Supplemental Information

Materials and Methods

Calculating the enrichment of genes bound by Sir2, Sum1 or Hst1 for differential regulation during the diauxic shift

Sir2, Sum1 and Hst1 bound ORFs (at least 60% covered) were compared to a set of genes that were previously identified as being differentially expressed during the diauxic shift using the Affymetrix Genechip platform [1]. The processed data was retrieved from dataset accession number E-TABM-496 at ArrayExpress. We used the differential $\log_2$ (fold-change) values to determine which genes were differentially expressed in the diauxic shift timepoint compared to log phase in WT strains. We then computed overlap of the Sir2, Sum1, or Hst1 bound genes with the differentially expressed gene list (either upregulated or downregulated). To calculate the p-value of association, we compared the overlap value with random overlaps of the dataset to account for enrichment or depletion over the random expectation (Figure S2b).

Identification of condensin and cohesin sites

419 condensin binding sites were retrieved from the D'Ambrosio C et al, 2008 study [2]. PeakFinder [3] was used to determine 1248 cohesin peaks from Dataset S1 (W303 strain arrested by *cdc16-ts* with ChIP performed for Mcd1-18Myc), and mapped from sacCer1 to sacCer2 genomic coordinates using the LiftOver tool downloaded from the UCSC genome browser.

Significance of overlaps between Sir2, Sum1 and Hst1 sites and condensin/cohesin sites, telomeric repeats and Pol III genes

Significance of overlaps of Sir2, Sum1 and Hst1 peaks with condensin and cohesin data (Table S5), telomeric repeats (Table S2), and Pol III transcribed genes (Table S4) was assessed using a random sampling model. All chromosomes were divided into mean peak size fragments. Thereafter, peaks were randomly sampled within each individual chromosome 10000 times. This approach preserved the total number and genomic coverage of peaks over the genome and each chromosome.

Significance of overlaps of Sir2, Sum1 and Hst1 bound ORFs

Significance of the high overlaps amongst Sir2, Sum1 and Hst1 bound ORFs (Figure 3C) was again assessed using a random sampling approach. Three different sets of lists were created by randomly sampling 105, 77 and 208 ORFs, corresponding to Sir2, Sum1 and Hst1 bound ORFs respectively, from all ORFs 10000 times. Mutual overlaps amongst the randomly selected ORFs were compared to the true overlaps to calculate the associated p-values and ratios of actual over mean random overlaps.

Supplemental References

1. Orzechowski Westholm J, Tronnersjo S, Nordberg N, Olsson I, Komorowski J, Ronne H: **Gis1 and Rph1 regulate glycerol and acetate metabolism in glucose depleted yeast cells.** *PLoS One* 2012, **7:**e31577.
2. D'Ambrosio C, Schmidt CK, Katou Y, Kelly G, Itoh T, Shirahige K, Uhlmann F: **Identification of cis-acting sites for condensin loading onto budding yeast chromosomes.** *Genes Dev* 2008, **22:**2215-2227.

3. Glynn EF, Megee PC, Yu HG, Mistrot C, Unal E, Koshland DE, DeRisi JL, Gerton JL: **Genome-wide mapping of the cohesin complex in the yeast Saccharomyces cerevisiae.** *PLoS Biol* 2004, **2:**E259.

Supplemental Figure Legends

Figure S1. ChIP-seq screenshots of Sirtuin and Sum1 binding to *HML*, *HMR*, and the rDNA genes. The sequence read number scale for each row is shown in brackets. Each horizontal bar represents 500 bp.

Figure S2. Confirmation ChIP and enrichment on genes downregulated during the diauxic shift. (a) Confirmation ChIP assays of untagged, Hst2-myc, Sir2-myc, Hst1-myc, and Sum1-myc strains at the *ADH1* and *TDH3* genes. **(b)** Statistical analysis of Hst1, Sum1, or Sir2 enrichment on Pol II-transcribed genes that are differentially regulated during the diauxic shift. The box plot shows a trend toward association with downregulated genes (compared to all differentially regulated genes), and an apparent depletion for genes that are activated during the shift. The association with downregulated genes (green) was highly significant for Hst1. There was a significant depletion of each factor from the activated genes (red).

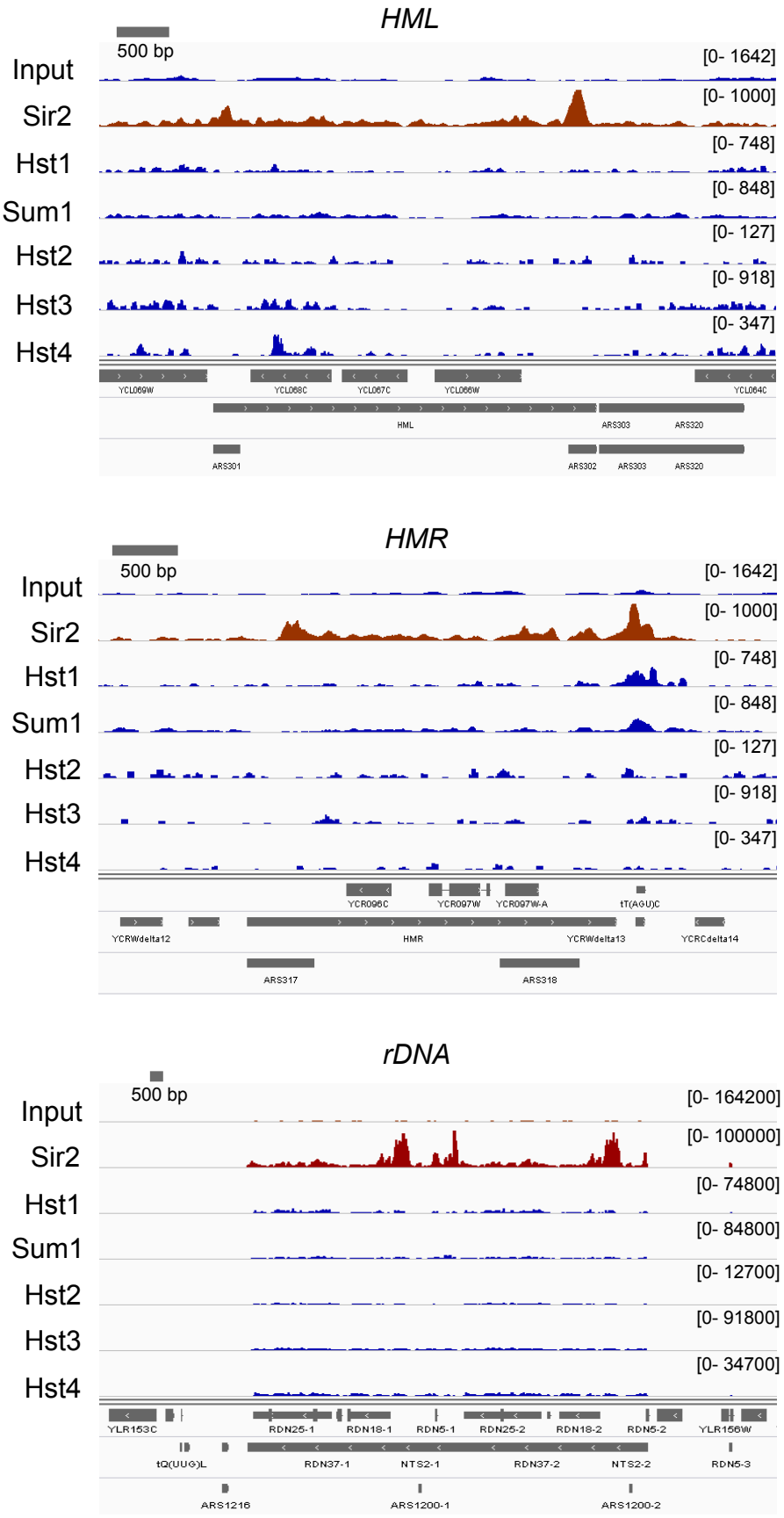
Figure S3. Sir2, Hst1, Sum1, and Npt1 are required for ENO2 and CDC19 repression during the diauxic shift. (a) RT-PCR analysis of *ENO2* expression relative to the *ACT1* control gene in WT, *sir2*Δ, *hst1*Δ, and *sum1*Δ strains growing exponentially. **(b)** RT-PCR analysis of *ENO2* expression during the diauxic shift in WT and the indicated mutant strains. **(c)** RT-PCR analysis of *ENO2* and *CDC19* expression during the diauxic shift in WT and *npt1*Δ strains.

