Integrative multi-omics profiling reveals cAMP-independent mechanisms regulating hyphal morphogenesis in *Candida albicans*

Kyunghun Min[1], Thomas F. Jannace[1,5], Haoyu Si[1,6], Krishna R. Veeramah[2], John D. Haley[3,4], and James B. Konopka[1]*

[1] Department of Microbiology and Immunology, Renaissance School of Medicine, Stony Brook University (SUNY), Stony Brook, NY, USA

[2] Department of Ecology and Evolution, Stony Brook University (SUNY), Stony Brook, NY, USA

[3] Department of Pathology, Renaissance School of Medicine, Stony Brook University (SUNY), Stony Brook, NY, USA

[4] Biological Mass Spectrometry Shared Resource, Renaissance School of Medicine, Stony Brook University (SUNY), Stony Brook, NY, USA

[5] Present address: Department of Quality Assurance, Biogen, Morrisville, NC, USA

[6] Present address: School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA

* Corresponding author: james.konopka@stonybrook.edu

ABSTRACT

Microbial pathogens grow in a wide range of different morphologies that provide distinct advantages for virulence. In the fungal pathogen *Candida albicans*, adenylyl cyclase (Cyr1) has been thought to be a master regulator of the switch to invasive hyphal morphogenesis and biofilm formation. However, faster growing *cyr1Δ*/Δ pseudorevertant (PR) mutants were identified that form hyphae in the absence of cAMP. Isolation of additional PR mutants revealed that their improved growth was due to loss of one copy of *BCY1*, the negative regulatory subunit of protein kinase A, from the left arm of chromosome 2. Furthermore, hyphal morphogenesis was improved in some of PR mutants by multigenic haploinsufficiency resulting from loss of large regions of the left arm of chromosome 2, including global transcriptional regulators. Interestingly, hyphal-associated genes were also induced in a manner that was independent of cAMP. This indicates that basal protein kinase A activity is an important prerequisite to induce hyphae, but activation of the cAMP pathway is not needed. Instead, phosphoproteomic analysis indicated that the Cdc28 cyclin-dependent kinase and the casein kinase Yck2 play key roles in promoting polarized growth. In addition, integrating transcriptomic and proteomic data reveals hyphal stimuli induce increased production of key transcription factors that contribute to polarized morphogenesis.

INTRODUCTION

Fungal pathogens are capable of transitioning between different morphologies that provide distinct advantages for virulence and survival in the host[1,2]. For example, the fungal pathogen *Candida albicans* switches from budding to hyphal growth, which promotes virulence as the long hyphal filaments mediate invasion into tissues, escape from immune cells, and biofilm formation[1-6]. A variety of stimuli promote hyphal morphogenesis, including serum, CO_2, alkaline pH, peptidoglycan breakdown products, N-acetylglucosamine (GlcNAc), and contact with a solid matrix[3,7,8]. In *C. albicans*, it has long been thought that adenylyl cyclase (Cyr1) is a master regulator of hyphal growth[3,5,9-11]. Deletion of adenylyl cyclase (*cyr1*Δ/Δ) blocks hyphal formation, and addition of millimolar levels of exogenous cAMP induces it[12]. However, interpreting the role of Cyr1 and cAMP is complicated by the fact that the *cyr1*Δ/Δ mutants grow very poorly[13]. Furthermore, a recent study showed that faster growing *cyr1*Δ/Δ pseudorevertant (PR) mutants form hyphae in the absence of Cyr1 and cAMP[14]. Thus, although cAMP is capable of inducing hyphae, it is not essential for most hyphal stimuli[14].

In *C. albicans*, cAMP formed from ATP by Cyr1 acts by binding to the negative regulatory subunit (Bcy1) of protein kinase A (PKA), thereby releasing the PKA catalytic subunits (Tpk1 and Tpk2) to phosphorylate target proteins[11]. Most current models propose that the cAMP-PKA pathway induces the expression of a special set of genes that promote hyphal growth[2,3,11,13,15,16]. This has been supported by the ability of many transcription factors (TFs) to regulate this switch. For example, PKA was reported to phosphorylate the Efg1 TF, which is required for hyphal induction[17,18]. However, transcriptional analysis of hyphal induced genes has not revealed the mechanism of hyphal induction[19,20]. The common core set of genes stimulated by a group of different hyphal inducers in *C. albicans* do not account for the transition to hyphal growth[19]. In addition, our recent studies showed that a mutant that cannot catabolize GlcNAc can be stimulated by GlcNAc to form hyphae without induction of hyphal-specific genes[20]. Other studies have shown that some hyphal regulatory TFs can be bypassed under

special conditions[21], such as altered expression of the Cak1 protein kinase[22] or in the absence of a variant histone H3[23]. This indicates that although TFs are important for creating the proper physiological environment for cells to undergo hyphal growth, the target genes are not directly involved in promoting filamentous morphogenesis.

Other studies have implicated several protein kinases that are not regulated by cAMP in hyphal signaling[2,3,24]. For example, the cyclin-dependent kinase Cdc28 promotes hyphal growth in part by phosphorylating several proteins involved in polarized morphogenesis[24-32]. Therefore, to better define the cAMP-dependent and independent mechanisms of hyphal signaling, we isolated a set of new *cyr1*Δ/Δ PR mutants that displayed variable levels of improved growth rates and ability to form hyphae. The wild type and PR mutant cells were compared with four omics approaches: genomics combined with gene-mapping by CRISPR-Cas9 to identify genetic changes in PR mutants, transcriptomics to better define the role of cAMP in hyphal gene regulation, proteomics and phosphoproteomics to reveal key kinases for hyphal induction. Furthermore, integrative transcriptomics and proteomics profiling indicates that there are increases in the levels of key transcription factors, possibly due to changes in their translation rate, that are induced by hyphal signaling. Altogether, these results reveal how multiple processes in the gene expression pathway can modulate cellular differentiation.

RESULTS

Large deletions in the left arm of chromosome 2 bypass the need for cAMP to improve the growth rate and to stimulate hyphal morphogenesis.

We previously reported that slow growing *cyr1*Δ/Δ mutant strains give rise to faster growing cells, which we termed pseudorevertants (PRs)[14]. Interestingly, these spontaneous PRs could form hyphae even though they lack Cyr1 and cAMP[14]. To better define the underlying mechanisms, we isolated additional PR strains and found that they differed in their growth rates and ability to be induced to form hyphae (Fig. 1a,b and Supplementary Fig. 1).

Based on these phenotypic differences, the new PR mutants could be grouped into 4 classes (Table 1). Surprisingly, the degree of improved growth rate of the PR mutants did not correlate with their ability to form hyphae, indicating that the mechanisms of suppression were complex. The faster growing Class 1 mutant doubled at a nearly wild-type rate (1.5 h) but only 74% of the cells formed hyphae. In contrast, the Class 2, Class 3, and Class 3+ PR mutants grew slower than the Class 1 mutants but were more efficient at forming hyphae. For example, Class 3 mutants grew at a doubling time of 2.3 h yet 93% of the cells could form hyphae.

Whole genome sequencing of the diploid *C. albicans* strains identified distinct genetic changes in the four classes of PR mutants. Interestingly, although they were different, all four classes of mutants contained genetic changes that resulted in loss of expression of one copy of *BCY1*, which encodes the negative regulatory subunit of cAMP-dependent PKA kinase. This suggested that reduced expression of *BCY1* increased PKA activity resulting in improved growth in the absence of cAMP. Similar results reported that a *bcy1*Δ mutant can rescue growth of a *cyr1*Δ mutant in *S. cerevisiae*[33]. Class 1 mutants exhibited the simplest genetic change, in that the improved growth correlated with a premature stop codon in *BCY1* on chromosome 2 (Fig. 1c, Extended data Table 1, and Source data 1). In contrast, the Class 2, 3, and 3+ PR mutants all lacked part of the left arm of one copy of chromosome 2 that includes *BCY1*.

Western blot analysis showed that the Bcy1 protein levels were reduced by 50% in the PR mutants, confirming that altered gene dosage leads to reduced production of Bcy1 (Extended Data Fig. 1). The reduction in Bcy1 did not impact the levels of Tpk2, one of the PKA catalytic subunits in the PR mutants compared to the WT. Interestingly, *TPK2* was located in the middle of the chromosome 2, which was duplicated in Class 3+ PRs. However, none of the other PKA pathway components were located on chromosome 2. This supports the conclusion that the haploinsufficiency of *BCY1* bypassed the need for cAMP for growth and hyphal induction in *C. albicans*.

In the Class 2 and 3+ PRs, similar breakpoints were identified in the independently isolated strains indicating that a specific DNA sequence induced the chromosomal deletion. To better understand how the large deletions of 270 kb and 590 kb were generated in the Class 2, 3, and 3+ PRs, we inspected the genome sequences for matches to the *C. albicans* 23-bp telomere repeat sequence (CACCAAGAAGTTAGACATCCGTA)[34] , which was found at the deletion end points (Extended Data Table 1). Analysis of the breakpoint regions in chromosome 2 revealed 4 to 9-bp matches to telomere seed sequences. However, the long repeat sequence, which was previously reported to drive genome rearrangements, was not found near the deletion sites[35]. As described previously, this suggests that chromosome break healing by *de novo* telomere addition contributes to the genome plasticity in *C. albicans*[36,37,38], which enables it to adapt to adverse conditions or deleterious mutations such as *cyr1*Δ/Δ.

Gene mapping by CRISPR-Cas9 identified general transcription factors are involved in hyphal regulation.

To confirm that the genetic changes in chromosome 2 improved growth and hyphal induction in the PR mutants, transient expression of the CRISPR-Cas9 system[39,40] was utilized to recreate the loss of one copy of *BCY1* and the large deletions present in the Class 2, 3, and 3+ PR mutants. To facilitate large deletions, two single guide RNAs (sgRNAs) were used to target Cas9 to cut immediately adjacent to the deletion end points detected in the spontaneous PR mutants (Fig. 2a). Analysis of these *cyr1*Δ/Δ mutants that were created to be heterozygous *bcy1*Δ, 270kbΔ, and 590kbΔ in chromosome 2 showed that they recapitulated the phenotypes of the corresponding spontaneous mutants PR13, PR12, and PR18, respectively (Fig. 2b,c,d). This confirmed that haploinsufficiency of *BCY1* improved growth, and that haploinsufficiency of the genes in the 270 kb region in the left arm of chromosome 2 was sufficient to improve hyphal induction in the PR mutants.

