowed the inclusion of *MET3*-cre within stable, *loxP*-flanked, *Clox* cassettes that carry *URA3* or *MAT1* markers (*URA3*-Clox and *MAT1*-Clox, respectively). These *URA3*-Clox and *MAT1*-Clox cassettes support gene disruption either via the sequential use and recycling of a single marker, or using multiple markers. The efficiency of this *Clox* system permits the accurate generation of resolved homozygous null mutants in less than two weeks, thereby significantly reducing the time required for gene disruption in *C. albicans*. Consequently, the *Clox* system will accelerate functional analysis programmes and provides a platform technology for other forms of genome manipulation in *C. albicans*.

**Results**

The *Clox* kit

The utility of the original Cre-*locP* system was compromised by the inability to construct stable cassettes carrying *MET3*-cre flanked by *loxP* sites because there was sufficient expression of Cre from *MET3*-cre in *E. coli* to catalyse *loxP* recombination [25]. Therefore, we designed a synthetic intron-containing cre gene that would prevent the expression of functional Cre in *E. coli*, whilst permitting the expression of functional Cre in *C. albicans* (Figure 1A). We selected the second intron from the *C. albicans TUB2* gene, because it is relatively short (164 nucleotides) and well characterized [30,31]. We then introduced two point mutations into the *TUB2* intron to create two in-frame stop codons that would prevent translational read-through of the intron in *E. coli*. This modified Ca*TUB2* intron sequence was inserted into the 343 codon cre gene open reading frame such that it interrupts codon 135. The cre open reading frame was then codon-optimized, all 18 CTG codons being replaced with preferred leucine codons during this process [25,32]. Synonymous non-preferred codons were used in places to remove inconvenient restrictions sites. Then a short 5′-untranslated region from *C. albicans* ADH1 was added, and transcriptional termination sequences from *S. cerevisiae CYC1* were introduced, because this terminator is well-characterized [33] and is functional in *C. albicans* [34]. Finally, *NdeI* and *XhoI* sites were designed at the 5′- and 3′-ends of the cre gene to facilitate its cloning into the *loxP*-URA3-*loxP* disruption cassette in the plasmid pLUL2 [25], and a 5′-*XhoI* site inserted to facilitate the subsequent insertion of the *C. albicans MET3* promoter. The structure of this synthetic, intron-containing, codon-optimized cre gene is illustrated in Figure 1A, and its complete sequence is presented in Figure S1. The cloning of this synthetic cre gene into pLUL2, and the subsequent insertion of *MET3* into the plasmid pLUMCL2, which carries the *URA3*-Clox disruption cassette (Figure 1B).

The *URA3*-Clox cassette is suitable for gene disruption in commonly used *C. albicans* *ura3*/*ura3* laboratory strains, but is not suitable for the manipulation of prototrophic clinical isolates, which require a dominant selectable marker. Therefore, we replaced the *URA3* sequence in pLUMCL2 with the *MAT1* sequence from pJK863 [19] to create a *MAT1*-Clox cassette in the plasmid pLNMC1 (Figure 1B). This cassette permits dominant selection via nourseothrycin resistance.

Previously we constructed a series of vectors to facilitate the construction of control *C. albicans* strains that have the relevant marker genes stably reintegrated into their genomes at the *RPS1* locus (Clp10, Clp20, Clp30: [25]). Therefore, we constructed an analogous plasmid for the reintegration of *MAT1* at *RPS1* (Clp-NAT) (Figure S2). We chose this locus because numerous laboratories have confirmed that the insertion of Clp plasmids at *RPS1* does not affect the phenotype or virulence of *C. albicans* [35].
**The Clox Strategy – Multi-marker Disruption**

The *NAT1-Clox* and *URA3-Clox* cassettes may be used alone or in combination with existing cassettes that carry alternative auxotrophic markers (Figure 1B). Hence the Clox cassettes are suitable for gene disruption in *C. albicans* using both multi-marker disruption and single marker recycling strategies (Figure 2).

