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NAR Breakthrough Article

Generating genomic platforms to study *Candida albicans* pathogenesis

Mélanie Legrand^{1,†}, Sophie Bachellier-Bassi^{1,†}, Keunsook K. Lee², Yogesh Chaudhari², Hélène Tournu^{3,4}, Laurence Arbogast¹, Hélène Boyer¹, Murielle Chauvel¹, Vitor Cabral^{1,5}, Corinne Maufrais^{1,6}, Audrey Nesseir^{1,5}, Irena Maslanka², Emmanuelle Permal¹, Tristan Rossignol¹, Louise A. Walker², Ute Zeidler¹, Sadri Znaidi¹, Floris Schoeters^{3,4}, Charlotte Majgier⁷, Renaud A. Julien⁷, Laurence Ma⁸, Magali Tichit⁸, Christiane Bouchier⁸, Patrick Van Dijck^{3,4}, Carol A. Munro^{2,*} and Christophe d'Enfert^{1,*}

¹Fungal Biology and Pathogenicity Unit, Department of Mycology, Institut Pasteur, INRA, Paris 75015, France, ²Medical Research Council Centre for Medical Mycology at the University of Aberdeen, Institute of Medical Sciences, Foresterhill, Aberdeen AB25 2ZD, UK, ³VIB-KU Leuven Center for Microbiology, Leuven 3001, Belgium, ⁴Laboratory of Molecular Cell Biology, KU Leuven, Leuven 3001, Belgium, ⁵Univ. Paris Diderot, Sorbonne Paris Cité, Cellule Pasteur, Paris 75015, France, ⁶Institut Pasteur-Bioinformatics and Biostatistics Hub-C3BI, USR 3756 IP CNRS-Paris 75015, France, ⁷Modul-Bio, Parc Scientifique Luminy Biotech II, Marseille 13009, France and ⁸Institut Pasteur-Biomics Pole-CITECH-Paris 75015, France

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ABSTRACT

The advent of the genomic era has made elucidating gene function on a large scale a pressing challenge. ORFeome collections, whereby almost all ORFs of a given species are cloned and can be subsequently leveraged in multiple functional genomic approaches, represent valuable resources toward this endeavor. Here we provide novel, genome-scale tools for the study of *Candida albicans*, a commensal yeast that is also responsible for frequent superficial and disseminated infections in humans. We have generated an ORFeome collection composed of 5099

ORFs cloned in a GatewayTM donor vector, representing 83% of the currently annotated coding sequences of *C. albicans*. Sequencing data of the cloned ORFs are available in the CandidaOrfDB database at <http://candidaorfeome.eu>. We also engineered 49 expression vectors with a choice of promoters, tags and selection markers and demonstrated their applicability to the study of target ORFs transferred from the *C. albicans* ORFeome. In addition, the use of the ORFeome in the detection of protein–protein interaction was demonstrated. Mating-compatible strains as well as GatewayTM-compatible two-hybrid vectors were en-

*To whom correspondence should be addressed. Tel: +33 0 140613257; Fax: +33 0 140613456; Email: denfert@pasteur.fr

Correspondence may also be addressed to Carol Munro. Tel: +44 0 1224 437 485; Fax: +44 0 1224 437 506; Email: c.a.munro@abdn.ac.uk

†The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

Present addresses:

Yogesh Chaudhari, Biosciences Department, University of Exeter, Exeter EX4 4QD, UK.

Hélène Tournu, Department of Clinical Pharmacy, University of Tennessee, Memphis, TN 38163, USA.

Laurence Arbogast, Brain plasticity in response to the environment Group, Institut Pasteur, Paris 75015, France.

Hélène Boyer, Laboratoire d'Immunologie, Hôpital Henri Mondor, Créteil 94000, France.

Vitor Cabral, Bacterial Signalling Group, Instituto Gulbenkian de Ciência, Oeiras 2780-156, Portugal.

Audrey Nesseir, Lycée Grégor Mendel, Vincennes, 94300, France; Emmanuelle Permal, Toulouse 31000, France.

Tristan Rossignol, MICALIS, INRA, Jouy-en-Josas 78352, France.

Ute Zeidler, Sandoz, Unterach 4866, Austria.

Sadri Znaidi, Laboratory of Molecular Microbiology, Vaccinology & Biotechnology Development, Institut Pasteur de Tunis, Tunis-Belvédère 1002, Tunisia.

Magali Tichit, Laboratoire Histopathologie Humaine et Modèles Animaux, Institut Pasteur, Paris 75015, France.

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gineered, validated and used in a proof of concept experiment. These unique and valuable resources should greatly facilitate future functional studies in *C. albicans* and the elucidation of mechanisms that underlie its pathogenicity.

INTRODUCTION

Over the last decade, there has been an exponential growth in the quantity of available genome sequence data due to the very rapid progress in sequencing technology. In 2004, the genome sequence of the human fungal pathogen *Candida albicans* was released as Assembly 19 (1). With the challenge of working with a heterozygous diploid organism, new computational methods had to be developed and resulted in the release in 2013 of Assembly 22, an assembly of a completely phased diploid genome sequence for the standard *C. albicans* reference strain SC5314 (2). This opened new perspectives to understand the genetic basis and functional mechanisms that underlie pathogenesis and evolution in this organism.

Although *C. albicans* gene sequences have been available to the community for more than a decade (3,4), only 1670 out of the 6198 predicted protein-coding genes have been characterized as of 31 January 31, 2018 according to the Candida Genome Database (5). Nowadays, the growing availability of whole-genome datasets has encouraged a shift towards the development of functional genomics and systems biology approaches, enabling analysis of high-throughput whole-genome assays to better understand biological networks. In this context, major efforts have been made to generate large-scale deletion (6–10) or overexpression (11–13) mutant collections. Genome-wide ORF libraries or ORFeomes represent useful resources for the implementation of approaches used to elucidate gene function (14). Besides, the development of collections of overexpression mutants (12), ORFeomes facilitate approaches aimed at evaluating protein subcellular localization and identifying protein–protein interactions (yeast two-hybrid) both at steady state and in response to environmental stimuli (15).

Large-scale cloning projects, with the goal of cloning all predicted ORFs into flexible recombinational vectors, have been described for several model organisms, including *Caenorhabditis elegans*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Escherichia coli* K-12, *Arabidopsis thaliana*, *Xenopus laevis* and *Drosophila melanogaster*, as well as infectious microorganisms such as *Brucella melitensis*, *Plasmodium falciparum*, *Helicobacter pylori*, *Chlamydia pneumonia*, *Staphylococcus aureus* and viruses (16–29). Human ORFeomes have also been generated and made publicly available, with the latest version containing sequence-confirmed ORFs for more than 11 000 human genes (30). Most ORFeome libraries are created using the highly versatile Gateway™ cloning approach (31). The Gateway™ technology employs the recombination system of bacteriophage lambda with two sets of reactions: the BP reaction, catalyzed by Gateway™ BP Clonase™, facilitates recombination between *attB* and *attP* sequences, and the LR reaction, catalyzed by Gateway™ LR Clonase™, promotes recombination between *attL* and *attR* sequences (31).

Previously, we have reported the development of a first generation *C. albicans* ORFeome, in which 644 full-length ORFs, encoding signaling proteins (transcription factors and kinases), as well as cell wall proteins and proteins involved in DNA processes (repair, replication and recombination), were cloned in the Gateway™ vector pDONR207 (32). Here, we describe the generation and validation of the latest *C. albicans* ORFeome collection, which consists of 5099 ORFs in pDONR207, allowing the transfer of the cloned genes into a variety of *C. albicans* Gateway™-compatible expression vectors. To this end, we also provide a panel of 15 expression vectors that differ in the combination of promoter/selection marker they are carrying, and give different options regarding the tagging of the cloned gene product. These 15 expression vectors have been validated using the filament-specific transcription factor gene *UME6*. In addition, we also provide a secondary collection of 34 expression vectors with additional options regarding the choice of the promoter and the tagging of the cloned gene product. Finally, among the numerous applications of ORFeome collections, we present a powerful association of the *C. albicans* ORFeome and a *C. albicans*-adapted two-hybrid system (33) that will allow systematic protein–protein interaction screening in *C. albicans*.

MATERIALS AND METHODS

Strains and growth conditions

Candida albicans strains used in this study are listed in Table 1. *Candida albicans* strains were routinely cultured at 30°C in YPD medium (1% yeast extract, 2% peptone, 2% dextrose), synthetic dextrose (SD) medium (0.67% yeast nitrogen base, 2% dextrose) or Nourseothricin-containing YPD medium (YPD + 200 µg/ml Nourseothricin). Solid media were obtained by adding 2% agar.

Escherichia coli strains were routinely cultured at 30°C or 37°C in LB or 2YT supplemented with 10 µg/ml gentamicin, 50 µg/ml kanamycin or 50 µg/ml ticarcillin. Solid media were obtained by adding 2% agar.

DH5α *E. coli* cells competent for transformation with DNA were prepared according to Hanahan *et al.* (34).

The ORFeome collection is being distributed by the Centre International de Ressources Microbiennes (CIRM). The 49 expression vectors are available from Addgene, while two-hybrid strains and vectors are now accessible from the Belgian Co-ordinated Collections of Micro-organisms (BCCM).

