

Supplementary Information

Proteins that physically interact with the phosphatase Cdc14 in *Candida albicans* have diverse roles in the cell cycle

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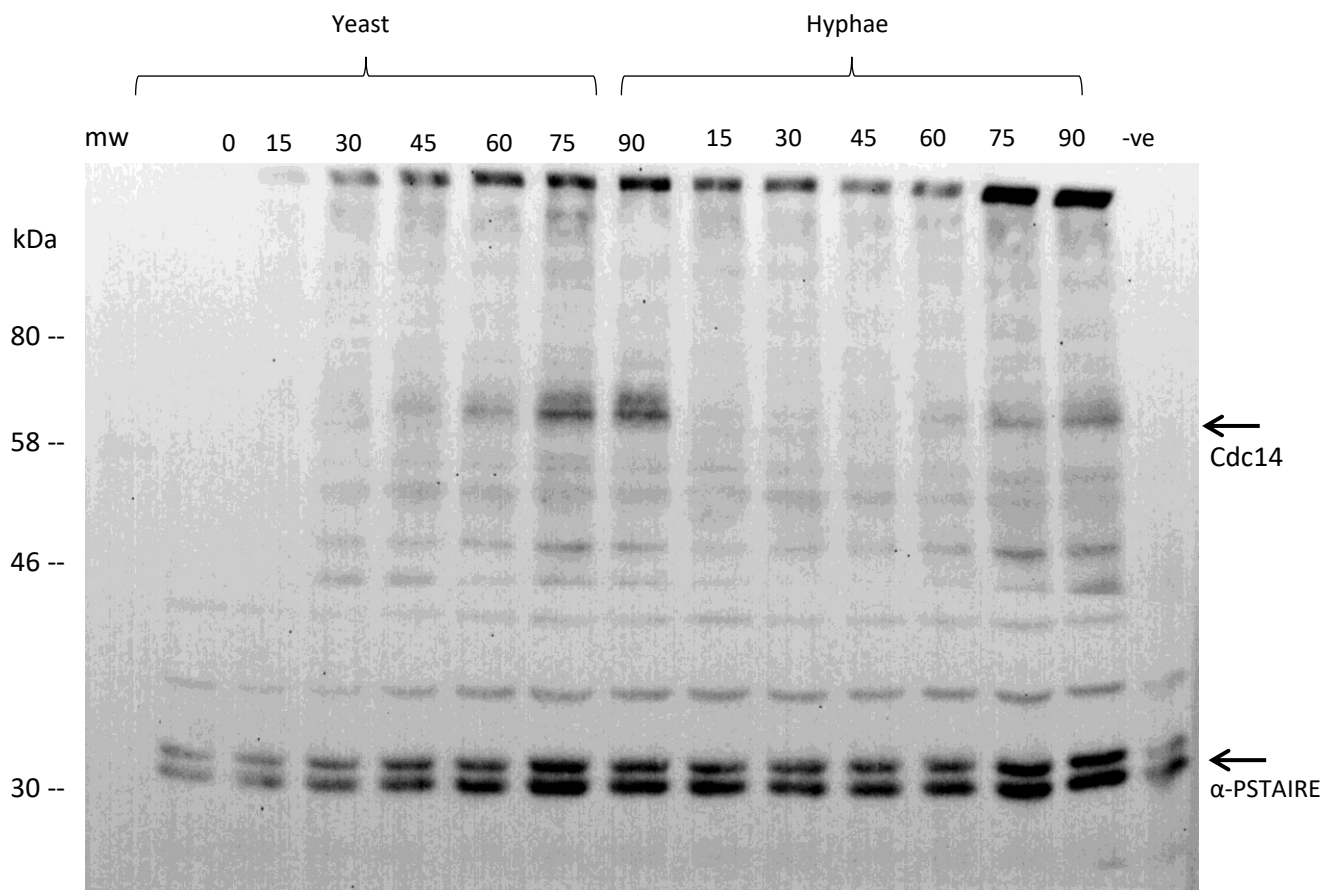
Supplementary Figure S1 Full length autoradiograms of the cropped panels shown in figure 1.

a: Samples were withdrawn at the indicated time in minutes after re-inoculation of a stationary phase culture into yeast or hyphal growth conditions. Lysates were fractionated by SDS gel electrophoresis and transferred to membrane by electroblotting. NEB Biolabs Prestained broad range protein markers were used for molecular weight markers which were also transferred and were visible on the membrane after blotting. The membrane was cut horizontally at the 46 kDa marker. The upper portion was probed with the α -Myc monoclonal antibody and the lower portion with the α -PSTAIRE monoclonal antibody as a loading control. The membranes portions were then rejoined and imaged together by ECL. After the chemiluminescence had been recorded the membranes were imaged with white light to record the migration of the molecular weight markers (mw). Specificity of the monoclonal antibodies is shown by the absence of a band in the negative controls (-ve), which were derived from parental MLO4 yeast cells in mid-log phase.