To validate the multi-marker disruption strategy (Figure 2), we used the LHL (*loxP*-HIS1-*loxP*) and *URA3-Clox* cassettes (Figure 3) to generate a homozygous *ade2/ade2* null mutation in *C. albicans* RM1000 (*his1- ura3-; Table 1*). The first *ADE2* allele was disrupted by targeted integration of an *ade2A::LHL* cassette. The resultant His*+* (*ADE2/ade2A::LHL*) strain was then transformed with an *ade2A::URA3-Clox* cassette to generate a His*+* Uri*+* (*ade2A::LHL/*ade2::URA3-Clox*) strain. At each stage, transformants were selected on medium containing methionine and cysteine to repress *MET3*-cre expression. Before marker recycling, transformants were single-celled on fresh medium containing methionine and cysteine to remove untransformed background cells. *MET3*-cre cassettes are stably maintained in the *C. albicans* genome as long methionine and cysteine are present to repress the *MET3* promoter. Then Cre resolves *loxP*-containing cassettes extremely efficiently once this repression is released [25]. Therefore it was important to maintain transformants in the presence of methionine and cysteine. Selecting for *URA3* and *HIS1* transformants when *MET3*-cre is derepressed led to the generation of non-resolvable mutants, essentially because this selects for *C. albicans* segregants that either express non-functional Cre or carry aberrant *loxP* sites.

Having selected His*+* Uri*+* cells, and confirmed their Ade-status, Cre-mediated recombination was induced by derepressing *MET3*-cre expression. Cells were grown for 4 h at 30°C in SC broth lacking methionine and cysteine and supplemented with adenine, histidine and uridine. Cells were then plated on the same medium. As before [25], over 90% resultant colonies were auxotrophic for uridine and histidine. Hence there was no need to select for resolved (*ura3-*) segregants with 5-FOA. The loss of *HIS1* and *URA3* sequences from these segregants (i.e. the resolution of the LHL and *URA3-Clox* cassettes) was demonstrated by diagnostic PCR (Figure 3B), confirming the functionality of the intron-containing *MET3*-cre gene in *C. albicans*. The strains generated at each stage of the gene disruption process displayed the expected auxotrophic requirements (Figure 3A), and their genotypes were confirmed by diagnostic PCR (Figure 3B).

**The Clox Strategy – Single Marker Recycling**

To validate the *URA3-Clox* cassette for single marker recycling (Figure 2), we used it to disrupt *GSH2* (*orf19.6404*), which encodes a putative glutathione synthase in *C. albicans* [36]. *C. albicans* RM1000 was transformed with a PCR-amplified *gsh2::URA3-Clox* cassette (Tables 1 and S1). Uri*+* transformants (*GSH2/*gh2A::URA3-Clox*) were selected on SC lacking uridine and containing methionine and cysteine, and then streaked on the same medium to select single colonies. The *URA3-Clox* cassette was then resolved by culturing transformants overnight in YPD containing uridine and without supplemental methionine and cysteine. The majority (>90%) of the resultant segregants were
Figure 2. Cartoons illustrating the exploitation of Clox cassettes for multi-marker gene disruption and single marker recycling. (see text).
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Uri- (GSH2/gsh2::loxP). The second GSH2 allele was then disrupted by retransforming Uri- cells with the same gsh2::URA3-Clox cassette. Uri+ transformants (gsh2D::loxP/gsh2D::URA3-Clox) were selected on SC lacking uridine and containing methionine and cysteine, and then streaked on the same medium to select single colonies. Transformants were then grown in YPD containing uridine to promote URA3-Clox resolution, and then streaked on YPD plates (without supplements) to obtain single colonies. Once again, large numbers of Uri- segregants (gsh2D::loxP/gsh2D::loxP) were generated, and 5-FOA selection was not required. The strains generated at each stage of the process displayed the expected auxotrophies and genotypes, the URA3-containing strains growing slightly better on YPD lacking uridine (Figure 4).

