Supplementary materials

Table S1. *Candida albicans* strains used in this study

Table S2. Plasmids used in this study

Table S3. Primers used in this study

Figure S1. Cell morphology of *yaf9* or *swr1* mutants and revertants. The strains were cultured overnight at 25 °C in YPD (up panels), and induced in YPD (middle panels) or YPD with 10% serum (down panels) at 37 °C for 3 hrs. Cell-morpha were observed and photographed.

Figure S2. Functional analysis of Eaf1 K173 mutants. (a) Effects of K to R, to Q, to N, or to H mutation at residue 173 of Eaf1 on Yaf9-Eaf1 interaction. HA tagged Eaf1, Eaf1^{K173R}, Eaf1K^{173Q}, Eaf1^{K173N} or Eaf1^{K173H} was co-expressed with Yaf9-myc, and cultured in YPD at 25 °C for Co-IP. **(b)** Cell morphology of wild-type, *eaf1*^{K173A}, *eaf1*^{K173N}, *eaf1*^{K173H}, *eaf1* mutants and *eaf1* revertant. Overnight cultured cells were inoculated into YPD and cultured at 37 °C with or without serum for 3 hrs.

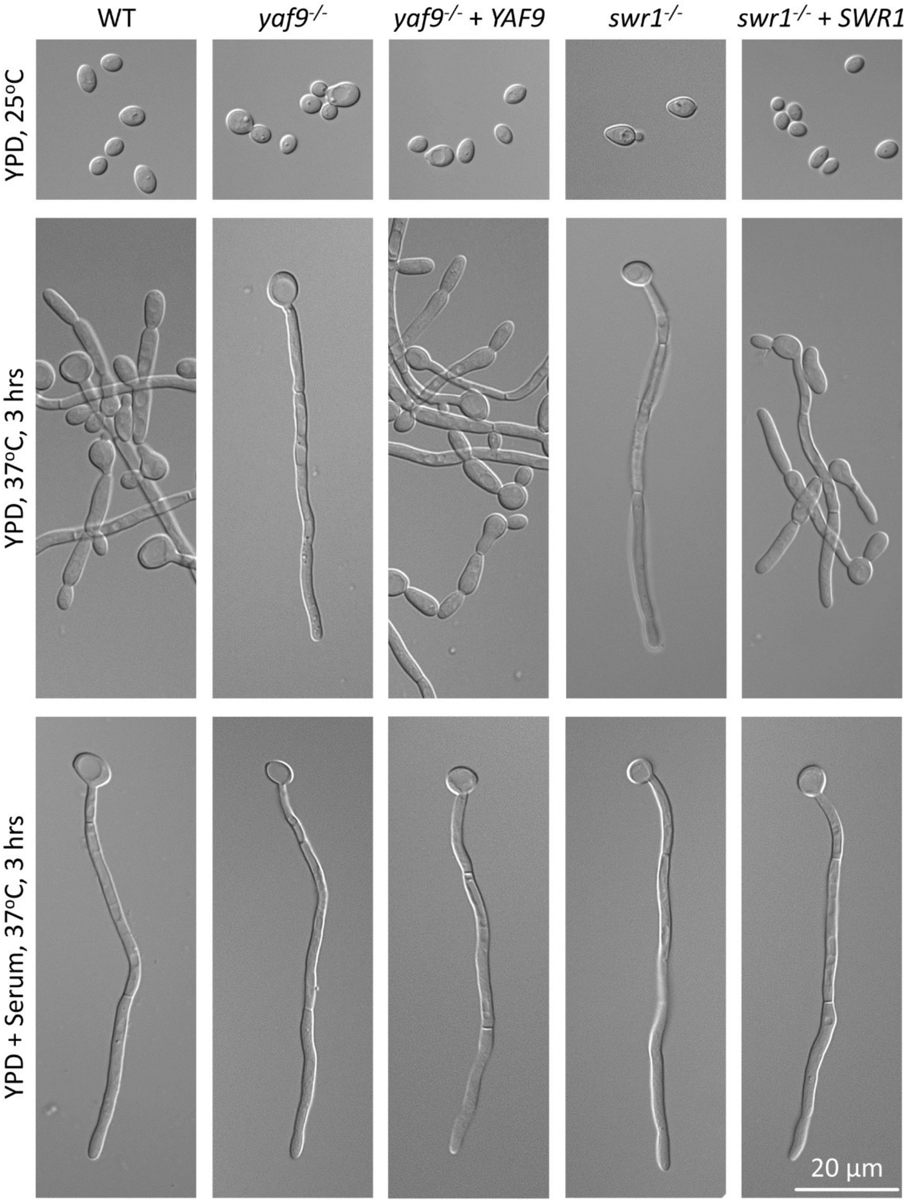
Figure S3. The role of auto-acetylation of Esa1 during hyphal development. (a) Sequence comparison of regions around auto-acetylated lysine residue of *C. albicans* Esa1 (CaEsa1) and *S. cerevisiae* Esa1 (ScEsa1). **(b)** CaEsa1 is auto-acetylated at lysine 296. Cells carring Esa1-Myc or Esa1^{K296R}-Myc were cultured in YPD at 25 °C and the WCEs were collected, immunoprecipitated with anti-Myc, and probed with anti-Ac-K. **(c)** The Eaf1 acetylation was abolished in *esa1*^{K296R} mutant, but enhanced in *esa1*^{K296Q} mutant. Eaf1-Myc was introduced into cells of wild-type, *esa1*, *esa1*^{K296R}, and *esa1*^{K296Q} mutant, cultured in YPD at 25 °C or in YPD plus 10% serum at 35 °C for Co-IP or IB. **(d)** The Esa1^{K296R} mutant blocks hyphal initiation, while the Esa1^{K296Q} mutant inhibits hyphal elongation. The cells of wild-type, *esa1*, *esa1*^{K296R}, *esa1*^{K296Q}, and *hda1* mutant were cultured in YPD at 25 °C for 6 hrs or in YPD plus 10% serum at 35 °C for 3 hrs, observed by microscopy.