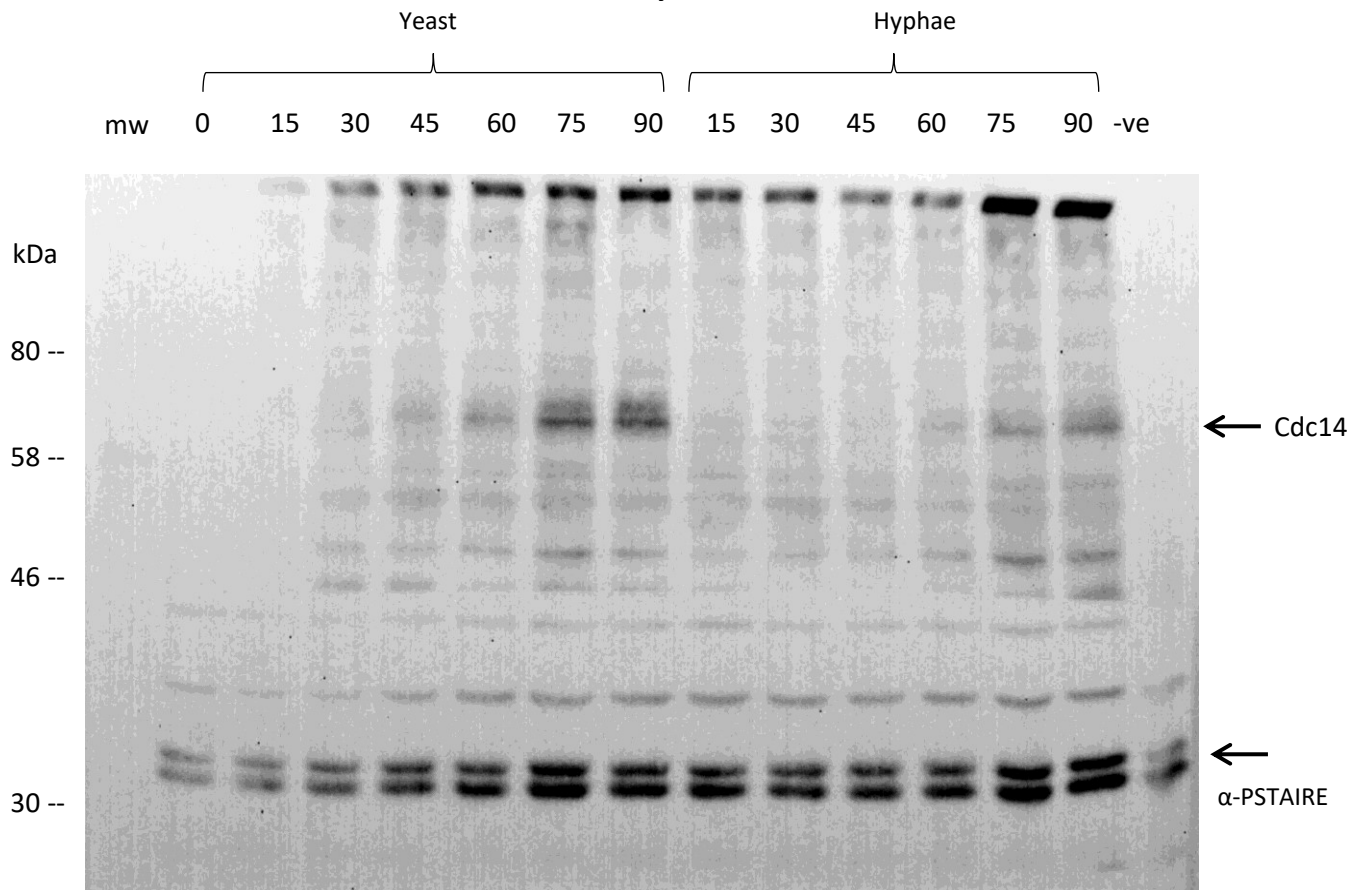
Figure S1b Full length autoradiograms of the cropped panels shown in figure 1b. A Lysate from *C. albicans cdc14^{PD}-Myc* cells was treated with λ phosphatase as indicated and the Western Blot probed with an α Myc antibody

Figure S1c Full length autoradiograms of the cropped panels shown in figure 1c. Cell lysates of the indicated strains were immunoprecipitated with an α Myc antibody. The Western blot was first probed with α GFP. After development with ECL the membrane was stripped and probed with an α Myc antibody. The stripping was not complete and bands corresponding to the GFP signal are still evident on the α Myc Autoradiograms. Lanes corresponding to samples from the IP, lysate serving to monitor the input, and the supernatant after the IP was pelleted are shown as indicated

Supplementary Fig. 2 *MET3-CDC14/cdc14^{PD}-MYC* cells were grown as yeast hyphae under *MET3*-repressing conditions. Yeast cells fail to separate and hyphal cells fail to form the long thin tubes characteristic of hyphal growth



Cdc14-Myc



Cdc14^{PD}-Myc

Figure S1a Full length autoradiograms of the cropped panels shown in figure 1a. NEB Biolabs Prestained broad range protein markers were used for molecular weight markers which were transferred to the membrane during the Western blotting. a: The membrane was cut horizontally at the 46 kDa marker. The upper portion was probed with the α -Myc monoclonal antibody and the lower portion with the α -PSTAIRE antibody as a loading control. The membranes portions were then rejoined and imaged together by ECL. After the ECL luminescence had been recorded the membranes were imaged with white light to record the migration of the molecular weight markers (mw). Negative controls were derived from mid-log phase parental MLO4 yeast cells. Specificity of the monoclonal antibodies is shown by the absence of a band in the negative controls (-ve) which were derived from parental MLO4 yeast cells in mid-log phase.

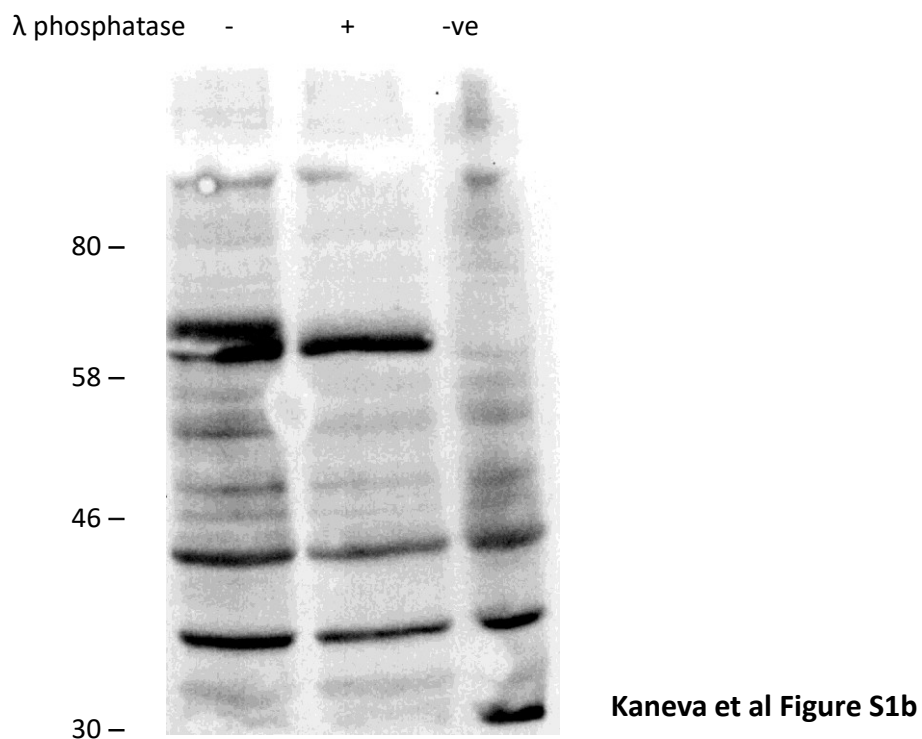


Figure S1b Full length autoradiograms of the cropped panels shown in figure 1b
A Lysate from *C. albicans* Cdc14^{PD}-Myc cells was treated with λ phosphatase and the Western blot probed with an α Myc antibody