Figure S4. Sir2, Hst2, and Npt1 do not regulate the *CLB1*, *RIF1*, and *RPB3* genes during the diauxic shift. (a) Screenshots of ChIP-seq reads across the ORF of each gene. No enrichment was observed compared to the Input control. **(b)** RT-PCR analysis of gene expression during the diauxic shift in WT, *sir2*Δ, *hst1*Δ, and *npt1*Δ strains.

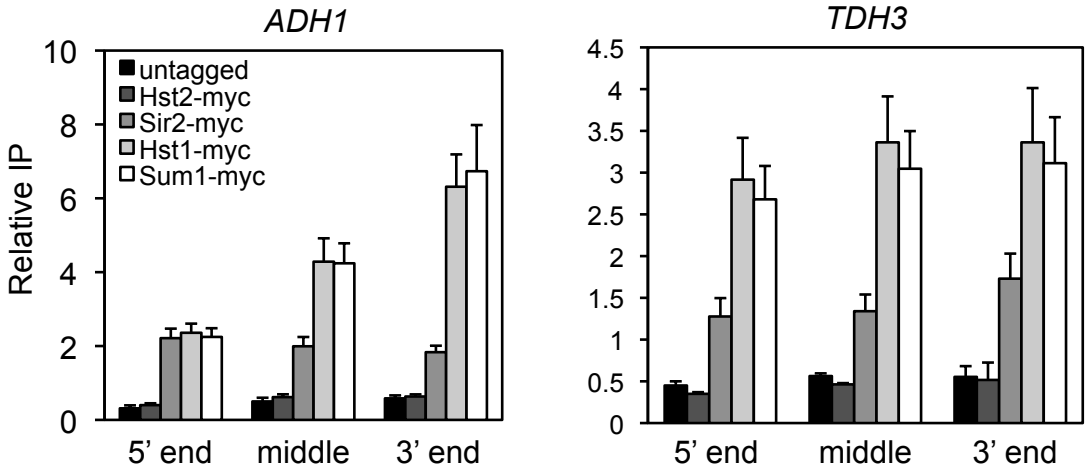
Figure S5. Quantitative ChIP assays of histone H4 and H3 acetylation levels in WT, *sir2*Δ *sum1*Δ, and *sir2*Δ *hst1*Δ double mutants. The immunoprecipitated signal for each sample is relative to a mock IP sample with no antibody added, and then normalized to H3 or H4 occupancy. No significant increases in acetylation were observed in the mutants, compared to WT, for any of the acetylation marks tested.

Figure S6. Venn diagram showing the number of Pol III-transcribed genes bound by Sir2, Hst1, or Sum1.

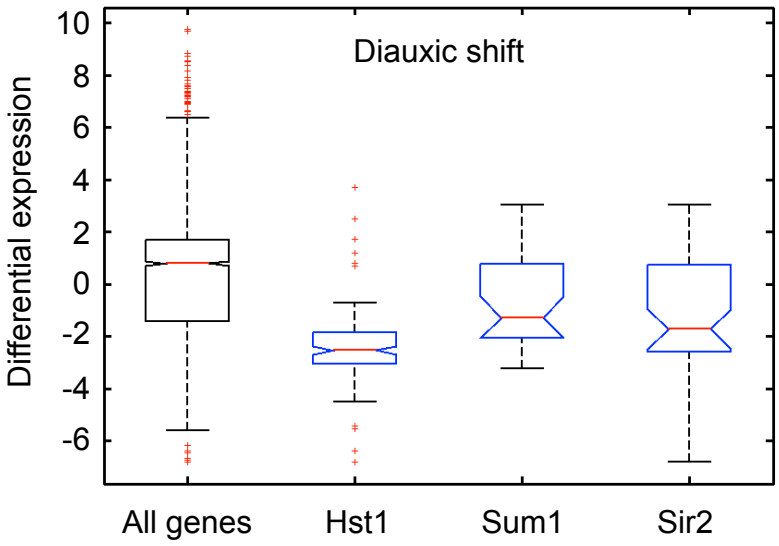
Figure S7. Condensin association with ribosomal protein genes. (a) Western blot showing the steady state expression levels of Myc-tagged versions of Smc4, Scc2, and Mcd1 proteins in the various deletion mutants used throughout this study. α-tubulin was used as a loading control. **(b)** ChIP-assay showing the relative binding of Smc4-myc and Brn1-myc at the ribosomal protein genes *RPL10* and *RPL25*. The cells were grown to log phase in YPD medium.


