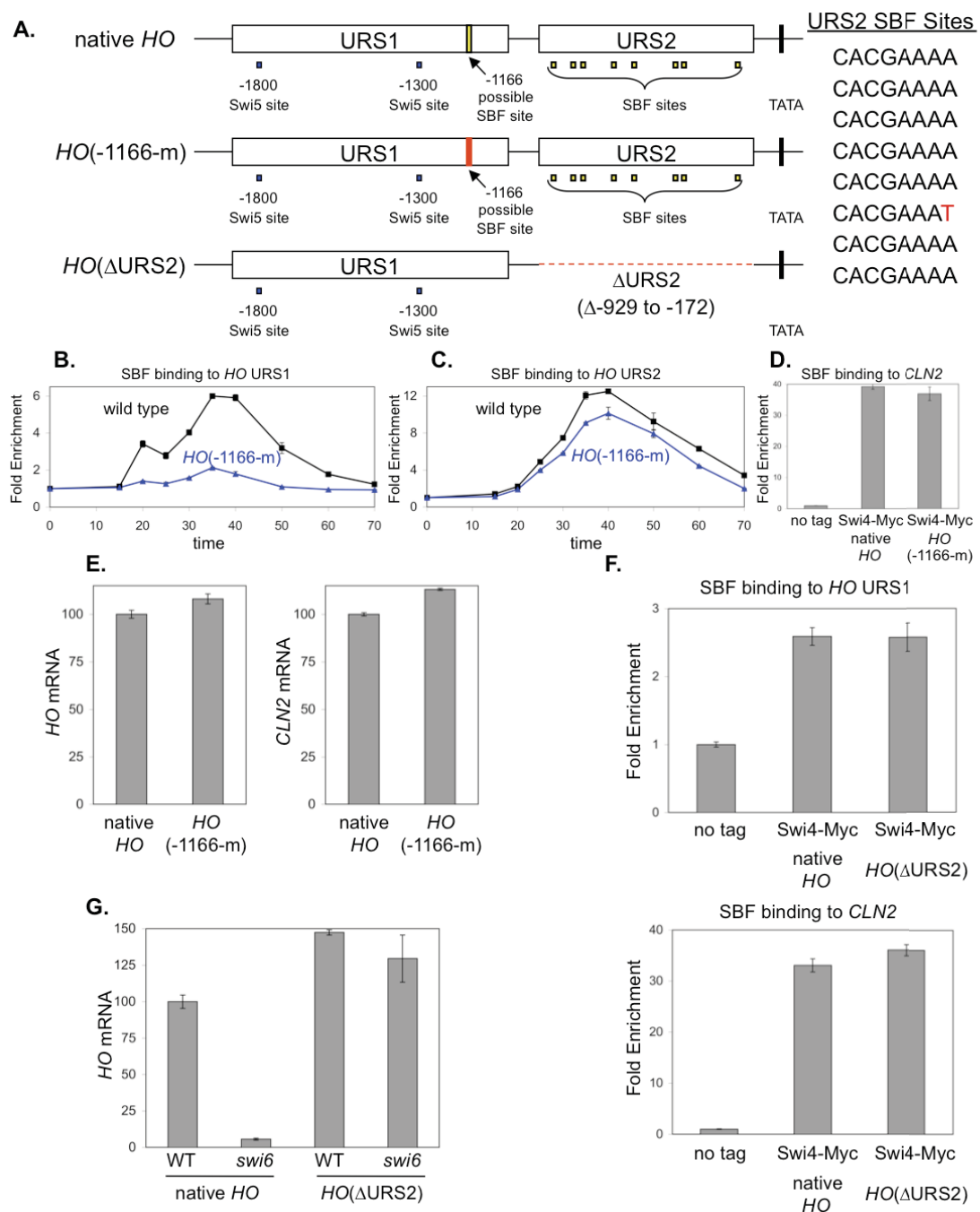


## Supplemental Information

### Repressive Chromatin Affects Factor Binding at the Yeast *HO* (Homothallic Switching) Promoter

Shinya Takahata, Yaxin Yu, and David J. Stillman

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### Supplemental Figure S1. SBF binds to a site in *HO* URS1.

**A.** Maps of the *HO* promoter showing URS1, URS2, and the binding sites for Swi5 and SBF, where the ATG represents +1 and the transcription start site is at -20. Maps are shown for native *HO*, *HO* with the -1166 mutation at a possible SBF binding site, and

*HO*( $\Delta$ URS2) with -929 to -172 deleted. The sequence CGCGTAAA is present at the -1166 site, and the figure also shows the sequence of the eight SBF sites present in URS2 region that conform to the CACGAAAA consensus.

**B.** Strains DY12794 (*GALp::CDC20 SWI4-Myc*) and DY13791 (*GALp::CDC20 SWI4-Myc HO(-1166-m)*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to *HO* URS1 was measured with primers that amplify from -1429 to -1139.