Figure S4. Cell morphology of Eaf1^{K173R}, Eaf1^{K173Q} and *brg1* carring Eaf1^{K173R} mutant induced in different media. An overnight culture of wild-type, Eaf1^{K173R}, Eaf1^{K173Q}, *brg1* and *brg1* carring Eaf1^{K173R} was induced at 37 °C in YPD for 3 hrs, YPD with 10% serum for 3 hrs, YPD with 5 nM rapamycin for 4 hrs, YEP with 2% GlcNAc for 4 hrs or Lee's with 2% mannitol for 6 hrs. Cell-morpha were observed and photographed.

Figure S5. Sequence alignment around the acetylable lysine in Eaf1

orthologues across eukaryotes. The acetylable residue K173 is conserved in Eaf1 orthologues among polymorphic fungi, but is occupied by a non-acetylable residue arginine (R) in non-dimorphic yeast-like fungi or glutamine (Q) in filamentous fungi. The lysine residue is neither conserved among Eaf1 orthologues from protista, nor the Eaf1 orthologues from higher eukaryotes or p400-like proteins.

Figure S1



WT
yaf9-/-
yaf9-/- + YAF9
swr1-/-
swr1-/- + SWR1
YPD, 25oC
YPD, 37oC, 3 hrs
YPD + Serum, 37oC, 3 hrs
20 µm

Figure S2

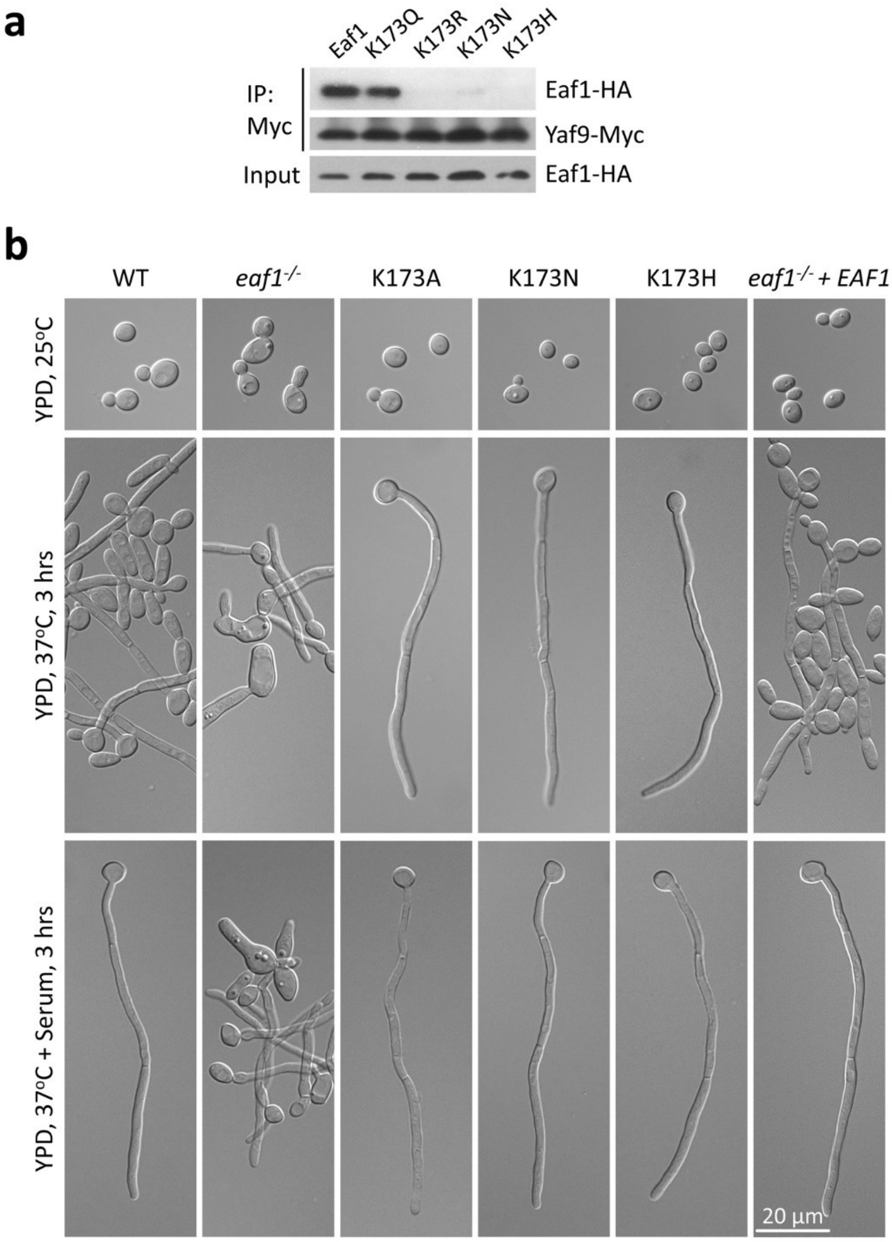

a
Eaf1
K173Q
K173R
K173N
K173H
IP:
Myc
Eaf1-HA
Yaf9-Myc
Input
Eaf1-HA
b
WT
eaf1-/-
K173A
K173N
K173H
eaf1-/- + EAF1
YPD, 25°C
YPD, 37°C, 3 hrs
YPD, 37°C + Serum, 3 hrs
20 µm

