Supplementary Text SI

Supplementary Table S1. List of *Candida albicans* genes in this study.

Gene name	Assembly 19 name	Assembly 22 Name	Source for Gene Name
TAF12L	19.470	CR_03910C_A	This work
TAF12	19.6820	C3_06820C_A	This work
TAF4	19.1885	C2_07460W_A	This work
TAF11	19.6923	C3_03930W_A	This work
ADA1	19.307	C3_03100C_A	This work
ADA2	19.2331	C1_10860C_A	CGD
TBP1	19.1837	C1_10660W_A	CGD

Supplementary Table S2. List of Plasmids

Plasmid	Relevant Description	Source
pSL301	Cloning vector, Amp^R	Invitrogen
pLITMUS28	Cloning vector, Amp^R	NEB
pET28b+	$T7_{lac}$ promoter with N- and C-terminal 6xHis tag	Novagen
pGEX-5X3	P_{tac} promoter with N-terminal GST tag	GE Healthcare
pRS413	*HIS3, CEN6-ARS4*	(1)
YEplac181	*LEU2*, 2μ	(2)
pESC-LEU	P_{GAL1}, *LEU2*	Stratagene
pKN56	y*TAF12, LEU2, CEN6-ARS*	(3)
pKN58	y*TAF12-HFD, LEU2, CEN6-ARS*	(3)
pESC-LEU-yTAF12	P_{GAL1}-y*TAF12, LEU2*	This work
pGAL1-470	P_{GAL1}-*CaTAF12L*, *LEU2*	This work
pGAL1-6820	P_{GAL1}-*CaTAF12, LEU2*	This work
YEplac181-470HF	*CaTAF12L-HFD, LEU2*, 2μ	This work
YEplac181-6820HF	*CaTAF12-HFD, LEU2*, 2μ	This work
pSN40	*C.m.LEU2*	(4)
pSN52	*C.d.HIS1*	(4)
pSN69	*C.d.ARG4*	(4)
pSFS2A	*SAT1* Flipper cassette	(5)
pNIM1	*C.a.SAT1 CaADH1* p*Tet-CaGFP*	(6)
pFA6a-3HA-HIS3Mx6	HA_3 tag, *S.p. his5*$^+$	(7)
pPK335	TAP tag, Ca*URA3*	(8)
pHAH1-P_{MAL2}	HAH1-P_{MAL2} cassette	(9)
pHAH1-P_{TET}	HAH1-P_{TET} cassette	(9)
pHAH1	HAH1 disruption cassette	(9)
Ip18	pSL301 with *C.m.LEU2* from pSN40	This work
Ip19	pSL301 with *C.d.HIS1* from pSN52	This work
Ip20	pRS413 with Act1 terminator from pNIM1	This work
Ip21	TAP tag, *C.m.LEU2*	This work
Ip22	TAP tag, *C.d.HIS1*	This work
Ip24	His-TAP-TBP	This work
Ip26	Leu-TAP-TBP	This work
Ip27	pLITMUS28 with *SAT1* flipper from pSFS2a	This work
Ip28	pFA6a-3HA-HIS3Mx6 with *SAT1* flipper in place of KanMAX	This work
Ip30	HA_3 tag, *SAT1* flipper in pLITMUS28	This work
Ip36	Ip30 with TAF12L up- and down-flank	This work
Ip38	Ip30 with TAF12 up- and down-flank	This work

Ip40	TAF12L in pGEX-5X-3	This work
Ip41	TAF12 in pGEX-5X-3	This work
Ip42	TAF4 in pGEX-5X-3	This work
Ip43	ADA1 in pGEX-5X-3	This work
Ip44	TAF12L in pET28b+	This work
Ip45	TAF12 in pET28b+	This work
Ip46	TAF4 in pET28b+	This work
Ip47	ADA1 in pET28b+	This work
Ip48	TAF12L *Δ*C in pET28b+	This work
Ip50	6xHis-3xFLAG, ACT1t in pRS413	This work
pSK1	6xHis-3xFLAG, ACT1t with *SAT1* flipper	This work
pPC16	pNIM1 bearing *ARG4* instead of *SAT1*	This work
pPC18	pNIM1-TAF12-3xFLAG-2xGly-6xHis	This work
pPC19	pNIM1-TAF12L-3xFLAG-2xGly-6xHis	This work
pPC22	pNIM1-TAF12L-3xFLAG-2xGly-6xHis-*ARG4*	This work

Supplementary Table S3. List of *C. albicans* and *S. cerevisiae* Strains

Strain	Relevant Genotype	Source
Candida albicans		
SN87	*leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	(4)
SN95	*arg4Δ/arg4Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	(4)
SN152	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	(4)
ISC3	SN87 *TBP::TAP-C.d.HIS1/TBP*	This work
ISC7	SN87 *TBP::TAP-C.d.HIS1/TBP::TAP-C.m.LEU2*	This work
ISC9	SN95 *HAH1-P$_{MAL2}$-TAF12L/TAF12L*	This work
ISC10	SN95 *HAH1-P$_{MAL2}$-TAF12/TAF12*	This work
ISC11	SN95 *HAH1-P$_{MAL2}$-TAF12L/HIS1-P$_{MAL2}$-TAF12L*	This work
ISC12	SN95 *HAH1-P$_{MAL2}$-TAF12/ HIS1-P$_{MAL2}$-TAF12*	This work
ISC13	SN95 *taf12lΔ::SAT1 FLP/TAF12L*	This work
ISC14	ISC7 *TAF12L::HA$_3$-SAT1 FLP/TAF12L*	This work
ISC16	ISC7 *TAF12::HA$_3$-SAT1 FLP/TAF12*	This work
ISC18	SN87 *TAF12L::HA$_3$-SAT1 FLP/TAF12L*	This work
ISC19	SN87 *TAF12::HA$_3$-SAT1 FLP/TAF12*	This work
ISC31	ISC14 *TAF12L::HA$_3$-FRT/TAF12L*	This work
ISC32	ISC16 *TAF12::HA$_3$-FRT/TAF12*	This work
ISC33	ISC31 *TAF12L::HA$_3$-FRT/TAF12L::HA$_3$-SAT1 FLP*	This work