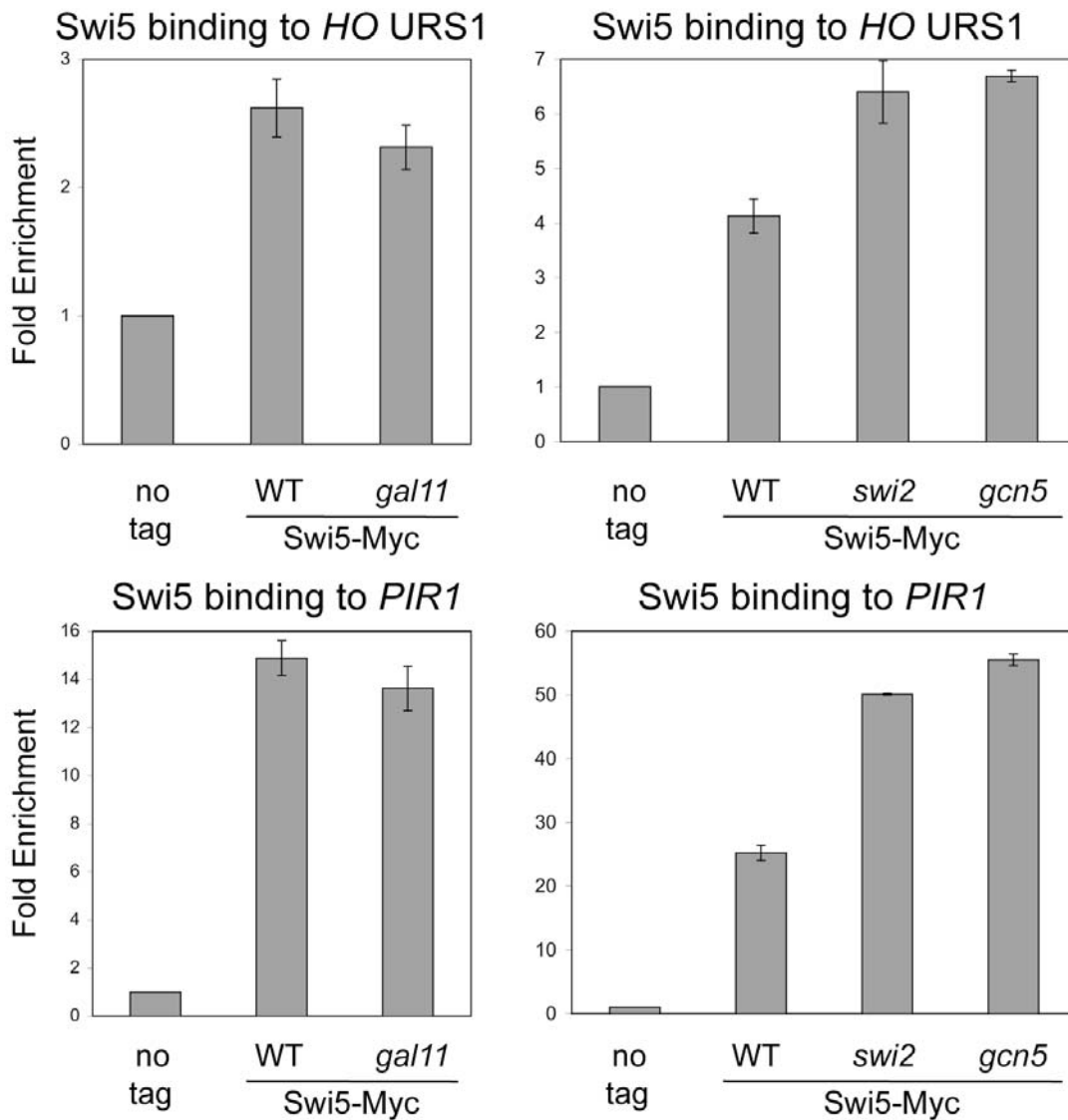
**C.** Strains DY12794 (*GALp::CDC20 SWI4-Myc*) and DY13791 (*GALp::CDC20 SWI4-Myc HO(-1166-m)*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to *HO* URS2 was measured with primers that amplify from -825 to -489.

**D.** ChIP experiments were performed with logarithmically growing strains DY150 (no tag), DY6241 (*SWI4-Myc*), and DY13787 (*SWI4-Myc HO(-1166-m)*). SBF binding to *CLN2* was measured with primers that amplify from -661 to -379.

**E.** *HO* and *CLN2* mRNA levels were measured by RT-qPCR from logarithmically growing cells: DY150 (wildtype) and DY13776 (*HO(-1166-m)*).