Generation of an entry clone collection

Primer design. The DNA sequence of *C. albicans* was obtained from the Candida Genome Database Release 21 (www.candidagenome.org), before Assembly 22 was released. Gene-specific forward primers were designed by adding the sequence 5'-GGGGACAAGTTTGTACAAA AAAGCAGGCTTG-3' to the 5' end of the first 30 nt of each ORF. Gene-specific reverse primers were designed by adding the sequence 5'-GGGGACCACTTTGTACAAG AAAGCTGGGTC-3' to the 5' end of the last 30 nt of each ORF excluding the Stop codon. Polymerase chain reaction

Table 1. *Candida albicans* strains used in this study

Strain	Source	Relevant Genotype	Reference
SC5314		Wild-type	(47)
BWP17		<i>ura3</i> Δ::λimm434/ <i>ura3</i> Δ::λimm434 <i>his1</i> Δ::hisG/ <i>his1</i> Δ::hisG <i>arg4</i> Δ::hisG/ <i>arg4</i> Δ::hisG <i>iro1</i> Δ::λimm434/ <i>iro1</i> Δ::λimm434	(40)
SN152		<i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434	(55)
CEC161	BWP17	<i>ura3</i> Δ::λimm434/ <i>ura3</i> Δ::λimm434 <i>his1</i> Δ::hisG/ <i>HIS1</i> <i>arg4</i> Δ::hisG/ <i>ARG4</i> <i>iro1</i> Δ::λimm434/ <i>iro1</i> Δ::λimm434	(38)
CEC369	CEC161	<i>ura3</i> Δ::λimm434/ <i>ura3</i> Δ::λimm434 <i>arg4</i> Δ::hisG/ <i>ARG4</i> <i>his1</i> Δ::hisG/ <i>HIS1</i> <i>iro1</i> Δ::λimm434/ <i>iro1</i> Δ::λimm434 <i>RPS1</i> / <i>RPS1</i> :: <i>Cip10</i>	(38)
CEC2907	CEC161	<i>ura3</i> ::λimm434/ <i>ura3</i> ::λimm434 <i>his1</i> ::hisG/ <i>HIS1</i> <i>arg4</i> ::hisG/ <i>ARG4</i> <i>ADH1</i> / <i>adh1</i> :: <i>P_{TDH3}</i> - <i>carTA</i> :: <i>SAT1</i>	(12)
SC2H3 (LMBP10469)*	SN152	<i>MTLa</i> / <i>MTLα</i> <i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434 5xLexAOp- <i>ADH1b</i> / <i>HIS1</i> 5xLexAOp- <i>ADH1b</i> / <i>lacZ</i>	(33)
SC2H3a	SC2H3	<i>MTLa</i> / <i>MTLα</i> :: <i>SAT1</i> - <i>FLP</i> <i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434 5xLexAOp- <i>ADH1b</i> / <i>HIS1</i> 5xLexAOp- <i>ADH1b</i> / <i>lacZ</i>	This study
SC2H3α	SC2H3	<i>MTLa</i> :: <i>SAT1</i> - <i>FLP</i> / <i>MTLα</i> <i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434 5xLexAOp- <i>ADH1b</i> / <i>HIS1</i> 5xLexAOp- <i>ADH1b</i> / <i>lacZ</i>	This study
SC2H3a-pWOR1 (LMBP10470)*	SC2H3a	<i>MTLa</i> / <i>MTLα</i> :: <i>FRT</i> <i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434 5xLexAOp- <i>ADH1b</i> / <i>HIS1</i> 5xLexAOp- <i>ADH1b</i> / <i>lacZ</i> <i>ADH1</i> / <i>adh1</i> ::(<i>P_{ADH1}</i> - <i>carTA</i> , <i>SAT1</i> , <i>P_{TET}</i> - <i>WOR1</i>)	This study
SC2H3α-pWOR1 (LMBP10469)*	SC2H3α	<i>MTLa</i> :: <i>FRT</i> / <i>MTLα</i> <i>arg4</i> Δ/ <i>arg4</i> Δ <i>leu2</i> Δ/ <i>leu2</i> Δ <i>his1</i> Δ/ <i>his1</i> Δ <i>URA3</i> / <i>ura3</i> Δ::λimm434 <i>IRO1</i> / <i>iro1</i> Δ::λimm434 5xLexAOp- <i>ADH1b</i> / <i>HIS1</i> 5xLexAOp- <i>ADH1b</i> / <i>lacZ</i> <i>ADH1</i> / <i>adh1</i> ::(<i>P_{ADH1}</i> - <i>carTA</i> , <i>SAT1</i> , <i>P_{TET}</i> - <i>WOR1</i>)	This study

*Strain number in the BCCM collection

(PCR) fragments amplified from these primers are compatible for C-terminal tagging with destination vectors containing the Gateway™ cassette A. A total of 6205 primer pairs were obtained from Invitrogen in a 96-well format and are listed in Supplementary Table S1.

Gateway™ cloning of the *C. albicans* ORFeome. The detailed method for the cloning of *C. albicans* ORFs in the pDONR207 vector has been described (35). Briefly, ORFs, ranging from 90 to 5295 bp, were amplified from genomic DNA of *C. albicans* strain SC5314 in 96-well plates using the Thermo Scientific Phusion High-Fidelity DNA Polymerase and 30 cycles of amplification, with elongation time varying from 1 to 3 min according to the ORF size. After ethanol precipitation, Gateway™-compatible amplified ORFs were recombined into pDONR207 (Invitrogen) using the Gateway™ BP Clonase™ II Enzyme Mix (Invitrogen). Reaction mixes containing pDONR207, the PCR products and BP Clonase™ were incubated overnight in 96-well plates, at room temperature. After adding proteinase K (Invitrogen) and incubating for 10 min at 37°C, the BP reactions were directly used for bacterial transformation. A total of 45–50 μl of chemically competent *E. coli* DH5α were added to the BP reactions and incubated for 30 min at 4°C. After heat-shock at 42°C for 35 s, 150 μl of recovery medium (20 ml YPD + 2 ml LB + 1 ml Hepes 1M) was added to the transformation reactions and the samples were covered with breathing films and incubated for 1.5 h at 37°C with shaking. Then 100 μl of each sample were plated onto LB agar containing 10 μg/ml Gentamicin and incubated overnight at 37°C. The remainder of the transformation reactions were stored at –80°C in 30% glycerol. A single colony from each transformation reaction was inoculated in 400 μl 2YT + 10 μg/ml Gentamicin in 96 deep-well

microplates. After 36 h-growth at 37°C, the cultures were used for plasmid extraction and for –80°C storage.

Validation of entry clones by DNA sequencing and bioinformatics analysis. Sanger sequencing of the 5'-end of each BP clone was performed with the 207VER-F oligonucleotide (see Supplementary Table S2 for oligonucleotide sequences except those used to amplify ORFs) to confirm that the expected ORF had been cloned. The 3'-ends were also sequenced with the 207VER-R oligonucleotide to ensure that the oligonucleotides did not carry deletions. All inserts validated by Sanger sequencing were systematically subjected to full-length sequence analysis using Illumina technology. Plasmid DNAs were fragmented using a Bioruptor sonicator. Sequencing libraries were prepared according to the KAPA LTP Library Preparation Kit protocol (KAPA Biosystems, catalogue number KK8232). The libraries were not made in duplicates and therefore pools (1–5) were sequenced only once. If nonsense or frameshift mutations were observed in a cloned ORF, another colony was checked or the ORF reamplified and cloned again. If these attempts were unsuccessful, cloning of the ORF was abandoned. Clones containing contiguous deletions or insertions of multiples of 3 bp were accepted. Missense mutations and those located within introns were accepted. It should be noted that further analysis of each mutation-containing ORF is required to determine whether or not mutations affect the function of the ORF. The fastq files have been deposited into NCBI-SRA and are available under the BioProject PRJNA472959. In Supplementary Table S1, the sequencing pool (pools 1–5) is given for each cloned ORF. Because of a server crash, the dataset for pool2 had been lost, but the reads could be recovered from CLC format, and the headers reconstructed based on the sequenc-

ing information provided by the Institut Pasteur sequencing platform.

CandidaOrfDB database

CandidaOrfDB was created to integrate the data of the *C. albicans* ORFeome project and is available at <http://candidaorfeome.eu>. The database is a relational database using the SQL database server Oracle with a web interface developed using J2EE. The alignment algorithm uses *biojava3-alignment* Java library, implemented with a NeedlemanWunsch aligner, configured with a gap open penalty of 5 and a gap extension penalty of 2. The substitution matrix used is named 'nuc-4_4' and was created by Todd Lowe (https://github.com/sbliven/biojava/blob/master/biojava3-alignment/src/main/resources/nuc-4_4.txt). The alignment algorithm was specifically customized for CandidaOrfDB to work on segments of 500 codons, which provides an optimized alignment performance for *C. albicans* average sequence length.

Clone access

The *C. albicans* ORFeome clones are available at the Centre International de Ressources Microbiennes (CIRM - https://www6.inra.fr/cirm_eng/).

Destination plasmids

All destination plasmids constructed in this study were derived from CIP- P_{TET} -GTW (12) and were confirmed by Sanger sequencing. Plasmid sequences have been submitted to GenBank. Accession numbers are given in Table 2. All oligonucleotides used for PCR and/or sequencing are listed in Supplementary Table S2.

SP cloning. First, a spacer sequence (SP) was amplified from the *E. coli kanR* gene borne on pCR-topo-blunt plasmid (Invitrogen) with primers SP3 and SP4. The PCR product was cloned in the *SacII* site of CIP- P_{TET} -GTW, yielding CIP- P_{TET} -GTW-SP, also referred to as pCA-Dest1100. This 390 bp-long sequence is flanked by the SP1 and SP2 Illumina paired-end sequencing primers 1 and 2 and can be used to insert molecular barcodes if expression plasmids are to be used in signature-tagged mutagenesis approaches.

