

Supporting Information

Lombardi et al. 10.1073/pnas.1116819108

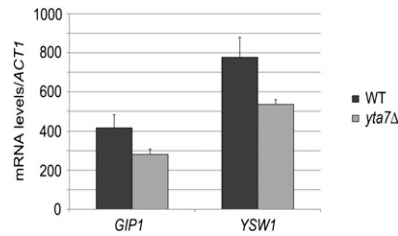


Fig. S1. Decreased mid-late meiotic gene induction without Yta7. RT-qPCR analysis of cDNA from SK1 WT and *yta7Δ* homozygotes. Cells were collected after 8 h in sporulation medium containing 1% potassium acetate. Values were normalized to *ACT1* and are relative to transcript levels in YPAcetate.

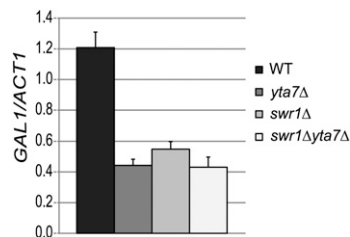


Fig. S2. Yta7 and H2A.Z functioned together for proper *GAL1* gene induction. RT-qPCR analysis of *GAL1* transcript levels after 1 h with galactose. *GAL1* gene induction was assayed in cells lacking both Yta7 and Swr1, the catalytic subunit of the H2A.Z deposition complex. The *swr1Δ* mutant was used in lieu of the *htz1Δ* mutant, because the *htz1Δ* mutant exhibits phenotypes due to both the loss of H2A.Z and problematic Swr1 activity in the absence of H2A.Z (1, 2). Cells were pregrown in YPRaffinose (2%, non-inducing).

- Halley JE, Kaplan T, Wang AY, Kobar MS, Rine J (2010) Roles for H2A.Z and its acetylation in *GAL1* transcription and gene induction, but not *GAL1*-transcriptional memory. *PLoS Biol* 8: e1000401.
- Morillo-Huesca M, Clemente-Ruiz M, Andújar E, Prado F (2010) The SWR1 histone replacement complex causes genetic instability and genome-wide transcription misregulation in the absence of H2A.Z. *PLoS ONE* 5:e12143.

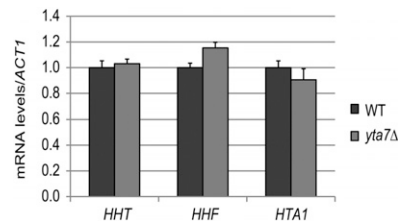


Fig. S3. Little or no changes to histone transcript levels in the *yta7Δ* mutant. RNA analysis was performed on asynchronously growing cells. *HHT* and *HHF* primer sets detect total H3 and H4 transcripts, respectively, whereas *HTA1* primers are specific to the H2A transcripts from the "copy 1" locus.

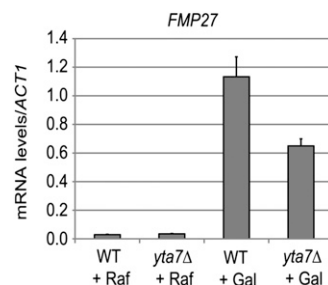


Fig. S4. Yta7 was required for proper *pGAL1::FMP27* induction. RT-qPCR analysis of *FMP27* transcript levels in raffinose (Raf; 2%, non-inducing) and after 1 h with galactose (Gal; 2%, inducing). The level of each transcript was normalized to *ACT1* mRNA levels. The error bars represent the SEM for four biological replicates.