HML
500 bp
Input
Sir2
Hst1
Sum1
Hst2
Hst3
Hst4
[0- 1642]
[0- 1000]
[0- 748]
[0- 848]
[0- 127]
[0- 918]
[0- 347]
YCL069W
YCL068C
YCL067C
YCL066W
YCL064C
HML
ARS303
ARS320
ARS301
ARS302
ARS303
ARS320
HMR
500 bp
Input
Sir2
Hst1
Sum1
Hst2
Hst3
Hst4
[0- 1642]
[0- 1000]
[0- 748]
[0- 848]
[0- 127]
[0- 918]
[0- 347]
YCR096C
YCR097W
YCR097W-A
tT(AGU)C
YCRWdelta12
HMR
YCRWdelta13
YCRCdelta14
ARS317
ARS318
rDNA
500 bp
Input
Sir2
Hst1
Sum1
Hst2
Hst3
Hst4
[0- 164200]
[0- 100000]
[0- 74800]
[0- 84800]
[0- 12700]
[0- 91800]
[0- 34700]
YLR153C
RDN25-1
RDN18-1
RDN5-1
RDN25-2
RDN18-2
RDN5-2
YLR156W
tQ(UUG)L
RDN37-1
NTS2-1
RDN37-2
NTS2-2
RDN5-3
ARS1216
ARS1200-1
ARS1200-2

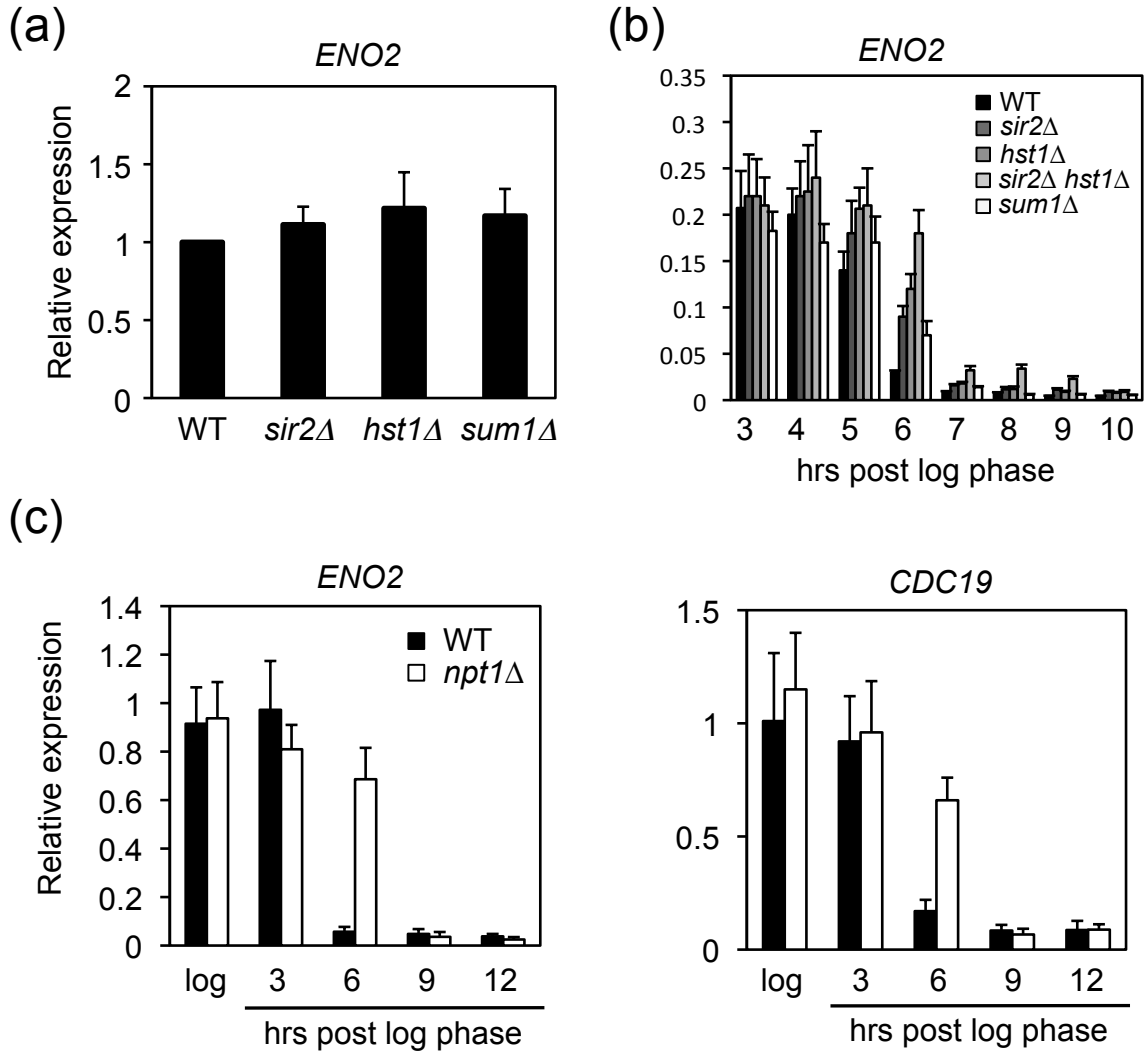
(a)



(b)



	All genes	Hst1	Sum1	Sir2
Genes with peaks	208	77	105
Repressed genes	113	19	32
p-values (enrichment)	**<0.0001**	0.14	0.46
Activated genes	6	10	14
p-values (depletion)	**<0.0001**	**<0.0001**	**<0.0001**


(a)
ENO2
Relative expression
2
1.5
1
0.5
0
WT
sir2Δ
hst1Δ
sum1Δ
(b)
ENO2
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
WT
sir2Δ
hst1Δ
sir2Δ hst1Δ
sum1Δ
3 4 5 6 7 8 9 10
hrs post log phase
(c)
ENO2
Relative expression
1.4
1.2
1
0.8
0.6
0.4
0.2
0
WT
npt1Δ
log 3 6 9 12
hrs post log phase
CDC19
1.5
1
0.5
0
log 3 6 9 12
hrs post log phase