Epitope tags. We then inserted in frame tags either upstream of attR1 or downstream of attR2 to allow N-terminal or C-terminal protein tagging, respectively. For the cloning of N-terminal tags, we used pUC-attR1-CmR, containing a *PciI*-*BglII* fragment from CIP-GTW cloned into the *PciI* and *BamHI* sites of pUC18. CIP-GTW was obtained after deleting P_{TET} from CIP- P_{TET} -GTW with *Acc65I* and *HpaI*. For cloning of the 3xHA coding sequence, two oligonucleotides (oligo1-*PciHABsrG* and oligo2-*PciHABsrG*) containing three HA epitopes were hybridized, gel purified and cloned into pUC-attR1-CmR cut with *PciI* and *BsrGI*. The resulting plasmid was then used as a PCR template with primers GTW02 and GTW03. The resulting PCR product was cut with *BspEI* and *HpaI*, and cloned into the same sites of pCA-Dest1100 to yield

pCA-Dest1110. For cloning of the GFP tag, the GFP gene was amplified from pFA-GFP-URA3 (36) with primers GTW04 and GTW05. The PCR product was cut with *PciI* and *EcoRV* and ligated into the same sites of pUC-attR1-CmR. The resulting plasmid was then used as a PCR template with primers GTW07 and GTW03. The resulting PCR product was cut with *ScaI* and *BspEI* and ligated into pCA-Dest1100 cut with *HpaI* and *BspEI*, yielding pCA-Dest1120. For cloning of the TAP-tag, the TAP-tag coding region was PCR amplified from pFA-TAP-URA3 (12) with primers GTW13 and GTW14. The resulting PCR product was then cut with *PciI* and *BsrGI*, and ligated into the same sites of pUC-attR1-CmR. The resulting plasmid was then digested with *EcoRV* and *BspEI* and the smallest restriction fragment was ligated into pCA-Dest1100 cut with *HpaI* and *BspEI* to yield pCA-Dest1130. For the cloning of C-terminal tags, we generated pUC-attR2 by inserting a *SalI*-*HindIII* fragment from pCA-Dest1100 into the same sites of pUC18. For cloning of the 3xHA epitope, pCaMPY-3xHA (37) was used as a PCR template with primers GTW20 and GTW21, and the resulting PCR product cut with *BsrGI* and *NsiI* was ligated in the same sites of pUC-attR2. The resulting plasmid was cut with *SalI* and *NsiI* and the fragment cloned in the same sites of pCA-Dest1100, yielding pCA-Dest1101. For cloning the GFP tag, the GFP gene was amplified from pFA-GFP-URA3 (36) with primers GTW11 and GTW12. The resulting PCR product was cut with *NsiI* and *EcoRV* and ligated into the same sites of pUC-attR2. The resulting plasmid was then cut with *SalI* and *NsiI* and the GFP-bearing fragment ligated into the same sites of pCA-Dest1100, yielding pCA-Dest1102. For cloning of the TAP-tag, the TAP-tag coding region was amplified from CIP10- P_{PCKI} -GTW-TAPtag (12) with primers GTW15 and GTW16. The PCR product was cut with *BsrGI* and *NsiI* and cloned in the same sites of pUC-attR2. The resulting plasmid was digested with *SalI* and *NsiI*, and the TAP-containing fragment ligated in the same sites of pCA-Dest1100, yielding pCA-Dest1103.

Promoters. We replaced P_{TET} with either P_{PCKI} (obtained from CIP10- P_{PCKI} -GTW-TAPtag, (12)), yielding the pCA-Dest12xx series; P_{TDH3} (cut from pKS- P_{TDH3} ; P_{TDH3} was PCR amplified from SC5314 genomic DNA with oligos SZ11 and SZ12, and the fragment inserted into pBluescript-KS (+) cut with *XhoI* and *EcoRV*) yielding the pCA-Dest13xx series; or P_{ACT1} , cut from CIP10:: P_{ACT1} -gLUC59 (38), yielding the pCA-Dest14xx series.

Selection markers. In all plasmids except the P_{TET} series, the auxotrophic marker *URA3* was replaced with the *NAT1* marker conferring nourseothricin resistance. Briefly, a *XbaI*-*DraIII* fragment or *SpeI*-*NaeI* fragment was cut from pUC-NAT1 and inserted into the similarly cut vectors. pUC-NAT1 was built by amplifying *NAT1* under the control of P_{TEF1} promoter with oligonucleotides UZ50 and UZ51, and using pFA6-SAT1 (39) as a template, and cloning the *AatII*-cut fragment into the same site of pUC18.

The 49 expression vectors are available from Addgene (<https://www.addgene.org>).

Table 2. Destination vectors for use with the *Candida albicans* ORFeome. Plasmid names are based on the combination of modules

Plasmid name*	Accession number	Selection marker	Promoter	N-Tag	C-Tag
pCA-DEST1100	MG188268	<i>URA3</i>	<i>P_{TET}</i>		
pCA-DEST1101	MG188269	<i>URA3</i>	<i>P_{TET}</i>		HA ₃
pCA-DEST1103	MG188271	<i>URA3</i>	<i>P_{TET}</i>		TAP
pCA-DEST1110	MG188272	<i>URA3</i>	<i>P_{TET}</i>	HA ₃	
pCA-DEST1130	MG188274	<i>URA3</i>	<i>P_{TET}</i>	TAP	
pCA-DEST1300	MG188282	<i>URA3</i>	<i>P_{TDH3}</i>		
pCA-DEST1301	MG188283	<i>URA3</i>	<i>P_{TDH3}</i>		HA ₃
pCA-DEST1303	MG188285	<i>URA3</i>	<i>P_{TDH3}</i>		TAP
pCA-DEST1310	MG188286	<i>URA3</i>	<i>P_{TDH3}</i>	HA ₃	
pCA-DEST1330	MG188288	<i>URA3</i>	<i>P_{TDH3}</i>	TAP	
pCA-DEST2300	MG188303	<i>NAT1</i>	<i>P_{TDH3}</i>		
pCA-DEST2301	MG188304	<i>NAT1</i>	<i>P_{TDH3}</i>		HA ₃
pCA-DEST2303	MG188306	<i>NAT1</i>	<i>P_{TDH3}</i>		TAP
pCA-DEST2310	MG188307	<i>NAT1</i>	<i>P_{TDH3}</i>	HA ₃	
pCA-DEST2330	MG188309	<i>NAT1</i>	<i>P_{TDH3}</i>	TAP	
pCA-DEST1102	MG188270	<i>URA3</i>	<i>P_{TET}</i>		GFP
pCA-DEST1120	MG188273	<i>URA3</i>	<i>P_{TET}</i>	GFP	
pCA-DEST1200	MG188275	<i>URA3</i>	<i>P_{PCK1}</i>		
pCA-DEST1201	MG188276	<i>URA3</i>	<i>P_{PCK1}</i>		HA ₃
pCA-DEST1202	MG188277	<i>URA3</i>	<i>P_{PCK1}</i>		GFP
pCA-DEST1203	MG188278	<i>URA3</i>	<i>P_{PCK1}</i>		TAP
pCA-DEST1210	MG188279	<i>URA3</i>	<i>P_{PCK1}</i>	HA ₃	
pCA-DEST1220	MG188280	<i>URA3</i>	<i>P_{PCK1}</i>	GFP	
pCA-DEST1230	MG188281	<i>URA3</i>	<i>P_{PCK1}</i>	TAP	
pCA-DEST1302	MG188284	<i>URA3</i>	<i>P_{TDH3}</i>		GFP
pCA-DEST2302	MG188305	<i>NAT1</i>	<i>P_{TDH3}</i>		GFP
pCA-DEST1320	MG188287	<i>URA3</i>	<i>P_{TDH3}</i>	GFP	
pCA-DEST2320	MG188308	<i>NAT1</i>	<i>P_{TDH3}</i>	GFP	
pCA-DEST1400	MG188289	<i>URA3</i>	<i>P_{ACT1}</i>		
pCA-DEST1401	MG188290	<i>URA3</i>	<i>P_{ACT1}</i>		HA ₃
pCA-DEST1402	MG188291	<i>URA3</i>	<i>P_{ACT1}</i>		GFP
pCA-DEST1403	MG188292	<i>URA3</i>	<i>P_{ACT1}</i>		TAP
pCA-DEST1410	MG188293	<i>URA3</i>	<i>P_{ACT1}</i>	HA ₃	
pCA-DEST1420	MG188294	<i>URA3</i>	<i>P_{ACT1}</i>	GFP	
pCA-DEST1430	MG188295	<i>URA3</i>	<i>P_{ACT1}</i>	TAP	
pCA-DEST2200	MG188296	<i>NAT1</i>	<i>P_{PCK1}</i>		
pCA-DEST2201	MG188297	<i>NAT1</i>	<i>P_{PCK1}</i>		HA ₃
pCA-DEST2202	MG188298	<i>NAT1</i>	<i>P_{PCK1}</i>		GFP
pCA-DEST2203	MG188299	<i>NAT1</i>	<i>P_{PCK1}</i>		TAP
pCA-DEST2210	MG188300	<i>NAT1</i>	<i>P_{PCK1}</i>	HA ₃	
pCA-DEST2220	MG188301	<i>NAT1</i>	<i>P_{PCK1}</i>	GFP	
pCA-DEST2230	MG188302	<i>NAT1</i>	<i>P_{PCK1}</i>	TAP	
pCA-DEST2400	MG188310	<i>NAT1</i>	<i>P_{ACT1}</i>		
pCA-DEST2401	MG188311	<i>NAT1</i>	<i>P_{ACT1}</i>		HA ₃
pCA-DEST2402	MG188312	<i>NAT1</i>	<i>P_{ACT1}</i>		GFP
pCA-DEST2403	MG188313	<i>NAT1</i>	<i>P_{ACT1}</i>		TAP
pCA-DEST2410	MG188314	<i>NAT1</i>	<i>P_{ACT1}</i>	HA ₃	
pCA-DEST2420	MG188315	<i>NAT1</i>	<i>P_{ACT1}</i>	GFP	
pCA-DEST2430	MG188316	<i>NAT1</i>	<i>P_{ACT1}</i>	TAP	

* In bold: vectors validated with *UME6*

Validation of 15 expression plasmids

Construction of *C. albicans* *UME6*-overexpression strains. Detailed methods for the transfer of *C. albicans* ORFs from pDONR207 into the expression plasmids as well as the integration of the resulting expression plasmids at the *RPS1* locus have been described (35). Briefly, the *UME6* ORF was transferred from the entry clone into each one of 15 expression vectors using the Gateway™ LR Clonase™ II Enzyme Mix (Invitrogen). After *E. coli* transformation, the plasmids were verified by EcoRV digestion. The *NAT1*- and *URA3*-bearing expression plasmids were digested by StuI and transformed into *C. albicans* strain CEC369 (38) (that derives from CEC161 (38) = BWP17 (40) +HIS+ARG) or CEC2907 (12), respectively, accord-

ing to Walther and Wendland (41). Transformants were selected for prototrophy or nourseothricin resistance, respectively, and verified by PCR using primer CIPUL with (i) primer CIPUR for the *URA3*-bearing plasmids and (ii) primer CgSAT1-rev for the *SAT1*-bearing plasmids, that yield 1 kb and 1.6 kb products, respectively, if integration of the OE plasmid has occurred at the *RPS1* locus.