Figure S3

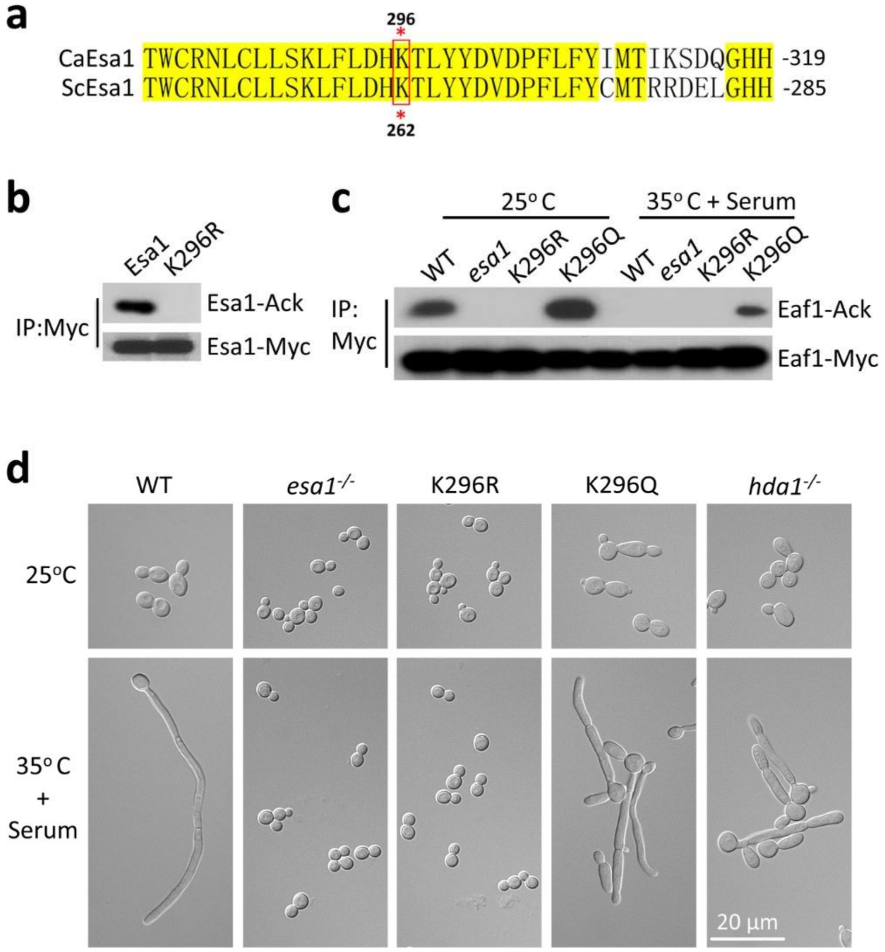

a
296
CaEsa1 TWCRNLCLLSKLFLDHKTLYYDVDPFLFYIMTIKSDQGHH -319
ScEsa1 TWCRNLCLLSKLFLDHKTLYYDVDPFLFYCMTRRDELGHH -285
262
b
Esa1
K296R
IP:Myc
Esa1-Ack
Esa1-Myc
c
25° C
35° C + Serum
WT
esa1
K296R
K296Q
WT
esa1
K296R
K296Q
IP:
Myc
Eaf1-Ack
Eaf1-Myc
d
WT
esa1-/-
K296R
K296Q
hda1-/-
25°C
35° C
+
Serum
20 μm