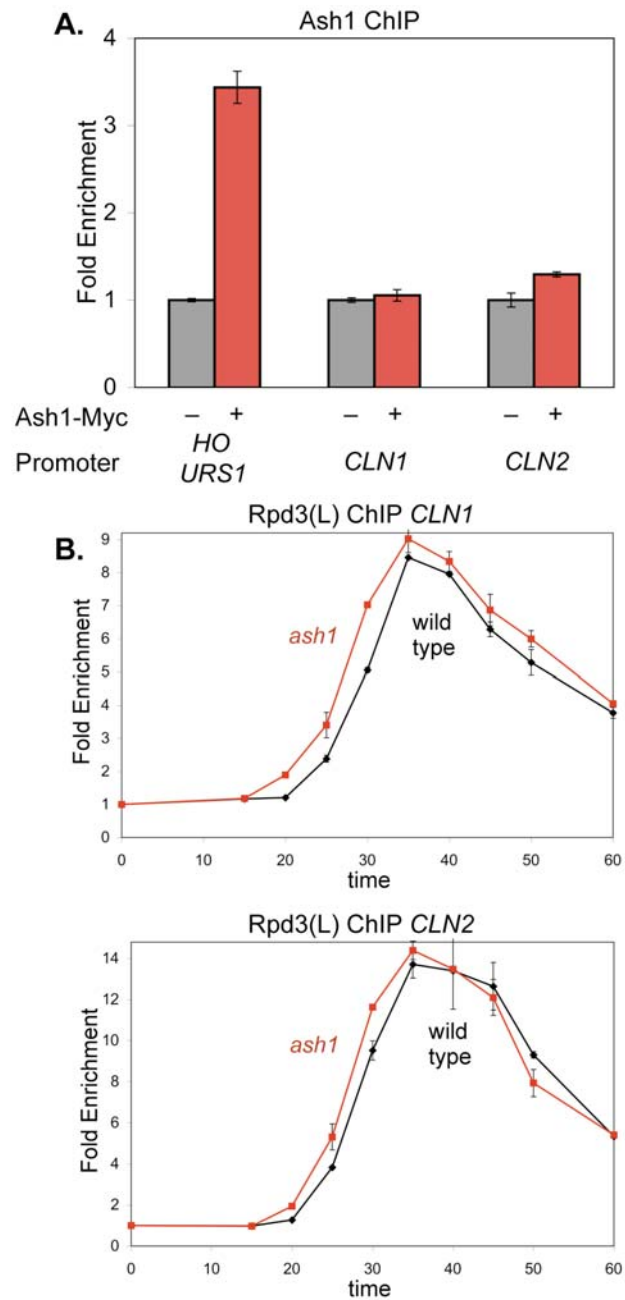
**F.** ChIP experiments were performed with logarithmically growing strains: DY150 (no tag), DY13776 (no tag, *HO(-1166-m)*), DY6241 (*SWI4-Myc*), and DY13787 (*SWI4-Myc HO(-1166-m)*).

**G.** *HO* mRNA levels were measured by RT-qPCR from logarithmically growing cells: DY150 (wildtype), DY13357 (*swi6*), DY11392 (*HO(-1166-m)*), and DY13751 (*swi6 HO(-1166-m)*).



**Supplemental Figure S2. Swi5 still binds to *HO* URS1 in coactivator mutants.**

ChIP experiments were performed with logarithmically growing untagged control strains (DY150, wildtype; DY5628, *gal11*; DY12761, *swi2(E834K)*; and DY5199, *gcn5*) and *SWI2-Myc* strains (DY6270, *SWI5-Myc::URA3MX*; DY13221, *SWI5-Myc::URA3MX gal11*; DY5832, *SWI5-Myc::KanMX*; DY13352, *SWI5-Myc::KanMX swi2(E834K)*; and DY5844, *SWI5-Myc::KanMX gcn5*). Binding to *HO* URS1 and to *PIR1* were measured with primers that amplify from -1429 to -1139 and from -600 to -362, respectively.