Strain	Relevant Genotype	Source
ISC34	ISC32 *TAF12::HA$_3$-FRT/TAF12::HA$_3$-SAT1 FLP*	This work
ISC35	SN95 *taf12lΔ::FRT/TAF12L*	This work
ISC36	SN95 *taf12l Δ::FRT/ taf12lΔ::SAT1 FLP*	This work
ISC37	SN95 *taf12Δ::SAT1 FLP/TAF12*	This work
ISC38	SN95 *taf12Δ::FRT/TAF12*	This work
ISC39	SN152 *ADA2::TAP-C.d.HIS1/ADA2*	This work
ISC40	SN152 *TAF11::TAP-C.d.HIS1/TAF11*	This work
ISC41	ISC18 *ADA2::TAP-C.d.HIS1/ADA2*	This work
ISC42	ISC18 *TAF11::TAP-C.d.HIS1/TAF11*	This work
ISC43	ISC19 *ADA2::TAP-C.d.HIS1/ADA2*	This work
ISC44	ISC19 *TAF11::TAP-C.d.HIS1/TAF11*	This work
ISC45	SN95 *taf12Δ::HAH1/TAF12*	This work
ISC46	ISC41 *ADA2::TAP-C.d.HIS1/ADA2::TAP-C.m.LEU2*	This work
ISC47	ISC42 *TAF11::TAP-C.d.HIS1/TAF11::TAP-C.m.LEU2*	This work
ISC48	ISC43 *ADA2::TAP-C.d.HIS1/ADA2::TAP-C.m.LEU2*	This work
ISC49	ISC44 *TAF11::TAP-C.d.HIS1/TAF11::TAP-C.m.LEU2*	This work
SKC3	SN87 *TAF12L::His6-Gly2-FLAG$_3$-FRT/TAF12L::His6-Gly2-FLAG$_3$-SAT1-FLP*	This work
SKC6	SN87 *TAF12::His6-Gly2-FLAG$_3$-FRT/ TAF12::His6-Gly2-FLAG$_3$-SAT1-FLP*	This work
SKC7	SN87 *ADA1::His6-Gly2-FLAG$_3$-SAT1-FLP/ADA1*	This work
SKC10	SN87 *TAF4::His6-Gly2-FLAG$_3$-SAT1-FLP/TAF4*	This work
SDC3	ISC11 *ADH1/adh1* <pNIM1>	This work
SDC6	ISC12 *ADH1/adh1*<pNIM1>	This work
SDC12	ISC36 *ADH1/adh1*<pPC16>	This work
SDC13	ISC11 *ADH1/adh1*<pPC19>	This work
SDC16	ISC12 *ADH1/adh1*<pPC18>	This work
SDC17	ISC36 *ADH1/adh1*<pPC22>	This work
Saccharomyces cerevisiae		
YSS19	*MATα G418^R his3Δ1 leu2Δ0 lys2Δ0 met15Δ0 ura3Δ0 taf12Δ::KanMX4 [TAF12-URA3-pRS416]*	This work
ISC20	YSS19 [pESC-LEU]	This work
ISC21	YSS19 [pESC-LEU-yTAF12]	This work
ISC22	YSS19 [pESC-LEU-470]	This work
ISC23	YSS19 [pESC-LEU-6820]	This work
ISC24	YSS19 [YEplac181]	This work

Strain	Relevant Genotype	Source
ISC25	YSS19 [yTAF12-LEU2-pRS415]	This work
ISC26	YSS19 [yTAF12 HFD-LEU2-pRS415]	This work
ISC27	YSS19 [470 HF-LEU2- YEplac181]	This work
ISC28	YSS19 [6820 HF-LEU2- YEplac181]	This work

Supplementary Table S4. List of Oligonucleotides

Primer	Sequence (5'-3')	Notes	Locus/Gene
ONC26	5'-CGGATCCCAGTGCAAGAATGAATAATG-3'	5' primer for *TAF12L* ORF; -10 to +10 with respect to ATG.	*19.470/TAF12L*
ONC27	5'-CTCTCGAGAGCATTATCATCATTCACA-3'	3' primer for *TAF12L* ORF; +2255 to +2232 with respect to ATG including the stop codon.	*19.470/TAF12L*
ONC28	5'-ACTGTCGACTAAATCATGGATTCATCAGCA-3'	5' primer for *TAF12* ORF; -6 to +14 with respect to ATG	*19.6820/TAF12*
ONC29	5'-GCCCGCGTCGACTTGATCTTTATTTAATTT-3'	3' primer for *TAF12* ORF; +1545 to +1525 with respect to ATG including the stop codon.	*19.6820/TAF12*
ONC42	5'-TGCCCACAATCACCACATTT-3'	5' primer for *TAF12L* HFD; +1741 to +1759 with respect to ATG.	*19.470/TAF12L*
ONC43	5'-GTTAATTAATGTTACATGCGTACAC-3'	3' common primer within the pESC-*LEU2* vector	pESC-*LEU*
ONC44	5'-TGACAACATCGACCTCAGCT-3'	5' primer for *TAF12* HFD; +1043 to +1063 with respect to ATG.	*19.6820/TAF12*
ONC66	AAC CTT TCC ACA AAC TGA CG	Internal primer pSFS plasmid; Binds to *FLP* gene in reverse orientaion; universal for *SAT1* flipper from 680nt in FLP region	*SAT1*-Flipper cassette
ONC71	AAATTCTGGAAATCTGGA	5' primer for *ACT1* terminator.	pNIM1
ONC72	GAAGATCTTATGATGGAATG	3' primer for *ACT1* terminator.	pNIM1
ONC73	CCTTTCAATGCTAAATTTTGT	5' primer for amplifying *19.1837* upflank; +436 to +453 with respect to ATG.	*19.1837/TBP*
ONC74	ATGGATCCATTTTTACGAAATTCATT	3' primer for amplifying *19.1837* upflank; +714 to +696 w.r.t. ATG excluding the stop codon.	*19.1837/TBP*
ONC75	GGGTTTCAACACAAGCCATAT	5' primer for amplifying *19.1837* downflank; +1 to +18 w.r.t. stop codon.	*19.1837/TBP*
ONC76	CATACTCCTTTCGAAACTTAC	3' primer for amplifying *19.1837* downflank; +322 to +304 w.r.t. stop codon.	*19.1837/TBP*
ONC93	TCTgGTACCAGTGGACGAG	5' Primer for orf*19.470* Up Flank (+1889 to +2253 ORF) with internal KpnI site	*19.470/TAF12L*
ONC94	ccttaattaaAGCATTATCATCATTCA	3' Primer for orf*19.470* Up Flank (+1889 to +2253 ORF) with PacI site in frame with the 3xHA or 13xMyc tag	*19.470/TAF12L*
ONC95	cctctAGATGATAGTACAGATGG	5' Primer for orf*19.470* Down Flank with XbaI site	*19.470/TAF12L*
ONC96	GATTCcGTACGAAAGACTC	3' Primer for orf*19.470* Down Flank with BsiWI site	*19.470/TAF12L*
ONC97	ACAGCTGATCCAAAAGTA	5' Primer for orf*19.6820* Up Flank(+1161 to +1546 ORF) with internal PvuII site	*19.6820/TAF12*
ONC98	ccttaattaATTGATCTTTATTTAATT	3' Primer for orf*19.6820* Up Flank(+1161 to +1546 ORF) with PacI site in frame with the 3xHA or 13xMyc tag	*19.6820/TAF12*
ONC99	TCCCCGGAGCTGCCTGTA	5' Primer for orf*19.6820* Down Flank	*19.6820/TAF12*
ONC100	GGAtcgcgATCGATAGTGCTACTAGT	3' Primer for orf*19.6820* Down Flank with PvuI and NruI sites	*19.6820/TAF12*
ONC103	5'- AAT CTA TTA CTC AAT CGA G -3'	6125 to 6144 bp in pNIM1	
ONC104	5'- TAA AAA TAT CGC ACT CAC -3'	+1374 to +1356 w.r.t. ATG of orf19.3997	
ONC109	TGGATAACAAACCGTTCTTC	3' primer for diagnostic PCR.	*C.m.LEU2*