Gene mapping strategies to identify the basis for the improved hyphal growth of the PR mutants showed that this effect is due to multiple genetic changes (Fig. 2e). In the first approach, smaller 90 kb sections of the 270 kb region were deleted from one copy of chromosome 2 in a *bcy1*Δ *cyr1*Δ/Δ strain. However, these mutants were not better at producing filamentous hyphal cells than the parental strain, suggesting that the improved hyphal morphogenesis is multigenic. Heterozygous deletion of a larger segment of chromosome 2 from 90kb→260kb made the cells more filamentous, which partially narrowed the key region. Smaller deletions designed to map the right end of the critical region of chromosome 2 showed that a 90kb→250kb deletion mutant did not exhibit better hyphal growth. Haploinsufficiency of the 10-kb region was therefore necessary to improve hyphal induction (although it was not sufficient on its own). Further mapping by deletion of the genes in this 10-kb region identified *SRB9* and *SPT5* to be involved in the improved hyphal phenotype (Extended Data Fig. 2). *SRB9* encodes a subunit of the RNA polymerase II mediator complex and *SPT5* encodes a transcription elongation factor complex subunit. Interestingly, the double heterozygous mutation of *SRB9* and *SPT5* in the 90kb→250kb deletion strain promoted improved hyphal growth, while the single heterozygous mutations of each gene did not. Thus, the gene mapping results indicate that global transcriptional regulators are important for creating a physiological state in the cell that is more conducive to induction of the switch of hyphal morphogenesis. This finding is consistent with the previous study[41] that protein components of Mediator, an important transcriptional coregulatory protein complex, were highly phosphorylated in *C. albicans* hyphae.

cAMP signaling is not necessary for transcriptional induction of hyphal regulated genes

Based in part on previous studies of *cyr1*Δ/Δ mutant strains, cAMP signaling was thought to be central to inducing the expression of a variety of genes, including virulence factors such as adhesins and hyphal-specific genes that promote filamentous growth[2,3,13,15,16]. To examine this role of cAMP signaling, we performed RNA sequencing (RNA-seq) analysis of the

WT and PR mutants before and after stimulation with the hyphal inducer GlcNAc (Fig. 3a and Source Data 2). Heatmap clustering and principal component analysis (PCA) of the normalized RNA-seq dataset revealed that WT and PRs showed similar patterns in transcriptomes, indicating that cAMP is not required to induce the broad range of hyphal genes (Fig. 3b and Supplementary Fig. 2). In contrast, the *cyr1*Δ/Δ mutant clustered separately due to its expected defect in regulating hyphal genes (Fig. 3b). Data for a subset of hyphal genes, as well as controls are shown in Fig. 3c. The transcriptomic profile of PR13 (*bcy1**/*BCY1 cyr1*Δ/Δ) was highly similar to the WT. However, PR12 (270kbΔ *cyr1*Δ/Δ) expressed a higher basal level of hyphal genes even in the absence of the hyphal inducer GlcNAc (Fig. 3c), which also correlates with a higher basal level of filamentous cell morphology (Fig. 1b). The PR12 transcriptome was also distinct as the levels of the genes in the 270-kb region were around 2-fold less than the WT level due to the haploinsufficiency (see Source Data 2). GlcNAc catabolic genes were highly expressed in all the strains tested, including *cyr1*Δ/Δ (Fig. 3c), which is consistent with previous studies showing that their regulation is cAMP independent[42,43]. Altogether, these data indicate that an appropriate basal level of PKA activity is needed for cells to respond transcriptionally to a hyphal inducer, rather than a requirement for stimulation of Cyr1 to produce cAMP.

Quantitative phosphoproteomics identified protein kinases required for normal hyphal growth

To better understand how the switch to hyphal morphogenesis is regulated, we compared protein production and phosphorylation during hyphal induction. WT and PR13 strains were treated with or without GlcNAc to form hyphae (Fig. 4a), and then a label-free mass spectrometry approach (LC-MS/MS) was used to detect 3,434 proteins and 17,580 phosphopeptides (Source Data 3). To differentiate experimental variances from biological alterations, we compared the replicate data of WT cells treated with GlcNAc from both the whole proteome and the phosphoproteome. The null comparisons of the biological replicates showed

194 high correlations (r > 0.9) (Fig. 4b). Efg1 was reported as a target of PKA and CDC28 kinases
195 and the genetic studies implicated that T179 and T206 positions were the phosphosites[17,32].
196 However, phosphoproteome data did not detect the previously reported phosphosites in
197 consistent with the reports of Willger et al.[41] and Cao et al.[44] (see Source Data 3). This
198 suggests that the phosphorylation mechanism of Efg1 is different from the previous models.
199 Interestingly, Efg1 was dephosphorylated during hyphal induction in the C-terminal prion-like
200 domain (PrLD), which supports the assembly of TF complexes by formation of phase-separated
201 condensates[45].

202 We next used gene set enrichment analysis[46] to infer the activity of specific protein
203 kinases. The algorithm was based on the levels of phosphorylated peptides containing amino
204 acid sequence motifs characteristic of the substrate specificity of known protein kinases (Fig.
205 4c). Strikingly, in contrast to the current models[2,3,5], this analysis revealed PKA activity was not
206 significantly different before and after hyphal induction in the WT or PR13 strains (Fig. 4d).
207 Furthermore, control studies showed that PKA subunit (Bcy1 and Tpk2) levels remained
208 constant during hyphal induction (Extended Data Fig. 1). Thus, there was no evidence to
209 support the stimulation of PKA in the PR mutants during hyphal induction. In contrast, Cdc28
210 kinase activity was increased during hyphal induction in the WT strain (Fig. 4d), consistent with
211 previous studies implicating this cyclin dependent kinase in hyphal regulation[25,26,32,47]. To
212 examine the role of Cdc28 further, we deleted the hyphal-induced cyclin *HGC1*. The *hgc1*Δ/Δ
213 mutation caused a stronger hyphal defect in the PR13 mutant compared to the WT control cells
214 (Extended Data Fig. 3a), indicating that PR13 cells are more reliant on cyclin-dependent activity
215 for hyphal induction than are the WT cells.

216 Interestingly, many of the Cdc28 phosphosites also contained a second motif indicating
217 they are targets for yeast casein kinase 1 (Yck2) (Fig. 4e,f,g). Recent studies in *C. albicans*
218 have characterized the role of Yck2 in modulating morphogenesis, virulence, fungal cell-wall
219 stress responses, and resistance to clinical antifungals[48-50]. Deletion of *YCK2* strongly affected

hyphal growth in both the WT and PR13 strains (Extended Data Fig. 3a). The *yck2*Δ/Δ cells displayed an elongated cell morphology, but did not switch to a true hyphal morphology in the presence of the hyphal inducers serum or GlcNAc. Interestingly, both kinases phosphorylated 11 sites in 8 genes and they are all thought to have a role in polarized growth (Extended Data Table 2). We created phospho-site mutations of *BNI1* and *MOB2* because they were required for normal hyphal growth[30,51]. However, phospho-mutation of the individual phosphorylation sites did not cause any hyphal defect, suggesting that it may require mutations of additional target proteins to cause a strong defect in hyphal morphogenesis (Extended Data Fig. 3b).

Hyphal stimulation induces translation of TFs that regulate morphological switching

The transcriptomic and proteomic data sets were examined to determine how the abundance of mRNAs and their corresponding proteins correlated during the switch to hyphal morphogenesis. There was a relatively weak correlation (Pearson correlation coefficient, r = 0.39) between mRNA and protein abundances in *C. albicans* (Fig. 5b). Typical Pearson correlation coefficients (r) for mammalian cells are about 0.6 and *S. cerevisiae* is about 0.7[52]. This indicated that *C. albicans* has dynamic post-transcriptional regulatory mechanisms. Since protein levels are a function of mRNA abundance, translation rate, and protein turnover (Fig. 5a), we approximated the translation rate with the protein/mRNA level ratio (this approximation neglects protein degradation, see Fig. 5c). Integration of RNA-seq and label-free LC-MS/MS data gave an opportunity to estimate the translation rate of 3267 genes (Source Data 4). The translation rate spanned over five orders of magnitude across genes (Fig. 5d). There was a negative correlation between mRNA abundance and translation rate, while there was a positive correlation between protein abundance and translation rate. Although it has been reported that 5' UTR length plays an important role in translation efficiency[53-55], there was no correlation between 5' UTR length and translation rate in our analysis.

We next examined whether the translation rate changed for TFs that are known to regulate hyphal morphogenesis. Strikingly, translation rates of some hyphal regulator TFs increased dramatically during hyphal growth while the mean translation rates of ribosomal proteins and total proteins were similar (Fig. 5e). However, mRNA levels of the hyphal regulator TFs did not change much compared to the translation rate (Fig. 5f). The Ume6, Sfl1, Brg1, Tec1, and Fkh2 proteins were not detected in the uninduced cells while their mRNA levels were similar to the median of total mRNAs (Source Data 4). Further work will be required to confirm whether these effects are due to translation or another mechanism, such as increased protein stability[56,57]. However, the results demonstrate that a post-transcriptional mechanism regulates key transcription factors that are important for hyphal morphogenesis.

DISCUSSION

The ability of *C. albicans* to switch between budding and hyphal morphologies contributes to virulence by promoting invasive growth, escape from immune cells, and biofilm formation[1-6]. The prevailing model has been that adenylyl cyclase acts as a master regulator by integrating signals from different hyphal inducers[3,5,9-11]. Although high levels of exogenous cAMP[12] or hyperactive *CYR1* mutants[58] can induce filamentous growth, the failure of *cyr1*Δ/Δ cells to form hyphae does not provide strong support for an essential role of adenylyl cyclase as this mutant displays abnormal physiological properties and grows slowly[12-14]. Furthermore, treatment of *cyr1*Δ/Δ cells with low levels of cAMP to improve their growth enabled them to be stimulated to form hyphae[12,14]. Isolation of *cyr1*Δ/Δ PR mutants provided strong proof that inducers including serum, GlcNAc, and alkaline pH can stimulate hyphae in the total absence of cAMP[14]. We therefore identified the underlying mechanisms for this by demonstrating that the improved growth of the PR mutants is due to mutation or deletion of one of the two copies of *BCY1*, which encodes the negative regulatory subunit of PKA (Fig.1 and Fig. 2). The lower level of Bcy1 in the PR mutants was confirmed by Western blot analysis (Extended Data Fig. 1)

and RNA-seq data (Fig. 3). Consistent with this, the PR mutants grew better and displayed a transcriptomic profile similar to WT cells. These results are also interesting in that genomic analysis revealed that the different classes of PR mutants showed distinct mechanisms for mutation of *BCY1* or deletion of parts of the left arm of chromosome 2 (Extended Data Table 1), which underscore how the plasticity of the *C. albicans* genome enables it to adapt to different kinds of stress from mutations or antifungal drugs[35,36,59,60].