Figure S4

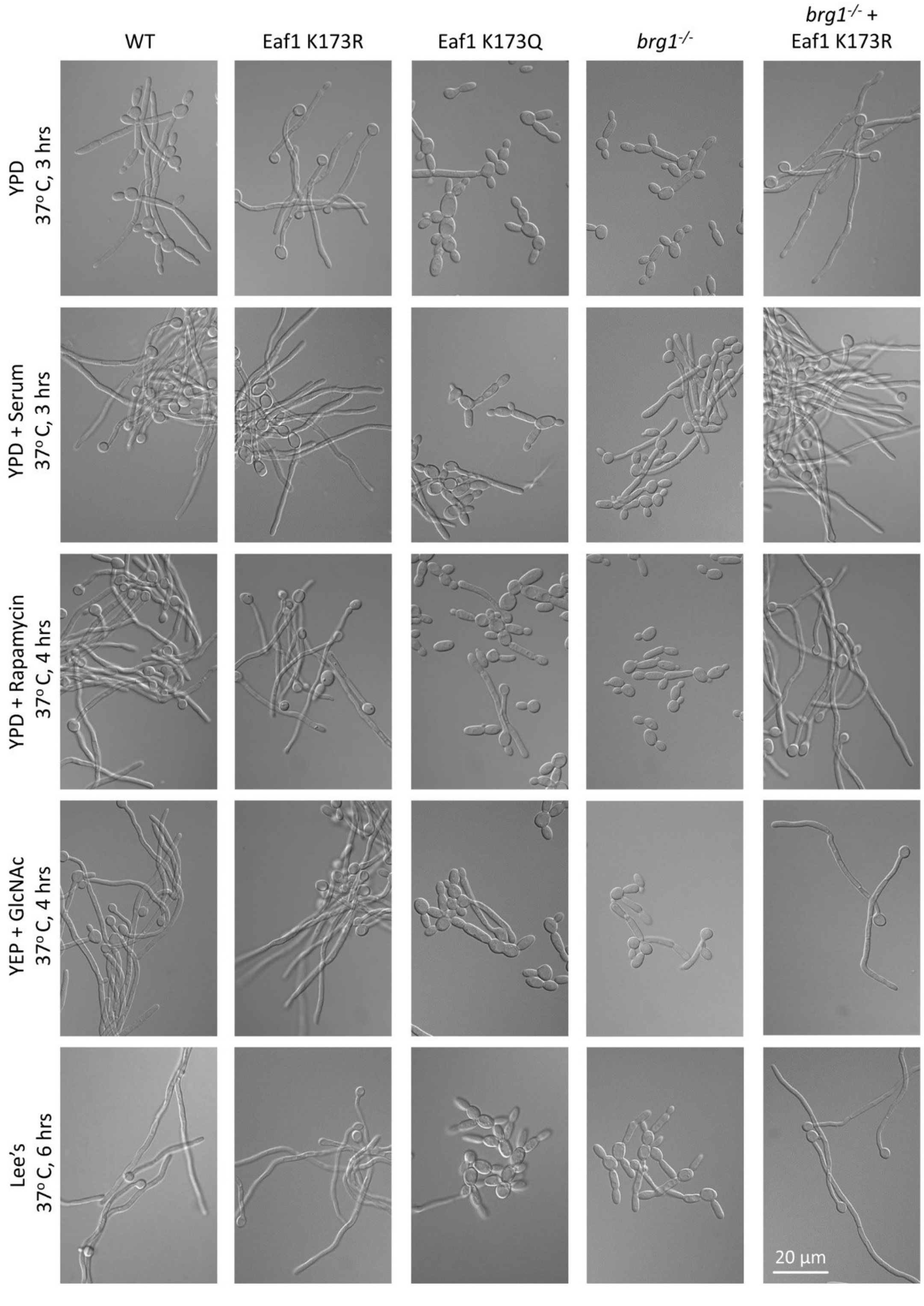
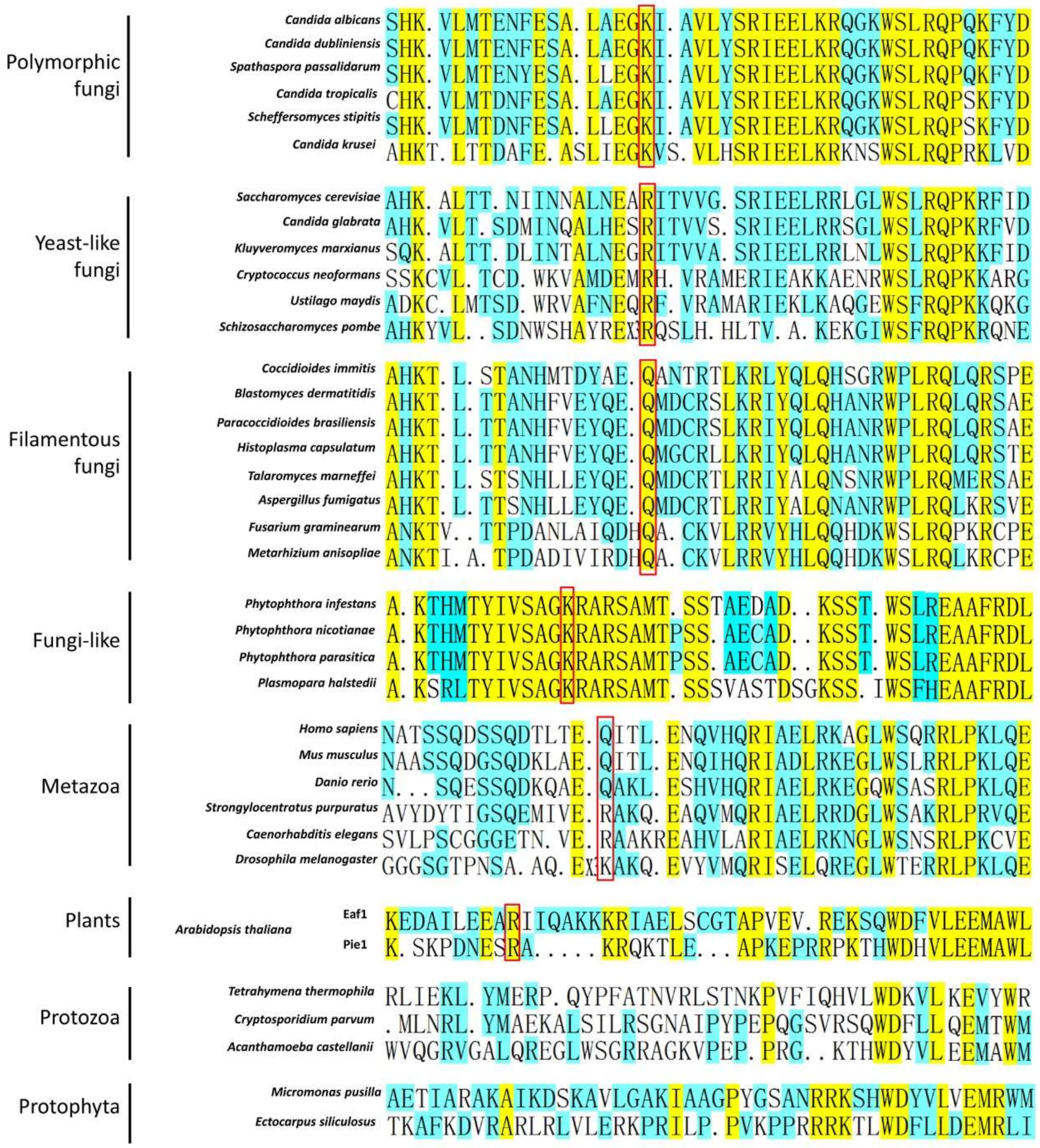

WT
Eaf1 K173R
Eaf1 K173Q
brg1-/-
brg1-/- + Eaf1 K173R
YPD 37º C, 3 hrs
YPD + Serum 37º C, 3 hrs
YPD + Rapamycin 37º C, 4 hrs
YEP + GlcNAc 37º C, 4 hrs
Lee's 37º C, 6 hrs
20 μm

