Supplemental Information

Primer pairs used for ChIP analysis using TaqMan approach

The primers and probe used to analyze the 5' end of *STE11* were designed to amplify *STE11* between 397 bp and 492 bp downstream of the start codon and are the sequences are as follows:

STE11 5'_F (+397 bp): 5' GTTAATGTAAATGGTTGCTTTAATGCAGATTCT 3'

STE11 5'_R (+492 bp): 5' TTCTCCATTGGAGTTTGTGGCTAAT 3'

STE11 5'_M (+449 bp — +464 bp): 5' TCATGTGGCAATCTTC 3'

The primers and probe used to analyze the 3' end of *STE11* were designed to amplify *STE11* between 1644 bp and 1748 bp downstream of the start codon and are the sequences are as follows:

STE11 3'_F (+1644 bp): 5' CGGTCCATTTGAGGAATCACTGATTAC 3'

STE11 3'_R (+1748 bp): 5' GCACCCTTGATATCTCTGTGAATAATGT 3'

STE11 3'_M (+1690bp — +1705 bp): 5' ACGCAACCCCAATCAG 3'

The primers and probe used to analyze the 5' end of *Flo8* were designed to amplify *Flo8* between 437 bp and 540 bp downstream of the start codon and are the sequences are as follows:

Flo8 5'_F (+437 bp): 5' GGGACATCTTTAATACCAGTTCTTCCA 3'

Flo8 5'_R (+540 bp): 5' GCTTCTATATATTTGTTCCTGCCTTTGTTC 3'

Flo8 5'_M (+474 bp — +489 bp): 5' TTGCTGAGCGAACTCT 3'

The primers and probe used to analyze the 3' end of *Flo8* were designed to amplify *Flo8* between 1899 bp and 1973 bp downstream of the start codon and are the sequences are as follows:

Flo8 3' F (+1899 bp): 5' CTCTAAAATAATCACTTCACAGAATAATACAGTATCCC 3'

Flo8 3'_R (+1973 bp): 5' TGCGCCTCCAGTATGTTTCC 3'

Flo8 3'_M (+1937bp — +1952 bp): 5' CCATTCGGCAATTCTT 3'

Supplemental Tables

Table S1. Yeast Strains

Yeast Strain	Genotype	Source
WZY42	*MATa; ura3−52;lys2−801; ade2−101; trp1Δ63; his3Δ200; leu2Δ1; hht1-hhf1::pWZ405-F2F9-LEU2; hht2-hhf2::pWZ403-F4F10-HIS3*	(1)
SDBY1001	as WZY42 with pJH18	(2)
SDBY1005	as WZY42 with pHCL55	(2)
SDBY1155	*MATa*; *ura3−52*,;*lys2−801*; *ade2−101*; *trp1Δ63*; *his3Δ200*; *leu2Δ1*; *hht1-hhf1*::*pWZ405-F2F9-LEU2*; *hht2-hhf2*::pWZ403-F4F10-HIS3; *set2Δ::KanMX*	This Study
FY406	MATa; *his3Δ200*; *trp1Δ63*; *lys2-128ξ*; *ura3-52*; and *leu2Δ1; (hta1-htb1)Δ::*LEU2 *(hta2-htb2)Δ::*TRP1 <*pSAB6*>	(3)
SDBY1156	as FY406 with pJH23	This Study
SDBY1157	as FY406 with pHND09	This Study
SDBY1158	as FY406 with pHND10	This Study
SDBY1159	as FY406 with pHND11	This Study
SDBY1160	as FY406 with pHND12	This Study
SDBY1161	as FY406 with pHND13	This Study
SDBY1162	as FY406 with pHND14	This Study
SDBY1163	as FY406 with pHND15	This Study
SDBY1164	as FY406 with pHND16	This Study
SDBY1165	as FY406 with pHND17	This Study
SDBY1166	as FY406 with pHND18	This Study
SDBY1167	as FY406 with pHND19	This Study
JHY205	*MATa;his3Δ1; leu2Δ0; met1Δ0; ura3Δ0; hht1-hhf1::KAN; hhf-2hht2::NAT; hta1-htb1::HPH; hta2-htb2::NAT pJH33*[CEN URA3 HTA1-HTB1 HHT2-HHF2]	(4)
SDBY1168	as JHY205 with pHND20 and pJH23	This Study
SDBY1169	as JHY205 with pHND21 and pJH23	This Study
SDBY1170	as JHY205 with pHND22 and pJH23	This Study
SDBY1171	as JHY205 with pHND20 and pHND16	This Study
SDBY1172	as JHY205 with pHND20 and pHND19	This Study
SDBY1173	as JHY205 with pHND22 and pHND16	This Study
SDBY1174	as JHY205 with pHND22 and pHND19	This Study
BY4741	*MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0*	Open Biosystems
set2Δ	*MAT*a; *his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; set2Δ*	Open Biosystems
ppr2Δ	*MAT*a; *his3Δ1; leu2Δ0; met15Δ0; ura3Δ0*	Open Biosystems
SDBY1055	as BY4741 *set2Δ* with pRS415	(5)
SDBY1056	as BY4741 *set2Δ* with pRS415-Set2-HA 1-733	(5)
SDBY1057	as BY4741 *set2Δ* with pRS415-Set2-HA Δ11-15	(5)
SDBY1058	as BY4741 *set2Δ* with pRS415-Set2-HA Δ31-39	(5)
SDBY1060	as BY4741 *set2Δ* with pRS415-Set2-HA 1-618	(5)
SDBY1175	as BY4741 *set2Δ* with pHND23	This Study
SDBY1176	as FY406 with pHND27	This Study
SDBY1177	as FY406 with pHND28	This Study
SDBY1178	as FY406 with pHND29	This Study
SDBY1179	as FY406 with pHND30	This Study
SDBY1180	as FY406 with pHND31	This Study
SDBY1181	as WZY42 with pHND32	This Study
SDBY1182	as WZY42 with pHND33	This Study
SDBY1183	as WZY42 with pHND34	This Study