ONC110	CGGTGGCACATTTCACAC	3' primer for diagnostic PCR.	*C.d.HIS1*
ONC111	GCTTCGGGGAAAATGGTT	5' primer for *19.1837*-TAP diagnostic PCR, +343 to +360 w.r.t. ATG.	*19.1837/TBP*
ONC114	GGTGCCACTGATCCATTG	5' primer for down-split marker.	*HAH1*
ONC115	GCCAACATATCCATAGTTAAAGC	3' primer for up-split marker.	*HAH1*
ONC116	CCGTATTCCATGATTGCTATG	5' primer for diagnostic PCR.	P_{MAL2}
ONC117	TACATAAACATATAACGGTCCCCATTTAATCTACCAA CGGTTTAATACTCCAGTGCAAGACTTCGTACGCTGCA GGTC	5' primer for amplifying pHAH1-P_{MAL2} cassette with 60bp homology to the region upstream of *19.470* ATG.	*19.470/TAF12L*
ONC118	GGTTTAACTAATAATCAACTACAATGAATAATGGATC TCAGAATCAAAGTGCCAATAATGGCCAACAACCTCAA CAGCAAATCAAT	3' primer for amplifying pHAH1-P_{MAL2} cassette with 60bp homology to the region downstream of *19.470* ATG.	*19.470/TAF12L*
ONC119	CTAAAACCAGCTACATCCTTCTTTCTTTTCAGTACAAA TCATTCATTAGTAAATTAAATCCTTCGTACGCTGCAGG TC	5' primer for amplifying pHAH1-P_{MAL2} cassette with 60bp homology to the region upstream of *19.6820* ATG.	*19.6820/TAF12*
ONC120	GTTTAACTAATAATCAACTACAATGGATTCATCAGCA GCTTCATCACAGGAGAAAAGAGTCGGGACATCTACAC CAGAAGCAGAG	3' primer for amplifying pHAH1-P_{MAL2} cassette with 60bp homology to the region downstream of *19.6820* ATG.	*19.6820/TAF12*
ONC123	GCC CTT CTG CCT GGA GTA	Diagnostic PCR primer within the non repeat sequence of His	pHAH
ONC124	CGTACTATACTGCAAACAGC	5' primer for P_{MAL2}-*19.470* diagnostic PCR; -180 to -160 w.r.t. ATG	*19.470/TAF12L*
ONC125	ATCACCCTTAGATGAGGA	5' primer for P_{MAL2}-*19.6820* diagnostic PCR; -282 to -264 w.r.t. ATG	*19.6820/TAF12*
ONC126	GTCTTTCGGCCTCATTGG	3' primer for P_{MAL2}-*19.470* diagnostic PCR; +160 to +143 w.r.t. ATG.	*19.470/TAF12L*
ONC127	CCGTTCTTGAGGATCTGT	3' primer for P_{MAL2}-*19.6820* diagnostic PCR; +150 to +133 w.r.t. ATG.	*19.6820/TAF12*
ONC135	GGTCTAGAATGAATAATGGATCTCAG	5' primer for amplifying *19.470* ORF; +1 to +18 w.r.t. ATG.	*19.470/TAF12L*
ONC136	GCCTCGAGAGCATTATCATCATTCAC	3' primer for amplifying *19.470* ORF; +2256 to +2239 w.r.t. ATG, excluding the stop codon.	*19.470/TAF12L*
ONC137	GGTCTAGAATGGATTCATCAGCAGCT	5' primer for amplifying *19.6820* ORF; +1 to +18 w.r.t. ATG.	*19.6820/TAF12*
ONC138	GCCTCGAGTTGATCTTTATTTAATTTGG	3' primer for amplifying *19.6820* ORF; +1545 to +1526 w.r.t. ATG, excluding the stop codon	*19.6820*
ONC139	TATAAATTTATACATAAACATATAACGGTCCCCATTTA ATCTACCAACGGTTTAATACTCCAGTGCAAGAGAAGT TCCTATACTTTCTAG	5' primer for amplifying *SAT1* flipper cassette with 60bp homology to the region upstream of *19.470* ATG.	*19.470/TAF12L*
ONC140	TCTTGGTGAGAACAGCGACCGAAA	3' primer for *SAT*1 flipper up-split marker.	*SAT1*
ONC141	GGAGCGATAAGCGTGCTTCTGCCG	5' primer for *SAT1* flipper up-split marker.	*SAT1*
ONC142	TCGATAAACTTAAACAACAGCTAATTTTTTTTCTTTAC TAACCAACAATTTACCATCTGTACTATCATCTGAAGTT CCTATTCTCTAGAA	3' primer for amplifying *SAT1* flipper cassette with 60bp homology to the region downstream of *19.470* stop codon.	*19.470/TAF12L*
ONC151	gc gct agc ATG ACA AGT ACA CCT CAA	Forward primer for *Ca19.1885* with NheI site for in-frame insertion into pET 28b+ and 2 bp overhang for in frame insertion ino pGEX-5x-3.	*19.1885/TAF4*
ONC152	gct ctc gag ATC TTT CAA TTT TGC ATA	Reverse primer for *Ca19.1885* with XhoI site	*19.1885/TAF4*
ONC153	gc gct agc ATG ACA TCT CAA ATC GCT	Forward primer for *Ca19.307* with NheI site for in-frame insertion into pET 28b+ and 2 bp overhang for in frame insertion ino pGEX-5x-3.	*19.307/ADA1*