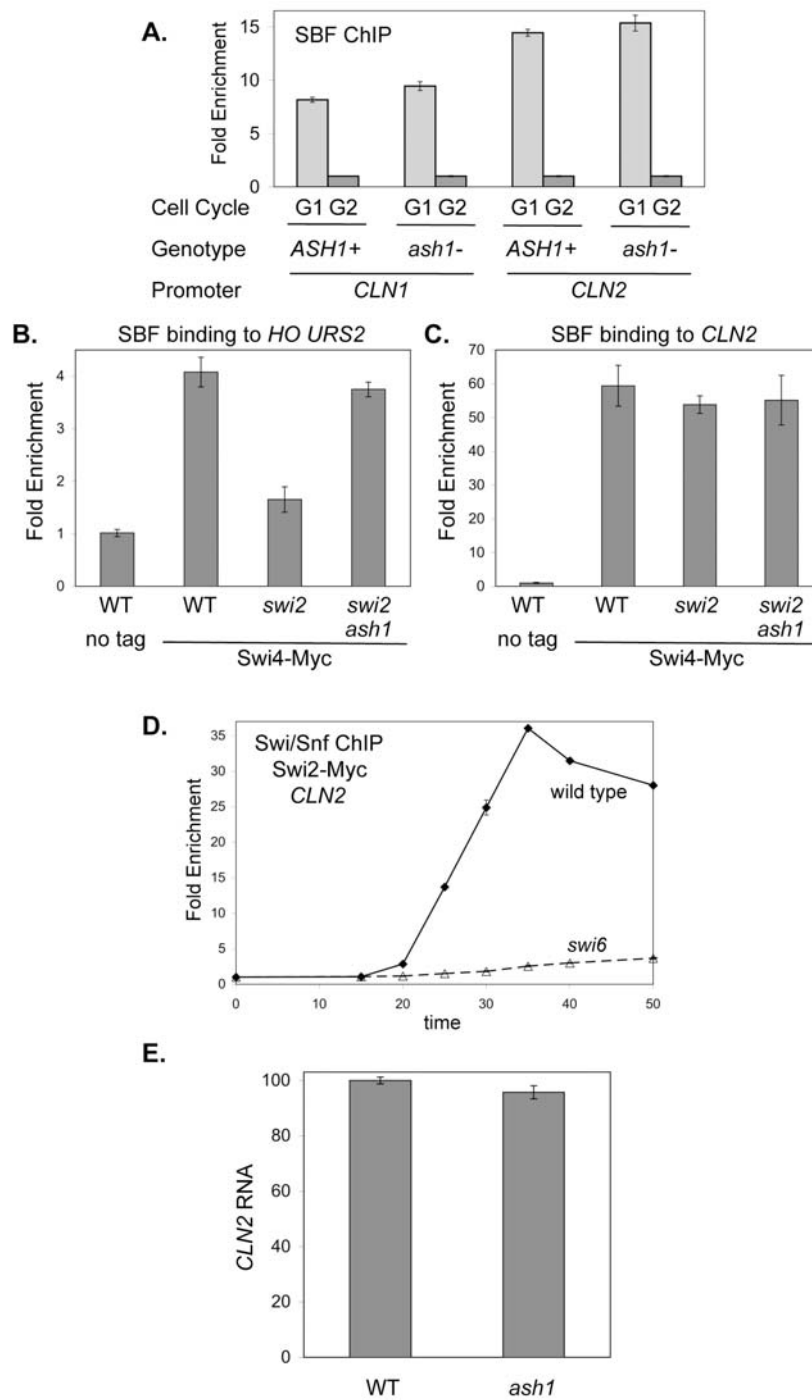


**Supplemental Figure S3. Ash1 does not bind to *CLN* genes and an *ash1* mutation does not affect Rpd3(L) Binding.**

**A.** ChIP experiments were performed with logarithmically growing strains DY150 (no tag control) and DY8309 (*ASH1-Myc*). Binding of Ash1 was determined for *HO URS1* (-1429 to -1139), *CLN1* (-645 to -373), and *CLN2* (-661 to -379).

**B.** Strains DY12247 (*GALp::CDC20 SDS3-Myc*) and DY12251 (*GALp::CDC20 SDS3-Myc ash1*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to *CLN1* was measured with primers that amplify from -645 to -373.

**C.** Strains DY12247 (*GALp::CDC20 SDS3-Myc*) and DY12251 (*GALp::CDC20 SDS3-Myc ash1*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to *CLN2* was measured with primers that amplify from -661 to -379.



**Supplemental Figure S4. Coactivator mutants do not affect SBF binding to *CLN2*.**

**A.** Strains DY12794 (*GALp::CDC20 SWI4-Myc*) and DY12795 (*GALp::CDC20 SWI4-Myc ash1*) were synchronized and a G2 ChIP sample was taken at the *CDC20* arrest and

a G1 sample at 35 min following release from the *CDC20* arrest. Binding of SBF was determined for *CLN1* (-645 to -373) and *CLN2* (-661 to -379).

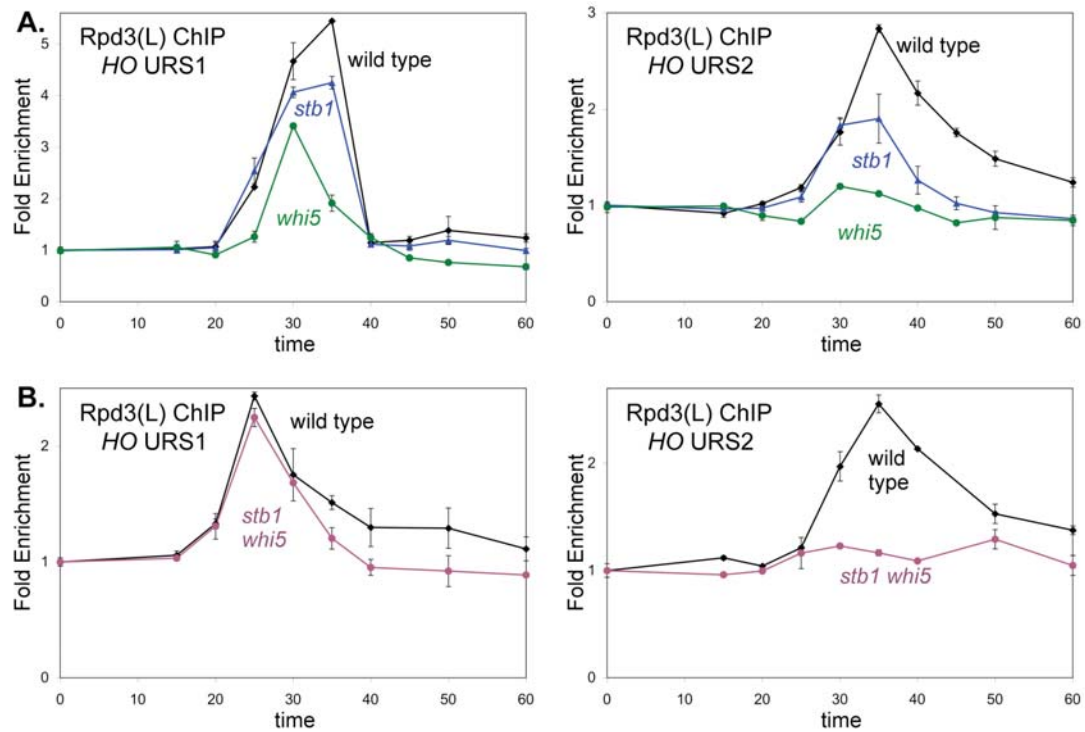
**B.** ChIP experiments were performed with logarithmically growing strains DY150 (no tag control), DY6241 (*SWI4-Myc*), DY11262 (*SWI4-Myc swi2(E834K)*), and DY11264 (*SWI4-Myc swi2(E834K) ash1*). SBF binding to *HO* URS2 was measured with primers that amplify from -825 to -489.