Current models also predict that PKA phosphorylates the Efg1 TF to stimulate it to induce expression of hyphal genes[2,3,11,13,15,16]. However, we failed to detect phosphorylation of Efg1 in WT or PR13 cells, consistent with previous studies[41,44]. In spite of this, the PR mutants were not only able to form hyphae, but they also induced the expression of the expected set of hyphal associated genes that includes many virulence factors (Fig. 3c). A further limitation of the current models is that several studies now question the role of transcriptional induction in promoting hyphal growth. For example, the common core set of genes stimulated by a group of different hyphal inducers in *C. albicans* do not account for the transition to hyphal growth[19]. In addition, under certain conditions GlcNAc can stimulate hyphae without induction of hyphal-specific genes[20]. There also appears to be a lack of TF specificity, as some hyphal regulatory TFs can be bypassed under special conditions[21], such as altered expression of the Cak1 protein kinase[22] or the absence of a variant histone H3[23]. In addition, filamentous growth is induced by deletion of the global transcriptional repressor *TUP1*[61]. Consistent with this, we found that haploinsufficiency of two global transcriptional regulators, *SRB9* and *SPT5*, contributed to the improved filamentous growth of the Class 2 mutants (Extended Data Fig. 2). Altogether, these data suggest a new model that TFs are important for creating the proper physiological environment for cells to undergo hyphal growth, but that the target genes are not directly involved in promoting filamentous morphogenesis.

To identify new mechanisms that promote hyphal growth, we carried out a multi-omics comparison of WT and PR cells (Extended Data Fig. 4). The phosphoproteomics analysis

identified a role of the Cdc28 cyclin dependent kinase and the Yck2 casein kinase 1 (Fig. 4). In fact, a subset of 8 proteins was dually phosphorylated by these protein kinases, although mutation of the phosphosites in two of these proteins (Bni1 and Mob2) did not cause a significant phenotype, perhaps because there are redundant mechanisms that contribute to hyphal growth (Extended Data Table 2 and Extended Data Fig. 3). Interestingly, deletion of *HGC1*, the hyphal-induced cyclin subunit of Cdc28, caused stronger defects in PR13 than in WT cells, suggesting that Cdc28 activity is more important for cAMP-independent induction of hyphal morphogenesis. In addition, integrative analysis of transcriptomic and proteomic data revealed that a set of transcription factors that are important for hyphal induction are produced at higher levels relative to their mRNA levels after hyphal induction, suggesting that differential translation of these factors represents a novel mechanism that contributes to hyphal growth (Fig. 5). Altogether, theses results indicate that future studies on hyphal signaling should focus on the roles that post-transcriptional and post-translational regulation play in promoting the changes in the morphogenesis pathways that mediate highly polarized hyphal growth.

METHODS

Strains, culture conditions, and hyphal analysis

The *C. albicans* strains used in this study are described in Supplementary Table 1. *C. albicans* strains were streaked fresh from storage at -80°C onto YPD (1% yeast extract, 2% peptone, 2% glucose) agar plates and then grown in rich YPD medium or in complete synthetic medium (SC) made with yeast nitrogen base, select amino acids, and uridine. *C. albicans* transformants were selected on YPD plus 200 µg/ml nourseothricin (NAT; Gold Biotechnology). NAT-sensitive derivatives of cells carrying the SAT flipper were then obtained by growing cells on maltose agar medium (1% yeast extract, 2% peptone, 2% maltose) for 2 days, and then several colonies were spread on YPD plates containing 25 µg/ml of NAT and incubated for 2

days at 30°C[40]. NAT-sensitive cells formed smaller colonies than NAT-resistant parental strains.

Strain doubling times were determined from growth curves in YPD at 30°C. Fresh overnight cultures were diluted to a final concentration of ~0.05 OD_{660} in 5 ml YPD in test tubes and then incubated at 30°C on a tube roller. The OD_{660} was measured hourly for ~8 hours until OD_{660} was >1.0. The reported doubling times are the averages of two biological replicates each performed in duplicate.

To analyze hyphal formation in liquid media, cells were grown overnight at 30°C in YPD, and then inoculated into SC + 50 mM glucose + 10% bovine calf serum, or SC + 50 mM GlcNAc medium. Samples were then incubated at 37°C for the indicated time and then images were captured using a Zeiss Axio Observer 7 inverted microscope equipped with a 40× objective differential interference contrast (DIC) optics and a Zeiss AxioCam 702 digital camera. *C. albicans* cells were grown and induced to make hyphae in the same conditions for transcriptome, proteome, and phosphoproteome analyses. *C. albicans* cells were grown at 37°C to log phase (OD_{660} of 0.2 ~ 0.4) in SC + 50 mM galactose medium. For hyphal induction, pre-warmed 0.5 M GlcNAc solution was added into the culture to make final concentration of 50 mM and the cultures were incubated for 2 h at 37°C. Cells were harvested by centrifugation, washed three times with ice-cold ultrapure water, snap frozen on dry ice, and stored at −80°C. Replicate experiments were conducted independently on different days.

Strain construction

Deletion mutant strains were created using transient expression of CRISPR-Cas9 to facilitate the genome engineering and limit transformation-induced genomic changes in *C. albicans*[39,62]. The methods were performed essentially as described previously[39,63]. Briefly, *CaCAS9* expression and sgRNA expression cassettes were co-transformed into cells along with a repair template. The *CaCAS9* gene was codon optimized for expression in *C. albicans*[64]. The

CaCAS9 expression cassette was PCR amplified from the plasmid pV1093, which was a kind gift from Dr. Valmik Vyas[64]. The sgRNA expression cassette was constructed through single-joint PCR from the plasmid pV1093[39]. We used 20-bp target sequences of the sgRNA, as reported previously by Vyas et al.[65] to target Cas9 to make a DNA double strand break at the target site (Supplementary Methods). When deleting large regions of chromosome 2 for gene mapping, two sgRNAs were used to cut each side of the target region. Repair templates were synthesized using the plasmid pGR-NAT as a template, which contains the *SAT1* flipper cassette[40]. The primers were designed to include 60 to 80 bases of homology to the sequences upstream or downstream from the target region. The oligonucleotides used in this study are listed in Supplementary Methods. PCR was conducted with Ex Taq (TaKaRa Bio, Inc.) in accordance with the CRISPR protocol (Supplementary Methods).

BNI1 and *MOB2* were mutated to prevent phosphorylation at the indicated sites using the CRISPR-Cas9 method developed by Vyas et al.[64] The 20-bp target sequence of sgRNA was cloned into pV1093 and correct clones were verified by DNA sequencing. The CRISPR expression plasmids were linearized by digestion with *Kpn1* and *Sac1* before transformation for efficient targeting to the *ENO1* locus. Repair templates were generated with two 60-base oligonucleotides containing a 20-base overlap at their 3′ ends centered on the desired site to mutate a phosphorylation site. The repair templates were constructed by PCR primer extension to contain the desired phospho-site mutation as well as a unique restriction site facilitate identification of appropriate transformants.

PCR products and linearized plasmids for transformation were purified and concentrated using a GeneJET PCR purification kit (Thermo Fisher Scientific, Inc.). Electroporation was used to introduce the DNA into cells following a previously described method[66]. An electrocompetent cell suspension (40 μl) was added to aliquoted DNA, placed in 0.1 cm-gap electroporation cuvettes, and electroporated on a Bio-Rad Gene Pulser at 1.5 kV. One milliliter of 0.5× YPD

containing 1 M sorbitol was added immediately to the cuvette, and then the cell mixture was incubated for 3 h at 30°C before plating onto YPD + 200 µg/ml NAT agar. Nat^r transformants were selected, and PCR genotyping of the transformants verified the genome editing.

Genome analysis

A 1 µg aliquot of the genomic DNA was prepared using the Illumina TruSeq PCR-free DNA HT sample preparation kit with 450 bp insert size. Intact genomic DNA was sheared using the Covaris sonicator (adaptive focused acoustics), followed by end-repair and bead-based size selection of fragmented molecules. The size selected fragments then had adenines added to the 3' ends of the DNA, Illumina sequence adaptors ligated onto the fragments, followed by PCR amplification and final library QC. A majority of the steps in this process were performed on the Caliper SciClone NGSx workstation (PerkinElmer), a robotics system developed and validated for automated library preparation. The library QC included a measurement of the average size of library fragments using the Agilent BioAnalyzer, estimation of the total concentration of DNA by PicoGreen (ThermoFisher), and a measurement of the yield and efficiency of the adaptor ligation process with a quantitative PCR assay (Kapa) using primers specific to the adaptor sequence. Sequencing was performed on the Illumina MiSeq instrument at 2 × 150 bp read length.

Reads were first trimmed and quality filtered using skewer v0.1.127[67] with the following parameters (-q 20 -Q 20 -l 50 -n yes). Reads were then mapped to the *C. albicans* SC5314 genome (Assembly 21)[68] using BWA mem v0.7.15[69]. Duplicates were marked and read groups added using the PICARD MarkDuplicates and AddOrReplaceReadGroups programs. Indels were realigned using GATK 3.3 RealignerTargerCreator and IndelRealigner[70]. A set of high-quality variants with variant scores of >100 were identified using GATK 3.3 HaplotypeCaller on all samples simultaneously. These were then set as known sites when performing base quality recalibration using GATK 3.3 PrintReads, AnalyzeCovariates and BaseRecalibrator to produce

finished bam files. GATK 3.3 HaplotypeCaller was then used again to call variants across samples to produce a final vcf file. snpEff 4.2 was used to annotate variants using a custom built database based on the *C. albicans* SC5314 genome (Assembly 21)[68].