Figure S5



Group	Species	Sequence
Polymorphic fungi	*Candida albicans*	SHK.VLMTENFESA.LAEGKI.AVLYSRIEELKRQGKWSLRQPQKFYD
	Candida dubliniensis	SHK.VLMTENFESA.LAEGKI.AVLYSRIEELKRQGKWSLRQPQKFYD
	Spathaspora passalidarum	SHK.VLMTENYESA.LLEGKI.AVLYSRIEELKRQGKWSLRQPQKFYD
	Candida tropicalis	CHK.VLMTDNFESA.LAEGKI.AVLYSRIEELKRQGKWSLRQPSKFYD
	Scheffersomyces stipitis	SHK.VLMTDNFESA.LLEGKI.AVLYSRIEELKRQGKWSLRQPSKFYD
	Candida krusei	AHKT.LTTDAFE.ASLIEGKVS.VLHSRIEELKRKNSWSLRQPRKLVD
Yeast-like fungi	*Saccharomyces cerevisiae*	AHK.ALTT.NIINNALNEARITVVG.SRIEELRRLGLWSLRQPKRFID
	Candida glabrata	AHK.VLT.SDMINQALHESRITVVS.SRIEELRRSGLWSLRQPKRFVD
	Kluyveromyces marxianus	SQK.ALTT.DLINTALNEGRITVVA.SRIEELRRLNLWSLRQPKKFID
	Cryptococcus neoformans	SSKCVL.TCD.WKVAMDEMRH.VRAMERIEAKKAENRWSLRQPKKARG
	Ustilago maydis	ADKC.LMTSD.WRVAFNEQRF.VRAMARIEKLKAQGEWSFRQPKKQKG
	Schizosaccharomyces pombe	AHKYVL..SDNWSHAYREXRQSLH.HLTV.A.KEKGIWSFRQPKRQNE
Filamentous fungi	*Coccidioides immitis*	AHKT.L.STANHMTDYAE.QANTRTLKRLYQLQHSGRWPLRQLQRSPE
	Blastomyces dermatitidis	AHKT.L.TTANHFVEYQE.QMDCRSLKRIYQLQHANRWPLRQLQRSAE
	Paracoccidioides brasiliensis	AHKT.L.TTANHFVEYQE.QMDCRSLKRIYQLQHANRWPLRQLQRSAE
	Histoplasma capsulatum	AHKT.L.TTANHFVEYQE.QMGCRLLKRIYQLQHANRWPLRQLQRSTE
	Talaromyces marneffei	AHKT.L.STSNHLLEYQE.QMDCRTLRRIYALQNSNRWPLRQMERSAE
	Aspergillus fumigatus	AHKT.L.TTSNHLLEYQE.QMDCRTLRRIYALQNANRWPLRQLKRSVE
	Fusarium graminearum	ANKTV..TTPDANLAIQDHQA.CKVLRRVYHLQQHDKWSLRQPKRCPE
	Metarhizium anisopliae	ANKTI.A.TPDADIVIRDHQA.CKVLRRVYHLQQHDKWSLRQLKRCPE
Fungi-like	*Phytophthora infestans*	A.KTHMTYIVSAGKRARSAMT.SSTAEDAD..KSST.WSLREAAFRDL
	Phytophthora nicotianae	A.KTHMTYIVSAGKRARSAMTPSS.AECAD..KSST.WSLREAAFRDL
	Phytophthora parasitica	A.KTHMTYIVSAGKRARSAMTPSS.AECAD..KSST.WSLREAAFRDL
	Plasmopara halstedii	A.KSRLTYIVSAGKRARSAMT.SSSVASTDSGKSS.IWSFHEAAFRDL
Metazoa	*Homo sapiens*	NATSSQDSSQDTLTE.QITL.ENQVHQRIAELRKAGLWSQRRLPKLQE
	Mus musculus	NAASSQDGSQDKLAE.QITL.ENQIHQRIADLRKEGLWSLRRLPKLQE
	Danio rerio	N...SQESSQDKQAE.QAKL.ESHVHQRIAELRKEGQWSASRLPKLQE
	Strongylocentrotus purpuratus	AVYDYTIGSQEMIVE.RAKQ.EAQVMQRIAELRRDGLWSAKRLPRVQE
	Caenorhabditis elegans	SVLPSCGGGETN.VE.RAAKREAHVLARIAELRKNGLWSNSRLPKCVE
	Drosophila melanogaster	GGGSGTPNSA.AQ.EXKAKQ.EVYVMQRISELQREGLWTERRLPKLQE
Plants	*Arabidopsis thaliana* Eaf1	KEDAILEEARIIQAKKKRIAELSCGTAPVEV.REKSQWDFVLEEMAWL
	Arabidopsis thaliana Pie1	K.SKPDNESRA.....KRQKTLE...APKEPRRPKTHWDHVLEEMAWL
Protozoa	*Tetrahymena thermophila*	RLIEKL.YMERP.QYPFATNVRLSTNKPVFIQHVLWDKVL KEVYWR
	Cryptosporidium parvum	.MLNRL.YMAEKALSILRSGNAIPYPEPQGSVRSQWDFLL QEMTWM
	Acanthamoeba castellanii	WVQGRVGALQREGLWSGRRAGKVPEP.PRG..KTHWDYVL EEMAWM
Protophyta	*Micromonas pusilla*	AETIARAKAIKDSKAVLGAKIAAGPYGSANRRKSHWDYVLVEMRWM
	Ectocarpus siliculosus	TKAFKDVRARLRLVLERKPRILP.PVKPPRRRKTLWDFLLDEMRLI

Table S1. *Candida albicans* strains used in this study

Strain	Genotype	Source
SC5314	Wild type	[1]
CAI4	*ura3::λ imm434/ ura3:: λ imm434*	[1]
BWP17	*ura3::λimm434/ura3::λ imm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG*	[2]
CWX1	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG ESA1/esa1::HIS1*	[3]
CWX2	*ura3::λimm434/ura3::λ imm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG esa1::HIS1/esa1 ::hisG-URA3-hisG*	[3]
CWX3	*ura3::λimm434/ura3::λ imm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG esa1::HIS1/esa1 ::hisG*	[3]
CLY3	*ura3::λ imm434/ura3::λ imm434 yng2:: hisG /yng2::hisG-URA3-hisG*	[4]
CLY4	*ura3::λ imm434/ura3::λ imm434 yng2:: hisG /yng2::hisG*	[4]
CWX10	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG SWR1/swr1::HIS1*	This study
CWX11	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG swr1::HIS1/swr1 ::hisG-URA3-hisG*	This study
CWX12	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG swr1::HIS1/swr1 ::hisG*	This study
CWX13	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG EAF1/eaf1::HIS1*	This study
CWX14	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/eaf1 ::hisG-URA3-hisG*	This study
CWX15	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/eaf1 ::hisG*	This study
CSC1	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf7::HIS1/eaf7 ::ARG4*	[4]
CWX16	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG bdf1::HIS1/bdf1 ::hisG-URA3-hisG*	This study
CWX17	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG bdf1::HIS1/bdf1 ::hisG*	This study
CWX18	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG YAF9/yaf9::HIS1*	This study
CWX19	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG yaf9::HIS1/yaf9 ::hisG-URA3-hisG*	This study
CWX20	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG yaf9::HIS1/yaf9 ::hisG*	This study
CWX21	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG htz1::HIS1/htz1 ::hisG-URA3-hisG*	This study
CWX22	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG htz1::HIS1/htz1 ::hisG*	This study
CWX23	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG*	This study