**C.** ChIP experiments were performed with logarithmically growing strains DY150 (no tag control), DY6241 (*SWI4-Myc*), DY11262 (*SWI4-Myc swi2(E834K)*), and DY11264 (*SWI4-Myc swi2(E834K) ash1*). SBF binding to *CLN2* was measured with primers that amplify from -661 to -379.

**D.** Strains DY8602 (*GALp::CDC20 SWI2-Myc*) and DY13529 (*GALp::CDC20 SWI2-Myc ash1*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Swi/Snf binding to *CLN2* was measured with primers that amplify from -661 to -379.

**E.** *CLN2* mRNA levels were measured by RT-qPCR from logarithmically growing DY150 (wild type) and DY5266 (*ash1*).





**Supplemental Figure S5. Rpd3(L) binding to *HO* URS2 requires *Whi5* and *Stb1*.**

**A.** Strains DY12247 (*GALp::CDC20 SDS3-Myc*), DY13500 (*GALp::CDC20 SDS3-Myc stb1*), and DY13498 (*GALp::CDC20 SDS3-Myc whi5*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to URS1 and URS2 were measured with primers that amplify from -1429 to -1139 and from -825 to -489, respectively. Sds3 is a subunit specific to Rpd3(L).

**A.** Strains DY12248 (*GALp::CDC20 SDS3-Myc*) and DY13502 (*GALp::CDC20 SDS3-Myc stb1 whi5*) were synchronized and ChIP samples were taken at various times following release from *CDC20* arrest. Binding to URS1 and URS2 were measured with primers that amplify from -1429 to -1139 and from -825 to -489, respectively. Sds3 is a subunit specific to Rpd3(L).

**Supplemental Table S1. Strain List.**

All strains are in the W303 strain background (1), and contain these mutations: *ade2-1 can1-100 his3-11,15 leu2-3,112 trp1-1 ura3-1*. Additionally, some of the W303 strains contain *lys2Δ25* and *met15Δ0* mutations.

DY150	<i>MATa ade2 can1 his3 leu2 trp1 ura3</i>
DY161	<i>MATa swi5::LEU2 ade2 can1 his3 leu2 trp1 ura3</i>
DY4394	<i>MATa ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3</i>
DY4846	<i>MATa ash1::LEU2 swi5::hisG-URA3-hisG ade2 can1 his3 leu2 trp1 ura3</i>
DY5199	<i>MATα gcn5::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3</i>
DY5266	<i>MATa ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3</i>
DY5628	<i>MATa gal11::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3</i>
DY5832	<i>MATa SWI5-Myc::KanMX ade2 can1 his3 leu2 trp1 ura3</i>
DY5840	<i>MATa swi2::LEU2 ade2 can1 his3 leu2 trp1 ura3</i>
DY5844	<i>MATa SWI5-Myc::KanMX gcn5::TRP1 ade2 can1 his3 leu2 trp1 ura3</i>
DY5925	<i>MATa gcn5::HIS3 ade2 can1 his3 leu2 trp1 ura3</i>
DY6067	<i>MATa GCN5-Myc::KanMX swi5::hisG ade2 can1 his3 leu2 trp1 ura3</i>
DY6148	<i>MATα GAL11-Myc::HIS3MX ade2 can1 his3 leu2 lys2 trp1 ura3</i>
DY6151	<i>MATa SWI2-Myc::TRP1 ade2 can1 his3 leu2 trp1 ura3</i>
DY6197	<i>MATa GAL11-Myc::HIS3MX swi5::LEU2 ade2 can1 his3 leu2 trp1 ura3</i>
DY6241	<i>MATa SWI4-Myc::TRP1 ade2 can1 his3 leu2 trp1 ura3</i>
DY6270	<i>MATα SWI5-Myc::URA3MX ade2 can1 his3 leu2 trp1 ura3</i>
DY6378	<i>MATa SWI2-Myc::TRP1 swi5::hisG-URA3-hisG ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3</i>