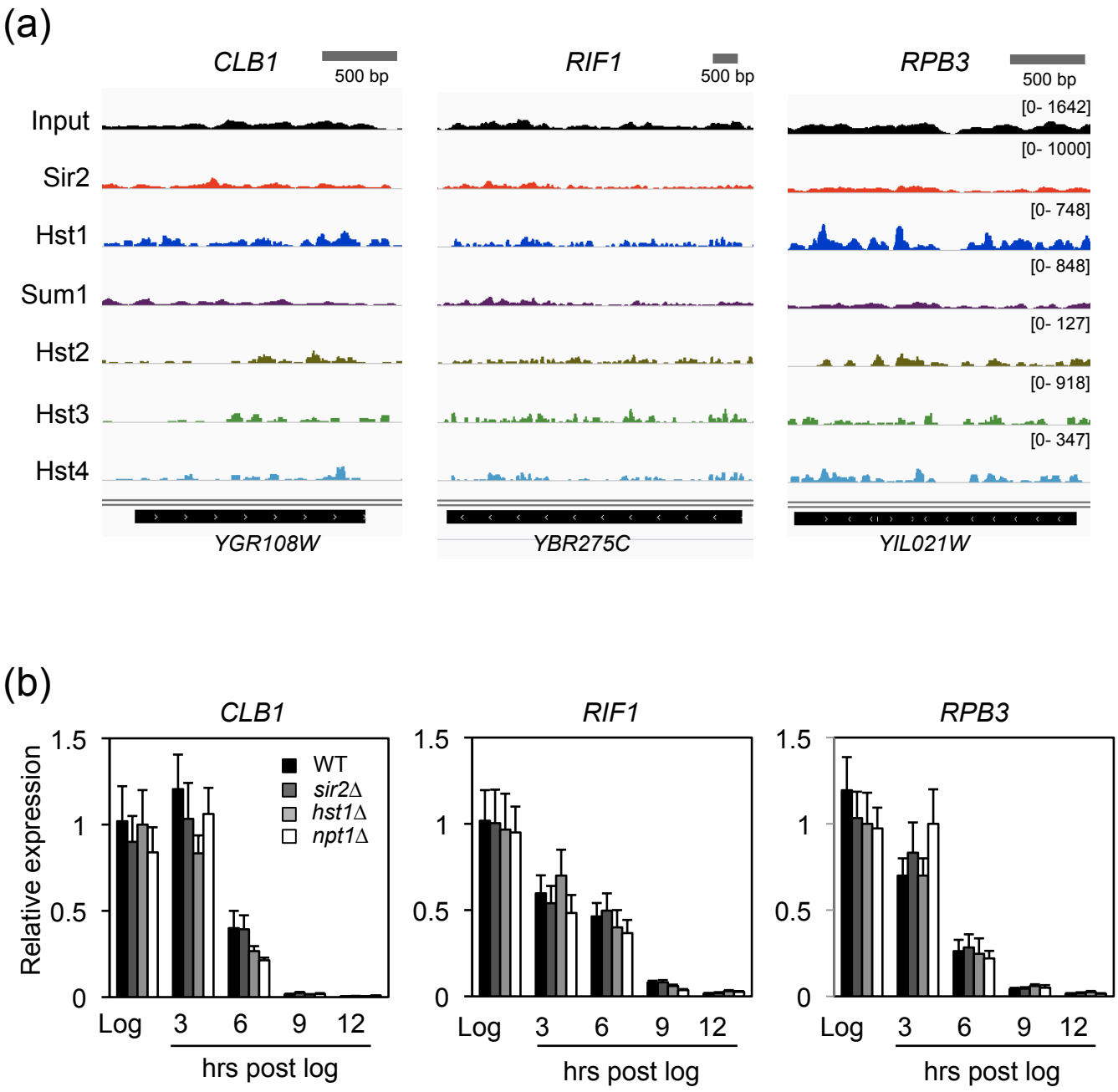

(a)
CLB1
500 bp
RIF1
500 bp
RPB3
500 bp
Input
Sir2
Hst1
Sum1
Hst2
Hst3
Hst4
[0- 1642]
[0- 1000]
[0- 748]
[0- 848]
[0- 127]
[0- 918]
[0- 347]
YGR108W
YBR275C
YIL021W
(b)
CLB1
RIF1
RPB3
Relative expression
1.5
1
0.5
0
WT
sir2Δ
hst1Δ
npt1Δ
Log
3
6
9
12
hrs post log