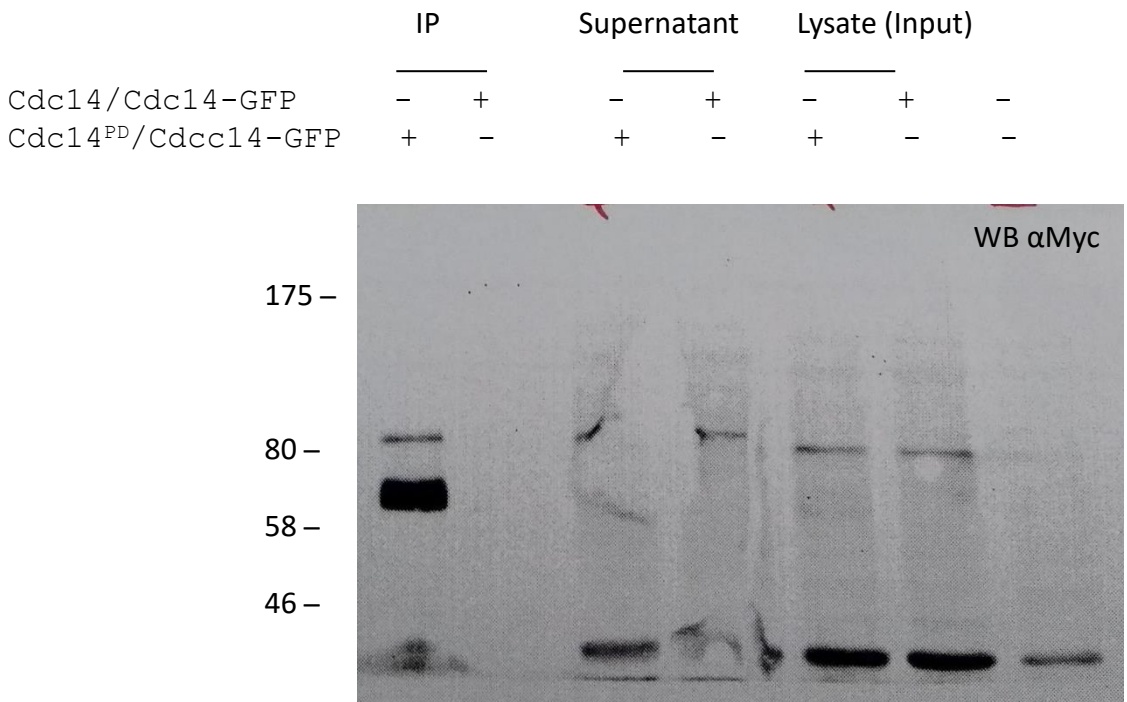
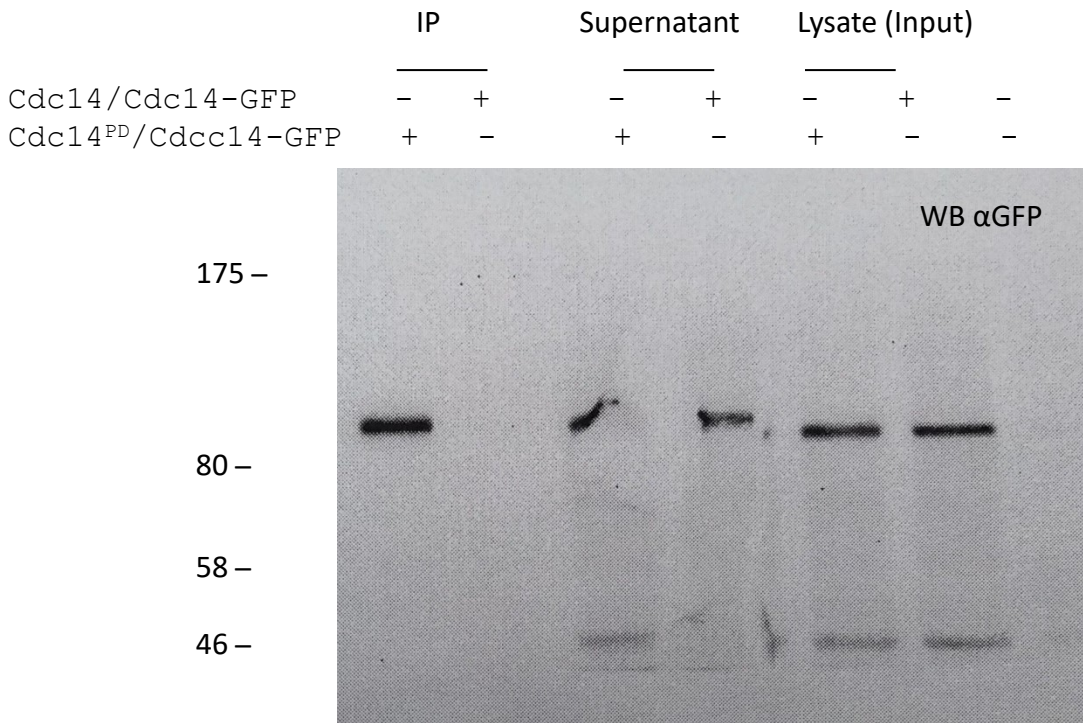
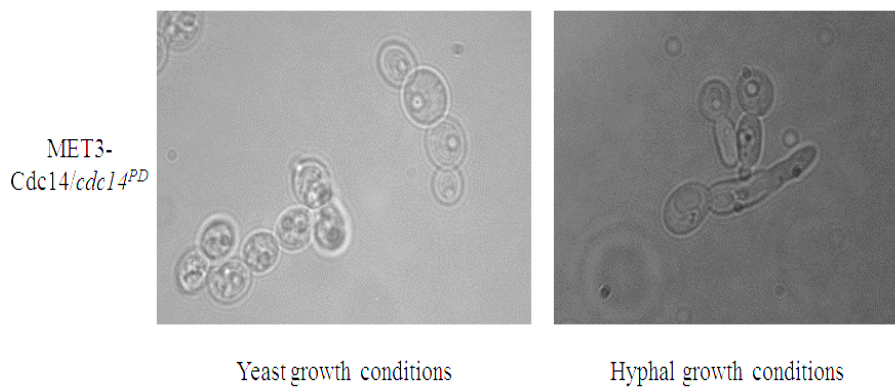