	hda1::HIS1/hda1 ::hisG-URA3-hisG	
CWX24	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG hda1::HIS1/hda1 ::hisG*	This study
CWX25	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG rpd3::HIS1/rpd3::hisG-URA3-hisG*	This study
CWX26	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG rpd3::HIS1/rpd3::hisG*	This study
CWX27	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG rpd31::HIS1/rpd31::hisG-URA3-hisG*	This study
CWX28	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG rpd31::HIS1/rpd31::hisG*	This study
CWX29	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/eaf1*^{K173R} *::URA3*	This study
CWX30	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/ eaf1*^{K173Q} *::URA3*	This study
CWX31	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/eaf1*^{K489R} *::URA3*	This study
CWX32	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG eaf1::HIS1/EAF1-YAF9::URA3*	This study
CWX33	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG yaf9::HIS1/yaf9 dYEATS::URA3*	This study
CWX34	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG esa1::HIS1/esa1*^{K296R} *::URA3*	This study
CWX35	*ura3::λimm434/ura3::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG esa1::HIS1/ esa1*^{K296Q} *::URA3*	This study
brg1	*his1/his1 leu2/leu2 arg4/arg4 URA3/ura3::λimm434 IRO1/iro1::λimm434 brg1::CdHIS1/brg1::CmLEU2*	[5]
CWX36	*his1/his1 leu2/leu2 arg4/arg4 ura3::λimm434/ura3::λimm434 IRO1/ iro1::λimm434 brg1::CdHIS1/brg1::CmLEU2 eaf1::hisG/eaf1*^{K173R} *::URA3*	This study

Table S2. Plasmids used in this study

Plasmid	Description	Source
pCUB6	Replacement of *S. cerevisiae URA3* by *C. albicans URA3* in pNKY50	2
pSWR1-KO	0.50 kb and 0.55 kb KO fragments of *C. albicans SWR1* and *hisG-URA3-hisG* in pBluescript SK(+)	This study
pEAF1-KO	0.53 kb and 0.6 kb KO fragments of *C. albicans EAF1* and *hisG-URA3-hisG* in pBluescript SK+	This study
pYAF9-KO	0.55 kb and 0.50 kb KO fragments of *C. albicans YAF9* and *hisG-URA3-hisG* in pBluescript SK(+)	This study
pBDF1-KO	0.56 kb and 0.53 kb KO fragments of *C. albicans BDF1* and *hisG-URA3-hisG* in pBluescript SK(+)	This study
pHTZ1-KO	0.50 kb and 0.50 kb KO fragments of *C. albicans HTZ1* and *hisG-URA3-hisG* in pBluescript SK(+)	This study
pPR671	*C. albicans ACT1* promoter,13×myc-FLAG, *HIS1*, for gene expression under *ACT1* promoter control at *RP10* locus in genome	4
p671-ARG4	*C. albicans ACT1* promoter,13×myc-FLAG, *ARG4*	3
pPR673	*C. albicans ACT1* promoter, 13×myc-FLAG, *URA3*	4
p671-YAF9	1.42 kb containing 5' region and ORF of *YAF9* in p671, for *YAF9-MYC* expression from its own promoter at *YAF9* locus	This study
p673-YAF9	1.42 kb containing 5' region and ORF of *YAF9* in p673	This study
p671-ARG4-YAF9	1.42 kb containing 5' region and ORF of *YAF9* in p671-ARG4	This study
p671-EAF1	3.4 kb containing 5' region and ORF of *EAF1* in p671	This study
p673-EAF1	3.4 kb containing 5' region and ORF of *EAF1* in p673	This study
p671-ARG4-EAF1	3.4 kb containing 5' region and ORF of *EAF1* in p671-ARG4	This study
p671-SWR1	5.4 kb containing 5' region and ORF of *SWR1* in p671	This study
p673-SWR1	5.4 kb containing 5' region and ORF of *SWR1* in p673	This study
p671- ARG4-SWR1	5.4 kb containing 5' region and ORF of *SWR1* in p671-ARG4	This study
p671-ESA1	2.18 kb containing 5' region and ORF of *ESA1* in p671	This study
p673-ESA1	2.18 kb containing 5' region and ORF of *ESA1* in p673	This study
p671-ARG4-ESA1	2.18 kb containing 5' region and ORF of *ESA1* in p671-ARG4	This study
P673-HDA1	2.5 kb containing 5' region and ORF of *HDA1* in p673	This study
pBES116	*C. albicans URA3* vector for integration at *ADE2* locus in genome	6
pBES116-YAF9	0.765 kb full length *YAF9* in pBES116 for *YAF9* expression from its own promoter at *YAF9* locus	This study
pBES116-YAF9 dYEATS	0.549 kb Yaf9 fragment lacking YEATS domain in pBES116	This study