Transcriptome analysis

RNA extraction, library preparations, and sequencing reactions were conducted at GENEWIZ, LLC. (South Plainfield, NJ, USA). Total RNA was extracted from fresh frozen cell pellets using Qiagen RNeasy Plus Universal mini kit following manufacturer's instruction (Qiagen). Extracted RNA samples were quantified using Qubit 2.0 Fluorometer (Life Technologies) and RNA integrity was checked using Agilent TapeStation 4200 (Agilent Technologies). RNA sequencing libraries were prepared using the NEBNext Ultra II RNA Library Prep Kit for Illumina following manufacturer's instructions (NEB). Briefly, mRNAs were first enriched with Oligo(dT) beads. Enriched mRNAs were fragmented for 15 min at 94°C. First strand and second strand cDNAs were subsequently synthesized. cDNA fragments were end repaired and adenylated at 3' ends, and universal adapters were ligated to cDNA fragments, followed by index addition and library enrichment by limited-cycle PCR. The sequencing libraries were validated on the Agilent TapeStation (Agilent Technologies), and quantified by using Qubit 2.0 Fluorometer (Invitrogen) as well as by quantitative PCR (KAPA Biosystems). The sequencing libraries were pooled and clustered on 1 lane of a flowcell. After clustering, the flowcell was loaded on the Illumina HiSeq instrument (4000 or equivalent) according to manufacturer's instructions. The samples were sequenced using a 2 $\times$ 150bp Paired End (PE) configuration. Image analysis and base calling were conducted by the HiSeq Control Software (HCS). Raw sequence data (.bcl files) generated from Illumina HiSeq was converted into fastq files and de-multiplexed using Illumina's bcl2fastq 2.17 software. One mismatch was allowed for index sequence identification.

We performed quality profiling, adapter trimming, read filtering, and base correction for raw data using an all-in-one FASTQ preprocessor, *fastp*[71]. The high-quality paired-end reads were mapped to the *C. albicans* SC5314 genome (Assembly 22)[72] using HISAT2[73]. StringTie[74] was used to assemble the read alignments obtained in the previous step and estimate transcript abundances. Absolute mRNA abundance was expressed as fragments per kilobase of transcript per million mapped reads (FPKM). Differential expression analyses were conducted using DESeq2[75] package from Bioconductor[76] on R.

Western blotting

The fresh frozen cell pellets were lysed using the same volume of 2× SDS lysis buffer (5% SDS, 20% glycerol, 125 mM Tris-HCl, pH 6.8) supplemented with cOmplete EDTA-free protease inhibitor cocktail (Roche), 10 mM activated sodium orthovanadate, 2.5 mM sodium pyrophosphate, 1 mM β-glycerophosphate, 1% phosphatase inhibitor cocktail 2 (Millipore-Sigma), 1% phosphatase inhibitor cocktail 3 (Millipore-Sigma). Zirconia beads were added, and the cells were mechanically disrupted by 3 rounds of 1-min bead beating and 1-min cooling on ice. The samples were boiled at 95°C for 5 min. After centrifugation at 14,000 rpm for 5 min at 4°C to remove cellular debris, the supernatant was transferred to a new tube and this step was repeated. The protein concentration was measured using a BCA protein assay kit (Thermo Fisher Scientific). 2-Mercaptoethanol and bromophenol blue were added to 5% and 0.002% final concentration, respectively. The samples were boiled at 95°C for 5 min. Equal amounts of proteins were resolved by SDS-PAGE using the Mini-PROTEAN Tetra Cell system (Bio-Rad) and Tris/glycine/SDS running buffer. Subsequently, proteins were transferred to a nitrocellulose membrane (Amersham) using a semi-dry transfer apparatus. The membranes were blocked with 5% nonfat dry milk in TBS-T buffer (20 mM Tris-HCl, pH 7.6, 150 mM NaCl, 0.2% Tween-20) for 30 min and probed with CaBcy1 rabbit polyclonal antibody (GenScript) or CaTpk2 rabbit polyclonal antibody (GenScript), at 1:1,000 dilution in 5% nonfat dry milk in TBS-T buffer plus

0.5% sodium azide for 2 hours at room temperature. The membranes were then washed three times with TBS-T and incubated with an IRDye 800CW goat anti-rabbit IgG secondary antibody (LI-COR Biosciences) diluted at 1:10,000 in TBS-T. The membranes were washed three times with TBS-T, stored in TBS buffer, and visualized by scanning with an Odyssey CLx infrared imaging system (LI-COR Biosciences). For Coomassie stained gels, SDS-PAGE gels were performed as described and then stained in Coomassie Brilliant Blue solution (0.1% Coomassie R-250, 50% methanol, 40% water, 10% glacial acetic acid) overnight. Gels were incubated for 6 h in destaining solution (50% water, 40% methanol, 10% glacial acetic acid), rinsed with water, and analyzed by scanning with an Odyssey CLx infrared imaging system (LI-COR Biosciences). Resulting images were analyzed and quantified using ImageStudio software (LI-COR Biosciences).

Preparation of samples for mass spectrometry

The frozen cell pellet samples were processed by Tymora Analytical Operations (West Lafayette, IN). For lysis, 200 µL of lysis buffer (8M urea in 50mM Tris-Cl pH 7.5, supplemented with phosphatase inhibitor cocktail 3 [Millipore-Sigma]) was added to each of the pellets and pipetted up and down several time to lyse a portion of the pellet. The samples were incubated for 10 min at 37°C, pulse-sonicated several times with a sonicator probe, and incubated again for 10 min at 37°C. The lysed samples were then centrifuged at 16,000 g for 10 min to remove debris and the supernatant portions collected. BCA assay was carried out to calculate the protein concentration and all samples were normalized by protein amount to 200 µg each. Then 5 mM dithiothreitol was added and the proteins were incubated at 37°C for 15 min to reduce the cysteine residues, and then alkylated by incubation in 15 mM iodoacetamide at room temperature for 45 min in the dark. The samples were diluted 3-fold with 50 mM triethylammonium bicarbonate and digested with Lys-C (Wako) at 1:100 (w/w) enzyme-to-protein ratio for 3 h at 37°C. The samples were further diluted 3-fold with 50 mM

triethylammonium bicarbonate and trypsin was added to a final 1:50 (w/w) enzyme-to-protein ratio for overnight digestion at 37°C. After digestion, the samples were acidified with trifluoroacetic acid to a pH < 3 and desalted using Top-Tip C18 tips (Glygen) according to manufacturer's instructions. A 1% portion of each sample was used for direct proteomics analysis and the remainder of each sample was used for phosphopeptide enrichment. The samples were dried completely in a vacuum centrifuge and stored at -80°C. The 99% portion of each sample was used for phosphopeptides enrichment using PolyMAC Phosphopeptide Enrichment Kit (Tymora Analytical) according to the manufacturer's instructions.

Liquid chromatography with tandem mass spectrometry (LC-MS/MS) analysis

The full phosphopeptide sample and 1 µg of the peptide sample each was dissolved in 10.5 µl of 0.05% trifluoroacetic acid with 3% (v/v) acetonitrile containing spiked-in indexed Retention Time Standard artificially synthetized peptides (Biognosys). The spiked-in 11-peptides standard mixture was used to account for any variation in retention times and to normalize abundance levels among samples. Ten microliters of each sample was injected into an Ultimate 3000 nano UHPLC system (Thermo Fisher Scientific). Peptides were captured on a 2-cm Acclaim PepMap trap column and separated on a heated 50-cm Acclaim PepMap column (Thermo Fisher Scientific) containing C18 resin. The mobile phase buffer consisted of 0.1% formic acid in ultrapure water (buffer A) with an eluting buffer of 0.1% formic acid in 80% (v/v) acetonitrile (buffer B) run with a linear 90-min gradient of 6–30% buffer B at flow rate of 300 nL/min. The UHPLC was coupled online with a Q-Exactive HF-X mass spectrometer (Thermo Fisher Scientific). The mass spectrometer was operated in the data-dependent mode, in which a full-scan MS (from m/z 375 to 1,500 with the resolution of 60,000) was followed by MS/MS of the 15 most intense ions (30,000 resolution; normalized collision energy - 28%; automatic gain control target [AGC] - 2E4, maximum injection time - 200 ms; 60 sec exclusion).

LC-MS data processing

The raw files were searched directly against the *C. albicans* database updated in 2019 with no redundant entries, using Byonic (Protein Metrics) and Sequest search engines loaded into Proteome Discoverer 2.3 software (Thermo Fisher Scientific). MS1 precursor mass tolerance was set at 10 ppm, and MS2 tolerance was set at 20ppm. Search criteria included a static carbamidomethylation of cysteines (+57.0214 Da), and variable modifications of phosphorylation of S, T and Y residues (+79.996 Da), oxidation (+15.9949 Da) on methionine residues and acetylation (+42.011 Da) at N terminus of proteins. Search was performed with full trypsin/P digestion and allowed a maximum of two missed cleavages on the peptides analyzed from the sequence database. The false-discovery rates of proteins and peptides were set at 0.01. All protein and peptide identifications were grouped and any redundant entries were removed. Only unique peptides and unique master proteins were reported.

Label-free quantitation analysis

All data were quantified using the label-free quantitation node of Precursor Ions Quantifier through the Proteome Discoverer v2.3 (Thermo Fisher Scientific). For the quantification of proteomic and phosphoproteomic data, the intensities of peptides were extracted with initial precursor mass tolerance set at 10 ppm, minimum number of isotope peaks as 2, maximum ΔRT of isotope pattern multiplets – 0.2 min, PSM confidence FDR of 0.01, with hypothesis test of ANOVA, maximum RT shift of 5 min, pairwise ratio-based ratio calculation, and 100 as the maximum allowed fold change. The abundance levels of all peptides/phosphopeptides and proteins/phosphoproteins were normalized to the spiked-in internal iRT standard. For calculations of fold-change between the groups of proteins, total protein or phosphoprotein abundance values were added together and the ratios of these sums were used to compare proteins within different samples. When the protein abundance could not be determined, pseudo value (1) was given for logarithm.

Phosphoproteomic data analysis

Phosphopeptide abundance values were normalized by protein abundance values[77,78]. Fifteen-amino acid sequences around the phosphorylation site was extracted from the phosphoproteome using a custom Microsoft Excel spreadsheet. rmotifx[79] package on R was used to find overrepresented patterns from the 15-aa sequence set. Potential substrates of 6 kinases (Cdc28, PKA, Yck2, MAPK, Cbk1, and Gin4) were predicted from the phosphoproteome based on their consensus phosphorylation motifs. The following consensus motifs were retrieved from the Scansite 4.0 database[80]; Cdc28 ([S/T]-P-x-K/R); PKA (R/K-R/K-x-[S/T]); Yck2 ([S/T]-x-x-[S/T]); MAPK (P-x-[S/T]-P); Cbk1 (H-x-K/R-x-x-[S/T] or H-x-x-K/R-x-[S/T]); Gin4 (R-S-x-[S/T]). We next utilized a gene set enrichment analysis algorithm, GSEA[46,81], to infer kinase activity based on the substrate phosphorylation levels from the phosphoproteome.