Figure S1b Full length autoradiograms of the cropped panels shown in figure 1c. Cell lysates of the indicated strains were immunoprecipitated with an αMyc antibody. The Western blot was first probed with αGFP. After development with ECL the membrane was stripped and probed with an αMyc antibody. The stripping was not complete and bands corresponding to the GFP signal are still evident on the αMyc Autoradiograms. Lanes corresponding to samples from the IP, lysate serving to monitor the input, and the supernatant after the IP was pelleted are shown as indicated



Supplementary Fig. S2 *MET3-CDC14/cdc14^{PD}-MYC* cells were grown as yeast hyphae under *MET3*-repressing conditions. Yeast cells fail to separate and hyphal cells fail to form the long thin tubes characteristic of hyphal growth

Supplementary Table S1 126 Cdc14-interacting proteins

Common Gene name	Protein_IDs	Yeast hit	Hyphae hit	Description
	orf19.2381	+	+	Protein of unknown function; possibly an essential gene, disruptants not obtained by UAU1 method; no domains
	orf19.2826	+	+	No domains
	orf19.3091	+		No domains
	orf19.3296	+		No domains
	orf19.3362/orf19.2671*	+		Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity and role in oxidation-reduction process
	orf19.4101	+		No domains
	orf19.520	+		No domains
	orf19.5246	+		No domains
	orf19.5491	+	+	ADIP domain Afadin- and alpha -actinin-Binding; This family is found in mammals where it is localized at cell-cell adherens junctions, and in Sch. pombe and other fungi where it anchors spindle-pole bodies to spindle microtubules. It is a coiled-coil structure, and in pombe, it is required for anchoring the minus end of spindle microtubules to the centrosome equivalent, the spindle-pole body
	orf19.5518	+	+	No domains
	orf19.557	+		No domains
	orf19.6030	+		No domains
	orf19.6583	+	+	No domains
	orf19.7060	+		No domains
	orf19.7406	+		No domains
<i>ACD99</i>	orf19.7288	+		Protein with predicted oxidoreductase and dehydrogenase domains
<i>ACE2</i>	orf19.6124	+	+	Transcription factor; similar to <i>S. cerevisiae</i> Ace2 and Swi5; regulates morphogenesis, cell separation, adherence, virulence in a mice; mutant is hyperfilamentous
<i>ACO1</i>	orf19.6385	+		Aconitase; induced in high iron; 2 upstream CCAAT motifs; amino acid starvation (3-AT),

				amphotericin B, phagocytosis, farnesol induced; Hap43, fluconazole-repressed; Gcn4-regulated
<i>ANT1</i>	orf19.6254	+		Peroxisomal adenine nucleotide transporter; role in beta-oxidation of medium-chain fatty acid and peroxisome proliferation;
<i>ARG1</i>	orf19.7469	+		Argininosuccinate synthase; arginine synthesis; Gcn4, Rim101 regulated
<i>ASK1</i>	orf19.4675	+	+	Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>BAS1</i>	orf19.3809	+		Putative Myb-like transcription factor; ortholog <i>S. cerevisiae</i> Bas1, a regulator of purine biosynthetic genes; mutant exhibits adenine auxotrophy and abnormal colony morphology
<i>BIR1</i>	orf19.643		+	Subunit of chromosomal passenger complex (CPC); CPC is comprised of Ipl1p-Sli15p-Bir1p-Nbl1p and regulates chromosome segregation; required for chromosome bi-orientation and for spindle assembly checkpoint activation upon reduced sister kinetochore tension; relative distribution to shortened microtubules increases upon DNA replication stress; sumoylated in an Mms21p-dependent manner; human survivin homolog
<i>CBR1</i>	orf19.1801	+		Putative cytochrome B5 reductase; plasma membrane-localized
<i>CDC16</i>	orf19.1792	+		Subunit of the anaphase-promoting complex/cyclosome (APC/C); which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition; required for sporulation; relocalizes to the cytosol in response to hypoxia
<i>CDC27</i>	orf19.3231	+		Putative ubiquitin-protein ligase; periodic mRNA expression, peak at cell-cycle S/G2 phase; Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C)
<i>CDC28</i>	orf19.3856	+		Cyclin-dependent protein kinase; interacts with regulatory subunit Cyb1; determination of cell morphology during the cell cycle
<i>CDC5</i>	orf19.6010	+	+	Polo-like kinase; member of conserved Mcm1 regulon; depletion causes defects in spindle elongation and Cdc35-dependent filamentation
<i>CDC7</i>	orf19.3561	+	+	Catalytic subunit of Dbf4p-regulated serine/threonine protein kinase; negative regulator of hyphal development; cell-cycle regulated periodic mRNA expression
<i>CDC9</i>	orf19.6155	+		DNA ligase I found in nucleus and mitochondria; essential enzyme that joins Okazaki fragments during DNA replication; also acts in ribonucleotide excision repair, base excision repair, and recombination; DNA ligase I mutants trigger ubiquitination of PCNA at K107, facilitating Rad59p-mediated bypass of unligated Okazaki fragments; human homolog LIG1 can complement yeast <i>cdc9</i> temperature-sensitive mutant at restrictive temperature
<i>CDH1</i>	orf19.2084	+	+	Protein involved in regulation of mitosis; similar to <i>S. cerevisiae</i> Cdh1, which is an APC/C component; transcriptionally induced by Mnl1 under weak acid stress
<i>CHT4</i>	orf19.1515	+	+	Chitinase; similar to <i>S. cerevisiae</i> sporulation-specific Cts2p
<i>CLB2</i>	orf19.1446	+		B-type mitotic cyclin (cyclin-dependent protein kinase regulatory subunit); essential; required for