- DY6669 *MATa GALp::CDC20::ADE2 ade2 can1 his3 leu2 trp1 ura3*
- DY6739 *MATa GAL11-Myc::HIS3MX ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY6741 *MATa GAL11-Myc::HIS3MX ash1::LEU2 swi5::hisG-URA3-hisG ade2 can1 his3  
leu2 lys2 trp1 ura3*
- DY6999 *MATa swi6::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY7194 *MATa GCN5-Myc::KanMX ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY7196 *MATa GCN5-Myc::KanMX ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY7240 *MATa GCN5-Myc::KanMX gal11::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY7387 *MATa gcn5::HIS3 ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY7379 *MATa pob3(L78R) ade2 can1 his3 leu2 lys2 met15 trp1 ura3*
- DY7403 *MATa SWI2-Myc::TRP1 ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY7874 *MATa ho::URA3(promoter)::KanMX(3') ade2 can1 his3 leu2 trp1 ura3*
- DY8309 *MATa ASH1-Myc::KanMX ade2 can1 his3 leu2 trp1 ura3*
- DY8312 *MATa GALp::CDC20::ADE2 ASH1-Myc::KanMX ade2 can1 his3 leu2 trp1 ura3*
- DY8602 *MATa SWI2-Myc::TRP1 GALp::CDC20::ADE2 ade2 can1 his3 leu2 trp1 ura3*
- DY8736 *MATa SWI2-Myc::TRP1 ash1::LEU2 gcn5::HIS3 ade2 can1 his3 leu2 trp1 ura3*
- DY8738 *MATa SWI2-Myc::TRP1 gcn5::HIS3 ade2 can1 his3 leu2 trp1 ura3*
- DY9395 *MATa SWI2-Myc::TRP1 swi5::hisG-URA3-hisG ade2 can1 his3 leu2 trp1 ura3*
- DY9559 *MATa whi5::HphMX ade2 can1 his3 leu2 lys2 met15 trp1 ura3*
- DY9711 *MATa swi2(E834K) ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY10204 *MATa taf1::HphMX YCp(URA3)-TAF1 ade2 can1 his3 leu2 trp1 ura3*
- DY10366 *MATa taf1::HphMX YCp(URA3)-TAF1 ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY10598 *MATa taf1(ΔTAND)::HphMX ade2 can1 his3 leu2 lys2 met15 trp1 ura3*

- DY11262 *MATa SWI4-Myc::TRP1 swi2(E834K) ade2 can1 his3 leu2 trp1 ura3*
- DY11264 *MATa SWI4-Myc::TRP1 swi2(E834K) ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY11278 *MATa GCN5-Myc::KanMX swi2(E834K) ash1::LEU2 ade2 can1 his3 leu2 trp1 ura3*
- DY11348 *MATa taf1::HphMX YCp(TRP1)-TAF1 ade2 ade2 can1 his3 leu2 trp1 ura3*
- DY11349 *MATa taf1::HphMX YCp(TRP1)-TAF1(Y570N) ade2 can1 his3 leu2 trp1 ura3*
- DY11392 *MATa ho( $\Delta$ URS2[-929 to -172]) ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY11570 *MATa ash1::LEU2 taf1::HphMX + YCp(TRP1)-TAF1 ade2 can1 his3 leu2 trp1 ura3*
- DY11571 *MATa ash1::LEU2 taf1::HphMX + YCp(TRP1)-TAF1(Y570N) ade2 can1 his3 leu2  
trp1 ura3*
- DY11574 *MATa whi5::KanMX taf1::HphMX + YCp(TRP1)-TAF1 ade2 can1 his3 leu2 trp1  
ura3*
- DY11575 *MATa whi5::KanMX taf1::HphMX + YCp(TRP1)-TAF1(Y570N) ade2 can1 his3 leu2  
trp1 ura3*
- DY12247 *MATa GALp::CDC20::ADE2 SDS3-Myc::His3MX ade2 can1 his3 leu2 lys2 trp1  
ura3*
- DY12248 *MATa GALp::CDC20::ADE2 SDS3-Myc::His3MX ade2 can1 his3 leu2 lys2 trp1  
ura3*
- DY12251 *MATa GALp::CDC20::ADE2 SDS3-Myc::His3MX ash1::LEU2 ade2 can1 his3 leu2  
lys2 trp1 ura3*
- DY12303 *MATa taf1::HphMX + YCp(HIS3)-TAF1-HA ade2 can1 his3 leu2 trp1 ura3*
- DY12305 *MATa taf1::HphMX + YCp(HIS3)-TAF1(N568 $\Delta$ )-HAplasmid ade2 can1 his3 leu2  
trp1 ura3*
- DY12711 *MATa GAL11-Myc::HIS3MX gcn5::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3*

- DY12729 *MATa GAL11-Myc::HIS3MX swi2(E834K) ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY12761 *MATa swi2(E834K) ade2 can1 his3 leu2 trp1 ura3*
- DY12794 *MATa GALp::CDC20::ADE2 SWI4-Myc::TRP1 ade2 can1 his3 leu2 trp1 ura3*
- DY12795 *MATa GALp::CDC20::ADE2 SWI4-Myc::TRP1 ash1::LEU2 ade2 can1 his3 leu2  
trp1 ura3*
- DY12795 *MATa GALp::CDC20::ADE2 SWI4-Myc::TRP1 ash1::LEU2 ade2 can1 his3 leu2  
trp1 ura3*
- DY12830 *MATa GALp::CDC20::ADE2 SDS3-Myc::His3MX ash1::LEU2 swi6::TRP1 ade2  
can1 his3 leu2 lys2 trp1 ura3*
- DY12861 *MATa GCN5-Myc::KanMX swi2(E834K) ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY13020 *MATa CDC28-Myc::KanMX ade2 can1 his3 leu2 lys2 met15 trp1 ura3*
- DY13197 *MATa GALp::CDC20::ADE2 ASH1-Myc::KanMX SIN3-HA::TRP1 ade2 can1 his3  
leu2 lys2 trp1 ura3*
- DY13221 *MATa SWI5-Myc::URA3MX gal11::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY13352 *MATa SWI5-Myc::KanMX swi2(E834K) ade2 can1 his3 leu2 trp1 ura3*
- DY13357 *MATa swi6::TRP1 ade2 can1 his3 leu2 trp1 ura3*
- DY13454 *MATa stb1::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3*
- DY13498 *MATa GALp::CDC20::ADE2 SDS3-Myc::HIS3MX whi5::KanMX ade2 can1 his3  
leu2 trp1 ura3*
- DY13500 *MATa GALp::CDC20::ADE2 SDS3-Myc::HIS3MX stb1::TRP1 ade2 can1 his3 leu2  
trp1 ura3*
- DY13502 *MATa GALp::CDC20::ADE2 SDS3-Myc::HIS3MX stb1::TRP1 whi5::KanMX ade2  
can1 his3 leu2 trp1 ura3*