Data availability

Requests for materials should be addressed to the corresponding author. The datasets generated in this study can be found under NCBI BioProject PRJNA706677, including whole-genome sequence data and RNA-seq data. Source data are provided with this paper.

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AUTHOR CONTRIBUTIONS

K.M. and J.B.K conceived the study. K.M., T.F.J., H.S., K.R.V., J.D.H., and J.B.K. investigated the study. K.M., K.R.V., and J.D.H. formally analyzed the study. K.M. and J.B.K. wrote the original draft of the manuscript. K.M., T.F.J., H.S., K.R.V., J.D.H., and J.B.K reviewed and edited the manuscript. J.B.K supervised the study.

COMPETING INTERESTS STATEMENT

The authors declare no competing interests.

767 **Table 1. Phenotypic and genetic variations of *cyr1*Δ/Δ pseudorevertants (PRs)**
768

Strain	PR class	Doubling time (h)[†]	Filamentation (%)[‡]	Short genotype[§]
WT		1.4 ± 0.07	98 ± 2.3	Prototrophic wild type strain
*cyr1*Δ/Δ		3.4 ± 0.36[b]	0[b]	*cyr1*Δ/Δ (parental strain)
PR13, PR19	Class 1	1.5 ± 0.19	74 ± 4.4[b]	*bcy1*/BCY1 cyr1*Δ/Δ
PR12, PR14	Class 2	1.8 ± 0.09[a]	93 ± 2.3	Monosomy of ~276 kb of Chr2L; *cyr1*Δ/Δ
PR18	Class 3	2.3 ± 0.06[b]	93 ± 4.2	Monosomy of ~590 kb of Chr2L; *cyr1*Δ/Δ
PR16	Class 3+	2.4 ± 0.18[b]	82 ± 16.4[a]	Monosomy of ~557 kb of Chr2L; trisomy of ~1.3 Mb of Chr2; *cyr1*Δ/Δ

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770 [†] Doubling times were measured in liquid YPD medium at 30°C. Shown is the mean ± SD of 4 independent experiments.

771 [‡] The percent of filamentous cells was measured 3 h after growth in GlcNAc medium at 37°C. Shown is the mean ± SD of at least 3

772 independent experiments with at least 100 cells counted for each condition.

773 [†‡] The p-value was calculated using one-way ANOVA with Dunnett's multiple comparisons test comparing the strains with the WT

774 control; [a] $p < 0.01$, [b] $p < 0.0001$.

775 [§]An asterisk indicates a nonsense mutation. Chr2L, left arm of chromosome 2.

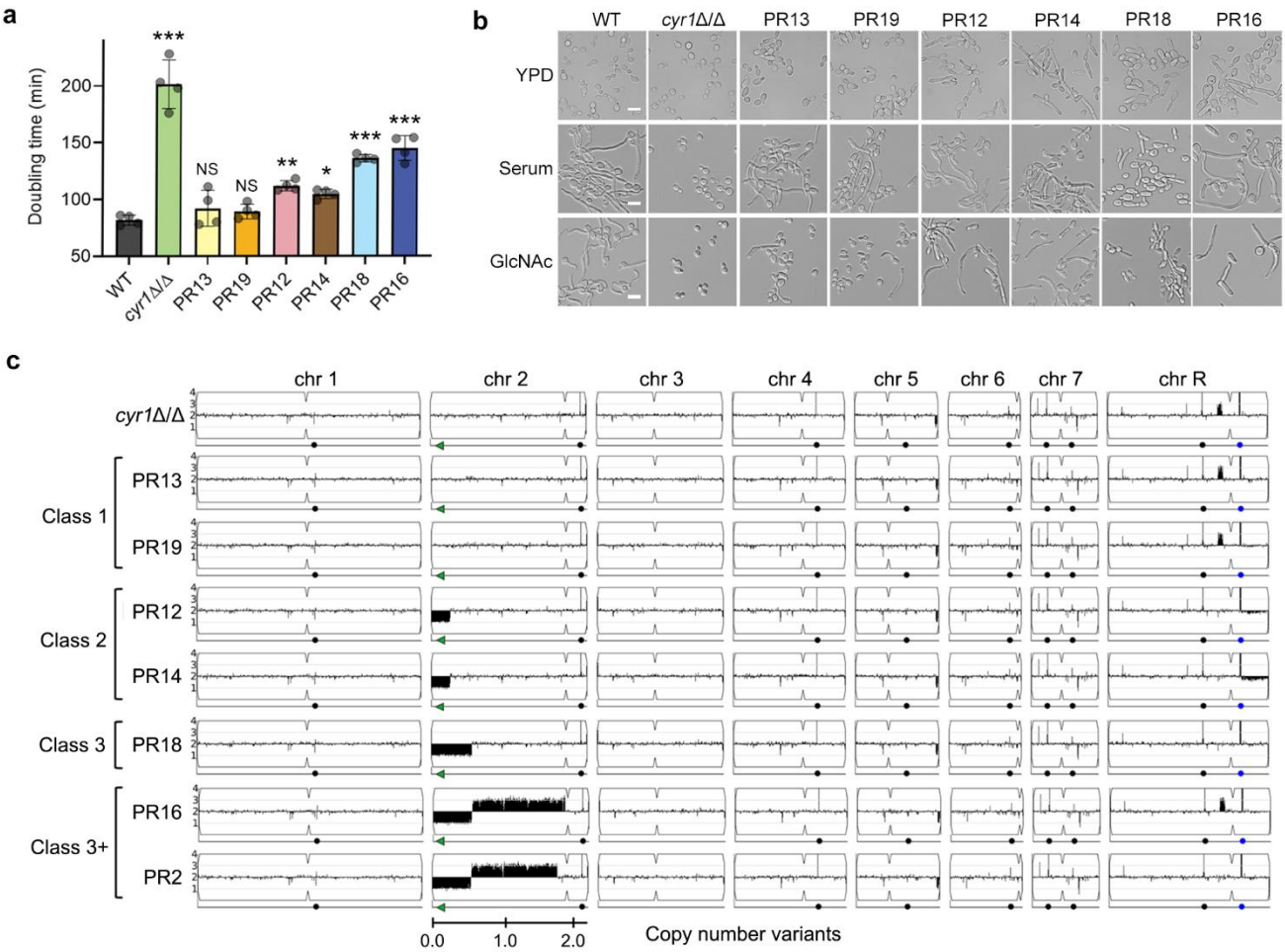


Fig. 1. Genetic changes in chromosome 2 bypassed the need for cAMP to improve growth and hyphal induction in *cyr1*Δ/Δ PR mutants.

a, Doubling times were measured in liquid YPD medium at 30°C. Shown is the mean ± SD (standard deviation) of 4 independent experiments. Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparisons test comparing the strains with the wild-type control (WT); ^{NS} $p > 0.05$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

b, The strains indicated at the top were grown in the liquid medium indicated on the left, and then hyphal induction was assessed microscopically. Cells were grown in liquid medium containing 15% serum or 50 mM N-acetylglucosamine (GlcNAc) to induce hyphal growth. Cells were incubated at 37°C for 3 h and then photographed. Scale bar, 10 μm.

c, Copy number variation analysis based upon read depth across the genome. Copy number estimates scaled to genome ploidy (Y-axis) and chromosome location (X-axis) were plotted using YMAP[82]. Numbers and symbols below chromosomes indicate chromosomal position (Mb), *BCY1* gene (green arrows), centromere locus (indentations in the chromosome cartoon), major repeat sequence position (black circles), and rDNA locus (blue circles, ChrR).

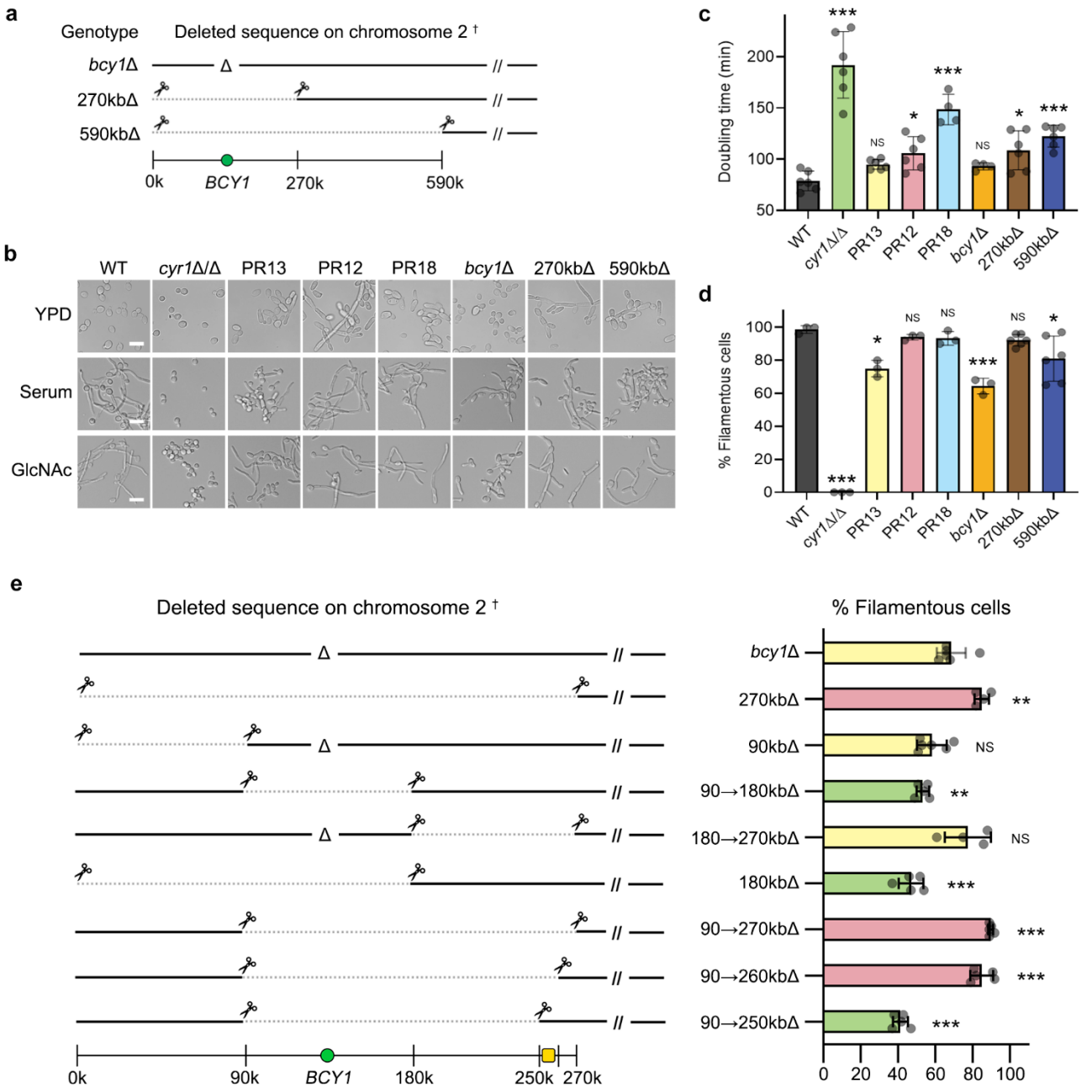


Fig. 2. Gene mapping by CRISPR-Cas9 demonstrates that haploinsufficiency of genes in chromosome 2 improved hyphal induction in *cyr1*Δ/Δ PR mutants.