				wild-type mitotic exit; role in cell polarization; interacts with catalytic subunit Cdk1
<i>CPA2</i>	orf19.3221	+		Putative arginine-specific carbamoylphosphate synthetase
<i>CSI2</i>	orf19.3535	+		Protein of unknown function; green fluorescent protein (GFP)- fusion protein localizes to the mother side of the bud neck and the vacuole
<i>CSM1</i>	orf19.7663	+		Putative component of the monopolin complex with role in rDNA silencing, homologous chromosome segregation, protein localization to nucleolar rDNA repeats
<i>DAD2</i>	orf19.3551	+	+	Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>DAD3</i>	orf19.3871	+		Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>DAK2</i>	orf19.4777	+		Putative dihydroxyacetone kinase; repressed by yeast-hypha switch
<i>DAL81</i>	orf19.3252	+		Zn(II)2Cys6 transcription factor; ortholog of <i>S. cerevisiae</i> Dal81, involved in the regulation of nitrogen-degradation genes; required for yeast cell adherence to silicone substrate
<i>DAM1</i>	orf19.4837	+	+	Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>DBF2</i>	orf19.1223	+		Essential serine/threonine protein kinase involved in mitotic spindle formation and cytokinesis; required for septum formation, exit from mitosis, and normal hyphal morphogenesis
<i>DBF4</i>	orf19.5166	+	+	
<i>DCI1</i>	orf19.6443	+		Protein with an enoyl-CoA hydratase related domain
<i>DUO1</i>	orf19.1428	+	+	Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>EHT1</i>	orf19.3040	+		Putative acyl-coenzymeA:ethanol O-acyltransferase; regulated by Sef1, Sfu1, and Hap43
<i>ERG1</i>	orf19.406	+		Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in the ergosterol biosynthesis pathway
<i>ERG2</i>	orf19.6026	+		Verified ORF; C-8 sterol isomerase; enzyme of ergosterol biosynthesis pathway; converts fecosterol to episterol.
<i>ERG24</i>	orf19.1598	+		C-14 sterol reductase, has a role in ergosterol biosynthesis;
<i>ERG26</i>	orf19.2909	+		C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis
<i>ERG27</i>	orf19.3240	+		3-Keto sterol reductase of ergosterol biosynthesis;acts in C-4 sterol demethylation with Erg25p and Erg26p
<i>ERG6</i>	orf19.1631	+		Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in ergosterol biosynthesis
<i>ERG7</i>	orf19.1570	+		2,3-epoxysqualene-lanosterol cyclase (lanosterol synthase), conversion of 2,3-oxidosqualene to lanosterol in sterol biosynthesis

<i>ESP1</i>	orf19.3356	+		Putative caspase-like cysteine protease; mutation confers increased sensitivity to nocodazole; periodic mRNA expression, peak at cell-cycle S/G2 phase; mRNA binds She3; Separase, a caspase-like cysteine protease; promotes sister chromatid separation by mediating dissociation of the cohesin Scc1p from chromatin; inhibits protein phosphatase 2A-Cdc55p to promote mitotic exit
<i>EXO1</i>	orf19.926	+		Putative exodeoxyribonuclease; cell-cycle regulated periodic mRNA expression
<i>FAA21</i>	orf19.272	+		Predicted acyl CoA synthetase; upregulated upon phagocytosis; transcript regulated by Nrg1 and Mig1
<i>FCY21</i>	orf19.1357	+		High affinity, high capacity, hypoxanthine-adenine-guanine-cytosine/H ⁺ symporter
<i>FDH1</i>	orf19.638	+		Formate dehydrogenase; oxidizes formate to CO ₂ ; Mig1 regulated; induced by macrophages; fluconazole-repressed; repressed by Efg1 in yeast, not hyphal conditions
<i>FKH2</i>	orf19.5389	+	+	Forkhead transcription factor; morphogenesis regulator; required for wild-type hyphal transcription, cell separation, and for virulence in cell culture
<i>FMA1</i>	orf19.6837	+		Putative oxidoreductase
<i>FUN30</i>	orf19.6291	+		Ortholog(s) have DNA binding, DNA-dependent ATPase activity, chromatin binding activity
<i>GDH3</i>	orf19.4716	+		NADP-glutamate dehydrogenase; Nrg1, Plc1 regulated
<i>GFA1</i>	orf19.1618	+		Glucosamine-6-phosphate synthase, homotetrameric enzyme of chitin/hexosamine biosynthesis
<i>GIN1</i>	orf19.658	+	+	Protein involved in regulation of DNA-damage-induced filamentous growth; putative component of DNA replication checkpoint; ortholog of <i>S. cerevisiae</i> Mrc1p, an S-phase checkpoint protein
<i>GLT1</i>	orf19.6257	+		Putative glutamate synthase; regulated by Sef1, Sfu1, and Hap43
<i>GRE24</i>	orf19.6868	+		Putative NADPH-dependent methylglyoxal reductase; homozygous transposon insertion causes decreased colony wrinkling under filamentous growth-inducing conditions, but does not block true hyphal formation in liquid media
<i>HAM1</i>	orf19.1108		+	Putative deoxyribonucleoside triphosphate pyrophosphohydrolase; caspofungin repressed; regulated by Gcn2p and Gcn4p
<i>HAT2</i>	orf19.7185	+		Subunit of the Hat1p-Hat2p histone acetyltransferase complex; required for high affinity binding of the complex to free histone H4, thereby enhancing Hat1p activity; similar to human RbAp46 and 48; has a role in telomeric silencing
<i>IDP2</i>	orf19.3733	+		Isocitrate dehydrogenase; white-opaque switch regulated; morphology-regulation by Ssn6; protein in exponential and stationary phase yeast; Hap43-repressed; Spider biofilm repressed by Bcr1, Tec1, Ndt80, Rob1, Brg1; Spider biofilm induced
<i>IFD3</i>	orf19.3311	+		Putative aldo/keto reductase; Mig1-regulated
<i>IPI3</i>	orf19.6234		+	Putative U2 snRNP component
<i>IPL1</i>	orf19.3474		+	Putative Aurora kinase; Hap43-induced