DY13527 *MATa CDC28-Myc::KanMX pob3(L78R) ade2 can1 his3 leu2 lys2 met15 trp1 ura3*

DY13529 *MATa SWI2-Myc::TRP1 swi6::ADE2 GALp::CDC20::URA3 ade2 can1 his3 leu2  
trp1 ura3*

DY13640 *MATa whi5::HphMX stb1::TRP1 ade2 can1 his3 leu2 lys2 met15 trp1 ura3*

DY13723 *MATa CDC28-Myc::KanMX swi6::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3*

DY13729 *MATa CDC28-Myc::KanMX stb1::TRP1 ade2 can1 his3 leu2 lys2 met15 trp1 ura3*

DY13731 *MATa CDC28-Myc::KanMX whi5::HphMX ade2 can1 his3 leu2 lys2 met15 trp1  
ura3*

DY13733 *MATa CDC28-Myc::KanMX stb1::TRP1 whi5::HphMX ade2 can1 his3 leu2 lys2  
met15 trp1 ura3*

DY13751 *MATa ho( $\Delta$ URS2[-929 to -172]) swi6::TRP1 ade2 can1 his3 leu2 lys2 trp1 ura3*

DY13752 *MATa ho( $\Delta$ URS2[-929 to -172]) SWI4-Myc::TRP1 ade2 can1 his3 leu2 trp1 ura3*

DY13776 *MATa ho(-1166-m)::KanMX(3') ade2 can1 his3 leu2 trp1 ura3*

DY13787 *MATa ho(-1166-m)::KanMX(3') SWI4-Myc::TRP1 ade2 can1 his3 leu2 trp1 ura3*

DY13791 *MATa GALp::CDC20::ADE2 ho(-1166-m)::KanMX(3') SWI4-Myc::TRP1 ade2 can1  
his3 leu2 trp1 ura3*

DY14133 *MATa swi5::TRP1 ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3*

DY14137 *MATa GCN5-Myc::KanMX swi5::TRP1 ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1  
ura3*

DY14140 *MATa GCN5-Myc::KanMX gal11::LEU2 ash1::TRP1 ade2 can1 his3 leu2 lys2 trp1  
ura3*

DY14142 *MATa GAL11-Myc::HIS3MX gcn5::TRP1 ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1  
ura3*

DY14144 *MATa gal11::KanMX ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1 ura3*

DY14147 *MATa SWI2-Myc::TRP1 gal11::KanMX ade2 can1 his3 leu2 trp1 ura3*

DY14148 *MATa SWI2-Myc::TRP1 gal11::KanMX ash1::LEU2 ade2 can1 his3 leu2 lys2 trp1  
ura3*

DY14186 *MATa GAL11-Myc::HIS3MX swi2(E834K) ash1::LEU2 ade2 can1 his3 leu2 trp1  
ura3*

**Supplemental Table S2. Plasmid List.**

<u>Plasmid</u>	<u>Description</u>	<u>Source</u>
pLEJ009 (M5098)	YCp- <i>KanMX</i> Vector	(2)
M5220	<i>CDC28</i> (untagged) in YCp- <i>KanMX</i> plasmid	this work
M5056	<i>HA-CDC28</i> in YCp- <i>KanMX</i> plasmid	this work
pM34 (M5100)	<i>TAF1</i> in YCp- <i>TRP1</i> plasmid	(3)
pTM25 (M5101)	TAF1(Y570N) in YCp- <i>TRP1</i> plasmid	(3)
pM7089 (M5014)	TAF1-HA(x4) in YCp- <i>HIS3</i> plasmid	T. Kokubo
pM7111 (M5147)	TAF1(N568Δ)-HA(x4) in YCp- <i>HIS3</i> plasmid	T. Kokubo
pM7110 (M5148)	TAF1(T657K)-HA(x4) in YCp- <i>HIS3</i> plasmid	T. Kokubo



**Supplemental Table S3. Oligonucleotide List.**RT-qPCR oligos

F1066	<i>HO</i>	AAATGGAGCGCTCTAAAGGAGAA
F1067	<i>HO</i>	CTAACCACAGACCAAGCATCCAA
F2043	<i>CLN2</i>	AATTCTTGATTGATGTATCCGCGTGG
F2044	<i>CLN2</i>	GTTAGGAATGGAAACAATGCCGTTCA
F1070	<i>ACT1</i> (control)	CTGCCGGTATTGACCAAACACTTACAA
F1071	<i>ACT1</i> (control)	GTCAAAGAAGCCAAGATAGAACCACCAA
F2173	<i>RDN25</i> (control)	CGTTCCTTGTCTATGTTCCCTTG
F2174	<i>RDN25</i> (control)	CACTGTACTTGTTTCGCTATCG