Figure S5

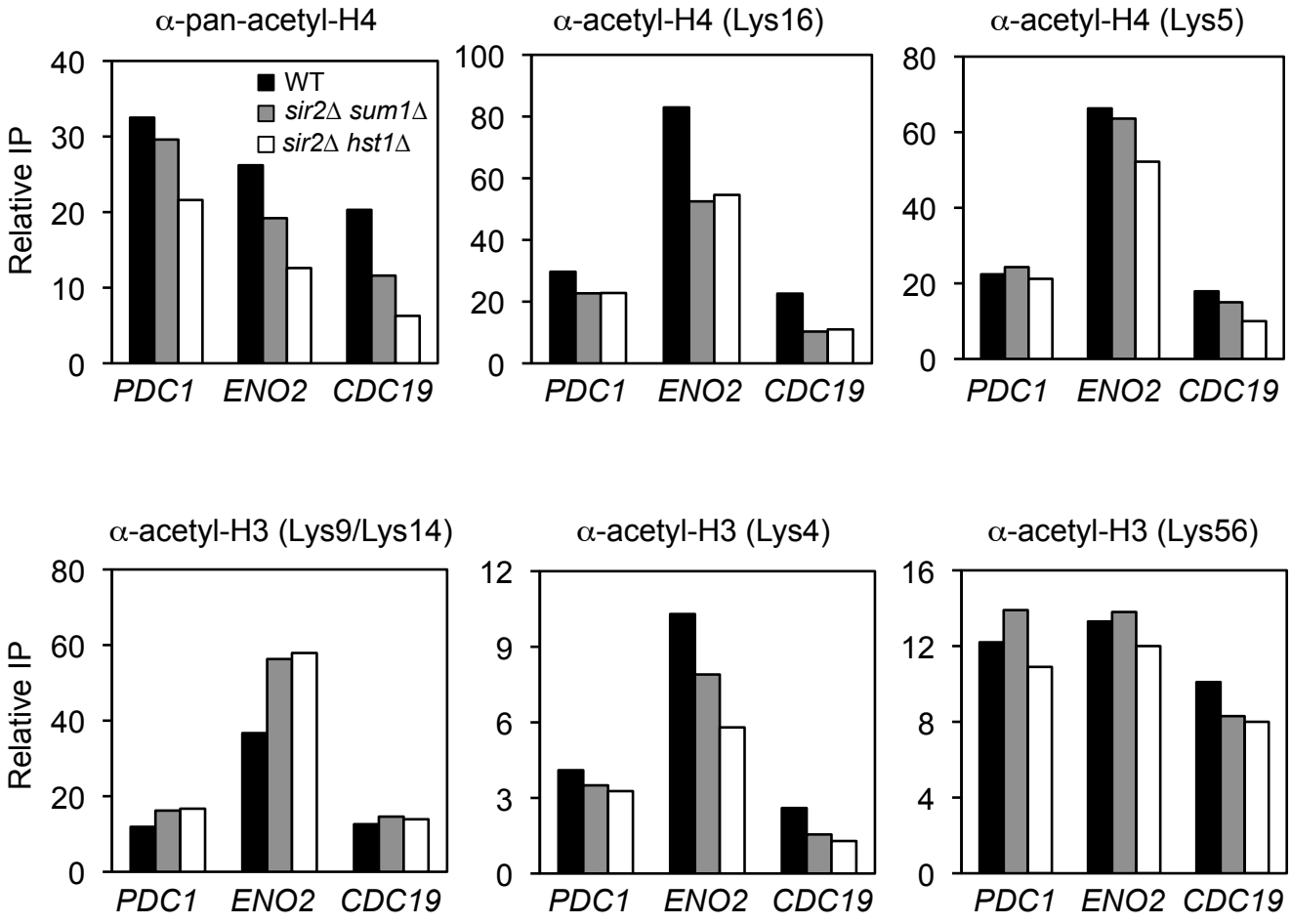
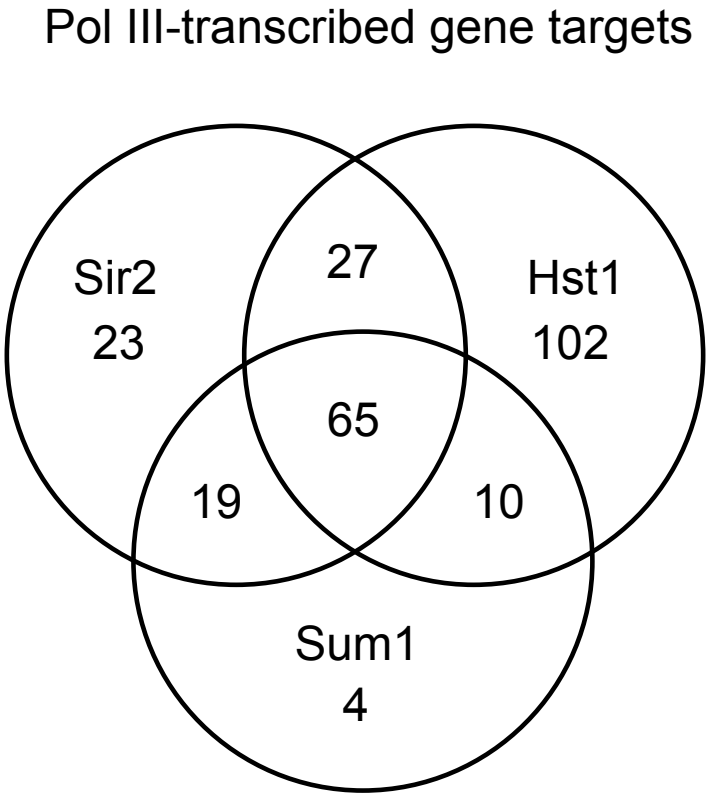
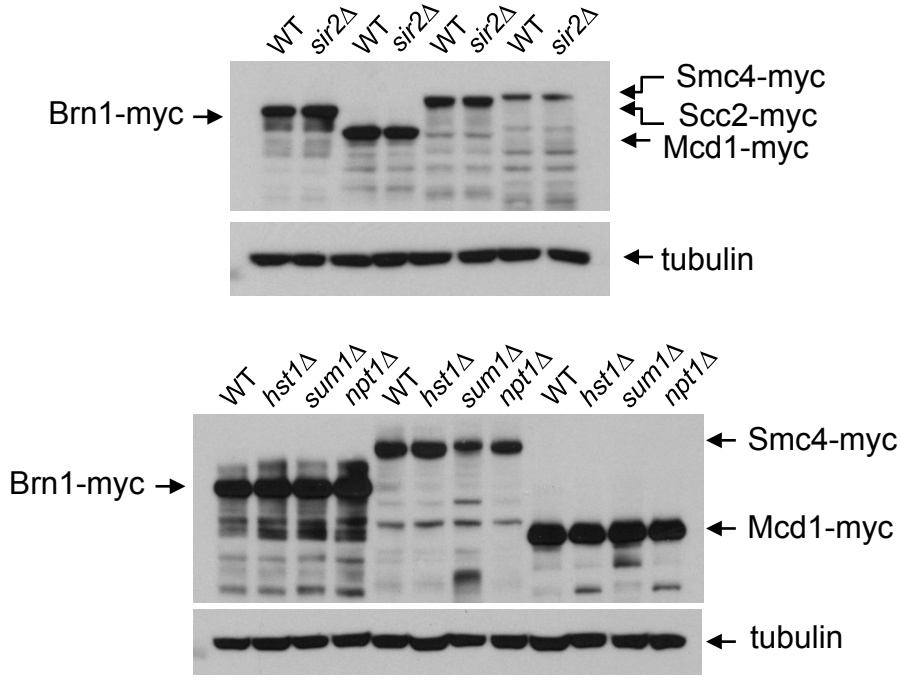

α-pan-acetyl-H4
α-acetyl-H4 (Lys16)
α-acetyl-H4 (Lys5)
α-acetyl-H3 (Lys9/Lys14)
α-acetyl-H3 (Lys4)
α-acetyl-H3 (Lys56)
Relative IP
WT
sir2Δ sum1Δ
sir2Δ hst1Δ
PDC1
ENO2
CDC19