<i>IQG1</i>	orf19.6536	+		Actomyosin ring component at bud neck; cell-cycle regulated ser phosphorylation at CDK sites regulate association with Bni1/Bnr1, Iqg1 degradation, and ring disassembly; mutation causes cytokinetic defects
<i>KRI1</i>	orf19.1609		+	Essential nucleolar protein required for 40S ribosome biogenesis; associate with snR30; physically and functionally interacts with Krr1p
<i>LPG20</i>	orf19.771	+		Aldo-keto reductase family protein; similar to aryl alcohol dehydrogenases
<i>MCR1</i>	orf19.3507	+		NADH-cytochrome-b5 reductase; soluble in hyphae
<i>MED1</i>	orf19.826	+		RNA polymerase II mediator complex subunit; RNA polymerase II transcription cofactor
<i>MLC1</i>	orf19.2416.1	+		Microtubule-dependent localized protein; at Spitzenkorper and cytokinetic ring in hyphae; cell-cycle dependent localization to tip polarisome, bud neck in yeast and pseudohyphae
<i>MSB1</i>	orf19.1133		+	Putative regulator of transcription; expression in <i>S. cerevisiae</i> flo8 and flo11 mutants suggests a role in regulation of adhesion factors
<i>NCB2</i>	orf19.5825		+	Beta subunit of NC2, heterodimeric regulator of transcription; activates CDR1 transcription
<i>NCP1</i>	orf19.2672	+		NADPH-cytochrome P450 reductase, acts with Erg11p in sterol 14 alpha-demethylation in ergosterol biosynthesis
<i>NDC80</i>	orf19.2827	+	+	Component of the kinetochore-associated Ndc80 complex; conserved coiled-coil protein involved in chromosome segregation, spindle checkpoint activity, and kinetochore assembly and clustering; evolutionarily conserved; complex members include Ndc80p, Nuf2p, Scp24p, and Spc25p; modified by sumoylation
<i>NET1</i>	orf19.267	+	+	Core subunit of the RENT complex; involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar structure
<i>NUF2</i>	orf19.1941	+		Kinetochore component; amount of Nuf2p and Mtw1p protein detected at each centromere is consistent with a single kinetochore microtubule attachment site
<i>ORC1</i>	orf19.3000	+	+	
<i>ORC2</i>	orf19.5358	+	+	
<i>ORC3</i>	orf19.6942	+	+	
<i>ORC4</i>	orf19.4221	+	+	
<i>ORC5</i>	orf19.2369	+		
<i>ORC6</i>	orf19.3289	+		
<i>OSM1</i>	orf19.6882	+		Putative flavoprotein subunit of fumarate reductase
<i>PSD2</i>	orf19.3954	+		Ortholog(s) have phosphatidylserine decarboxylase activity, role in phosphatidylcholine biosynthetic process and cell division site, cytosol, endosome localization
<i>PUS1</i>	orf19.3477	+		Putative pseudouridine synthase; predicted role in snRNA pseudouridine synthesis, tRNA

				pseudouridine synthesis
<i>RAD52</i>	orf19.4208	+	+	Required for homologous DNA recombination, repair of UV- or MMS-damaged DNA, telomere length, UV-induced LOH; constitutive expression, MMS-induced; weakly complements <i>S. cerevisiae</i> rad52 mutant
<i>RAD9</i>	orf19.4275	+	+	DNA damage-dependent checkpoint protein; involved in regulation of DNA-damage-induced filamentous growth
<i>RHR2</i>	orf19.5437	+		Glycerol 3-phosphatase; roles in osmotic tolerance, glycerol accumulation in response to salt; Spider/flow model biofilm induced; regulated by macrophage, stress, yeast-hyphal switch, pheromone, Gcn4, Hog1, Nrg1, Tup1
<i>RIF1</i>	orf19.427	+	+	Ortholog(s) have telomeric DNA binding activity, role in DNA double-strand break processing, DNA replication initiation, chromatin silencing at silent mating-type cassette, telomere capping and shelterin complex localization
<i>RNH1</i>	orf19.5614		+	Putative ribonuclease H1
<i>RTC4</i>	orf19.580	+		Protein of unknown function; mutants are viable
<i>SAE2</i>	orf19.4988	+	+	<i>S. cerevisiae</i> ortholog Sae2 is an endonuclease that processes hairpin DNA structures with the MRX complex, involved in meiotic and mitotic double-strand break repair; upregulated in a <i>cyr1</i> null mutant
<i>SIN3</i>	orf19.6011	+		Protein similar to <i>S. cerevisiae</i> Sin3p (transcriptional corepressor involved in histone deacetylase recruitment); has paired amphipathic helix PAH1 domain; interacts with ScOpi1p, not CaOpi1p; transposon mutation affects filamentous growth
<i>SLD2</i>	orf19.2389	+		Single-stranded DNA origin-binding and annealing protein; required for initiation of DNA replication; phosphorylated in S phase by cyclin-dependent kinases (Cdks), promoting origin binding, DNA replication and Dpb11p complex formation; component of the preloading complex; binds the Mcm2-7p complex to prevent inappropriate Mcm2-7p interaction with the GINS complex in G1; required for S phase checkpoint; relative distribution to the nucleus increases upon DNA replication stress
<i>SLI15</i>	orf19.6049	+	+	Subunit of the conserved chromosomal passenger complex (CPC); complex regulates kinetochore-microtubule attachments, activation of the spindle tension checkpoint, and mitotic spindle disassembly; other complex members are Ipl1p, Bir1p, and Nbl1p
<i>SLK19</i>	orf19.2684	+	+	SMC_N Superfamily domain involved in Chromosome segregation ATPase [Cell cycle control, cell division, chromosome partitioning]
<i>SLM1</i>	orf19.4043	+		Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; TORC2 complex substrate and effector; protein abundance increases in response to DNA replication stress; SLM1 has a paralog, SLM2, that arose from the whole genome duplication