ONC154	gct ctc gag CAT AGT CGA CAC TAA ATC	Reverse primer for *Ca19.307* with XhoI site	*19.307/ADA1*
ONC155	CGAGACCCAGTTTGACGG	5' primer for *19.470*-HA_3 diagnostic PCR	*19.470/TAF12L*
ONC156	CCCTACTGCTGCCGCTGC	5'primer for *19.6820*-HA_3 diagnostic PCR	*19.6820/TAF12*
ONC161	ATATGAAGAACTAAAACCAGCTACATCCTTCTTTCTTT TCAGTACAAATCATTCATTAGTAAATTAAATCGAAGT TCCTATACTTTCTAG	5' primer for amplifying *SAT1* flipper cassette with 60bp homology to the region upstream of *19.6820* ATG.	*19.6820/TAF12*
ONC162	GGAAATTATAGTTTACCCAAGTAAATAAGTTTTTGTGT ATATAGTGTAATTGTACAGGCAGCTCCGGGGAGAAGT TCCTATTCTCTAGAA	3' primer for amplifying *SAT1* flipper cassette with 60bp homology to the region downstream of *19.6820* stop codon.	*19.6820/TAF12*
ONC311	TTGATGTCAATAAAGCTTCTAAAATCTATGAATTCTTT GTGCATATGGGATGGTGTTCTCAGGGGGGATCCATGG AAAAGAGA	5' primer for amplifying TAP tag cassette with 65bp homology to the C-terminus of *19.2331* ORF excluding the stop codon.	*19.2331/ADA2*
ONC312	TGGTATTTAAATCCAATTATATAAATCTATGCAAAAC AAAAAAAAATGAAAAGAATATACTACATGTGTGATG GATATCTGCA	3' primer for amplifying TAP tag cassette with homology to 65bp region downstream of *19.2331* stop codon.	*19.2331/ADA2*
ONC313	TTGAGAACAGTGTATTTTCTGGAAGTCGGAAAAGAAA AATGGGAGACGATGGCCCTTTCTATGTTGGATCCATG GAAAAGAGA	5' primer for amplifying TAP tag cassette with 65bp homology to the C-terminus of *19.6923* ORF excluding the stopcodon.	*19.6923/TAF11*
ONC314	ATCTTAACAAACCAGAATACTGCCTAAGAAATACAAA ACAAAACTAAGCATTAGCAAAGCCATAAGTGTGATGG ATATCTGCA	3' primer for amplifying TAP tag cassette with homology to 65bp region downstream of *19.6923* stop codon.	*19.6923/TAF11*
ONC324	TTATAGTTTACCCAAGTAAATAAGTTTTTGTGTATATA GTGTAATTGTACAGGCAGCTCCGGGGACTGATATCAT CGATGAATTCGAG	3' primer for amplifying pHAH1 cassette with 65bp homology to the region downstream of *19.6820* stop codon.	*19.6820/TAF12*
ONC325	tta att aat CAT CAT CAC CAT CAT CAT GGT GGT GAT TAT AAA GAT CAT GAT GGT	Oligos for generating 6xHis-Gly-Gly-3xFLAG tag, with PacI site at the 5' end and a 5'overhang compatible with XhoI site at the 3' end. To be cloned upstream of *ACT1* terminator to make an intermediate construct and then with auxotrophic markers from pSN series to make the final *C.m.LEU2*-, *C.d.HIS1*-, or *C.d.ARG4*-marked tagging cassettes	Oligos for construction of 6xHis-Gly-Gly-3xFLAG tag
ONC326	GAT TAT AAA GAT CAT GAT ATT GAT TAT AAA GAT GAT GAT GAT AAA TAA C		
ONC327	TTT ATA ATC ACC ACC ATG ATG ATG GTG ATG ATG att aat taa		
ONC328	ATC TTT ATA ATC ACC ATC ATG ATC		
ONC329	tc gag TTA TTT ATC ATC ATC ATC TTT ATA ATC AAT ATC ATG		
ONC330	GGGCAATGGTACAGGCTCT	5' primer for *19.2331*-TAP diagnostic PCR; +957 to +975 w.r.t. ATG.	*19.2331/ADA2*
ONC331	TGGAAATCCCAACGGAAT	3' primer for *19.2331*-TAP diagnostic PCR; +300 to +283 w.r.t. stop codon.	*19.2331/ADA2*
ONC332	CAGGAACGCAATTCTAAAGG	5' primer for *19.6923*-TAP diagnostic PCR; +775 to +794 w.r.t. ATG.	*19.6923/TAF11*
ONC333	AGCCAGGCGGACATTACA	3' primer for *19.6923*-TAP diagnostic PCR; +292 to +275 w.r.t. stop codon.	*19.6923/TAF11*
ONC425	ATTGAAGATGAAAAAATGGGTACGAGAAATGCTGTA ATAAAAGGATATGCAAAATTGAAAGAT CAT CAT CAC CAT CAT CAT GGT	Fwd Primer_orf*19.1885* Assembly 21, Ca21chr2 1522380-1525471W (3092 nucleotides)	*19.1885/TAF4*
ONC426	TTA TCC GAA TCA TTA ACT AGT TTA ACA AAT ACC TAT AAC TAC ATC TAT TCA TTT CCT AAT GCT GGA GCT CCA CCG CGG TG	Rev Primer_orf*19.1885* Assembly 21, Ca21chr2 1522380-1525471W (3092 nucleotides)	*19.1885/TAF4*
ONC427	GCTCATATTGGAACCACCGATGAACTAAAATGGGTAT TGCACGATTTAGTGTCGACTATGCAT CAT CAC CAT CAT CAT GGT	Fwd Primer_orf*19.307* Assembly 21, Ca21chr3 657097-660569C (3473 nucleotides	*19.307/ADA1*
ONC428	CTA TTT AGT CAA GAA AAT AAA AAT ACA ATT TTT CTT TTT TTT AAA AAA AGT CTC ATA ATG GCT GGA GCT CCA CCG CGG TG	Rev Primer_orf*19.307* Assembly 21, Ca21chr3 657097-660569C (3473 nucleotides	*19.307/ADA1*
ONC504	G CAG GCG GTG GGT CAG AC	Up Check	*19.1885/TAF4*

ONC505	GAG AGG CTA AAA TCC ATT GGT AAG GG	Down Check	*19.1885/TAF4*
ONC506	GCA GCC ACT ACC AAT GAC GC	Up Check	*19.307/ADA1*
ONC507	GCC ACA TTA TCG CAA GAA ATC GCC	Down Check	*19.307/ADA1*
ONC939	GCC GTC GAC ATG AAT AAT GGA TCT CAG AAT C	Fwd Primer for *19.470* cloning for complementation with SalI site, ATG codon and 3bp 5' overhang	*19.470/TAF12L*
ONC940	GGA GTC GAC ATG GAT TCA TCA GCA GCT TC	Fwd Primer for *19.6820* cloning for complementation with SalI site, ATG codon and 3bp 5' overhang	*19.6820/TAF12*
ONC943	GGA AGA TCT CCC CGA AGA TCT TAT GAT GGA	Rev Primer (in the Act1-terminator region) for *19.470, 19.6820* cloning for complementation with BglII site	*19.470/TAF12L, 19.6820/TAF12*

Supplementary Table S5. List of Genomes used in Fig. 1D

Sequence Identifier	Organism
SACE|YDR224C/1-131=Histone_H2B	*Saccharomyces cerevisiae*
SACE|YBL002W/1-131=Histone_H2B	*Saccharomyces cerevisiae*
CAAL|orf19.6925/1-130=Histone_H2B	*Candida albicans*
CAAL|orf19.1052/1-130=Histone_H2B	*Candida albicans*
SKLU_c2172-g8.1/1-229=yTAF12	*Saccharomyces kluyveri*
SMIK_1070-g2.1/1-443=yTAF12	*Saccharomyces mikatae*
KLAC|XP_453782/1-490=yTAF12	*Kluyveromyces lactis*
SPAR_120-g4.1/1-509=yTAF12	*Saccharomyces paradoxus*
YLIP|XP_501393.1/1-511=yTAF12	*Yarrowia lipolytica*
SCAS_c693-g33.1/1-507=yTAF12	*Saccharomyces castelli*
KWAL_23916/1-478=yTAF12	*Kluyveromyces waltii*
SKUD_c1848-g6.1/1-511=yTAF12	*Saccharomyces kudriavzevii*
CAGL_XP_445749/1-513=yTAF12	*Candida glabrata*
SBAY_c591-g21.1/1-505=yTAF12	*Saccharomyces bayanus*
ERGO_NP_9864721.2/1-485=yTAF12	*Eremothecium gossypii*
dTAF12_isoform_C/1-196=Animal_TAF12	*Drosophila melanogaster*
Mus_TAF12/1-161=Animal_TAF12	*Mus musculus*
hTAF12/1-161=Animal_TAF12	*Homo sapiens*
Oryza_jap/1-272=Plant_TAF12	*Oryza japonica*
ATHAL_NM_111842/1-539=Plant_TAF12	*Arabidopsis thaliana*
ATHAL_NM_101605/1-683=Plant_TAF12	*Arabidopsis thaliana*
SACE_YDR145W/1-539=yTAF12	*Saccharomyces cerevisiae*