pBES116-EAF1	2.06 kb full length *EAF1* in pBES116 for *EAF1* expression from its own promoter	This study
pEAF1 muts	Eaf1 ^{K173R}, Eaf1 ^{K173Q}, Eaf1 ^{K173A}, Eaf1 ^{K173H}, Eaf1 ^{K173N} and Eaf1 ^{K489R} mutation in pBES116-EAF1	This study
pBES116-ESA1	2.18 kb *ESA1* in pBES116 for *ESA1* expression from its own promoter	[3]
pEAF1-YAF9	*EAF1* and *YAF9* fusion fragment in pBES116 for Eaf1-Yaf9 fusion expression from *EAF1* promoter	This study
pBA1	*C. albicans ADH1* promoter in BES116, for gene expression under *ADH1* promoter control at *ADE2* locus	[7]
pBA1-YAF9	0.765 kb full length *YAF9* in pBA1 for *YAF9* expression from *ADH1* promoter	This study
pEaf1-myc	Eaf1-Myc fusion in pBA1	This study
pEaf1-myc muts	Lysine to arginine substitution at K173, K447, K478, K481, K482, K489 and K552 in pEaf1-myc	This study
pEsa1-myc	Esa1-Myc fusion in pBA1	This study
pEsa1-K296R-myc	Lysine to arginine substitution at K296 in p Esa1-myc	
pEsa1-HA	Esa1 with 3HA at C-terminus from its own promoter, *URA3*	This study
pSwr1-HA	Swr1 with 3HA at C-terminus from its own promoter, *URA3*	This study
pYaf9-HA	Yaf9 with 3HA at C-terminus from its own promoter, *URA3*	This study
pEaf1-HA	Eaf1 with 3HA at C-terminus from its own promoter, *URA3*	This study
pEaf1-HA muts	Eaf1 ^{K173R}, Eaf1 ^{K173Q} , Eaf1 ^{K173A} and Eaf1 ^{K489R} mutation in pEaf1-HA	This study
pHda1-HA-URA	Hda1 with 3HA at C-terminus from its own promoter, *URA3*	This study
pHda1-HA-HIS	Hda1 with 3HA at C-terminus from its own promoter, *HIS1*	This study
pGST-Eaf1	2.06 kb full length *EAF1* in pGEX-4T1 for GST-Eaf1 expression in *E. coli*	This study
pGST-Eaf1 muts	Eaf1 ^{K173R} and Eaf1 ^{K173Q} mutation in pGST-Eaf1	This study
pMBP-Yaf9	0.765 kb full length *YAF9* in pSJ8 for MBP-Yaf9 expression in *E. coli*	This study
pMBP-dYEATS	0.549 kb Yaf9 fragment lacking YEATS domain in pSJ8	This study
pMBP-YEATS	0.218 kb Yaf9 fragment containing YEATS domain in pSJ8	This study

Table S3. Primers used in this study

Primers	Sequence	Purpose and features
F1	5'- ATTAGTAACACATCCCTCTCATATACCGCAATGGAGACCAGAAAATTTGGAAGACGGCAAgttttcccagtcacgacgtt	KO *SWR1* by PCR method
R1	5'- AACTTACCAAAGTAATCTGTAGTAAACTCTCCCTCTTGAATAACAACGTTATCCAACTGTtgtggaattgtgagcggata	
F2	5'- tgca agatct ctgcag CTGCAGGAAAAGTATCCGTA	pSWR1-KO-5’ region
R2	5'- tgca agatct GCTGGCTGGTTCGTTTCCCA	
F3	5’- cgat ggatcc GACTAGAAATACAGTGGCCA	pSWR1-KO-3’ region
R3	5’- cgat gcatgc ctgcag GTTCAAGTACACAACGTGCT	
F4	5'-GTGGCGAAATACTTGGCACAGTCTCTAAAACCACATACGCCAACCCAATGCCAAACACCAgttttcccagtcacgacgtt	KO *EAF1* by PCR method
R4	5'-AAAGAAATACAACGCCACCGAAATGGACCCGCCACAACCGCAACTATGAAAAGAAGTTTAtgtggaattgtgagcggata	
F5	5'- tgca agatct ctgcag CCAACCCTGCAAACCCTCTAA	pEAF1-KO-5’ region
R5	5'- tgca agatctGGTTTGGTTAAGAAGAAGAAG	
F6	5'- cgat ggatccGTCAGACAACGACCTTAAACA	pEAF1-KO-3’ region
R6	5'- cgat gcatgc ctgcagCTAACGGATAGTCTTGGGGGC	
F7	5'- CCAATGGTATAGATAGAGATGTTTTAAAGTAATAGGTAATTAGGATATGCAAATATAAATgttttcccagtcacgacgtt	KO *YAF9* by PCR method
R7	5'- CCCATGAATGATGATAGCACTAGTTCTAGTTCTAGTTCTAGTTCTAGTTGTTATTTTAAAtgtggaattgtgagcggata	
F8	5'-tgca agatct ctgcag GATAGAGATGTTTTAAAGTAA	pYAF9-KO-5’ region
R8	5'-tgca agatct GAATGAGTTGATGACATGGAT	
F9	5'-cgat ggatcc GAAAAATTAGCCCTCCTACAA	pYAF9-KO-3’ region
R9	5'-cgat gcatgc ctgcag GCACTAGTTCTAGTTCTAGTT	
F10	5'-CCATCAATTTATAATCTTTAATTAATAATTTAGAAAAAATTCCCTTTCTCATCAAACTGGgttttcccagtcacgacgtt	KO *BDF1* by PCR method
R10	5'GTCTCTCGTTTTTGTTGGAATCTTCGGAGTTTTGAAACCTTAAGCTTTTTTTTTTAATTTtgtggaattgtgagcggata	
F11	5'- tgca agatct ctgcag GCTTGTTAAGAATGCTATCA	pBDF1-KO-5’ region
R11	5'- tgca agatct GATGTGAACTTTGTTGGTTA	
F12	5'- cgat ggatcc GGTCAGCAAGGGTCCGACAA	pBDF1-KO-3’ region
R12	5'- cgat gcatgc ctgcag GGTTAATTGTTGTTTATCTA	
F13	5'- CCAAAATTATTGCACTGGACACCACCTCTGTTCACTGCAAACCAATTACGGTTTGGGTGGCGCGGTGGCGGCCGCATCTTT	Endogenous Esa1-HA
R13	5'- CGATAAAAGTATTAGAATATGGGGAACATCCTATTAAATATATATCTATATATATATTTAGGGGGATCCACTAGTTCTAGA	
F14	5'-GATGGCATTGGTCACATTGATGAGTATATGTTACGGTTTATTTCGGATGGATATTATTTACGCGGTGGCGGCCGCATCTTT	Endogenous Swr1-HA
R14	5'-GCAAGAGATTTTTATAAAAGAAAGGGCCATTTGCTTAATATGTAATACAAGGAGTAACTAGGGGGATCCACTAGTTCTAGA	
F15	5'- ATGTCATCAACTCATTCAAGAAGAATAAAATTTGTATCGATATCAGTACCTATATTATATCGCGGTGGCGGCCGCATCTTT	Endogenous Yaf9-HA