<i>SPC19</i>	orf19.4473	+	+	Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>SPC34</i>	orf19.3788	+	+	Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to spindle microtubules
<i>SPS19</i>	orf19.3684	+		Putative oxidoreductase
<i>SQS1</i>	orf19.2400	+		Protein that stimulates the ATPase and helicase activities of Prp43p; acts with Prp43p to stimulate 18s rRNA maturation by Nob1p; overexpression antagonizes the suppression of splicing defects by spp382 mutants; component of pre-ribosomal particles; relocalizes from nucleus to nucleolus upon DNA replication stress
<i>SRB9</i>	orf19.1451	+		Subunit of the RNA polymerase II mediator complex; transposon mutation affects filamentous growth
<i>STU1</i>	orf19.4435	+	+	Ortholog(s) have structural constituent of cytoskeleton activity, role in microtubule nucleation and spindle pole body localization
<i>STU2</i>	orf19.6610	+		Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p
<i>THP1</i>	orf19.5276	+		Putative nuclear pore-associated protein; Hap43p-induced gene; induced upon low-level peroxide stress; possibly an essential gene, disruptants not obtained by UAU1 method
<i>TNA1</i>	orf19.2397	+		High affinity nicotinic acid plasma membrane permease; responsible for uptake of low levels of nicotinic acid; expression of the gene increases in the absence of extracellular nicotinic acid or para-aminobenzoate (PABA)
<i>TRS33</i>	orf19.6496	+		Putative TRAPP complex subunit; constitutive expression independent of MTL or white-opaque status
<i>YAK1</i>	orf19.147	+		Predicted serine-threonine protein kinase; involved in hyphal growth regulation and biofilm formation
<i>YDJ1</i>	orf19.6408		+	Putative DnaJ-like heat shock/chaperone
<i>YEN1</i>	orf19.652	+	+	Holliday junction resolvase; promotes template switching during break-induced replication (BIR), causing non-reciprocal translocations (NRTs); localization is cell-cycle dependent and regulated by Cdc28p phosphorylation; homolog of human GEN1; similar to <i>S. cerevisiae</i> endonuclease Rth1p
<i>YHB1</i>	orf19.3707	+		Nitric oxide dioxygenase; acts in nitric oxide scavenging/detoxification; role in virulence in mouse; transcript activated by NO, macrophage interaction; Hap43, hypha repressed; mRNA binds She3
<i>YHR045W</i>	orf19.4013	+		Putative protein of unknown function; possible role in iron metabolism and/or amino acid and carbohydrate metabolism; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum
<i>YJL068C</i>	orf19.6596	+		Putative esterase; possibly transcriptionally regulated by Tac1; induced by Mnl1 under weak acid

				stress; protein present in exponential and stationary growth phase yeast cultures
<i>YNK1</i>	orf19.4311	+		Nucleoside diphosphate kinase (NDP kinase)
<i>YPL247C</i>	orf19.384	+		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; similar to the petunia WD repeat protein an11; overexpression causes a cell cycle delay or arrest
<i>YPR127W</i>	orf19.7306	+		Aldo-keto reductase; increased transcript associated with MDR1 overexpression, benomyl or long-term fluconazole treatment; overexpression does not affect drug or oxidative stress sensitivity; stationary phase enriched
<i>ZDS1</i>	orf19.3823	+		Protein with a role in regulating Swe1p-dependent polarized growth; involved in maintaining Cdc55p in the cytoplasm where it promotes mitotic entry; involved in mitotic exit through Cdc14p regulation; interacts with silencing proteins at telomeres; has a role in Bcy1p localization; implicated in mRNA nuclear export

* Orf19.336 and orf19.2671 are 98% identical and therefore could not be distinguished from each other.

Supplementary Table S2 Oligonucleotides used

Primer	Sequence in direction 5' ->3'
Ask1-XFP_F	CAAAAGATTTATCAAAAGATTTAACAGAAAATTCAACTACTGATTTAGG TCCATTTAGAGAAAGATGGAAGAAATTGACAAGAAAAGgtgctggcgcagg tgcttc
Ask1-XFP_R	AGGAGGCAATTATCTAACTAGAAGGTTCTAATGTTGAAACTCTTTCTTTC TTTCTTTCTTTCTTTTTGCACCCAATTAGTGATATCtctgatatcatcgatgaatt cgag
Ask1_chk_F	CAATCAACTCCAAGATCGAGTG
Ask1-HA_F	ATTTAACAGAAAATTCAACTACTGATTTAGGTCCATTTAGAGAAAGATG GAAGAAATTGACAAGAAAAGgtcgacggatccccgggtataccatacatgattcct gac
Ask1-HA_R	AGGAGGCAATTATCTAACTAGAAGGTTCTAATGTTGAAACTCTTTCTTTC TTTCTTTCTTTCTTTTTGCACCCAATTAGTGATATCtctgatgaattcgagctcgtt
S1-Cdc14-XFP	GGATTGCTTCTGGAAACTCACAAACATCAAGAGCACACTCTGGTGGTGT GAGAAAGTTAAGTGGAAAGAAACATggtgctggcgcagggtgcttc
S2-Cdc14*-XFP	CCGACTTGGCCAAGCCTAGATCCCGACTAATAGGAATTGATTTGGATGG TATAAACGGAAACAAAAAAGAGCTGGTACTACTctgatatcatcgatgaat tcgag
S2-Cdc14-XFP	GGATTTGATATATTGGCTTTTGCATATGGTTCGGAAGAACAATTGAA ATTGTTGAACCAGCTTATGAAGAAGACTAATTTAGtctgatatcatcgatgaat tcgag
Cdc14-TAP-MYC_F	CTCACAAACATCAAGAGCACACTCTGGTGGTGTGAGAAAGTTAAGTGG AAAGAAACATggtcgacggatccccgggttagaacagaagcttatatccgaa
Cdc14-TAP-HA-MYC_R	CGAGTGGCCTATCCAAAAGATTCAACTCAGCCTTATTCCAATAACTGGA TTGAATTGAGTGAAGATAGTGATATTGCTGtctgatgaattcgagctcgtt
Cdc14-chk_F	GACATCTCCACTTGCTGATTCTTCTG
Cdc14-chk-myc_R	GGCTTTTGCATATGGTTCGGAAGAAC