Table S1. Yeast Strains (continued)

Yeast Strain	Genotype	Source
SDBY1184	as WZY42 with pHND35	This Study
SDBY1185	as WZY42 with pHND36	This Study
SDBY1186	as WZY42 with pHND37	This Study

Table S2. Histone Plasmids

Plasmid	H3	H4	H2A	H2B	Parent	Source
pJH18	WT	WT	None	None	pRS314	(6)
pHCL55	K36R	WT	None	None	pJH18	(2)
pHCL94	WT	K44Q	None	None	pJH18	(5)
pJH23	None	None	WT	WT	pRS313	(3)
pHND09	None	None	L116A	WT	pRS313	This study
pHND10	None	None	L116I	WT	pRS313	This study
pHND11	None	None	L116Q	WT	pRS313	This study
pHND12	None	None	L117A	WT	pRS313	This study
pHND13	None	None	L117Q	WT	pRS313	This study
pHND14	None	None	K119Q, K120Q	WT	pRS313	This study
pHND15	None	None	ΔL116, L117	WT	pRS313	This study
pHND16	None	None	L116A, L117A	WT	pRS313	This study
pHND17	None	None	L116E, L117E	WT	pRS313	This study
pHND18	None	None	L116K, L117K	WT	pRS313	This study
pHND19	None	None	L116Q, L117Q	WT	pRS313	This study
pHND20	WT	WT	None	None	pRS415	This study
pHND21	K36R	WT	None	None	pRS415	This study
pHND22	WT	K44Q	None	None	pRS415	This study
pHND27	None	None	I112A	WT	pRS313	This study
pHND28	None	None	H113A	WT	pRS313	This study
pHND29	None	None	Q114A	WT	pRS313	This study
pHND30	None	None	N115A	WT	pRS313	This study
pHND31	None	None	P118A	WT	pRS313	This study
pHND32	R52A	WT	None	None	pRS314	This study
pHND33	I112A	WT	None	None	pRS314	This study
pHND34	N108A	WT	None	None	pRS314	This study
pHND35	N108D	WT	None	None	pRS314	This study
pHND36	V117A	WT	None	None	pRS314	This study
pHND37	V117Q	WT	None	None	pRS314	This study

Table S3. Other Plasmids

Plasmid	Inserted Gene	Restriction sites in cloning	Promoter	Vector	Source
pHND23	Set2-HA 1-261	*BamH*I, *Xho*I	Endogenous	pRS415	This Study
pHND24	Set2	*Nhe*I, *Kpn*I	T7	pCAL-n	(5)
pHND25	Histone H4 24-50	*EcoR*I, *BamH*I	AmpR	pGEX-2T	(5)
pHND26	Histone H2A 107-131	*BamH*I, *Xho*I	AmpR	pGEX-4T	This study