R15	5'-TTATTGTAGGAGGGCTAATTTTTCTTGTTCGAGTAATTTATATTGATTTCGTTGATTTTC GGGGGATCCACTAGTTCTAGA	
F16	5'- ATGAACGATACTTGGAGGTCTCGATTAAAGGAGATTCTGCATATCACTGCAGACCCATTCCGCGGTGGCGGCCGCATCTTT	Endogenous Eaf1-HA
R16	5'-CTACTTACGCGTTGTTTGGCGACCCTGACATGGGCGATGCAGTTTGGTTTTTTTGGTGTG GGGGGATCCACTAGTTCTAGA	
F17	5'- gct ggatcc GACGAAAATTTTTCCTTGATA	Endogenous Esa1-myc
R17	5'- ggag acgcgt cg GATAATGGCTTTTCTGGCGAA	
F18	5'- gct ggatcc GAGATGAGTATAATACAATCA	Endogenous Swr1-myc
R18	5'- ggag acgcgt cg TAAATAATATCCATCCGAAATA	
F19	5'- gct ggatcc TTGATGAAAAATTATCTACTC	Endogenous Yaf9-myc
R19	5'- ggag acgcgt cgTTGTAGGAGGGCTAATTTTTCT	
F20	5'- gct ggatcc GACAATACCAACGACGAAGA	Endogenous Eaf1-myc
R20	5'- ggag acgcgt cg CGCGTTGTTTGGCGACCCTGA	
F21	5'-gat gcggccgc GACAATACCAACGACGAAGACA	pBES116-EAF1
R21	5'-gat ggtacc TTACGCGTTGTTTGGCGACCC	
F22	5'-gat gcggccgc TTGATGAAAAATTATCTACTC	pBES116-YAF9
R22	5'-gat ggtaccTCATGTAGGAGGGCTAATTTTTCT	
F23	5'-GTGACATTTAAATTACATGAAACTTATGAAAATCCA	pBES116-YAF9 dYEATS
R23	5'-ATGTAATTTAAATGTCACTCTTGAATGAGTTGATGACAT	
F24	5'-gat gcggccgcGACAATACCAACGACGAAGACA	pEAF1-YAF9
R24	5'- TCAGGGTCGCCAAACAACGCG ATGTCATCAACTCATTCAAGA	
F25	5'-TCTTGAATGAGTTGATGACATCGCGTTGTTTGGCGACCCTGA	
R25	5'-gatggtaccTCATGTAGGAGGGCTAATTTTTCT	
F26	5'-ACAGTCTGCCAGACTTCATCTGCTCTCCATTGACG	Hda1-HA
R26	5'-CTGACTGACTGACTGCTGGTGGAAGTTTCAAAGCA	
F27	5'-CTTGCCTTACCTCGGTTTGAAAAATAAAAGAACGAGCCTA	
R27	5'-TGTGTACGAGTTGCAATCTTCGGAAGAGGAGTAGTCTTCA	
F28	5'-GTATGGCAAGAGACCATCAAACG	
R28	5'-TCAGCACAGGGATATGGGAAGTA	
F29	5'- gct ggatcc TTATAGAGAAGAATGACTCA	Hda1-Myc
R29	5'- ggag acgcgt cgATCTTCGGAAGAGGAGTAGT	
F30	5'-gatc agatct ATGGCGGTAGCAGAAATCAAA	pBA1-YAF9
R30	5'-gatc atcgat TTACCACCCAAACCGTAATTG	
F31	5'-CAGTCAGTCAGTCAGGATAACGCAGGAAAGAACAT	PUC18 backbone
R31	5'-AGTCTGGCAGACTGTCTTAAGGGATCCAAGCTTCCCGGGTTCTTAGACGTCAGGTGGCA	
F32	5'-TGCAACTCGTACACAAGCGCGCCAATTAGATCCGTG	URA3 amplification
R32	5'-CCGAGGTAAGGCAAGTTCTTTCCTGCGTTATCCTG	
F33	5'-gatgaattcATGTCATCAACTCATTCAAGA	pMBP-Yaf9
R33	5'-gatctcgagTCATGTAGGAGGGCTAATTTTTCT	
F34	5'-gctggatccATGAACGATACTTGGAGGTCT	pGST-Eaf1
R34	5'-ggagacgcgtctaGTTGTTTGGCGACCCTGACAT	
F35	5'-CCAGTTACTTCTGGATCATC	*HWP1*, qRT PCR

R35	5'-TCGGTACAAACACTGTTAGA	
F36	5'-TGGTGTTGCGTGGTCATTG	*EAF1*, qRT PCR
R36	5'-ATCGGTGGTTCTCTGGAGTC	
F37	5'-GCTCAGTACCTCGCCAGTT	*EAF1-YAF9*, qRT PCR
R37	5'-GTTCTGGTGGTGTTGTTGGTT	
F38	5'-GCTTTTGGTGTTTGACGAGTTTCT	*ACT1*, qRT PCR
R38	5'-GTGAGCCGGGAAATCTGTATAGTC	

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