Induction of the Tet-On system. Overexpression from *P_{TET}* was achieved by the addition of anhydrotetracycline (ATc, 3 µg/ml; Fisher Bioblock Scientific) in YPD at 30°C (42). Overexpression experiments were carried out in the dark, as ATc is light sensitive.

Microscope analysis for filamentation. Cells were observed with a Leica DM RXA microscope (Leica Microsystems) with an x40 oil-immersion objective.

Analysis of TAP- and 3HA-tagged proteins by western blots.

For the P_{TET} and P_{TDH3} strains, a 30 ml culture in YPD or YPD+ATc3 was inoculated at $OD_{600} = 0.2$ or 2×10^6 cells/ml with a freshly grown colony and incubated at 30°C with shaking until OD_{600} reached ~1.

For the 3HA-tagged strains, 750 µl of cultures were collected by centrifugation, resuspended in 25 µl of water and diluted in 25 µl of 2× Laemmli sample buffer. After 10 min at 100°C, proteins were stored at –80°C or directly submitted to electrophoresis.

For the TAP-tagged strains, 20 ODs of exponentially growing cells were collected by centrifugation and resuspended in lysis buffer (9M Urea, 1.5% w/v dithiothreitol, 2–4% w/v CHAPS, and 1.5 M Tris pH9.5). Homogenization of the cells was achieved using a FastPrep bead beater. After homogenization, the lysed cells were centrifuged at 13 000 rpm for 10 min at room temperature, and the supernatant containing the solubilized proteins was used directly or stored at –80°C.

Proteins were separated on an Invitrogen 8% Nu-Page gel, transferred onto nitrocellulose. TAP- and 3HA-tagged proteins were detected using peroxidase-coupled anti-peroxidase and anti-HA-peroxidase antibodies (Sigma and Roche, respectively) and an ECL kit (GE Healthcare).

Construction of opaque mating-compatible two-hybrid strains and GatewayTM-compatible two-hybrid vectors

Mating-compatible strains were generated by deletion of *MTLa* or *MTLα* locus using the *SAT1* flipper cassette (39) in the two-hybrid strain background SC2H3 (33). To delete the *MTLa* locus, flanking regions were amplified with primers *MTLa*-5'F and *MTLa*-5'R, and with *MTLa*-3'F and *MTLa*-3'R. To delete the *MTLα* locus, homologous regions were amplified with primers *MTLα*-5'F and *MTLα*-5'R, and with *MTLα*-3'F and *MTLα*-3'R. Both fragments for each locus were cloned into pSAT1 (39), at *SacI*/*NotI* and *XhoI*/*KpnI* sites respectively. *SacI*/*KpnI* deletion constructs were transformed in SC2H3 (33) and transformants were selected on YPD medium containing 200 µg/ml of nourseothricin. Positive SC2H3a and SC2H3α strains were subsequently grown in maltose medium for induction of the recombinase and loss of the *SAT1* flipper cassette.

For induction of opaque switching, a *WOR1* fragment was amplified with primers *WOR1*F and *WOR1*R and cloned into pNIM1 vector (42) at *Sall* and *BglII* sites. SC2H3a and SC2H3α strains were transformed with pNIM1-*WOR1* with selection on nourseothricin-containing medium. The resulting strains, SC2H3a-p*WOR1* and SC2H3α-p*WOR1*, were grown in the presence of doxycycline (50 µg/ml) to induce the opaque state (43). Opaque mating-compatible strains were finally transformed with prey or bait plasmid and selected on SC-ARG or SC-LEU respectively.

Bait and prey two-hybrid vectors, pC2HB and pC2HP, respectively (33) were converted into GatewayTM destination vectors using the GatewayTM Vector Conversion System

to generate pC2HB-GC and pC2HP-GC, respectively. The genes encoding the bait protein Hst7 (Orf19.469) and the prey Cek1 (Orf19.2886) were transferred by LR reactions from the donor collection of vectors into pC2HB-GC and pC2HP-GC destination vectors, respectively.

Mating approach and protein–protein interaction detection

Opaque cells of SC2H3a and SC2H3α, expressing VP16-Cek1 (Arg+) and *lexA*-Hst7 (Leu+) respectively, were crossed as follows. Opaque cells of both types were mixed at 1×10^6 cells each in Spider medium (44) and incubated at 23°C for 24 h. Resulting tetraploid cells were selected on SC-LEU-ARG medium for 48 h incubation at 30°C, and transferred to SC-HIS-MET medium for protein–protein interaction detection. Chromosome loss was induced on pre-sporulation medium at 37°C for 10 days as described previously (45).

RESULTS

Establishment of a sequence-validated *Candida albicans* OR-Feome

Our objective was to develop a *C. albicans* ORFeome encompassing as many of the 6205 ORFs predicted in Assembly 21 of the *C. albicans* genome as possible (46). To this aim, forward and reverse oligonucleotides with, respectively, *attB* and *attP* sequences at their 5' ends were synthesized for each of the 6205 ORFs (Supplementary Table S1), used in independent PCR reactions with genomic DNA of *C. albicans* strain SC5314 (47) and the resulting PCR products were cloned in pDONR207 using GatewayTM recombinational cloning (31). The resulting plasmids were then subjected to Sanger sequencing at the 5' and 3' ends of the cloned ORFs and to Illumina sequencing throughout the cloned ORFs.

Among the 6205 ORF sequences (from Assembly 21) used for oligonucleotide design, 6 are no longer present in Assembly 22 while 20 are annotated as mitochondrial genes in Assembly 22. Among the 6179 remaining ORFs, 5099 (83%) were successfully cloned and full-length sequence-validated. Sequences were validated by comparing the entire sequence of each cloned ORF against the reference sequences for haplotype A and B of the *C. albicans* SC5314 genome available at the Candida Genome Database (CGD; version_A22-s07-m01-r18; (48)). We defined 4 groups: (i) 4061 sequences that are 100% identical with a reference sequence (**No SNP, no DIP**; where SNP stands for Single Nucleotide Polymorphism and DIP stands for Deletion/Insertion Polymorphism); (ii) 108 sequences that do not carry any SNP but carry DIPs (**No SNP, DIPs**); (iii) 843 sequences that carry SNPs but no DIP (**SNPs, no DIP**); and (iv) 87 sequences that carry both SNPs and DIPs (**SNPs and DIPs**) (Figure 1A and Supplementary Table S1). DIPs, multiples of 3, vary from 3 to 33 nt in length. ORFs with DIPs non-multiples of three were also retained when present within introns.

Overall, 4061/6179 variation-free *C. albicans* ORFs (65.7%) are now available to the community. Among the 930 SNP-containing ORFs, 460 contain 1 SNP, 131 contain 2 SNPs, 78 contain 3 SNPs, 74 contain 4 SNPs and 187