a, A schematic diagram showing deleted sequences on chromosome 2.

b, The strains indicated at the top were grown in the liquid medium indicated on the left, and then hyphal induction was assessed microscopically. Cells were grown in liquid medium containing 15%

serum or 50 mM GlcNAc to induce hyphal growth at 37°C for 3 h and then photographed. Scale bar, 10 μm.

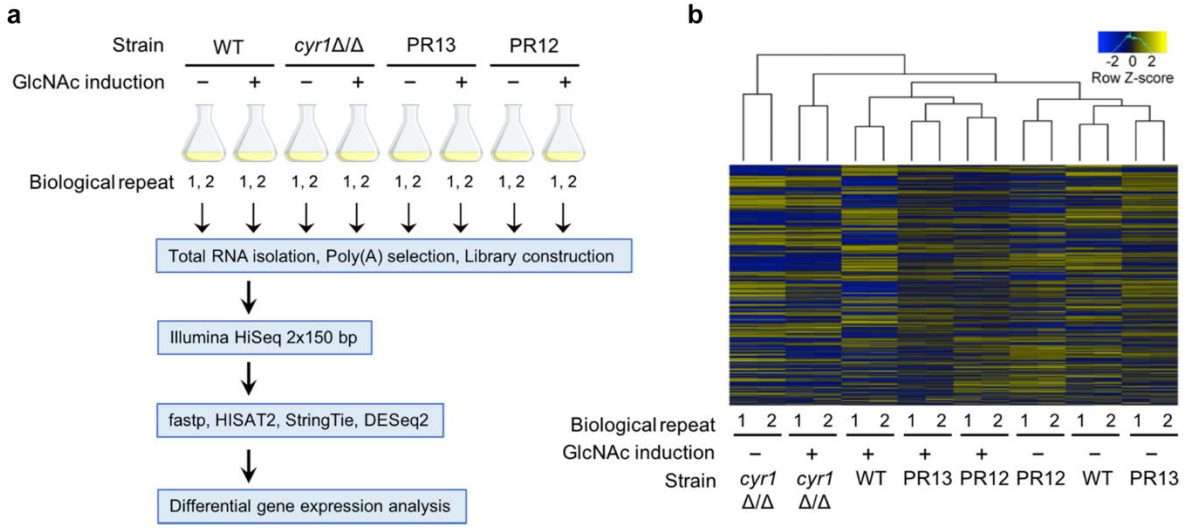
c, Doubling times were measured in liquid YPD medium at 30°C. Shown is the mean ± SD of 6 independent experiments.

d, Graph indicating the percent of filamentous cells after growth in GlcNAc medium described in panel **b**. Shown is the mean ± SD of at least 3 independent experiments with at least 100 cells counted for each condition.

e, Gene mapping by CRISPR-Cas9 identified a 10-kb region (yellow square) that is involved in the filamentous phenotype. The left panel shows deleted sequences on chromosome 2. The right panel shows the percent of filamentous cells in liquid GlcNAc medium at 37°C; green, weak hyphal induction; yellow, intermediate hyphal induction; pink, strong hyphal induction.

a,**e**, † Note that deletions are heterozygous; the cells retain a wild type version of chromosome 2. Numbers and symbols indicate gene deletion (Δ), CRISPR cut site (scissors), large genomic deletion (dotted line), *BCY1* gene (green circles), and chromosomal position (kb).

c,**d**,**e** Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparisons test comparing the strains with the WT or parental strain; ^{NS} $p > 0.05$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



c

GlcNAc	WT −	WT +	cyr1Δ/Δ −	cyr1Δ/Δ +	PR13 −	PR13 +	PR12 −	PR12 +	
NAG1	0.0	5.8	-0.4	5.6	-0.3	5.8	0.2	5.6	GlcNAc catabolic genes
NGT1	0.0	5.6	-0.3	5.9	0.1	6.1	0.3	5.3	
DAC1	0.0	5.5	-0.2	5.4	-0.1	5.4	0.3	5.2	
HXK1	0.0	4.4	0.2	4.4	-0.2	4.3	-0.3	4.1	
ECE1	0.0	4.9	-4.9	-4.7	0.1	4.5	2.9	4.8	Hyphae-specific genes
HWP1	0.0	3.2	-5.8	-5.1	0.2	3.4	3.0	4.2	
HYR1	0.0	2.7	-1.9	-3.0	-0.8	2.0	2.0	2.5	
ALS3	0.0	1.7	-2.0	-1.8	-0.6	0.9	-0.1	1.3	
HGC1	0.0	1.6	-0.1	0.2	1.0	1.8	0.4	1.6	
UME6	0.0	1.4	-4.4	-5.0	-1.2	0.6	-0.4	0.6	Hyphal regulator transcription factors
BRG1	0.0	1.1	0.3	-0.2	0.9	0.6	0.6	1.1	
BCR1	0.0	0.4	0.7	1.0	0.2	0.6	-0.5	0.2	
EFG1	0.0	0.2	0.3	-0.2	0.1	0.2	-0.4	-0.2	
NDT80	0.0	-0.1	-0.5	-0.4	0.1	-0.3	-1.4	-1.1	
CYR1	0.0	0.2	-10.2	-9.4	-16.3	-12.3	-11.7	-9.9	cAMP-PKA pathway genes
BCY1	0.0	0.1	0.5	0.3	-0.2	-0.4	-1.1	-0.9	
TPK1	0.0	-0.2	-0.6	-0.5	-0.1	-0.2	-0.1	-0.1	
TPK2	0.0	-0.3	1.2	0.9	0.6	0.3	0.2	0.3	
ACT1	0.0	0.3	0.2	0.2	0.1	0.2	-0.2	0.2	Housekeeping genes
TEF1	0.0	-0.2	-0.2	-0.3	0.0	-0.3	-0.5	-0.5	

Fig. 3. cAMP signaling is not necessary in transcriptional regulation of the genes during hyphal induction.

a, Experimental scheme of transcriptomic analysis. Cells were grown at 37°C in liquid galactose medium and then 50 mM GlcNAc was added for 2 h to induce hyphae.

b, Cluster analysis of differentially expressed genes (DEGs).

c, Summary of differential expression analysis. The numbers in colored boxes are $\log_2$ difference of transcript levels compared to the wild-type −GlcNAc condition. Grey boxes indicate the difference is not significantly different (adjusted $p > 0.1$).

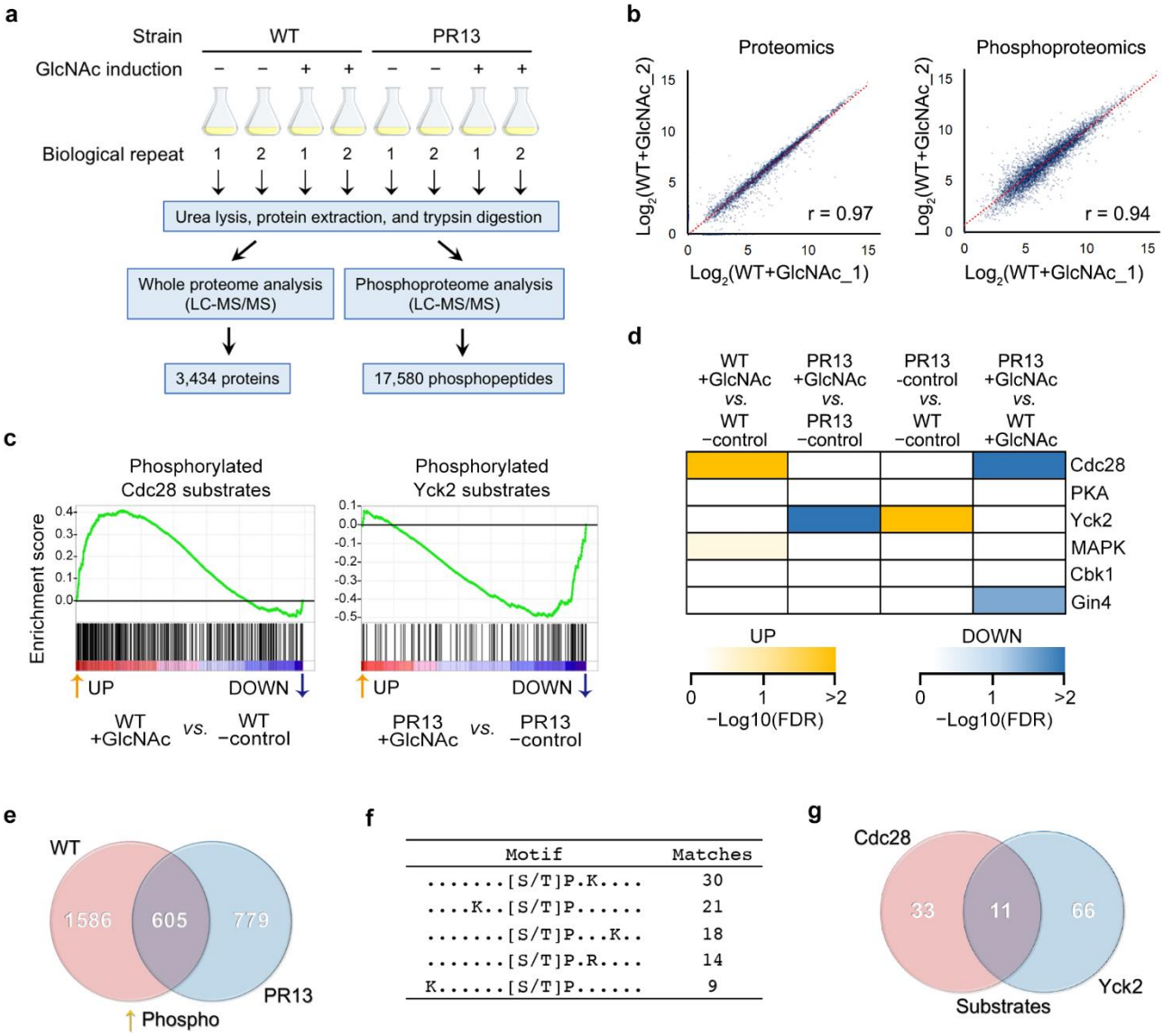


Fig. 4. Quantitative phosphoproteomics detected activity of two key kinases in hyphal induction.