Sequence Identifier	Organism
orf19.470/1-750=CaTAF12L	*Candida albicans*
CAWG_01728/1-742=CaTAF12L	*Candida albicans WO-1*
CD36_29190/1-739=CaTAF12L	*Candida dubliniensis*
CTRG_00709/1-803=CaTAF12L	*Candida tropicalis*
CPAR2_202430/1-787=CaTAF12L	*Candida parapsilosis*
CORT0D02480/1-771=CaTAF12L	*Candida orthopsilosis*
DEHA2F04664g/1-525=CaTAF12L	*Debaryomyces hansenii*
PICST_91503/1-771=CaTAF12L	*Pichia stipitis*
CANTEDRAFT_130715/1-524=CaTAF12L	*Candida tenuis*
SPAPADRAFT_59700/1-361=CaTAF12L	*Spathaspora passalidarum*
PGUG_01313/1-515=CaTAF12L	*Pichia guilliermondii*
CLUG_01450/1-500=CaTAF12L	*Candida lusitaniae*
orf19.6820/1-515=CaTAF12	*Candida albicans*
CD36_86790/1-513=CaTAF12	*Candida dubliniensis*
CTRG_05681/1-589=CaTAF12	*Candida tropicalis*
CPAR2_808600/1-516=CaTAF12	*Candida parapsilosis*
CORT0C00560/1-491=CaTAF12	*Candida orthopsilosis*
LELG_03005/1-601=CaTAF12	*Lodderomyces elongisporus*
PICST_70126/1-568=CaTAF12	*Pichia stipitis*
SPAPADRAFT_62384/1-469=CaTAF12	*Spathaspora passalidarum*

Construction of *S. cerevisiae* strains bearing either full length or histone-fold domain of Ca*TAF12L* or Ca*TAF12*

Construction of *TBP-TAP* tagged *C. albicans* strain

Construction of *C. albicans* strains bearing 3xHA-tagged *TAF12L* and *TAF12*

Construction of TAP-tagged *TAF11* and *ADA2* strains

Construction of His_6-$FLAG_3$ tagged *TAF4* and *ADA1* strains

Construction of P_{MAL2}-regulatable *TAF12L* and *TAF12* strains

Construction of *taf12lΔ* and *taf12bΔ* null mutants

Construction of *TAF12*-complemented *C. albicans* strain

Construction of *TAF12L*-complemented *C. albicans* strain

Generation of TAF12L, Taf12b, Ada1 and Taf4 polyclonal antibodies

Construction of *S. cerevisiae* strains bearing either full length or histone-fold domain of Ca*TAF12L* or Ca*TAF12*

The *C. albicans* full length ORFs *orf19.470*/*TAF12L* was PCR-amplified using ONC26 and ONC27, and *orf19.6820/TAF12* was amplified with ONC28 and ONC29 from SC5314 genomic DNA, and cloned downstream of the P_{GAL1} promoter in the vector pESC-Leu (Stratagene/Agilent) to obtain plasmids pGAL1-470 and pGAL1-6820. To express TAF12L and TAF12 histone fold domains, the y*TAF12* ORF in the plasmid pKN56 (3) was replaced with the HF domains of *TAF12L* and *TAF12* as follows. Using plasmids pGAL1-470 and pGAL1-6820 as templates and reverse primer ONC43 with either ONC42 or ONC44 respectively as forward primers, the *TAF12L* and *TAF12* HF domain coding sequences were PCR amplified, and inserted into pKN56 to obtain plasmids pRS416-470HF and pRS416-6820HF. Finally, the *TAF12L* and *TAF12* HF domain coding sequences along with the y*TAF12* upstream and downstream sequences were subcloned as BamHI-BglII fragments into BamHI-cut YEplac181 to obtain plasmids YEplac181-470HF and YEplac181-6820HF.

Plasmids pKN56, pKN58, YEplac181-470HF, YEplac181-6820HF and YEplac181 (empty vector) were transformed into *S. cerevisiae* strain YSS19 and obtained strains ISC25, ISC26, ISC27, ISC28 and ISC24 respectively. They were then replica printed onto SC-Leu+Ura+5-FOA or as control SC-Leu-Ura plates and tested for complementation of *taf12Δ* deletion. To examine complementation by full-length *TAF12L* and *TAF12*, the plasmids pESC-Leu-yTAF12, pGAL1-470 and pGAL1-6820 and empty vector pESC-Leu were transformed into *S. cerevisiae* strain YSS19 and obtained strains ISC20, ISC21, ISC22 and ISC23 respectively. The transformants were then replica printed onto SC-Leu+Ura+5-FOA media containing either 2%

raffinose alone (Raf) or 2% galactose + 2% raffinose (Gal/Raf) as carbon source and tested for complementation of *taf12Δ* deletion.

Construction of *TBP-TAP* tagged *C. albicans* strain

The heterologous auxotrophic markers *C.m.LEU2* and *C.m.HIS1* from pSN40 and pSN52 respectively (10) were subcloned into pSL301 vector (Invitrogen) as BamHI/ApaI fragments to produce intermediate plasmids Ip18 and Ip19 respectively. The *ACT1* terminator (*ACT1*t) sequence was PCR amplified from plasmid pNIM1 (11) using ONC71/72 to introduce a BglII site at its 3' end, and cloned into SmaI-cut pRS413 as a blunt-end fragment to obtain Ip20. The BamHI-EcoRV fragment containing the TAP tag from pPK335 (8) and the EcoRV-BglII *ACT1*t fragment from Ip20 were ligated to BamHI-cut Ip18 and Ip19 to obtain plasmids Ip21 and Ip22. *C. albicans TBP1* (orf19.1837) upstream and downstream regions of the stop codon were PCR amplified and inserted into the TAP-tagging cassette in Ip21 and Ip22. The Upflank fragment containing the 3' end of *TBP1* ORF (279bp) was PCR amplified using primers ONC73/74 and cloned into Ip21 and Ip22. The Downflank fragment was similarly amplified using primers ONC75/76 and cloned into compatible sites in Ip21 and Ip22 derivatives bearing the Upflank fragment to generate plasmids Ip24 and Ip26.

The *TBP-TAP-C.d.HIS1* tagging construct from plasmid Ip24 was excised with StuI-BstBI digestion and purified DNA was transformed into *C. albicans* strain SN87 and obtained strain ISC3 (*TBP::TAP-C.d.HIS1/TBP*). Locus-specific integration was confirmed by diagnostic PCR using primers ONC111/110. Further, two independent clones of ISC3 were transformed with the *C.m.LEU2*-marked TAP tagging cassette from Ip26 and transformants were selected for Leu^+ His^+ prototrophy and screened for the correct integration of the *LEU2*-marked tagging cassette

using ONC111/109. The resulting strain ISC7 expressed a ~45 kDa TBP-TAP protein as judged by Western blot. Presence of an untagged *TBP1* ORF was ruled out using primers ONC111/76.