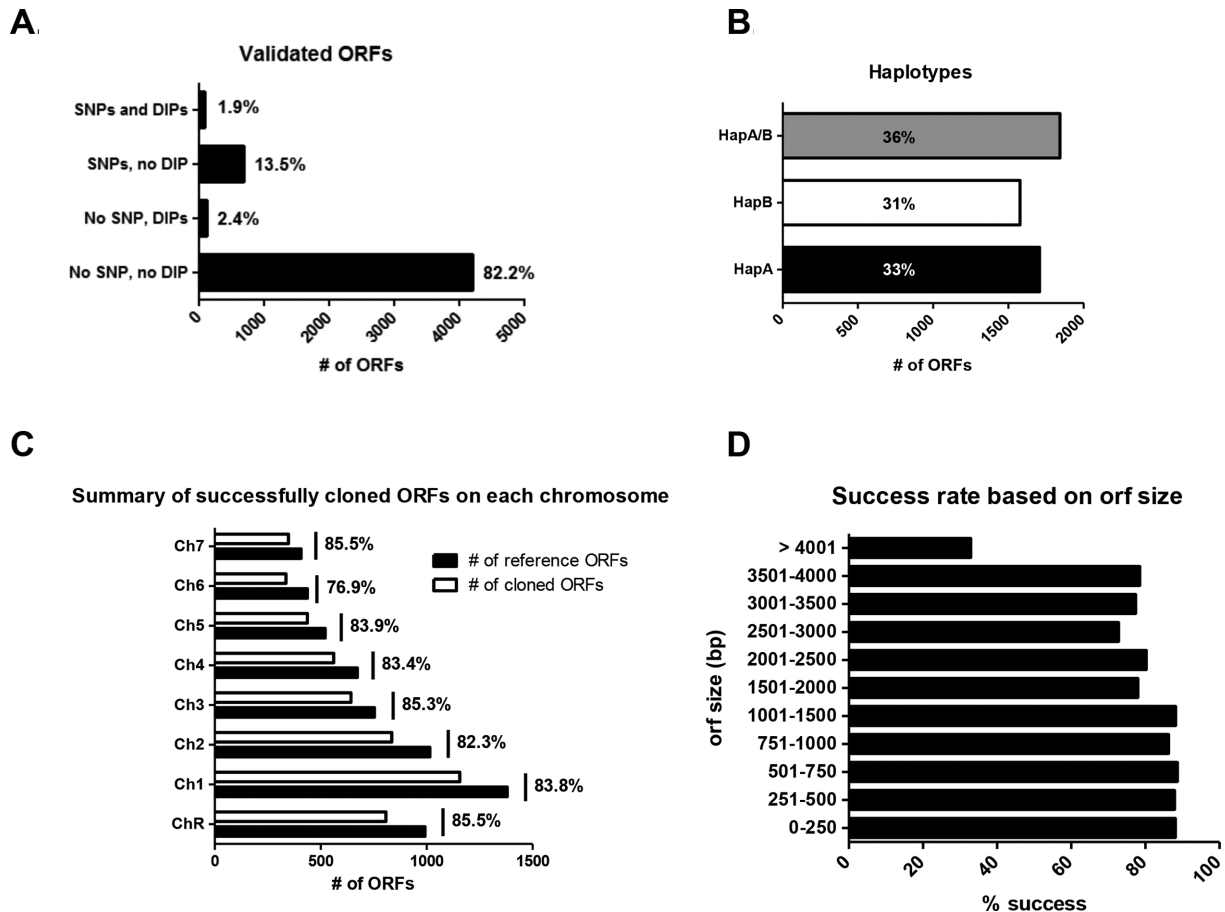


Figure 1. Statistics on the *Candida albicans* ORFeome. (A) Percentage of successfully cloned ORFs that are identical to the reference sequence (No SNPs, no DIPs) or that contain SNPs and/or DIPs. Only SNPs that do not introduce a STOP codon and DIPs multiple of 3 bp have been accepted. (B) Haplotypes distribution. Each cloned ORF has been assigned to HapA or HapB when there are differences between the two alleles of the ORF, and HapA/B when the two alleles of the ORF are identical (as defined in Assembly22). (C) Success rate on each chromosome. The graphs represent the number of reference ORFs and the number of successfully cloned ORFs on each chromosome, as well as the overall percentage of success for each chromosome. (D) Percentage of success based on ORF size.

ORFs contain 5 or more SNPs (up to 72 SNPs). For 36% of the validated ORFs, there was no difference between the two alleles in the reference sequences (**HapA/B**; Figure 1B). When nucleotide differences were present in the two alleles of the reference ORF sequence, we did not notice any bias in the haplotype that was cloned: haplotype A ORFs were cloned in 33% of cases (**HapA**; Figure 1B) and haplotype B ORFs were cloned in 31% of cases (**HapB**; Figure 1B). On chromosomes R, 1, 2, 3, 4, 5 and 7, ORF cloning was uniformly successful, with a cloning success rate ranging from ~82% to ~86%. Chromosome 6 ORFs were slightly underrepresented (76.9%) (Figure 1C). Although ORFs up to 1.5 kb could be cloned with a success rate around 87% and ORFs between 1.5 and 4 kb could be cloned with a success rate around 77%, we observed a decreased success rate for the longer ORFs (Figure 1D). GC content did not seem to be the cause for either lack of PCR amplification or cloning failure as we did not see a statistically significant difference in GC content when comparing successfully cloned and failed-ORFs (data not shown).

Analysis of the 6875211 nucleotides of the 5099 sequence-validated ORFs revealed 3029 SNPs. The ratio of non-

synonymous to synonymous changes due to SNPs was around 1. These nucleotide substitutions could be either real SNPs between our strain and the reference strain, or due to poor quality of some reference sequences, or mutations in the primers or PCR-induced mutations. Overall, the resulting maximum error rate amounted to 4.4×10^{-4} i.e. 1 SNP every 2270 cloned nucleotides. Notably, the *C. albicans* SC5314 genome sequence available at CGD (version_A22-s07-m01-r18) contained 272 ORFs with sequence ambiguities for at least one of the alleles. These ambiguities included stretches of 'Ns' or IUPAC code nucleotides (Y, R, S, M, K, W). The ORFeome-generated sequencing data resolved sequence ambiguities for 110 of these ORFs (Supplementary Tables S3 and 4). In this study, we also detected recombinant haplotypes for 116 of the cloned ORFs (Supplementary Table S5) that displayed characteristics of both reference haplotypes.

Taken together, our study provides an extensive, extremely high quality *C. albicans* ORFeome.

CandidaOrfDB: a database for the *C. albicans* ORFeome

CandidaOrfDB was created to integrate the data of the *C. albicans* ORFeome project and is available at <http://candidaorfeome.eu>. CandidaOrfDB enables the scientific community to search for availability and quality of the clones. All data pertinent to the cloning process are stored in the database. This information includes the name and sequence of the primers used to amplify the ORFs from *C. albicans* SC5314 genomic DNA, the coordinates of the primers in their 96-well storage plates and any sequencing information available on the clones. SNPs and DIPs, their location in the ORF and their influence on the corresponding amino acid sequences are shown (Figure 2). Nucleotide sequence of the cloned ORF and the corresponding amino acid sequence are displayed with highlights of SNPs or DIPs relative to the closest haplotype sequence (Figure 2). The reference sequence data have been extracted from CGD (48). The database can be queried through the ORF number (orf19.xxxx or 19.xxxx; (5)), the Assembly 22 name (Ci_XXXXXW or Ci_XXXXXC; (5)) or the gene name.

A collection of destination vectors for exploiting the *C. albicans* ORFeome

The *C. albicans* ORFeome described above was developed in pDONR207 as this allows subsequent transfer of the cloned ORFs to Gateway™-adapted destination vectors. While destination vectors for ORF expression in hosts such as *E. coli* or *S. cerevisiae* are available (49,50), only a few destination vectors for ORF expression in *C. albicans* have been reported (12). Therefore, we set out to establish a collection of Gateway™-adapted destination vectors for constitutive or conditional expression of untagged or tagged ORFs in *C. albicans*. Our primary collection of 15 *C. albicans* destination vectors derived from CIP10S (12) provides a choice of two promoters, either the constitutive promoter P_{TDH3} or the inducible promoter P_{TET} , and the option for N- or C-terminal fusion to various epitope tags (3xHA or TAP) (Table 2 and Figure 3). Integration of the destination vectors and their derivatives at the *RPS1* locus in the *C. albicans* genome is promoted by *StuI* or *I-SceI* linearization. These CIP10-derived vectors carry either the auxotrophic marker *URA3* or the *NAT1* marker that confers resistance to nourseothricin and can be used with clinical isolates. However, P_{TET} -bearing plasmids cannot carry the *NAT1* marker since the transactivator needed for tetracycline-mediated induction of P_{TET} is borne on the *NAT1*-carrying pNIMX plasmid (12). All vectors harbor a so-called spacer sequence (SP) originating from the *E. coli* kanamycin resistance gene, for barcode insertion and subsequent Illumina-based barcode sequencing. A second set of 34 plasmids was also generated with the constitutive promoters P_{ACT1} or the inducible promoter P_{PCK1} , and the option for N- or C-terminal fusion to GFP (Table 2). All 49 destination vectors were designated with a standardized nomenclature, pCA-DESTijkl, whereby i stands for the transformation marker (1, *URA3*; 2, *NAT1*); j stands for the promoter (1, P_{TET} ; 2, P_{PCK1} ; 3, P_{TDH3} ; 4, P_{ACT1}); k stands for N-terminal tagging (0, no tag; 1, 3xHA; 2, GFP; 3, TAP); and l stands for C-terminal tagging (0, no tag; 1, 3xHA; 2,

GFP; 3, TAP) (Table 2 and Figure 3). All destination vectors are available from Addgene (<https://www.addgene.org>).

In order to validate that the primary set of 15 destination vectors could drive constitutive or conditional expression of untagged or tagged ORFs, the *UME6* ORF was transferred into each of them using LR Clonase™. *UME6* encodes a transcription factor whose overexpression has been shown to force filamentation in *C. albicans* (51,52). The validation criteria for the destination vectors were (i) success of the LR reaction, (ii) integration in the *C. albicans* genome at the *RPS1* locus, (iii) filamentation phenotype and/or (iv) detection of the 3xHA- or TAP-tagged Ume6 protein by western blot. The LR reaction was successfully used to transfer *UME6* from the pDONR207::*UME6* plasmid to all 15 destination vectors. The resulting expression plasmids were successfully integrated at the *C. albicans* *RPS1* locus. The five strains containing P_{TET} were induced overnight at 30°C by adding 3 µg/ml anhydrotetracycline (ATc3) to the culture medium, while the 10 strains containing P_{TDH3} were grown overnight at 30°C in YPD. As previously described (12,51,52), overexpression of Ume6 led to hyperfilamentation. This phenotype was observed for all strains, regardless of the tag used (Figure 4A and B). Nevertheless, the C-terminal TAP-tag appeared to hinder Ume6 function. Indeed, protein tags can potentially alter protein localization and/or protein function. One strength of our system is that it provides a choice of tagging, that could minimize the effect of the tag on a specific protein function. 3xHA- or TAP-tagged Ume6 was detected in the relevant strains and under the appropriate growth conditions (Figure 5A and B). We noticed extra bands migrating faster than the 3HA-tagged Ume6 protein, which are likely to result from protein degradation. The 3HA-tagged Ume6 protein was extracted by resuspending the cells in 2× Laemmli sample buffer and boiling at 100°C for 10 min. This rapid protocol might be responsible for the observed protein degradation.

Taken together, these data present a collection of 49 available destination vectors and validate 15 of those for application with the *C. albicans* ORFeome.