a, Experimental scheme of parallel proteomic and phosphoproteomic analyses. Cells were grown at 37°C in liquid galactose medium and then 50 mM GlcNAc was added for 2 h to induce hyphae. For phosphorylation analysis, phosphopeptides were enriched by polymer-based metal-ion affinity capture (PolyMAC).

b, Representative null comparisons of the biological replicates show high reproducibility. We compared the replicate data of WT+GlcNAc_1 and WT+GlcNAc_2 from both whole proteome and phosphoproteome.

c, Representative results of kinase-substrate enrichment analysis. Gene set enrichment analysis (GSEA) algorithm[46] was used to identify significantly enriched or depleted groups of phosphorylated substrates.

d, The color-coded diagram illustrates changes of the selected kinase activities indicated by the scale bar at the bottom (< 25% false discovery rate [FDR]). Kinase activity inference was based on the collective phosphorylation changes of their identified substrates.

e, Venn diagrams of phosphopeptides upregulated during hyphal induction ($\log_2$ fold change > 0.5). Note that 605 phosphopeptides were upregulated in both WT and PR13 strains.

f, Overrepresented motifs were extracted from the 605 phosphopeptides, using the motif-x algorithm[79] ($p < 10^{-6}$). 44 phosphopeptides had the Cdc28 consensus motif ([S/T]-P-x-K/R) indicating they were potential substrates.

g, Venn diagrams of the upregulated Cdc28 substrates ([S/T]-P-x-K/R) or Yck2 substrates (S/T-x-x-[S/T]). 11 phosphopeptides were potential substrates of both Cdc28 and Yck2 kinases.

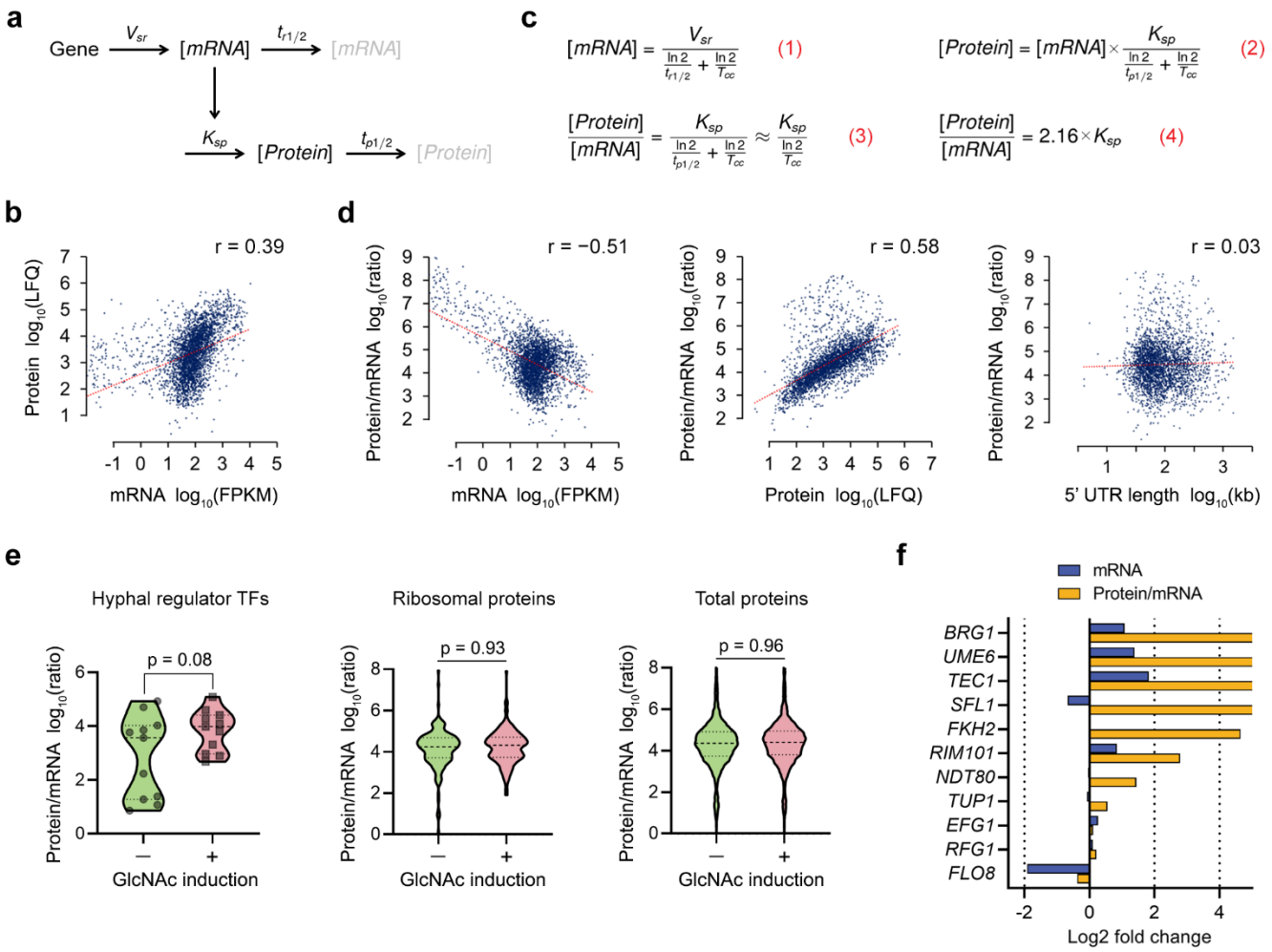


Fig. 5. Integrated transcriptomic and proteomic analyses indicate that hyphal stimulation induces translation of hyphal regulator TFs.

a, A basic gene expression model with key parameters (adopted from REF.[52,83]). The mRNA is transcribed with rate V_{sr} and degraded with a half-life represented by $t_{r1/2}$. The protein is translated proportionally to the mRNA abundance with the rate constant K_{sp} and degraded with a half-life of $t_{p1/2}$. **b**, An across-gene correlation analysis comparing estimates of absolute mRNA abundance (expressed in fragments per kilobase of transcript per million mapped reads (FPKM)) to protein abundance (expressed as label free quantitation (LFQ)) in exponentially growing WT cells. r, Pearson correlation coefficient.

c, Mathematical expression of mRNA (Equation 1) and protein abundances (Equation 2) as a function of key gene expression parameters, including cell doubling time T_{cc}, as detailed in REF.[83]. Rearranging Equation 2 yields the dependency of protein-mRNA abundance ratio on the translation rate constant K_{sp}, cell doubling time T_{cc}, and protein half-life $t_{p1/2}$ (Equation 3). We neglected protein degradation assuming that protein replacement is generally driven by dilution due to cell division in exponentially growing *C. albicans* cells ($t_{p1/2} >> T_{cc}$). Substituting the cell doubling time (T_{cc} = 1.5 h in *C. albicans*) yields Equation 4. Therefore, we can approximate the translation rate with the protein-to-mRNA level ratio.

d, Across-gene correlation analyses comparing protein-to-mRNA ratio versus mRNA abundance, protein abundance, and 5' UTR length (from left to right). r, Pearson correlation coefficient.

e, Protein-to-mRNA ratios of 11 selected hyphal regulator transcription factors (TFs) during GlcNAc induction. The protein-to-mRNA ratios of the 5 hyphal regulators were two orders of magnitude lower than the median in −GlcNAc control, indicating their translation rate was very low before hyphal induction. The p-value was calculated using two-sided unpaired t-test (hyphal regulator TFs) and z-test (ribosomal proteins and total proteins).

f, The relative change in protein-to-mRNA ratio for the selected 11 hyphal regulators is shown in yellow, relative changes in mRNA expression are shown in blue. The protein-to-mRNA ratio of *UME6*, *SFL1*, *BRG1*, *TEC1*, and *FKH2* increased dramatically (log2 fold change > 4) during hyphal induction while mRNA levels did not.

Extended Data Table 1. Genome analysis summary

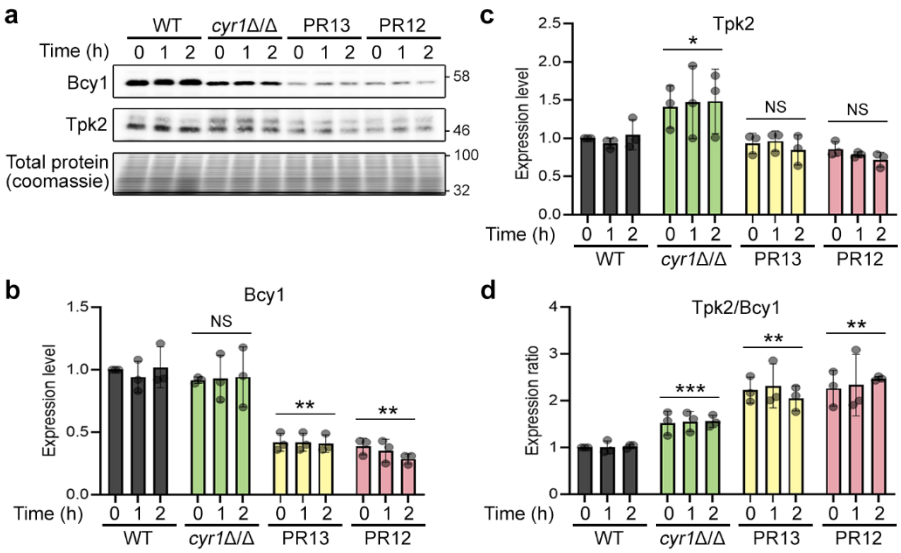
Strain	PR Class	Short genotype	*de novo* telomere addition†	Telomere seed sequence
*cyr1*Δ/Δ	-	*cyr1*Δ/Δ	-	-
PR13	1	*bcy1-Q82*/BCY1 cyr1*Δ/Δ	-	-
PR19	1	*bcy1-E19*/BCY1 cyr1*Δ/Δ	-	-
PR12	2	*Monosomy of ~276 kb of Chr2L cyr1*Δ/Δ	Detected at Chr2: 276,278	ACATCCGTA
PR14	2	*Monosomy of ~276 kb of Chr2L cyr1*Δ/Δ	Detected at Chr2: 276,278	ACATCCGTA
PR18	3	*Monosomy of ~590 kb of Chr2L cyr1*Δ/Δ	Detected at Chr2: 590,175	CATCCG
PR16	3+	*Monosomy of ~557 kb of Chr2L* *Trisomy of ~1342 kb of Chr2 cyr1*Δ/Δ	Detected at Chr2: 1,899,373	GAAG
PR2	3+	*Monosomy of ~557 kb of Chr2L* *Trisomy of ~1239 kb of Chr2 cyr1*Δ/Δ	Detected at Chr2: 1,796,423	CGTACA