Construction of *C. albicans* strains bearing 3xHA-tagged *TAF12L* and *TAF12*

The 3xHA-tagged *TAF12L* and *TAF12* in the background of the TBP-TAP strain ISC7 were constructed as follows. The plasmids Ip36 and Ip38, bearing C-terminal HA_3-tagging cassette for *TAF12L* and *TAF12* respectively were constructed as follows. The *SAT1* flipper cassette from pSFS2A (5) was subcloned between the Acc65I-SacI sites of pLITMUS28 (New England Biolabs) to obtain Ip27. The *SAT1* flipper cassette was then excised with BglII-StuI, cloned into BglII-EcoRV cut pFA6a-3HA-His3MX6 plasmid (7) resulting in plasmid Ip28. The tagging cassette was excised with SmaI-Acc65I, end-filled and subcloned into a fresh pLITMUS28 vector backbone cut with StuI to obtain the final 3xHA tagging construct Ip30. The Upflanks of *TAF12L* (364bp, +1890 to +2254 with respect to ATG) and *TAF12* (385bp, +1162 to +1546 with respect to ATG) were PCR amplified using Pfu DNA Polymerase and ONC93/94 and ONC97/98 primer pairs respectively. The Downflank regions were similarly amplified using Pfu Polymerase and primer pairs ONC95/96 for *TAF12L* and ONC99/100 for *TAF12*. The Upflank and Downflank sequences were cloned into Ip30 and plasmids Ip36 and Ip38 were obtained.

The *TAF12L* gene-specific tagging cassette was excised from plasmid Ip36, fragments gel purified, quantitated and equimolar DNA amounts (~0.5μg) transformed into strain ISC7. The *TAF12*-specific tagging cassette was excised from plasmid Ip38 and transformed into strain ISC7. The transformants were selected for nourseothricin resistance and screened for correct integration of the cassettes using gene-specific upstream primers (ONC155 or ONC156 for *TAF12L-HA_3* and *TAF12-HA_3* respectively) with the cassette-specific reverse primer (ONC140), resulting in strains ISC14 and ISC16. The tagging cassettes were also transformed into wild-

type strain SN87 and screened to obtain strains ISC18 and ISC19.

Tagging of the second *TAF12L* and *TAF12* alleles in strains ISC14 and ISC16 respectively was carried out using the same tagging cassette used for tagging each of the first allele. Nourseothricin-sensitive (Nou^S) segregants for both the *TAF12L* and *TAF12* single allele tagged strains were obtained resulting in strains ISC31 and ISC32. The *TAF12L-HA$_3$* and *TAF12-HA$_3$* tagging cassettes from Ip36 and Ip38 were used to transform two independent Nou^S clones of ISC31 and ISC32 respectively. Transformants were again selected for nourseothricin resistance and screened for the correct integration by PCR. Untagged Ca*TAF12L* and Ca*TAF12* were ruled out by PCR using primer pairs ONC93/96 and ONC97/100 respectively. The resultant strains ISC33 and ISC34 expressed 3xHA-tagged TAF12L and TAF12 proteins respectively as judged by Western blot.

Construction of TAP-tagged *TAF11* and *ADA2* strains

The tagging cassettes were used PCR for amplification using plasmid Ip22 as template to generate for *ADA2* (orf19.2331) and *TAF11* (orf19.6923) with primer pairs ONC311/312 and ONC313/314 respectively using Phusion DNA polymerase. The amplicons were transformed into *C. albicans* strain SN152, ISC18 and ISC19 and transformants selected on medium lacking histidine. Locus-specific integration of the cassettes was confirmed by PCR using gene-specific upstream primers (ONC330 or ONC332 for ADA2-TAP and TAF11-TAP respectively) with the cassette-specific reverse primer (ONC110). The resulting strains ISC39, ISC41 and ISC43 carried TAP tag at one of the two native *ADA2* loci, while strains ISC40, ISC42 and ISC44 carried TAP tag at one of the two native *TAF11* loci in SN152, ISC18 and ISC19 strain backgrounds respectively.

We next used Ip21 (*LEU2*-marked) as the template for PCR amplification of the *ADA2*-

and *TAF11*-specific cassettes with the same primer pairs ONC311/312 and ONC313/314 respectively. The purified *ADA2*-specific amplicons were transformed into two independent single-allele tagged transformants of strains ISC41 and ISC43, while the *TAF11*-specific amplicons were transformed into strains ISC42 and ISC44 for second allele tagging. All transformants were selected for Leu^+ His^+ prototrophy and screened for the correct integration of the *LEU2*-marked tagging cassette using specific primers for *ADA2* (ONC330) or *TAF11* (ONC332) with ONC109. The resulting strains ISC46 and ISC48 expressed the ~75 kDa Ada2-TAP protein, while strains ISC47 and ISC49 expressed the ~65 kDa TAF11-TAP protein. We also ascertained that these strains, as expected, also expressed either TAF12L-HA_3 or TAF12-HA_3 proteins as indicated. Furthermore, ORF-specific PCR reactions using primers ONC330/331 and ONC332/333 ensured that the strains were devoid of untagged *ADA2* and *TAF11* ORFs respectively.

Construction of His_6-$FLAG_3$ tagged *TAF4* and *ADA1* strains

The 6xHis-3xFLAG tagging construct was prepared as follows. The His_6-$FLAG_3$ tag sequence was constructed from synthetic oligonucleotides adapters, whose details would be provided upon request. The final annealed product was ligated to SalI cut, end-filled and XhoI cut Ip20 to generate plasmid Ip50. The plasmid pSK1 containing His_6-Gly_2-$FLAG_3$ tag followed by *ACT1* terminator and *SAT1*-marked flipper cassette was constructed as follows. The 5439bp vector backbone bearing His_6-Gly_2-$FLAG_3$ tag and the *ACT1*-terminator sequence was obtained by digesting plasmid Ip50 with BamHI, end-filled and digested with NotI, and was ligated to the *SAT1*-flipper cassette excised as a 4207bp StuI-NotI fragment from plasmid Ip27, and pSK1 plasmid was obtained.

The *HIS_6-$FLAG_3$* tagging cassette was amplified from pSK1 as up-split and down-split

fragments using gene specific long primers ONC425/ONC140 and ONC426/ONC141 for *TAF4*, and ONC427/ONC140 and ONC428/ONC141 for *ADA1*. The amplicons were purified by phenol extraction and ethanol precipitation and quantitated on agarose gel. Equimolar amounts of the two fragments for each gene were transformed into *C. albicans* strain SN87 and Nou^R transformants selected on YPD plates containing 200µg/ml nourseothricin. The correct integrations were confirmed by PCR using primers ONC151or ONC504 (*TAF4*) and ONC153 or ONC506 (*ADA1*) with cassette-specific reverse primer ONC66, and the resulting strains SKC7 and SKC10 expressed ~60kDa Taf4-His_6-$FLAG_3$ and ~65kDa ADA1-His_6-$FLAG_3$ proteins respectively.