ChIP oligos

F1093	<i>HO</i> URS1 (-1429 to -1139)	TATACCCAATCGCTGCGTGC
F1094	<i>HO</i> URS1 (-1429 to -1139)	AGCCGCCACGAATCAAACCTT
F1095	<i>HO</i> URS2 (-825 to -489)	GGCAAACCTAATGTGACCGT
F1096	<i>HO</i> URS2 (-825 to -489)	GGCAAACCTAATGTGACCGT
F1154	<i>HO</i> TATA (-43 to +175)	CCATATCCTCATAAGCAGCA
F1155	<i>HO</i> TATA (-43 to +175)	AAGCTCTGTGTTTGGTTTTT
F2127	<i>CLN1</i>	GACGATCCACTAGCGACTTCT
F2128	<i>CLN1</i>	CACGCTGCCTTTACTCCATTC
F996	<i>CLN2</i>	GTTATCAATTCATGCGCGCT
F997	<i>CLN2</i>	AGATCAACATTTTCGCAGGTT
F1759	<i>PIRI</i> UAS	CTGCCCAAATGCTTAAATACAGA
F1760	<i>PIRI</i> UAS	ATAATTCCTCGAAGCCAGAC
F1416	Chrom I control	GTTTATAGCGGGCATTATGCGTAGATCAG
F1417	Chrom I control	GTTCCCTCTAGAATTTTTCCACTCGCACATTC

ChIP oligos tiled along the *HO* promoter

F2083	<i>HO</i> Promoter -2033 to -1823	GAGTATTGTGTCATGTTTCGAGACAAAC
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F2084	<i>HO</i> Promoter -2033 to -1823	TTAAGTCCAAAGGCACAATTTTACG
F2085	<i>HO</i> Promoter -1872 to -1670	TTGATCTTTACCGTTTAGTTCCAAC
F2086	<i>HO</i> Promoter -1872 to -1670	GTAAAGCCTCCAGAACAGCTATG
F2087	<i>HO</i> Promoter -1742 to -1551	AAAGGCGGATCAAGATGTATGAAAG
F2088	<i>HO</i> Promoter -1742 to -1551	GGAACCATGTGATCTTACGTTGATATG
F2089	<i>HO</i> Promoter -1640 to -1416	TCCGAAAAGCAATTACTCTCTATGTT
F2090	<i>HO</i> Promoter -1640 to -1416	GCGATTGGGTATAATGAAGATTGTTA
F2091	<i>HO</i> Promoter -1471 to -1250	AAGCTAAGAATTTACATGTTGTTG
F2092	<i>HO</i> Promoter -1471 to -1250	GTTGAGGTCTTTTCTATTTCTGATTG
F2093	<i>HO</i> Promoter -1295 to -1121	AATGCTGGAGCAAAAATTTCAATCAG
F2094	<i>HO</i> Promoter -1295 to -1121	GGAGCCCCTCAGACATTAGCC
F2115	<i>HO</i> Promoter -1204 to -1014	TCTACGGATGATCTGTGAGAA
F2116	<i>HO</i> Promoter -1204 to -1014	CTACGTTAAGACCTGTAACCGA
F2117	<i>HO</i> Promoter -1063 to -859	GAAAGAACCGCAGAGTGCTT
F2118	<i>HO</i> Promoter -1063 to -859	GAACCTGGTACGTATATTGTGGC
F2097	<i>HO</i> Promoter -983 to -796	TCGATCCGTTTGGCGTCTTT
F2098	<i>HO</i> Promoter -983 to -796	TAATCGACGACGGTCACATTAGGTT
F2099	<i>HO</i> Promoter -839 to -619	TCATACCCTGACTTGGCAAAC
F2100	<i>HO</i> Promoter -839 to -619	CTTAAGCCCTGTGTAGGATTGATT
F2101	<i>HO</i> Promoter -677 to -481	ATGCAGTTGAAGACATGTGCGTC
F2102	<i>HO</i> Promoter -677 to -481	CATAGAAACAGGACTTGCGAACCC
F2103	<i>HO</i> Promoter -573 to -336	ACGATTACCATGGAAATTAACGTACCT
F2104	<i>HO</i> Promoter -573 to -336	TCTATGAAAATGAATTGTTGCTCTGC
F2105	<i>HO</i> Promoter -448 to -250	GGTTTACGAAATGATCCACGAAAATC
F2106	<i>HO</i> Promoter -448 to -250	TTTCACACCTAATAACGCCCAGC
F2119	<i>HO</i> Promoter -307 to -75	ACCATTGGTACCTACTACTTTGAAT
F2120	<i>HO</i> Promoter -307 to -75	GCCATTTAGAATAGGAATTGAATAC

Supplemental Information

Repressive Chromatin at the *HO* Promoter

F2109 *HO* Promoter -165 to +56

GTTGAAGCATGATGAAGCGTTCTAAAC

F2110 *HO* Promoter -165 to +56

GCGATGTCTTTAATTTACCGTTAGC

F1154 *HO* Promoter -43 to +175

CCATATCCTCATAAGCAGCA

F1155 *HO* Promoter -43 to +175

AAGCTCTGTGTTTGGTTTTT

**References.**

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3. Tsukihashi, Y., Miyake, T., Kawaichi, M., and Kokubo, T. (2000) *Mol. Cell. Biol.* **20**, 2385-2399