† 23-bp telomere repeat sequence, CACCAAGAAGTTAGACATCCGTA

Extended Data Table 2. Potential phosphorylation substrates of Cdc28 and Yck2 during hyphal induction

Gene	Phosphosite	Description*	Deletion phenotype*
BNI4	S523	Formin; Protein required for wild-type cell wall chitin distribution, morphology, hyphal growth	Hyphal induction: normal
FPK1	T143, S337	Serine/threonine protein kinase	Hyphal induction: normal
ZDS1	S272	Protein with a role in regulating Swe1p-dependent polarized growth	Hyphal induction: normal
INT1	S416, T1214	Bud site selection protein Bud4	Hyphal induction: normal
SOL1	T16	Cell cycle regulator	Hyphal induction: normal
BNI1	S1619	Formin; Role in cytoskeletal organization, cell polarity	Hyphal induction: abnormal
MOB2	S49	Cbk1 kinase activator protein	Hyphal induction: absent
ASK1	S249	Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules	Inviable

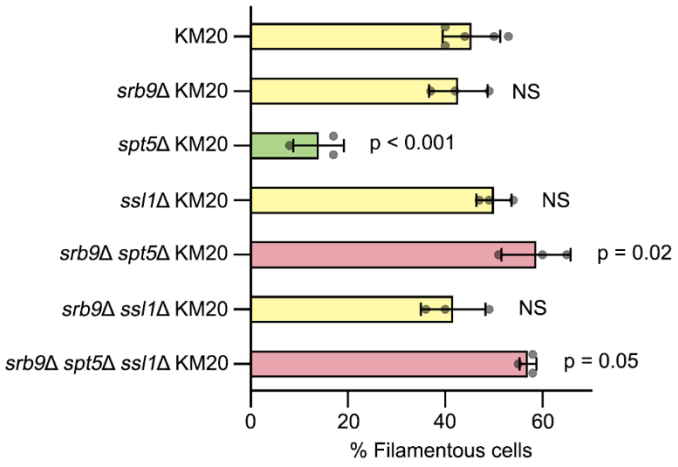
*Descriptions and deletion phenotypes were obtained from *Candida* Genome Database.



Extended Data Fig. 1. Expression levels of PKA subunits during hyphal induction.

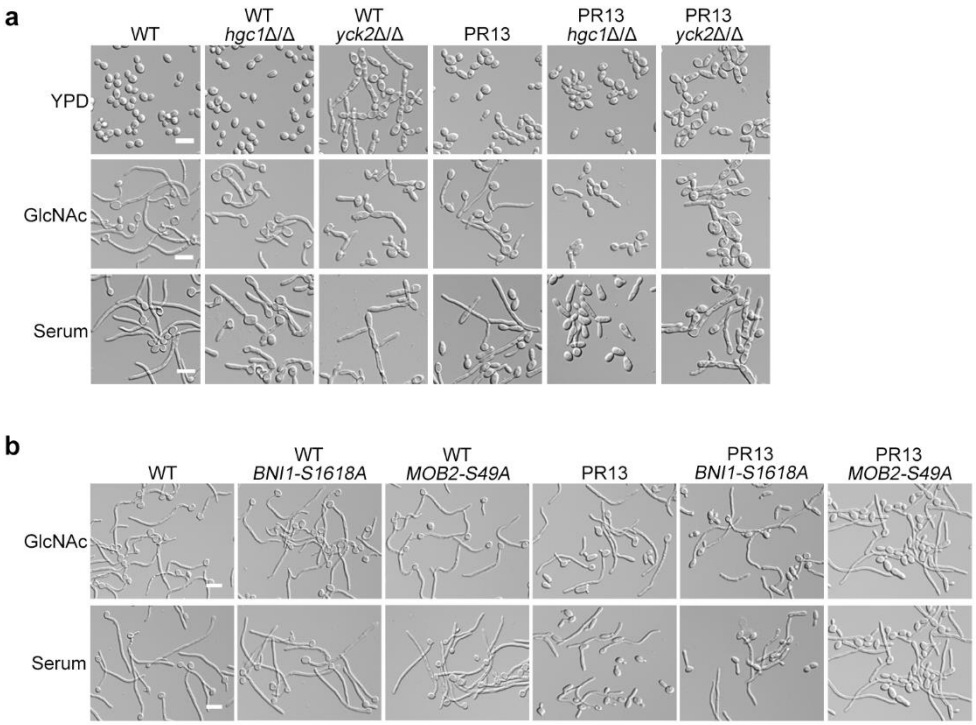
a, Western blot detection of the negative regulatory subunit (Bcy1) and the catalytic subunit (Tpk2) of PKA. Cells were grown at 37°C in liquid galactose medium and then 50 mM GlcNAc was added for 2 h to induce hyphae. The sizes of the protein standards (kDa) are indicated on the right of each blot. Images shown are representative of three independent experiments.

b,c,d, Relative levels of Bcy1 (**b**), Tpk2 (**c**), and TPK2/Bcy1 ratio (**d**) compared to the WT 0-h samples. Shown is the mean ± SD of 3 independent experiments. Expression levels were normalized to total proteins on Coomassie-stained gels. Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparisons test comparing the strains with the WT; ^{NS} $p > 0.05$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Extended Data Fig. 2. Gene-mapping analysis of the 10-kb region of chromosome 2 identified a role for *SRB9* and *SPT5* in hyphal induction in the PR mutants.

The single, double, and triple heterozygous deletion mutants of *SRB9*, *SPT5*, and *SSL1* were created in KM20 strain background (*Chr2L 90kb→250kbΔ bcy1Δ/BCY1 cyr1Δ/Δ*). The plot shows the percent of filamentous cells in liquid GlcNAc medium at 37°C; green, weak hyphal induction; yellow, intermediate hyphal induction; pink, strong hyphal induction. Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparisons test comparing the strains with the parental strain; ^{NS} $p > 0.05$.

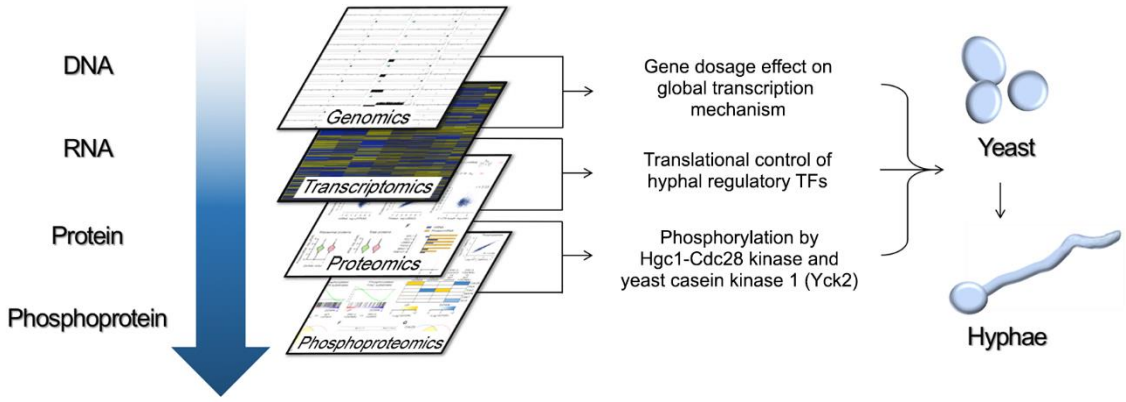


Extended Data Fig. 3. Deletion of Cdc28 cyclin (*HGC1*) and casein kinase 1 (*YCK2*) disrupt normal hyphal growth.

a, Deletion of Cdc28 cyclin (*HGC1*) and casein kinase 1 (*YCK2*) disrupt normal hyphal growth in WT and PR13 backgrounds.

b, Phospho-mutants of Mob2 and Bni1 did not show an obvious defect in hyphal growth.

a,b, The strains indicated at the top were grown in the liquid medium indicated on the left, and then hyphal induction was assessed microscopically. Cells were grown in liquid medium containing 15% serum or 50 mM N-acetylglucosamine (GlcNAc) to induce hyphal growth. Cells were incubated at 37°C for 3 h and then photographed. Scale bar, 10 μm.



Extended Data Fig. 4. Integrative multi-omics profiling revealed new pathways that induce *C. albicans* hyphal formation in a cAMP-independent manner.

We gained mechanistic insights into hyphal morphogenesis, by performing integrative multi-omics profiling in *C. albicans*. Genetic changes in PR mutants were identified by performing genome analysis, gene-mapping by CRISPR-Cas9, and transcriptome analysis. These studies showed that gene dosage effects on *BCY1* (negative regulator of PKA) and global transcription mechanisms promoted hyphal growth in the absence of cAMP. Integrating transcriptomic and proteomic data revealed that translation rate of some hyphal regulatory TFs increased dramatically during hyphal induction while their mRNA levels did not, suggesting a novel mechanism of translational regulation promotes hyphal growth. We revealed that phosphorylation by Hgc1-Cdc28 kinase and yeast casein kinase 1 (Yck2) plays a crucial role in hyphal induction by performing parallel comparisons of protein expression and phosphorylation. In conclusion, hyphal morphogenesis is regulated by multiple processes in a cAMP-independent manner.