Interestingly, the diagnostic PCR revealed that some gsh2D::URA3-Clox cells had undergone Cre-mediated recombination even during growth on media containing methionine and cysteine (Figure 4B). Therefore, under these growth conditions, leaky MET3p-cre expression appears to be sufficient to promote some Clox resolution. C. albicans gsh2A/gsh2A cells were sensitive to oxidative stress (Figure 4A), which is consistent with the predicted glutathione synthase activity of Gsh2 [36]. To confirm that the NAT1-Clox cassette can be used to inactivate loci in prototrophic clinical isolates via single marker recycling, we deleted the ADE2 locus in C. albicans SC5314 (Table 1). To inactivate the first ADE2 allele, cells were transformed with an ade2::NAT1-Clox cassette, nourseothricin resistant (NouR) transformants selected on YPD supplemented with nourseothricin, methionine and cysteine, and these transformants restreaked onto the same medium. To resolve the NAT1-Clox cassette, purified NouR isolates were grown overnight in YPD containing uridine to promote NAT1-Clox resolution, and then streaked on YPD plates (without supplements) to obtain single colonies. Once again, large numbers of Uri- segregants (ade2D::loxP/ade2D::loxP) were generated, and 5-FOA selection was not required. The strains generated at each stage of the process displayed the expected auxotrophic requirements for wild type (ADE2/ADE2), heterozygous (ade2D::LHL/ADE2), unresolved homozygous (ade2D::LHL/ade2D::UAR3-Clox) and resolved homozygous mutants (ade2D::loxP/ade2D::loxP). Growth media are specified on the right: w/o, without a specific supplement. (B) PCR confirmation of the genotypes for these mutants using primers specific for each allele (specified on the left of each panel). PCR product lengths are given on the right of each panel. ACT1 was used as a positive control, and a no-DNA control was included (Control).
Discussion

The accurate manipulation of specific chromosomal loci is critical for the molecular dissection of microbial development, pathogenicity and drug resistance. Therefore a range of elegant tools have been developed for gene disruption in C. albicans [8,10,15,16,18,19,22,23,25,37]. Despite the availability of these tools, gene deletion in C. albicans remains a relatively time-consuming process because this fungus is an obligate diploid, apparently unable to undergo meiosis [5–7]. Consequently, despite the valiant attempts of a number of groups [18,38–43] we lack a comprehensive collection of homologous C. albicans deletion mutants that is freely available to the academic community. Exciting recent developments suggest that a collection of haploid null mutants could be generated [4,37], but as things stand C. albicans haploids display fitness defects and are unstable [4,37]. Enhanced gene disruption tools would significantly increase the feasibility of generating a collection of deletion mutants, whether in haploids or diploids. The Clox toolkit (Figure 1) offers this enhancement by improving the efficiency with which selectable markers can be recycled, increasing the yields of desired mutants, reducing the number of requisite steps to generate these mutants, and significantly decreasing the time required to generate these mutants.