Proof of concept of a two-hybrid matrix approach of protein–protein interaction detection via mating in *C. albicans*

The availability of the ORFeome collection is a prerequisite to large, systematic two-hybrid (2H) screenings in *C. albicans*. The Candida 2H (C2H) system was developed for targeted one to one protein–protein interaction detection (33). Hence, there was a need to engineer the system for high throughput screening based on rapid and convenient recombination cloning systems for the generation of prey/bait arrays of proteins, and to use a mating approach to circumvent the low efficiency of transformation of this fungus. The former was obtained by adapting the prey and bait recipient vectors for Gateway™-mediated transfer of the ORFeome library, yielding pC2HB-GC and pC2HP-GC, respectively. The latter involved the combined processes of white-opaque switching and the preparation of mating-compatible 2H strains. The pleiomorphic fungus *C. albicans* is characterized by a parasexual cycle, with the possible mating of diploids, and generation of tetraploids, the absence of meiosis and the reversion to the diploid

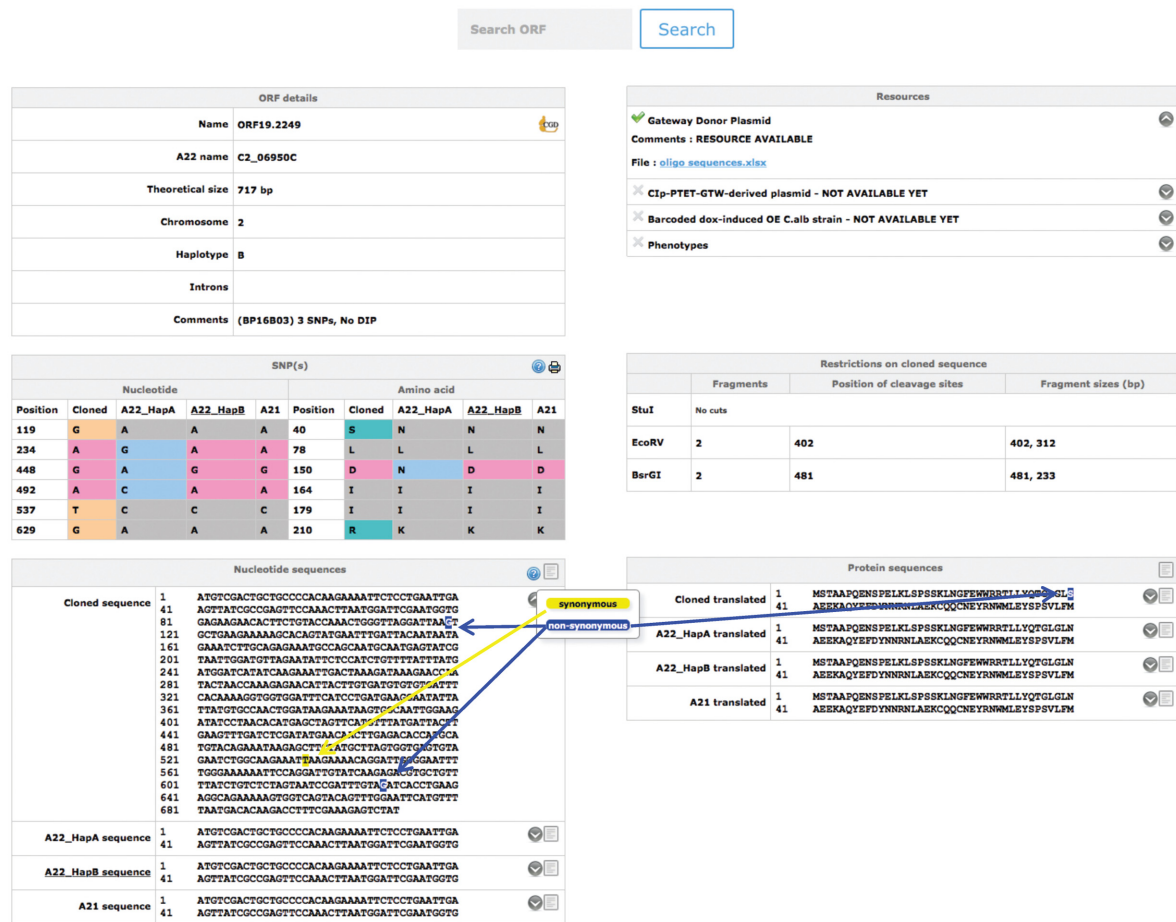


Figure 2. Snapshot of the CandidaOrfDB interface. An example of an ORF page is shown. In the 'ORF details' box, the different ID names, the length and the chromosome location of the ORF of interest are displayed. The haplotype assigned to the cloned ORF is noted (A, B or A/B if there is no allelic differences or equal number of differences against both haplotypes). The coordinates of introns are indicated when present. The summary results of the sequence analysis against the reference sequence are presented. The 'SNP(s)' box shows a table that lists the sequence differences between the cloned ORF and the reference sequences (Haplotypes A and B from Assembly22, and Assembly21 sequences). The 'Nucleotide and Protein sequences' boxes display the sequences with a color code for synonymous and non-synonymous SNPs. All sequences can be downloaded. The 'Resources' box displays links towards information that is relevant to each resource, i.e. oligonucleotide sequences for the BP clones, barcode sequence for the overexpression plasmids and the *C. albicans* overexpression strains, position of the clone in the different plates of the collection, plasmid sequences. The 'Restrictions on the cloned sequence' box indicates the existence of restriction sites, as well as the size of the expected fragments for enzymes that are used in regards to subsequent applications of these donor plasmids.

state by chromosome loss (reviewed in (53)). An essential pre-requisite to mating in *C. albicans* is the phenotypic switch from white to opaque, a stable but reversible switch regulated by environmental stimuli such as low temperatures, carbon dioxide and nutrients. The epigenetic switch is tightly linked to mating since the $\alpha 1/\alpha 2$ complex, encoded at the mating type like (*MTL*) loci, acts as a repressor of opaque switching (54). In that context, the two-hybrid strain SC2H3 originating from the diploid α/α SN152 strain (55) was deleted for the *MTL* α or *MTL* α locus to construct SC2H3 α and SC2H3 α strains. The efficient switch to opaque in the hemizygote strains was achieved by the doxycycline-controlled expression of *WOR1*, a major regulator of the white to opaque switch (43,56).

A proof of principle of the whole procedure for protein-protein detection is shown in Figure 6. The MAP kinase ki-

nase Hst7 was used as bait and linked to the DNA binding domain *lexA*, as part of the pC2HB-GC vector. Similarly, the Cek1 kinase was expressed as a prey protein, fused to the activation domain VP16, component of the pC2HP-GC vector. pC2HB-Hst7 and pC2HP-Cek1 were transformed into opaque SC2H3 α and SC2H3 α strains, respectively. Mating of the resulting transformants was achieved through selection for leucine and arginine prototrophy. Upon interaction of the two proteins, the reconstituted transcriptional module promoted the expression of the *HIS1* marker, allowing only the mating-derived strains to grow on histidine-free medium, whereas the original diploid strains could not (Figure 6B). It is possible that some strains reverted to the diploid state, but we did not perform FACS analysis to assess this as it is not relevant for the protein-protein interaction analysis. All transformants were able to grow in the

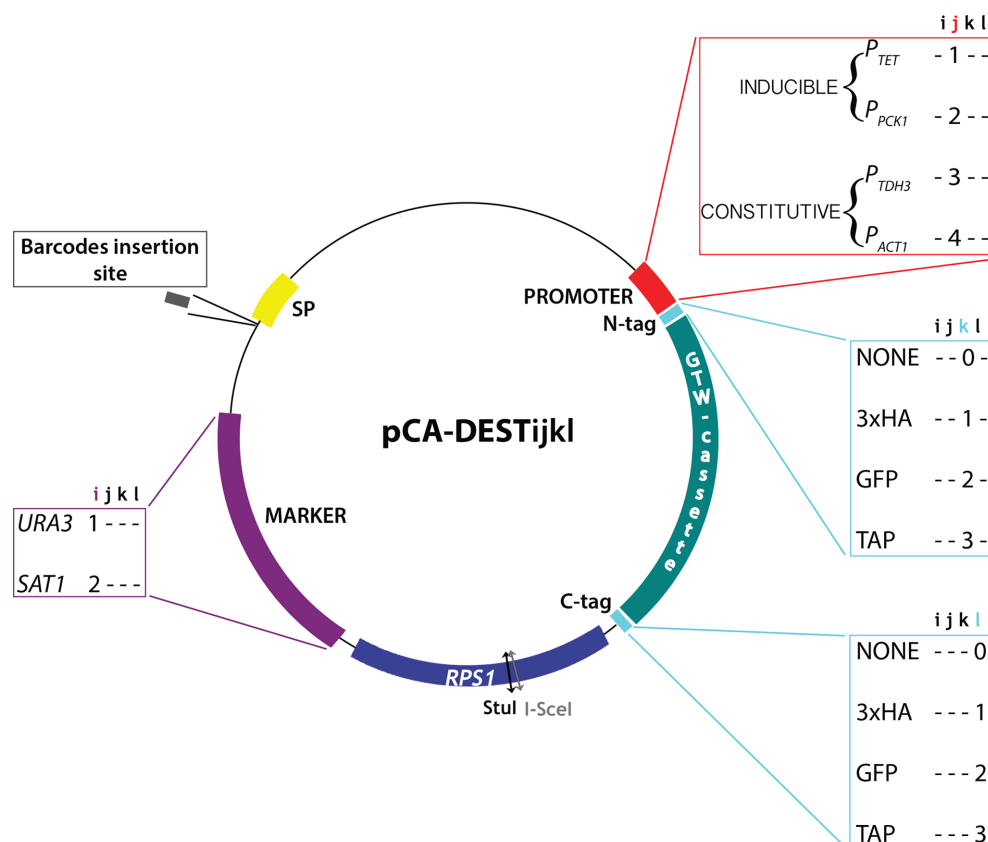


Figure 3. Structure of the destination vectors for use with the *Candida albicans* ORFeome. Schematic view of the 49 destination vectors, each designated with a standardized nomenclature, pCA-DESTijkl, whereby i stands for the transformation marker (1, *URA3*; 2, *NAT1*); j stands for the promoter (1, P_{TET} ; 2, P_{PCK1} ; 3, P_{TDH3} ; 4, P_{ACT1}); k stands for N-terminal tagging (0, no tag; 1, 3xHA; 2, GFP; 3, TAP); and l stands for C-terminal tagging (0, no tag; 1, 3xHA; 2, GFP; 3, TAP). The spacer sequence (SP), represented by the yellow box, is intended to facilitate subsequent Illumina-based barcode sequencing. The Gateway cassette (GTW), represented by the green box, requires working with *ccdB* resistant *Escherichia coli* strains. Integration of StuI-linearized plasmids (or at the nearby I-SceI site if the cloned ORF contains StuI sites) is targeted at the *RPS1* locus.

absence of arginine and leucine, indicating the presence of the prey and bait vectors respectively. In addition, all these strains were able to grow in absence of histidine, indicative of the targeted protein–protein interaction.