Construction of P_{MAL2}-regulatable *TAF12L* and *TAF12* strains

A maltose-regulatable promoter was inserted upstream of the *TAF12L* and *TAF12* ORFs using the pHAH1-P_{MAL2} construct (a gift from Dr. K. Ganesan, IMTECH). The pHAH1-P_{MAL2} plasmid was used as a template to generate gene-specific construct designed to insert the P_{MAL2} promoter upstream of the ATG of *TAF12L* and *TAF12* ORFs using a split-marker strategy (12) along with the single transformation strategy (9,13). Accordingly, we used the primer pairs ONC117/ONC115 (*TAF12L*) and ONC119/ONC115 (*TAF12*) for PCR amplification of the up-split fragments. For the down-split fragments, we first amplified the down-flank, encompassing +3 to +160 bp of *TAF12L* ORF and +3 to +150 bp of *TAF12* ORF using the primers ONC118/ONC126 and ONC120/ONC127 respectively. The down-flank amplicons also contained an extra 28 bp sequence complementary to the P_{MAL2} promoter at their 5' end. Next, a mutually primed PCR of the down-flank amplicons with the linearized pHAH1-P_{MAL2} and primer pairs ONC114/ONC126 and ONC114/ONC127 was carried out to generate the *TAF12L* and *TAF12* down-split marker fragments respectively.

The up-split and down-split fragments were introduced into *C. albicans* strain SN95 by electroporation (5) and Arg^+ transformants were selected. The genomic DNA from the transformants were screened by PCR for correct integration of the cassette using primers (ONC124 for *TAF12L* and ONC125 for *TAF12*) located upstream of the site of insertion in combination with cassette-specific reverse primer ONC115. The positive clones were further confirmed by another PCR using gene-specific reverse primers located within the ORF but downstream of the site of integration (ONC94 for *TAF12L* and ONC98 for *TAF12*) along with a cassette-specific forward primer located within P_{MAL2} (ONC116). Thus we obtained strains ISC9 and ISC10, bearing one allele of *TAF12L* or *TAF12* under the P_{MAL2} promoter respectively. We then selected for spontaneous Arg^+ His^+ segregants in maltose-containing medium, wherein the P_{MAL2} promoter was inserted upstream of both the alleles. Using gene-specific upstream and downstream primers (ONC124-ONC126 for *TAF12L* and ONC125-ONC127 for *TAF12*) we confirmed that the resultant strains ISC11 and ISC12 contained *HIS1*-marked P_{MAL2} cassette, and using PCR, we ruled out the presence of the native promoter-bearing *TAF12L* and *TAF12* coding sequences.

Construction of *taf12lΔ* and *taf12Δ* null mutants

To construct *TAF12L* and *TAF12* deletion strains we carried out sequential deletion of both alleles using the recyclable *SAT1*-marked deletion cassette from pSFS2a (5). We used either *TAF12L*-specific primer pairs (ONC139/ONC140 and ONC141/ONC142), or *TAF12*-specific primer pairs (ONC161/ONC140 and ONC141/ONC162) to amplify the respective up-split and down-split fragments. The corresponding up- and down-split fragments were transformed into strain SN95 and transformants selected for Nou^R. Correct integration was confirmed using gene-specific upstream primers ONC124 (*TAF12L*) or ONC125 (*TAF12*) with cassette-specific

reverse primer ONC140, as well as gene-specific downstream primers ONC96 (*TAF12L*) or ONC100 (*TAF12*) along with a cassette-specific forward primer ONC141. The resultant heterozygous Nou^R strains ISC13 (*taf12lΔ::SAT1-FLP/TAF12L*) and ISC37 (*taf12Δ::SAT1-FLP/TAF12*) were used to obtain Nou^S segregants as described previously (5). Because PCR reactions with gene-specific upstream primers ONC124 (*TAF12L*) or ONC125 (*TAF12*) and the cassette-specific reverse primer ONC141 did not yield amplicons, we confirmed the excision of the cassettes in strains ISC35 (*taf12lΔ::FRT/TAF12L*) and ISC38 (*taf12Δ::FRT/TAF12*).

To delete the second *TAF12L* and *TAF12* allele, we again transformed the same deletion cassettes into ISC35 and ISC38 respectively, and obtained viable *taf12lΔ* strain ISC36 that exhibited a rough colony morphology and slow growth defect. The *taf12Δ* null mutants could not be obtained by this approach. To determine the essentiality of *TAF12* gene, we used the *HIS1-ARG4-HIS1* deletion cassette pHAH1 similar to the method described earlier (13,14). We were unable to obtain any His^+ Arg^+ colonies despite screening several independent heterozygous (Arg^+) clones suggesting that deletion of both alleles of *TAF12* was lethal.

Construction of *TAF12*-complemented *C. albicans* strain

The plasmid pPC18 bearing *TAF12::3xFLAG-2xGly-6xHis* under the *TET1* promoter was constructed as follows. The tagged *TAF12* ORF was PCR amplified from *C. albicans* strain SKC6 genomic DNA using primers ONC940-ONC943 as SalI-BglII fragment, and cloned into similarly cut pNIM1 vector (6). The plasmid pPC18 was then digested with SacII and Acc65I and the Tet-regulatable, epitope-tagged *TAF12* coding sequence was then transformed into *C. albicans* strain ISC12, and successful integration confirmed by PCR using primers ONC103-ONC104 and constructed *C. albicans* strain SDC16. Similarly the control strain SDC6 was constructed by integrating pNIM1 vector alone.

Construction of *TAF12L*-complemented *C. albicans* strain

The plasmid pPC19 bearing *TAF12L::3xFLAG-2xGly-6xHis* under the *TET1* promoter was constructed as follows. The tagged *TAF12L* ORF was PCR amplified from *C. albicans* strain SKC3 genomic DNA using primers ONC939-ONC943, cut with BglII at its 3' end and ligated to SalI-cut and blunt ended, and BglII digested pNIM1 plasmid vector. The plasmid pPC19 was then digested with SacII and Acc65I and the Tet-regulatable, epitope-tagged *TAF12L* coding sequence was transformed into *C. albicans* ISC11 strain, and the correct integration was confirmed by PCR using primers ONC103-ONC104 to yield strain SDC13. Similarly the control strain SDC3 was constructed by integrating pNIM1 vector alone.

To complement the *taf12*Δ/Δ mutant strain ISC36 with wild-type *TAF12L*, the *SAT1* marker gene in pPC19 plasmid was replaced by the *ARG4* marker gene as follows. The *ARG4* coding sequence was excised from pSN69 by NotI digestion, end-filled using klenow, digested BamHI, and ligated to pPC19 digested with ApaI and end-filled using klenow and digested with BglII, and plasmid pPC22 was obtained. Similarly the *SAT1* marker gene of pNIM1 plasmid was replaced by *ARG4* marker gene and the plasmid pPC16 was constructed. Plasmid pPC22 was then digested with SacII and Acc65I and the Tet-regulatable, epitope-tagged *TAF12L* coding sequence was then transformed into strain ISC36. The resulting transformants were screened for the successful integration using PCR primers ONC103-ONC104 to yield strain SDC17. Similarly the pPC16 vector alone was digested with SacII and Acc65I and the fragment bearing Tet-regulatable, epitope-tagged *TAF12L* coding sequence was transformed into strain ISC36, successful integration confirmed with PCR primers ONC103-ONC104 to yield strain SDC12.