The recycling of selectable markers in C. albicans is desirable for two main reasons. Firstly, a narrow range of auxotrophic markers are available for laboratory strains (URA3, HIS1, ARG4, LEU2) [8,15,16,18], and few dominant antibiotic markers can be used in prototrophic clinical strains (MPA3, SAT1/NAT1, HygB) [19,23,44–47]). Therefore, the opportunities to dissect multigene families would be severely constrained without marker recycling. Secondly, marker position effects can influence virulence-related phenotypes in C. albicans [48–51], and therefore markers are generally reintegrated at a standard locus to control for these effects [35,52,53]. Initially, marker recycling in C. albicans was achieved via homologous recombination between relatively large direct repeats that flank the marker gene [8,10]. However, these ura3− segregrants arise infrequently, and therefore their isolation depends on positive 5-FOA selection, which is mutagenic [21]. The FLP-system displays markedly improved frequencies of marker recycling that are reported to yield 8–20% of marker-resolved segregants [22,23], but which can approach 100% resolution (Joachim Morschhauser, personal communication). No selection of Not− segregrants is required, but these smaller colonies must be carefully distinguished from larger Not− background colonies [23]. Cre-loxP also offers extremely high frequencies of marker resolution that can approach 100% in C. albicans [25]. However, the utility of the initial system was prejudiced by the inability to clone stable cre-containing loxP-flanked disruption cassettes in E. coli [25]. The construction of an intron-containing cre gene has successfully circumvented this problem (Figure 1). The leaky resolution of Clox cassettes even in C. albicans cells grown on methionine and cysteine, which is a consequence of the extreme efficiency of this system, represents a potential drawback (Figure 4B). Those researchers that need to retain unresolved versions of their mutants might utilise our earlier Cre-loxP system [25], or the current SAT1 flipper [24], which retains the original Candida-adapted FLP, a recombinase with lower activity than the mutated ecaFLP gene [54]. However, for most...
Figure 5. Validation of NAT1-Clox for single marker recycling in a prototrophic clinical isolate. NAT1-Clox was used to generate a homozygous ade2Δ/ade2Δ mutation in C. albicans SC5134. (A) Confirmation of the expected phenotypes for wild type (ADE2/ADE2), unresolved heterozygous (ADE2/ade2Δ::loxP), resolved heterozygous (ADE2/ade2Δ::loxP), unresolved homozygous (ade2Δ::loxP/ade2Δ::loxP) and resolved homozygous mutants (ade2Δ::loxP/ade2Δ::loxP). Growth media are specified on the right: w/o, without a specific supplement; nou, nourseothricin. (B) PCR confirmation of the genotypes for these mutants using primers specific for each allele (specified on the left). PCR product lengths are specified on the right. ACT1 was used as a positive control, and a no-DNA control was included (Control).

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researchers the high Cre efficiency is not an issue, because the desired endpoint is generally the resolved mutant. Furthermore, Clp10, Clp20, Clp30 and Clp-NAT facilitate stable reintegration of the desired markers into resolved mutants [25] (Figure S2).

We have validated the exploitation of Clox cassettes for single marker recycling and multi-marker disruption (Figure 2). Single marker recycling demands two cycles of transformation and marker recycling. Given the high yield of correctly resolved Clox mutants (>90%) following MET3p-cre induction ([25]; this study), we find that selections for resolved segregants are not required, and that PCR diagnosis can be left till the end of the disruption process (Figure S3). Therefore, having established the methodology, we proceed directly to the second round of disruption without waiting for PCR confirmation of heterozygous mutant genotypes (retrospective genotyping). The analysis of several segregants from several transformants is generally sufficient to yield the desired homozygous null mutants. As a result we are now able to routinely generate independent, resolved, homozygous null mutants in laboratory strains and clinical isolates within two weeks. The process is even more rapid for the multi-marker disruption strategy which requires only one round of Cre-mediated marker resolution (Figure 2). The notable exception is where inactivation of the target gene confers a significant fitness defect, which necessitates the construction of a conditional mutant [55–58]. In principle, one-step gene deletion in haploid C. albicans strains should be even faster, although current protocols, which include the cloning of disruption cassettes and flow cytometry to exclude autodiploidized segregants, takes nearly four weeks [37].

The Clox cassettes have been tested by other users. Several general points can be made based on their successful construction of over 50 C. albicans mutants with Clox cassettes (Figure 1). First, off-target integration with Clox cassettes does not appear to be a major issue. Off-target integration was rare for those mutants whose genotypes were confirmed by Southern blotting. Also, almost without exception, independently generated mutants have displayed identical or very similar phenotypes. Second, the re-disruption of the first allele is often observed during the second round of disruption when the same PCR primers were used to generate the second disruption cassette, and when it was not possible to impose a double selection (e.g. for LUL and LHL cassettes: Figure 2). However, the desired homozygous null mutant was usually obtained after screening about 20 second round transformants. Furthermore, this issue is circumvented by amplifying the second disruption cassette with primers that target the region deleted from the first allele. Indeed, this approach was successful for all 11 non-essential C. albicans loci where this strategy was employed. Third, the Clox system does not provide a magical solution to the problems associated with deleting essential loci. Attempts to delete both alleles of 3 C. albicans loci that appear to be essential using Clox cassettes were unsuccessful. As observed for other systems [10,15], triploid segregants containing a wild type allele were obtained, rather than the desired homozygous null mutant. We conclude that success rates with Clox appear similar to other disruption systems.