Table S4. Fold Change Analysis of *STE11* H3 K36 dimethylation ChIP Analysis (See Fig. 5*A*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	-13.1 +/- 0.04
H4 K44Q/ WT	5’	-1.6 +/- 0.05
H2A L116A, L117A / WT	5’	-2.1 +/- 0.06
H4 K44Q+H2A L116A, L117A / WT	5’	-3.6 +/- 0.13
H3 K36R / WT	3’	-15.3 +/- 0.05
H4 K44Q/ WT	3’	-1.5 +/- 0.20
H2A L116A, L117A / WT	3’	-1.7 +/- 0.17
H4 K44Q+H2A L116A, L117A / WT	3’	-3.7 +/- 0.14

*****Data represents three biological repeats with three technical repeats each.

Table S5. Fold Change Analysis of *FLO8* H3 K36 dimethylation ChIP Analysis (See Fig. 5*A*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	-12.0 +/- 0.04
H4 K44Q/ WT	5’	-1.8 +/- 0.03
H2A L116A, L117A / WT	5’	-2.0 +/- 0.05
H4 K44Q+H2A L116A, L117A / WT	5’	-2.9 +/- 0.04
H3 K36R / WT	3’	-10.4 +/- 0.04
H4 K44Q/ WT	3’	-1.8 +/- 0.17
H2A L116A, L117A / WT	3’	-1.9 +/- 0.14
H4 K44Q+H2A L116A, L117A / WT	3’	-2.9 +/- 0.08

*****Data represents three biological repeats with three technical repeats each.

Table S6. Fold Change Analysis of *STE11* H3 K36 trimethylation ChIP Analysis (See Fig. 5*B*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	-8.1 +/- 0.06
H4 K44Q/ WT	5’	-1.9+/- 0.04
H2A L116A, L117A / WT	5’	-4.3 +/- 0.05
H4 K44Q+H2A L116A, L117A / WT	5’	-9.6 +/- 0.03
H3 K36R / WT	3’	-10.9 +/- 0.04
H4 K44Q/ WT	3’	-2.0 +/- 0.11
H2A L116A, L117A / WT	3’	-4.2 +/- 0.11
H4 K44Q+H2A L116A, L117A / WT	3’	-9.4 +/- 0.05

*****Data represents three biological repeats with three technical repeats each.

Table S7. Fold Change Analysis of *FLO8* H3 K36 trimethylation ChIP Analysis (See Fig. 5*B*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	-9.4 +/- 0.03
H4 K44Q/ WT	5’	-1.9 +/- 0.05
H2A L116A, L117A / WT	5’	-4.2 +/- 0.02
H4 K44Q+H2A L116A, L117A / WT	5’	-10.1 +/- 0.03
H3 K36R / WT	3’	-12.9 +/- 0.04
H4 K44Q/ WT	3’	-1.9 +/- 0.11
H2A L116A, L117A / WT	3’	-4.3 +/- 0.13
H4 K44Q+H2A L116A, L117A / WT	3’	-11.9 +/- 0.02

*****Data represents three biological repeats with three technical repeats each.

Table S8. Fold Change Analysis of *STE11* H4 acetylation ChIP Analysis (See Fig. 6*A*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	1.2 +/- 0.12
H4 K44Q/ WT	5’	1.8 +/- 0.15
H2A L116A, L117A / WT	5’	1.8 +/- 0.27
H4 K44Q+H2A L116A, L117A / WT	5’	3.4 +/- 0.87
H3 K36R / WT	3’	2.1 +/- 0.42
H4 K44Q/ WT	3’	2.5 +/- 0.30
H2A L116A, L117A / WT	3’	2.9 +/- 0.88
H4 K44Q+H2A L116A, L117A / WT	3’	5.3 +/- 0.54

*****Data represents three biological repeats with three technical repeats each.

Table S9. Fold Change Analysis of *FLO8* H4 acetylation ChIP Analysis (See Fig. 6*B*)

Samples Compared	Location	Fold Change
H3 K36R / WT	5’	1.0 +/- 0.11
H4 K44Q/ WT	5’	1.3 +/- 0.21
H2A L116A, L117A / WT	5’	1.4 +/- 0.16
H4 K44Q+H2A L116A, L117A / WT	5’	2.6 +/- 0.11
H3 K36R / WT	3’	2.4 +/- 0.23
H4 K44Q/ WT	3’	2.6 +/- 0.16
H2A L116A, L117A / WT	3’	3.6 +/- 0.49
H4 K44Q+H2A L116A, L117A / WT	3’	5.0 +/- 0.51

*****Data represents three biological repeats with three technical repeats each.

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