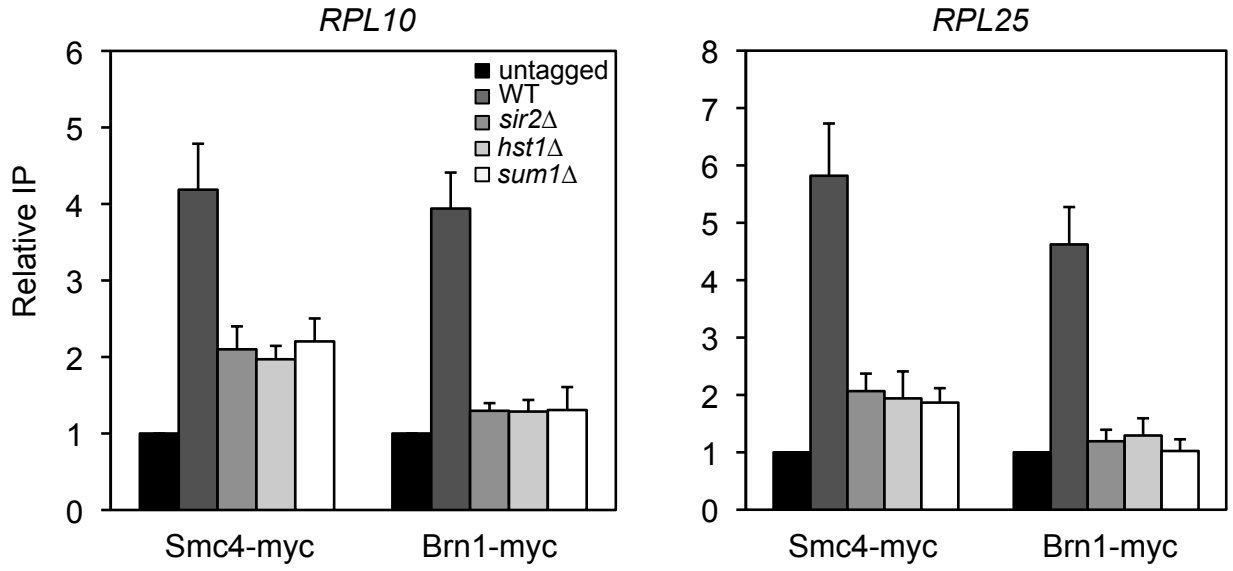
Figure S6


Pol III-transcribed gene targets
Sir2
23
27
Hst1
102
65
19
10
Sum1
4

(a)


WT
sir2Δ
WT
sir2Δ
WT
sir2Δ
WT
sir2Δ
Brn1-myc
Smc4-myc
Scc2-myc
Mcd1-myc
tubulin
WT
hst1Δ
sum1Δ
npt1Δ
WT
hst1Δ
sum1Δ
npt1Δ
WT
hst1Δ
sum1Δ
npt1Δ
Brn1-myc
Smc4-myc
Mcd1-myc
tubulin

(b)


RPL10
RPL25
Relative IP
untagged
WT
sir2Δ
hst1Δ
sum1Δ
0
1
2
3
4
5
6
7
8
Smc4-myc
Brn1-myc
Smc4-myc
Brn1-myc

Supplemental Table S1. Terminal TG1-3 peak locations and intensities.

	Sir2		Hst1		Sum1	
Chr[1]	coordinate[2]	reads[3]	coordinate	reads	coordinate	reads
IL	45	11492	45	3159	45	451
IR	230152	25441	230152	6848	230152	590
IIR	813147	13042	813147	4872	813147	665
IIIL	252	46874	252	14045	252	1506
IIIR	316564	20766	316564	6078	316564	710
IVL	117	25009	117	7795	119	705
VIR	270108	2549	270108	759	270107	120
VIIIL	52	14250	52	3853	52	1195
VIIIR	562525	35336	562525	14441	562525	1496
IXL	25-45	8098	25-45	2776	25-45	317
IXR	439841	6087	439841	1743	439835	245
XL	9-45	7341	9-45	2795	9-45	252
XR	745690	28255	745690	8953	745690	813
XIL	45	26123	45	9059	45	767
XIR	666290	65627	666290	23892	666290	2046
XIIL	80	30265	80	9210	80	3152
XIIIL	41-45	3037	41-45	1025	43	49
XIIIR	924334	16277	924334	6504	924334	458
XIVR	784202	39764	784201	14499	784201	1336
XVL	48	26828	48	9526	48	920
XVR	~1091268	6640	~1091268	1299	~1091268	395
average		21862		7292		866
Std. Dev.		15986		5768		734

[1]Chromosome termini with measureable TG_{1-3} repeats

[2]SGD coordinate of the nucleotide(s) with the highest number of reads.

[3]Number of reads at the peak.

Table S2. Non-random enrichment of Sir2, Hst1 and Sum1 for telomeric repeats.

	p value	No. of overlaps detected	Fold enrichment over random	Expected no. of overlaps (random)	SD random	z-score
Sir2	< 1e-04	35	41.65	0.84	1.09	31.33
Hst1	< 1e-04	37	33.78	1.10	1.25	28.77
Sum1	< 1e-04	30	46.32	0.65	0.97	30.15

Table S3. GO Terms of Genes with Overlapping Sir2, Hst1, and Sum1 Binding to ORFs[1].