Generation of TAF12L, TAF12, Ada1 and TAF4 polyclonal antibodies

The complete *TAF12L* and *TAF12* coding regions were PCR amplified using primers

ONC135/136 and ONC137/138 respectively and Phusion DNA polymerase (Finnzymes). The amplicons were cloned into vector pGEX-5X-3 (GE Healthcare) cut with SmaI-XhoI, to obtain plasmids Ip40 (GST-TAF12L) and Ip41 (GST-Taf12b). Next, the complete *TAF12L* and *TAF12* coding regions from plasmids Ip40 and Ip41 respectively were subcloned as XbaI-XhoI fragments into NheI-XhoI cut pET28b+ (Novagen) resulting in recombinant plasmids Ip44 (TAF12L-His_6) and Ip45 (Taf12b-His_6). The 3' region (864 bp) of *TAF12L* ORF in Ip44 was removed by SalI-XhoI digestion and the remaining plasmid was self ligated to yield Ip48 expressing TAF12LΔC-His_6.

The *TAF4* (orf19.1885) and *ADA1* (orf19.307) full length coding regions were PCR amplified using primers ONC151/152 and ONC153/154 respectively. The blunt-XhoI cut amplicons were cloned into pGEX-5X-3 cut with SmaI-XhoI, to obtain plasmids Ip42 (GST-TAF4) and Ip43 (GST-Ada1). Next, the *TAF4* and *ADA1* coding regions from Ip42 and Ip43 respectively were subcloned as NheI-XhoI fragments into similarly cut pET28b+ to generate recombinant plasmids Ip46 (TAF4-His_6) and Ip47 (Ada1-His_6).

The recombinant proteins expressed from plasmids Ip48 (TAF12LΔC-His_6), Ip45 (TAF12-His_6), Ip46 (TAF4-His_6) and Ip47 (Ada1-His_6) were purified using His-Trap affinity columns (GE Healthcare) as per manufacturer's instructions. The purified TAF12LΔC-His_6 and TAF12-His_6 proteins were used for immunization of rabbits, whereas Taf4-His_6 and Ada1-His_6 proteins were immunized into mice as per standard protocols (15). Polyclonal sera collected after the first and subsequent boosts were tested for the presence of protein-specific antibodies by western blot.

Supplemental Figure Legends:

Fig. S1. Altered growth and colony phenotype of *taf12a* mutant under pseudohyphae-inducing or hyphal-inducing conditions. (*A-H*) Colony phenotype of *taf12a* mutants in pseudo-hyphal medium. *C. albicans* strains SN95 (WT), ISC11 (*PMAL2-TAF12L*) and ISC36 (*taf12a*Δ) were grown on the indicated plates and isolated colonies were imaged using a Nikon stereozoom microscope SMZ1500 equipped with a Nikon digital camera DXM1200C on the indicated days of incubation. (*A*) YPD, 37°C (1x, day3); (*B*) YPD, 30°C (1x, day3); (*C*) YCB, 30°C (1x, day5); (*D*) YCB, 30°C (3x, day5); (*E*) YCB, 30°C, transmitted light (day7); (*F*) SLAD, 37°C (2x, day5); (*G*) SLAD, 30°C (2x, day5); (*H*) SLAD, 30°C, transmitted light (day7). The colony boundaries of WT strain in YCB (panel 'e') and SLAD media (panel 'h') are marked with white arrows. 1x and 3x refer to the Objective lens used and images acquired using transmitted light. (*I-K*) Colony phenotype of *taf12a* mutants in hyphae-inducing media. The *C. albicans* strains WT, ISC11 and ISC36 were grown on the indicated plates and isolated colonies were imaged on the indicated days. (*I*) YPD, 30°C (1x, day3); (*J*) GlcNAc, 37°C (day3); (*K*) serum, 37°C (day6). All images were taken at 1x objective magnification.

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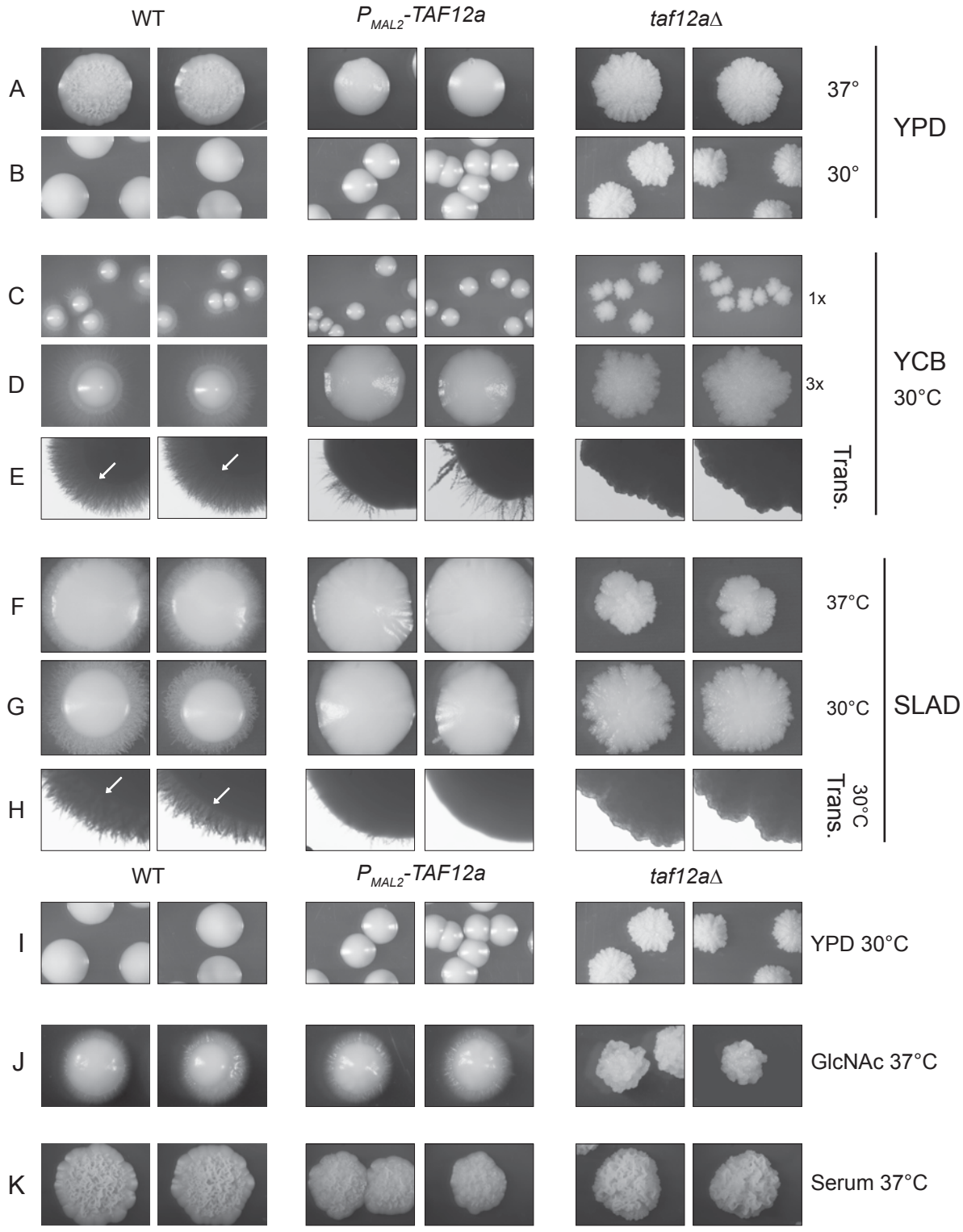

Fig. S1
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