DISCUSSION

A partial *C. albicans* GatewayTM-adapted ORFeome (ORFeomeV1; 644 ORFs) and the corresponding *C. albicans* overexpression strains have already been successfully used to investigate morphogenesis, biofilm formation and genome dynamics in *C. albicans* (12,32,57). In this study, we have now generated the *C. albicans* ORFeomeV2 within the GatewayTM recombination cloning system, as well as a collection of destination vectors suitable for expression in *C. albicans*.

This new *C. albicans* ORFeome resource encompasses 5099 ORFs (83% of the annotated ORFs) and will be made available to the community upon request. The resource is supported by the CandidaOrfDB database, providing information on the individual plasmids and their sequences. The *C. albicans* ORFeomeV2 is of unprecedented quality, as all ORFs in the collection are fully sequenced, which remains an exception in large-scale ORFeome projects where ORFs are rarely sequenced in their entirety and only the 5'- and

3'-ends of the cloned ORFs are sequenced to confirm identity and the absence of frameshift mutations in the primers (16,17,19,22,24,30). Nevertheless, it should be noted that further analysis of each mutation-containing ORF is required to determine whether or not mutations affect the function of the ORF. Given these high standards, the success rate of 83% that we achieved with the *C. albicans* ORFeomeV2 is quite remarkable.

In eukaryotes, ORFeomes are usually cloned from full-length cDNA libraries to account for the presence of introns and therefore splicing variants. However, only 6% of *C. albicans* genes have introns (58), rendering the generation of the *C. albicans* ORFeome more straightforward than for pluricellular eukaryotes. Indeed, ORFs were simply amplified from the genomic DNA of the reference strain SC5314 and therefore, 360 ORFs in the *C. albicans* ORFeomeV2 harbor introns, a matter that should be taken into consideration when expressing ORFs in a prokaryotic host and, possibly, eukaryotic hosts other than *C. albicans*. A second aspect to be taken into consideration when using the ORFeome in hosts other than *C. albicans* is the unusual codon usage in this species (59). Indeed, in *C. albicans*, CUG is decoded as a serine instead of a leucine the majority of the

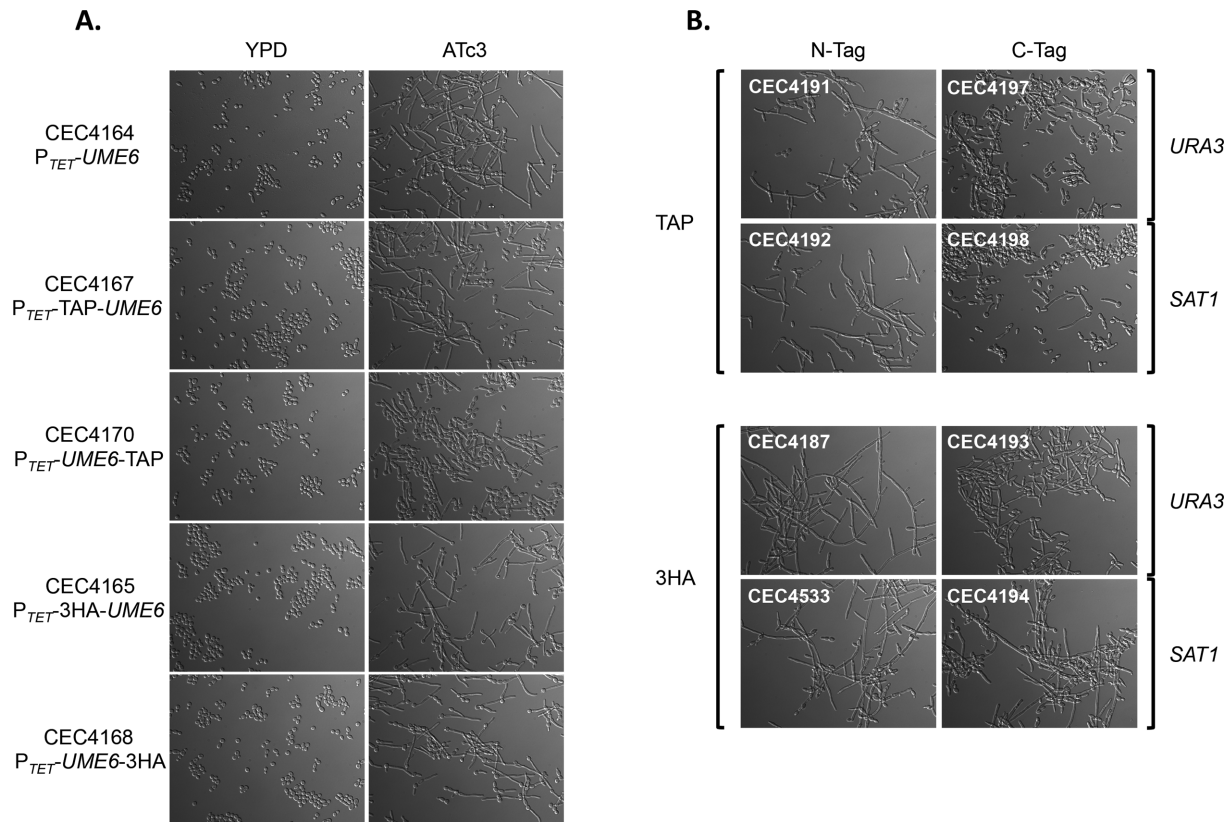


Figure 4. Ume6-driven filamentation validates the primary set of 15 destination vectors. Inducible (**A**) and constitutive (**B**) overexpression of *UME6* triggers filamentation. Isolates were grown in rich medium in presence or absence of ATc3 for 2–4 h at 30°C. Cells were observed with a Leica DM RXA microscope (Leica Microsystems) with an x40 oil-immersion objective.

time. Hence, improper translation in hosts with a standard genetic code may distort protein structure and function.

Sanger sequencing of both 5' and 3' ends was performed to confirm ORF identity and exclude clones containing primer or recombination errors. Previous studies have reported mutation rates in primers of 3–10% (27,30). Similar rates were observed in this work. Unlike other Gateway™ re-combinational cloning projects (16,30), we did not see major differences in cloning efficiency for ORFs up to 4 kb. A decrease in success rate was observed only for ORFs >4 kb. This size bias could be attributed to an increased difficulty to amplify the ORF by PCR, a reduced efficiency of the Gateway™ BP Clonase™ reactions with long PCR products, and the error rate of the PCR polymerase, which increases with longer products. In addition, we also corrected the sequences of 110 ORFs with sequence ambiguities (N-tracts and IUPAC code nucleotides) according to the Candida Genome Database and identified 116 ORFs that display a recombinant haplotype. Recombinant haplotypes could be explained by template switching during PCR cycles or by incorrectly phased SNPs in reference sequences. This could be addressed by performing long-read sequencing of the *C. albicans* SC5314 genome.

However, many challenges remain to be addressed. For heterozygous genes, only one allele is present in the ORFeome. Because functional differences have been reported between the two alleles of a heterozygous gene (60–62), it would be relevant to also clone and validate the second al-

lele in these instances. In addition, oligonucleotides have been designed based on annotation of the haploid set of Assembly 19 of the *C. albicans* genome. As a consequence, genes of the *MTLα* locus have not been included in the ORFeome. Despite our efforts, the collection is still missing 1081 clones. The next version of the *C. albicans* ORFeome could extend gene coverage by adding the missing ORFs, allelic variants or strain-specific variations.