These Clox trials confirmed a fourth point. Retrospective genotyping of Clox mutants is practical for loci without an anticipated phenotype. For the 14 C. albicans mutants where this approach was tested, no problems were experienced with retrospective genotyping. Independent homozygous null mutants were successfully generated for 11 of the 14 target loci. For these 11 mutants, 3 independent homozygous mutants were obtained by retrospective screening of 10 second round transformants from each of 5 first round transformants. Regarding the other 3 loci, their apparent essentiality was revealed more quickly by retrospective genotyping. We conclude that the high efficiency of Clox marker recycling makes retrospective PCR diagnosis of C. albicans Clox mutants a feasible option.

We note that the utility of the Clox system extends beyond rapid and convenient gene deletion. As for other cassettes [59,60], the Clox system could be adapted to construct fluorescent protein fusions or epitope-tag proteins in laboratory strains or clinical isolates. In principle, Clox could also be exploited to engineer large chromosomal deletions [61], or the induction of genetic alterations that allow the analysis of spatial and temporal patterns of gene expression and their role in development [62]. Therefore, the Clox
system represents a significant step forward in the development of the *C. albicans* molecular toolbox that should empower local and genome-wide analyses of this major opportunistic pathogen of humans.

**Materials and Methods**

**Strains and Growth Conditions**

*C. albicans* strains used in this study are listed in Table 1. Unless otherwise specified, all strains were grown in YPD [63]. In some cases strains were grown on YPDG (YPD containing 40 μg/ml glutathione) or YPDA (YPD containing 0.01% adenine). SD medium supplemented with auxotrophic requirements or SC medium lacking the appropriate supplement [60] were used to screen *C. albicans* cells transformed with Clox disruption cassettes. During all selections for Clox transformants, and for all phenotyping assays, media were supplemented with 2.5 mM methionine and 2.5 mM cysteine to repress the MET3 promoter and minimize Cre-loxP mediated recombination. Nourseothricin resistant (Nou\textsuperscript{K}) transformants were selected using 200 μg/mL nourseothricin (Werner Bioagents, Jena, Germany). For phenotyping assays, strains were grown overnight at 30°C, 200 rpm in SC medium containing the appropriate supplements plus 2.5 mM methionine and 2.5 mM cysteine. These cells were diluted in sterile water, and 10\textsuperscript{5} cells were spotted onto agar plates, which were then incubated at 30°C for two days before imaging.

**Clox Construction**

A synthetic, codon-optimized cre open reading frame, interrupted by a *C. albicans* TUB2 intron at codon 135, was designed in silico (Results), constructed by DNA2.0 (Menlo Park, CA, USA) and cloned between the NheI and NsiI sites in pLUL2 [25] to generate pLUCL2. The CaMET3 promoter region (1336 bp) was then PCR-amplified using Infusion cloning primers Clox-MET3p-F and Clox-MET3p-R (Table S1) and cloned between the NheI and XmnI sites in pLUCL2 in front of the cre gene using an InFusion HD cloning kit according to the manufacturer’s instructions (Clontech, California, USA) to generate the URA3-Clox cassette in the plasmid pLUMCL2. The URA3 marker in pLUMCL2 was then replaced with the NAT1 marker to generate the NAT1-Clox cassette in the plasmid pLUMCL. NAT1 was amplified from pJK863 [64] using the primers Clox-NAT1-F and Clox-NAT1-R (Table S1), and then cloned between the Bpu10I and NheI sites of pLUCL2 by In-Fusion cloning to create pLUMCL. The sequences of the URA3-Clox and NAT1-Clox cassettes were confirmed experimentally. The structures of all Clox cassettes are illustrated in Figure 1, and their sequences are available in GenBank:

- URA3-Clox (loxP-URA3-MET3p-cre-loxP): GenBank accession number KC999858
- NAT1-Clox (loxP-NAT1-MET3p-cre-loxP): GenBank accession number KC999859
- LAL (loxP-ARG4-cre-loxP): GenBank accession number DQ015897
- LHL (loxP-HIS1-cre-loxP): GenBank accession number DQ015898
- LUL (loxP-URA3-cre-loxP): GenBank accession number DQ015899

**Clp-NAT**

Clp-NAT is a *Candida albicans* integrating plasmid (Clp) based on pJK863 [19], a kind gift from Julia Kohler. pJK863 carries a FLP-recyclable, codon-optimized NAT1 gene. To create Clp-NAT, the RPS1 targeting sequence, including the SacI linearization sites, was amplified from Clp10 [52] using the primers RPS1-NAT1-F and RPS1-NAT1-R (Table S1). The resulting PCR product was cloned between the SacII and SacI sites in pJK863, thereby generating Clp-NAT (Figure S2). The plasmid was sequenced from m13F to m13R and the data were deposited in GenBank under accession number KJ174065.

**Gene Disruption Using URA-Clox and NAT-Clox**

The URA3-Clox and NAT1-Clox cassettes were PCR-amplified using Extensor master mix (Thermo scientific; MA, USA) with chimeric primers, the 5’-ends of which represented short (90–100 bp) flanking regions of homology to the target locus [59], and the 3’-ends of which hybridized to the PCR priming sites common to all Clox cassettes (Table S1). The resulting PCR products were used to transform *C. albicans* [64]. Transformants were selected on nourseothricin-containing or uridine-lacking medium that also contained 2.5 mM methionine and 2.5 mM cysteine to repress MET3p-cre expression and inhibit marker resolution. Fresh Nou\textsuperscript{K} and Uvr\textsuperscript{R} transformants were single-celled on fresh medium containing 2.5 mM methionine and 2.5 mM cysteine, and if necessary, their genotypes confirmed by diagnostic PCR with the primers described in Table S1.

**Cre-mediated Marker Resolution**

After streaking for single colonies, *C. albicans* transformants were grown overnight in 10 ml SC medium that contained 2.5 mM methionine and 2.5 mM cysteine (to repress MET3p-cre expression) and maintained marker selection (i.e. lacked uridine or contained nourseothricin). Cells were harvested by centrifugation, washed twice in sterile H2O, and resuspended in 10 ml SC that lacked methionine and cysteine (to induce MET3p-cre expression) and without marker selection (i.e. lacked nourseothricin or contained uridine, and if necessary, contained any supplement required to support the new gene knock-out). Cells were incubated in this medium at 30°C for 4 h, and then streaked onto plates containing the same growth medium. The genotypes of the resolved mutants were then confirmed by diagnostic PCR using the primers described in Table S1.

**Oxidative Stress Resistance**

The oxidative stress resistance of *C. albicans* control and gsh2/gsh2 strains was tested by growing the strains overnight at 30°C, 200 rpm in SC medium containing the appropriate supplements, plating 10\textsuperscript{5} cells on YPD containing 1 mM tert-butylhydroperoxide (tBOOH), and incubating the plates at 30°C for two days.

**Ethics Statement**

No ethical permissions were required for this work which involved no experimentation involving animals or human samples.

**Supporting Information**

- **Figure S1** Annotated DNA sequence of the synthetic, codon-optimized, intron containing cre gene. (PDF)
- **Figure S2** Structure of the Clp-NAT plasmid, for targeting NAT1 to the RPS1 locus. (PDF)
- **Figure S3** Protocol for multi-marker gene disruption using Clox cassettes. (PDF)
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Author Contributions

Conceived and designed the experiments: SS DSC ERB AJPB. Performed the experiments: SS DSC ERB AJPB. Analyzed the data: SS DSC ERB AJPB. Contributed reagents/materials/analysis tools: IB. Contributed to the writing of the manuscript: SS DSC ERB FCO NARG AJPB.

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