Cdc14-URAF_F	GTCTTTCATTCAAAAACACGTTTGTCTACCATACCGTTCTAAACTACCT AATAATCACAAACACCTTTTCCGctcgaggaagttcctatacttc
Cdc14-URAF_R	CGAGTGGCCTATCCAAAAGATTCAACTCAGCCTTATTCCAATAACTGGA TTGAATTGAGTGAAGATAGTGATATTGCTGctctagaactagtgatctgaagtt
NotI-Cdc14-3'_F	GGCGGG GCGGCCGC GTCTTCTTCATAAGCTGGTTCAAC
SacI-Cdc14-3'_R	GGCGGG GAGCTC CGGAGAATACAAGTACCATTCTCAAG
Cdc14-S1-MET3_F	AAATGTATATAACGAAGATGACTATCATCAATGGTCCGGTTAGTAAAGC GAACAAGCTTTATAAAAATAGTTATGCTGAACGTACCATgaagcttctgacg ctgcaggtc
Cdc14-S2-MET3_R	AAAGGTAGAACAATCAATTTGAAGTAGATTTTCCAACATACTTTTAAG AAACTCTATAAGAGGCACATGAACCAGTGAACATGcatgttttctggggagg gtatttac
MET3-chk_F	GCGCCCCTCTAAAACAATACCC
Cdc14-5'chk_R	GGTAATGCGTCTTCAACTGTG
Cdc14-TAP-MYC_F	CTCACAAACATCAAGAGCACACTCTGGTGGTGTGAGAAAGTTAAGTGG AAAGAAACATggtcgacggatccccgggtagaacagaagcttatatccgaa
Cdc14-TAP-HA-MYC_R	CGAGTGGCCTATCCAAAAGATTCAACTCAGCCTTATTCCAATAACTGGA TTGAATTGAGTGAAGATAGTGATATTGCTGctgatgaattcgagctcgtt
Cdc14-chk_F	GACATCTCCACTTGCTGATTCTTCTG
Cdc14-chk-myc_R	GGCTTTTGCATATGGTTCGGAAGAAC
Cdc14-URAF_F	GTCTTTCATTCAAAAACACGTTTGTCTACCATACCGTTCTAAACTACCT AATAATCACAAACACCTTTTCCGctcgaggaagttcctatacttc
Cdc14-URAF_R	CGAGTGGCCTATCCAAAAGATTCAACTCAGCCTTATTCCAATAACTGGA TTGAATTGAGTGAAGATAGTGATATTGCTGctctagaactagtgatctgaagtt
NotI-Cdc14-3'_F	GGCGGG GCGGCCGC GTCTTCTTCATAAGCTGGTTCAAC
SacI-Cdc14-3'_R	GGCGGG GAGCTC CGGAGAATACAAGTACCATTCTCAAG

Cdc14-S1-MET3_F	AAATGTATATAACGAAGATGACTATCATCAATGGTCCGGTTAGTAAAGC GAACAAGCTTTATAAAAATAGTTATGCTGAACGTACCATgaagcttcgtacg ctgcaggtc
Cdc14-S2-MET3_R	AAAGGTAGAACAATCAATTTGAAGTAGATTTTCCCAACATACTTTAAG AAACTCTATAAGAGGCACATGAACCAGTGAACATGcatgttttctggggagg gtatttac
S2-Cdc14-XFP	GGATTTGATATATTGGCTTTTGCATATGGTTCGGAAGAACAAATTGAA ATTGTTGAACCAGCTTATGAAGAAGACTAATTTAGtctgatcatcgatgaat tcgag
BamHI linker	GAT CCC TCC CAG AAC
XhoI linker	TCG AGT TCT GGG AGG
<u>XhoI-Cdc14_F</u>	GGC GGG CTC GAG GGC TTT CCT TTC CTT TGC TAT G
XbaI-Cdc14-MYC_R	GGC GGG TCT AGA CTA ATT TGT GAG TTT AGT ATA CAT GC
Cdc14-seq1_R	GAGGCACATGAACCAGTGAAC
Cdc14-seq2_F	GATGGAAGAGATCTTTTTGGAATTC
Cdc14-seq3_F	CCAGAATTGGGCTCCTCATCAAG
Cdc14-seq4_F	GGTTGTTTGATTGGAGCCCATC
Cdc14-seq5_F	GCTCACCAGCAAGGTATGACTC
Cdc14 C275S F	GCAGTACATTCTAAAGCAGGGTTAGG
Cdc14 C275S R	CCTAACCTGCTTTAGAATGTACTGC
Cdc14C275S_chk_ R	CCGGTTCTTCCTAACCTGCTTTAG

Supplementary Dataset S1 Excel file of the Statistical analysis of the peptide ratios carried out in Perseus v.1.2.5.6. Orf annotations are as downloaded from CGD. Separate worksheets are as follows

Hits lists proteins in which the H:L ratio was significantly different from a 1:1 ratio at an FDR of 0.05 after removal of proteins that were also significantly enriched in the combined lysates from the heavy and light cultures. A “+” in the yeast and/or hyphal column indicates the IP in which the H:L ratio was significantly elevated. For each morphological state, the data are combined from two biological replicates. Orf19.336 and Orf19.2671 are 98% identical and therefore could not be distinguished from each other.

Hits also significant in lysate Proteins that were also significantly elevated H:L ratio in the combined lysate before affinity purification. These proteins were removed from the initial list of proteins that showed significantly elevated HL ratio in the combined IP. Note some proteins have been removed from hyphal list but they remained the yeast list. These are encoded by orfs 19.1631, 19.1801, 19.3040, 19.3240 and 19.6837. So these 5 proteins are present in both worksheets of removed hits and confident hits.

Initial hit list shows the hits including proteins where the H:L ratio was also elevated in the combined lysate. Highlighted cells shows where the H:L ratio was significantly elevated in both the IP and combined lysate

Complete list of proteins- yeast Lists all proteins detected in the combined yeast IPs. Significance at three different FDR values are shown for each protein

Complete list of proteins- hyphae Lists all proteins detected in the combined hyphal IPs. Significance at three different FDR values are shown for each protein.

Supplementary Dataset S2 Proteins enriched in the yeast IP that were not detected in the lysate

Dataset S3 GO analysis of proteins showing significant heavy peptide enrichment in the IP. Excel file of *C. albicans* GO Term finder Process analysis using the GO Term Finder tool on the CGD website (<http://www.candidagenome.org/>). The query set was the list of 126 proteins in S1 Table. The default background gene set was used.

Supplementary Dataset S4 Canonical Cdc14 dephosphorylation motifs in Cdc14-interacting proteins

Dataset S5 Datasets, notebooks of statistical procedures followed and computer code used for further statistical analysis of the following

- Further verification of yeast-specific hits that are significantly enriched in the IP
- Enrichment of genes annotated as Ergosterol synthesis
- Cdc14 target sites
- Concordance with other surveys of Cdc14 interactors
- Motif enrichment in the list of 126 hit