ORFeomes are essential to bridge the gap between genome annotation and systems biology and allow large-scale gene and protein characterization. The development of a collection of *C. albicans* constitutive or conditional overexpression strains is one of the applications of the *C. albicans* ORFeome that we have successfully explored (12,32,57). In this respect, the *C. albicans* ORFeome project is currently completing its second and third phases, which consist of transferring the 5099 cloned ORFs into barcoded destination vectors and generating a collection of *C. albicans* barcoded overexpression mutants, each mutant carrying one of the 5099 cloned ORFs under the control of the inducible P_{TET} promoter. CandidaOrfDB already provides information on the available overexpression plasmids and strains. In this study, we have paved the way for a second application of the *C. albicans* ORFeome through the development of tools for a 2H matrix approach of protein–protein interaction detection via mating in *C. albicans*. Our data show that mating of diploid *C. albicans* expressing a bait fused to the LexA DNA binding domain and a prey

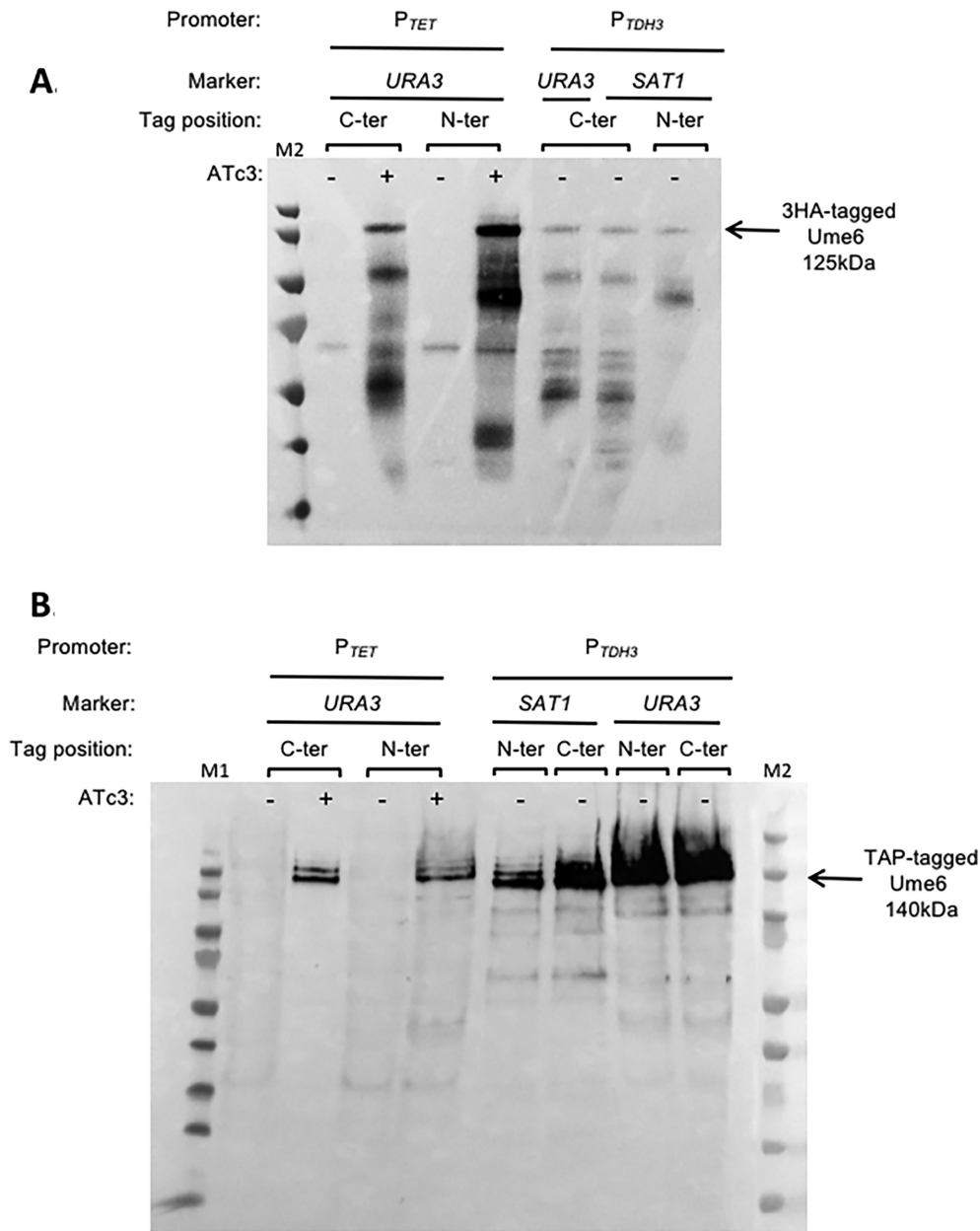


Figure 5. Detection of 3xHA- or TAP-tagged Ume6 protein by western blot. Production of 3xHA-tagged (**A**) and TAP-tagged (**B**) Ume6 proteins. *Candida albicans* strains harboring the P_{TET} and P_{TDH3} constructions were grown in YPD $\pm$ ATc3 for 2 and 4 h, respectively. Whole cell extracts were separated by SDS-PAGE and probed with a peroxidase-coupled antibody, allowing the detection of the 3xHA-tagged and TAP-tagged Ume6 protein. The tagged Ume6 proteins are indicated by an arrow along with their deduced sizes. M1: PageRuler Prestained Protein Ladder (Thermo Scientific) and M2: Precision Plus Protein™ Dual Color Standards (Bio-Rad).

fused to the VP16 activation domain, respectively, allows protein–protein interactions to be tested. In *S. cerevisiae*, large-scale 2H screens can be performed in a matrix design whereby haploid strains expressing baits and preys are mated and protein–protein interactions are scored in the resulting diploids. Our toolkit now enables the implementation of such a matrix design for large-scale 2H screens in *C. albicans*. To this aim, a collection of 1500 prey clones has already been generated. As mentioned above, *C. albicans* codon usage is unusual, which limits the development of applications of the *C. albicans* ORFeome in species that use

standard decoding such as *S. cerevisiae*. Our development of tools for large-scale 2H screens in *C. albicans* circumvents this limitation, opening the path for the characterization of the *C. albicans* interactome. Defining the *C. albicans* interactome will undoubtedly impact our understanding of *C. albicans* pathogenesis in humans.

In summary, high-level gene coverage coupled with the versatility of the Gateway™ recombinational cloning, *C. albicans*-adapted functional genomics tools and full access to clones, make the *C. albicans* ORFeomeV2 a unique and

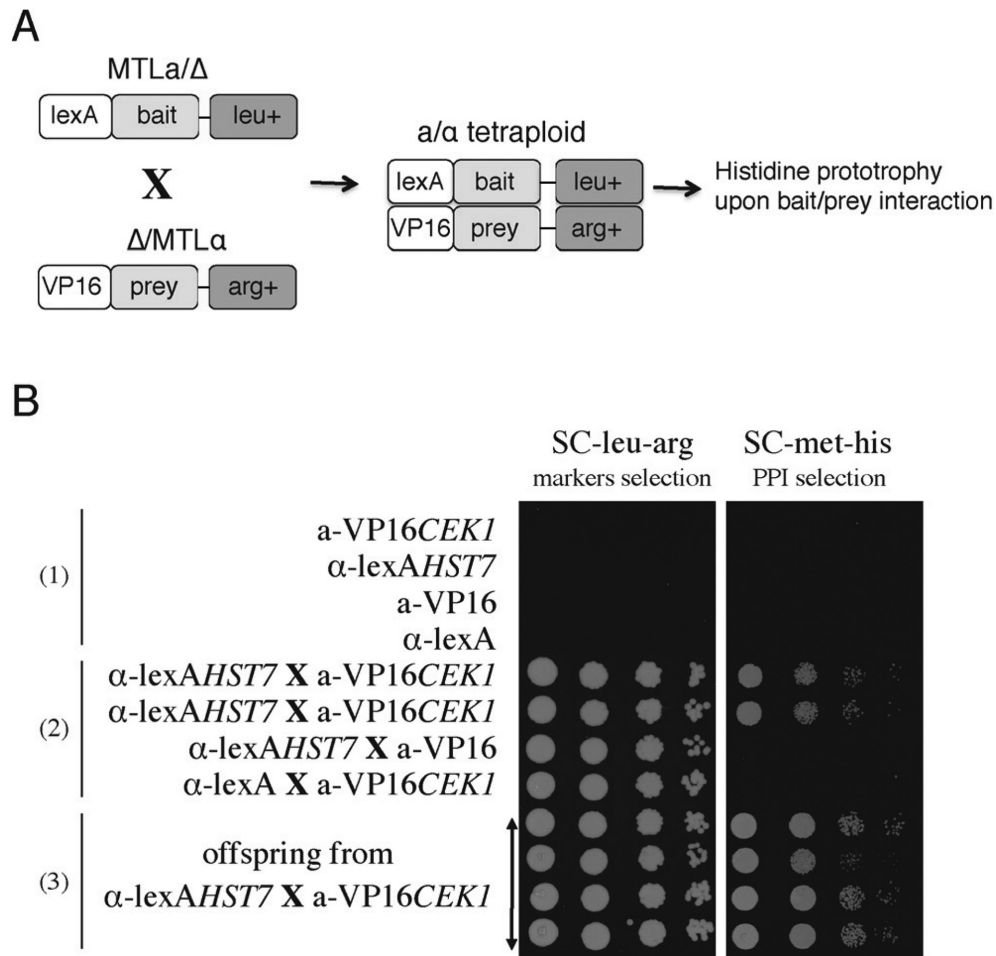


Figure 6. Proof of principle of two-hybrid based PPI detection via mating in *Candida albicans*. **(A)** Schematic representation of the concept. Diploid opaque *MTLa* bait-expressing cells were mixed with opaque *MTLa* prey-expressing cells to obtain tetraploids, as selected on leucine and arginine-free medium. Detection of protein-protein interaction was observed on medium lacking histidine as an indicator of expression of the two-hybrid readout marker. **(B)** Proof of principle using Hst7 as a bait and Cek1 as a prey, previously shown to interact (31). Cells of each type were spotted in a dilution series and growth was monitored on SC-leu-arg, which allowed growth of the tetraploid and diploid offspring and on SC-met-his, which allowed detection of PPI, only in those cells that are expressing both bait and prey proteins. As negative controls, tetraploids derived from the crossing of bait-expressing strains with empty prey vector transformed strains, and from the crossing of prey-expressing strains with strains expressing the empty bait vector grew on SC-leu-arg but not on SC-met-his.

valuable resource for the scientific community that should greatly facilitate future functional studies in *C. albicans*.

DATA AVAILABILITY

Plasmid sequences have been submitted to GenBank. Accession numbers are given in Table 2.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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