GOBPID	Pvalue	OddsRatio	Expect	Count	Size	Term
GO:0006417	0	16.441	1	7	194	regulation of translation
GO:0010608	0	15.106	1	7	210	posttranscriptional regulation of gene expression
GO:0032268	0	14.586	1	7	217	regulation of cellular protein metabolic process
GO:0051246	0	11.02	1	7	282	regulation of protein metabolic process
GO:0006007	0	27.893	0	4	57	glucose catabolic process
GO:0019320	0	25.033	0	4	63	hexose catabolic process
GO:0046365	0	23.059	0	4	68	monosaccharide catabolic process
GO:0046164	0	21.371	0	4	73	alcohol catabolic process
GO:0019660	0	133.284	0	2	7	glycolytic fermentation
GO:0019655	0	133.284	0	2	7	glucose catabolic process to ethanol
GO:0044282	0	10.448	1	5	189	small molecule catabolic process
GO:0006090	0	26.91	0	3	42	pyruvate metabolic process
GO:0009063	0	24.976	0	3	45	cellular amino acid catabolic process
GO:0044275	0	13.698	0	4	111	cellular carbohydrate catabolic process
GO:0009310	0.001	22.79	0	3	49	amine catabolic process
GO:0016052	0.001	12.728	0	4	119	carbohydrate catabolic process
GO:0000955	0.001	74	0	2	11	amino acid catabolic process via Ehrlich pathway
GO:0006006	0.001	12.617	0	4	120	glucose metabolic process
GO:0006067	0.001	66.589	0	2	12	ethanol metabolic process
GO:0034308	0.001	66.589	0	2	12	monohydric alcohol metabolic process
GO:0046395	0.001	19.033	0	3	58	carboxylic acid catabolic process
GO:0016054	0.001	19.033	0	3	58	organic acid catabolic process
GO:0031323	0.001	4.598	3	10	1056	regulation of cellular metabolic process
GO:0019318	0.001	10.974	0	4	137	hexose metabolic process
GO:0010468	0.001	4.681	3	9	884	regulation of gene expression
GO:0006113	0.001	47.534	0	2	16	fermentation
GO:0010556	0.001	4.607	3	9	896	regulation of macromolecule biosynthetic process
GO:0005996	0.001	9.838	1	4	152	monosaccharide metabolic process
GO:0046165	0.001	15.833	0	3	69	alcohol biosynthetic process
GO:0019752	0.001	6.032	1	6	400	carboxylic acid metabolic process
GO:0043436	0.001	6.032	1	6	400	oxoacid metabolic process
GO:0031326	0.001	4.507	3	9	913	regulation of cellular biosynthetic process
GO:0006091	0.001	7.245	1	5	267	generation of precursor metabolites and energy

[1]Only GO terms with p-values 0.001 or lower.

Table S4. Statistically significant enrichment of Sir2, Hst1 and Sum1 for Pol III transcribed genes.

	p value	No. of overlaps detected	Fold enrichment over random no.	Expected no. of overlaps (random)	SD random	z-score
Sir2	< 1e-04	151	119.80	1.26	1.29	116.01
Hst1	< 1e-04	250	169.20	1.48	1.39	178.54
Sum1	< 1e-04	118	109.79	1.07	1.22	95.96

Table S5. Statistical analysis of condensin and cohesin overlap with Sir2, Hst1 and Sum1.

	p value	No. of overlaps detected	Fold enrichment over random no.	Expected no. of overlaps (random)	SD random	z-score
Condensin						
Sir2	< 1e-04	97	173.28	0.56	0.76	126.49
Hst1	< 1e-04	170	208.82	0.81	0.92	184.33
Sum1	< 1e-04	65	139.49	0.47	0.70	91.86
Cohesin						
Sir2	< 1e-04	40	28.85	1.39	1.23	31.28
Hst1	< 1e-04	47	24.07	1.95	1.46	30.90
Sum1	< 1e-04	34	28.94	1.17	1.15	28.58

Table S6. Yeast Strains.

Strains	Genotype	Source
ML1	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167*	[1]
ML2	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 npt1Δ::kanMX4*	[1]
ML28	*MAT*α *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 sir2Δ::kanMX4*	[1]
ML29	*MAT*α *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 hst1Δ::kanMX4*	[1]
ML30	*MAT*α *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 sir2Δ::kanMX4 hst1Δ::kanMX4*	[1]
ML31	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 sum1Δ::kanMX4*	[1]
ML44	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SIR2::13xMyc-kanMX4*	[1]
ML54	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 HST1::13xMyc-kanMX4*	[1]
ML65	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SUM1::13xMyc-kanMX4*	[1]
ML96	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 HST2::13xMyc-kanMX4*	This study
ML149	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 BRN1::13xMyc-kanMX4*	This study
ML150	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 MCD1::13xMyc-kanMX4*	This study
ML152	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SMC4::13xMyc-kanMX4*	This study
ML155	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SMC4::13xMyc-kanMX4 hst1Δ::natMX4*	This study
ML157	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 BRN1::13xMyc-kanMX4 hst1Δ::natMX4*	This study
ML158	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 MCD1::13xMyc-kanMX4 hst1Δ::natMX4*	This study
ML160	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SMC4::13xMyc-kanMX4 sir2Δ::natMX4*	This study
ML161	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 BRN1::13xMyc-kanMX4 sir2Δ::natMX4*	This study
ML163	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 MCD1::13xMyc-kanMX4 sir2Δ::natMX4*	This study
ML166	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SMC4::13xMyc-kanMX4 sum1Δ::natMX4*	This study
ML168	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 MCD1::13xMyc-kanMX4 sum1Δ::natMX4*	This study
ML169	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167*	This study

	BRN1::13xMyc-kanMX4 sum1Δ::natMX4	
ML183	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SMC4::13xMyc-kanMX4 npt1Δ::natMX4*	This study
ML184	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 MCD1::13xMyc-kanMX4 npt1Δ::natMX4*	This study
ML185	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SCC2::13xMyc-kanMX4 npt1Δ::natMX4*	This study
ML187	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SIR2::13xMyc-kanMX sir3Δ::natMX*	This study
ML188	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 SIR2::13xMyc-kanMX si4Δ::natMX*	This study
JS306	*MAT*a *his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 RDN1(18S)::mURA-HIS3 RDN1(NTS2)::Ty1-MET15*	[2]
JS1142	*MATα his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 RDN1 (NTS2)::Tyl-MET15*	This study
JS1143	*MATα his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 RDN1 (NTS2)::Tyl-MET15 sir2Δ::kanMX4*	This study
JS1144	*MATα his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 RDN1 (NTS2)::Tyl-MET15 hst1Δ::kanMX4*	This study
JS1145	*MATα his3Δ200 leu2Δ1 met15Δ0 trp1Δ63 ura3-167 RDN1 (NTS2)::Tyl-MET15 sir2Δ::kanMX4 hst1::kanMX4*	This study
DSY364	JS306 with *hst1Δ::kanMX4*	This study
DSY366	JS306 with *hst2Δ::kanMX4*	This study
DSY368	JS306 with *hst3Δ::kanMX4*	This study
DSY370	JS306 with *hst4Δ::kanMX4*	This study
YG62	*MATα RAP1 leu2-3,112 trp1 ade2-1 ura3-1 his3 adh4::ura3/ADE2-TELVIIL*	[3]
YG64	*MAT***a** *rap1-17 leu2-3,112 trp1 ade2-1 ura3-1 his3 adh4::ura3/ADE2-TELVIIL*	[3]
SY675	YG62 with *SIR2::13xMyc-kanMX4*	This study
SY676	YG64 with *SIR2::13xMyc-kanMX4*	This study
SY677	YG62 with *SUM1::13xMyc-kanMX4*	This study
SY679	YG64 with *SUM1::13xMyc-kanMX4*	This study
SY680	YG62 with *HST1::13xMyc-kanMX4*	This study
SY681	YG64 with *HST1::13xMyc-kanMX4*	This study

1. Li M, Petteys BJ, McClure JM, Valsakumar V, Bekiranov S, Frank EL, Smith JS: Thiamine biosynthesis in *Saccharomyces cerevisiae* is regulated by the NAD^+-dependent histone deacetylase Hst1. *Mol Cell Biol* 2010, 30:3329-3341.

2. Smith JS, Caputo E, Boeke JD: A genetic screen for ribosomal DNA silencing defects identifies multiple DNA replication and chromatin-modulating factors. *Mol Cell Biol* 1999, 19:3184-3197.

3. Obtained from David Shore. These strains were FOA-selected, and are Ura^-. They are derived from strains AJL275-2a (for YG62) and AJL440-1c (for YG64) from Arthur Lustig's lab.

Table S7. Oligonucleotides for qPCR.

Target	DNA sequence
PDC1 (ORF-5' end) sense	CTTCGGTGTCGGTGAATTGTC
PDC1 (ORF-5' end) anti-sense	AGCTTGAGCAGAGATGGATGG
PDC1 (ORF-middle) sense	CGATGCTGAATCCGAAAAGG
PDC1 (ORF-middle) anti-sense	GACGTCGTGTCTGGAACAACA
PDC1 (ORF-3' end) sense	CCATTGGTTTCACCACTGGTG
PDC1 (ORF-3' end) anti-sense	TCAAGCCCCATCTGATCATG
PDC1 (3'- intergenic) sense	GCCGACAGTCTGTTGAATTGG
PDC1(3- intergenic) anti-sense	GAAGCGGACCCAGACTTAAGC
ENO2 (ORF-5' end) sense	TTTCGTCAAGGCCAACCTAGA
ENO2 (ORF-5' end) anti-sense	CCAAGATAGCGTTAGCACCCA
ENO2 (ORF-middle) sense	CTTGAACGTTTTGAACGGTGG
ENO2 (ORF-middle) anti-sense	TCGGAACCAATTCTCATGGCT
ENO2 (ORF-3' end) sense	CTAGAATTGCTACCG CCATCG
ENO2 (ORF-3' end) anti-sense	GTTGGCAGCGAAAGAGTCTTG
ADH1 (ORF-5' end) sense	TCACACTGACTTGCACGCTTG
ADH1 (ORF-5' end) anti-sense	CCAGCCCTTAACGTTTTCACC
ADH1 (ORF-middle) sense	AAGCCGCTCACATTCCTCAAG
ADH1 (ORF-middle) anti-sense	ACCGGCCATCAAGTTAGCAGA
ADH1 (ORF-3' end) sense	CAGCTGGTGCCAAGTGTTGTT
ADH1 (ORF-3' end) anti-sense	AACCTCTGGCGAAGAAGTCCA
TDH3 (ORF-5' end) sense	AACGGTTTCGGTAGAATCGGT
TDH3 (ORF-5' end) anti-sense	AGCAGCGTAGTCGTTGGTGAT
TDH3 (ORF-middle) sense	CCAACGCTTCTTGTACCACCA
TDH3 (ORF-middle) anti-sense	ATCGTTGATAACCTTGGCCAA
TDH3 (ORF-3' end) sense	AAGGCTGCCGCTGAAGGTA
TDH3 (ORF-3' end) anti-sense	GCGTCTTCGGTGTAACCCAA
CDC19 ORF sense	ACAACGCCAGAAAGTCCGAA
CDC19 ORF anti-sense	CAATGGCCAATGGTCTACCTG
PDC5 ORF sense	TCACAGTCGGCGCTCTATTG
PDC5 ORF anti-sense	GATCAAGTTCTTCAGCGGCC
CLB1 ORF sense	CGTCATTATGTGCCTCAGCG
CLB1 ORF anti-sense	TGCCCAGCATTTTTCTCGA
RIF1 ORF sense	AATTAGGCCAAGCCCACACAG
RIF1 ORF anti-sense	CGTTACCATCTCCCCCCAA
RPB3 ORF sense	GAAACTGACATGCGTTGCGA
RPB3 ORF anti-sense	CACTTGGCGTGCTCTTTGG
ALD2 ORF sense	CCAAGGTCGGTGGATTTGTG
ALD2 ORF anti-sense	CTTTAAGGTTCGATTGGCCG

BNA2 ORF sense	GTTGCTGACCTGCCCTCTCTT
BNA2 ORF anti-sense	GACGCTCCGCACCTTGTTAT
tQ(UUG)H sense	ACTTTCGGTTTTGATCCGGA
tQ(UUG)H anti-sense	AAAGGTCCTACCCGGATTCG
tE(UUC)E1 sense	TGTAACGGCTATCACATCACGC
tE(UUC)E1 anti-sense	GGAGTCGAACCCCGGTCT
SNR30 ORF sense	CAACGCTCGAGAGGCAGAG
SNR30 ORF anti-sense	AATACGTGAGGCCCATTGGA
RPL10 sense	GAAGAAGGCTACCGTCGATGA
RPL10 anti-sense	TGGCACAGATACGAGCAGCTT
RPL25 sense	TATTGACACTTTGGCAGCCG
RPL25 anti-sense	TCAGCCAACTTGGAGACGAAT
NTS1 sense	TGTTAGTGCAGGAAAGCGGG
NTS1 anti-sense	CTACACCCTCGTTTAGTTGC
NTS2 sense	GTATGTGGGACAGAATGTCG
NTS2 anti-sense	GACTTACGTTTGCTACTCTC
ChrVI_TEL_70bp sense	GCCATTTCCGTGTGTAGTGA
ChrVI_TEL_70bp anti-sense	CCATGACCCAGTCCTCATTT
ChrVI_TEL_7000bp sense	TGCCACAATGCTATGGATTC
ChrVI_TEL_7000bp anti-sense	GTGAAAGTTCAGCGCAACAA