Table S1. Genes significantly affected in the *yta7Δ* mutant

ID	Name	Fold change
REP1_2UM	REP1_2UM	0.18
REP2_2UM	REP2_2UM	0.20
FLP_2UM	FLP_2UM	0.21
YDL227C	HO	0.46
YDR428C	BNA7	0.49
YHR057C	CPR2	0.50
YHR029C	YHI9	0.54
YFR012W	YFR012W	0.56
YHR015W	MIP6	0.56
YAL067C	SEO1	0.56
YIR030C	DCG1	0.57
YFL053W	DAK2	0.58
YNL335W	YNL335W	0.60
YDR369C	XRS2	0.60
YGR201C	YGR201C	0.60
YJR025C	BNA1	0.61
YGR259C	YGR259C	0.61
YMR182C	RGM1	0.61
YNL012W	SPO1	0.61
YHR067W	HTD2	0.61
YOL141W	PPM2	0.1
YDR539W	YDR539W	0.61
YEL030W	ECM10	0.61
YHL022C	SPO11	0.62
YIL037C	PRM2	0.62
YIL015C-A	YIL015C-A	0.62
YJL028W	YJL028W	0.62
YGL104C	VPS73	0.62
YIL089W	YIL089W	0.63
YDR070C	YDR070C	0.64
YKL114C	APN1	0.64
YPL278C	YPL278C	0.64
YGR169C	PUS6	0.64
YKL053C-A	MDM35	0.64
YPL277C	YPL277C	0.64
Ty class*	Ty class*	0.65 ± 0.036
YER138W-A	YER138W-A	0.65
YML079W	YML079W	0.65
YGR122C-A	YGR122C-A	0.65
YOR338W	YOR338W	0.66
YGL258W	VEL1	0.66
YGL259W	YPS5	0.66
YPL165C	SET6	0.66
YBR045C	GIP1	0.66
YOR295W	UAF30	0.66
YGL027C	CWH41	0.67
YBR013C	YBR013C	0.67
YDL195W	SEC31	0.67
YBR261C	YBR261C	0.67
YDR258C	HSP78	0.67
YFL059W	SNZ3	0.68
YDR285W	ZIP1	0.68
YMR315W-A	YMR315W-A	0.68
YOL160W	YOL160W	0.68
YER093C-A	YER093C-A	0.68
YIL073C	SPO22	0.68
YNR064C	YNR064C	0.69
YBL098W	BNA4	0.69
YFR023W	PES4	0.69
YJL089W	SIP4	0.69
YGL240W	DOC1	0.69
YDR493W	YDR493W	0.69
YDR336W	YDR336W	0.70

Table S1. Cont.

ID	Name	Fold change
YBR192W	RIM2	0.80
YGR091W	PRP31	0.80
YDL030W	PRP9	0.80
YPL216W	YPL216W	0.80
YDL108W	KIN28	0.81
YKL165C	MCD4	1.27
YDR421W	ARO80	1.30
YMR147W	YMR147W	1.32
YFR018C	YFR018C	1.33
YER179W	DMC1	1.34
YOL110W	SHR5	1.34
YFR020W	YFR020W	1.35
YHR095W	YHR095W	1.35
YML100W-A	YML100W-A	1.36
YMR319C	FET4	1.36
YPR053C	YPR053C	1.37
YGR225W	AMA1	1.38
YIL162W	SUC2	1.39
YJR094C	IME1	1.39
YJL212C	OPT1	1.40
YGR203W	YGR203W	1.40
YJL217W	YJL217W	1.42
YGR280C	PXR1	1.42
YBR072C-A	YBR072C-A	1.42
YJL133C-A	YJL133C-A	1.43
YDR100W	TVP15	1.44
YBL012C	YBL012C	1.44
YCR024C-A	PMP1	1.44
YCL042W	YCL042W	1.45
YHL026C	YHL026C	1.46
YOR383C	FIT3	1.46
YNL145W	MFA2	1.46
YJR115W	YJR115W	1.47
YGR050C	YGR050C	1.47
YAR028W	YAR028W	1.47
YGR279C	SCW4	1.48
YBR182C-A	YBR182C-A	1.48
YPR013C	YPR013C	1.48
YBR183W	YPC1	1.49
YNL015W	PBI2	1.50
YGL089C	MF(ALPHA)2	1.53
YBR044C	TCM62	1.56
YDR033W	MRH1	1.56
YGR271W	SLH1	1.56
YPL092W	SSU1	1.58
YDL048C	STP4	1.58
NTS2-1	NTS2-1	1.59
YJL037W	IRC18	1.62
NTS1-2	NTS1-2	1.63
YOR318C	YOR318C	1.64
YGR146C-A	YGR146C-A	1.64
YBR147W	YBR147W	1.66
YGL158W	RCK1	1.67
YJL150W	YJL150W	1.68
YDR342C	HXT7	1.69
YJR004C	SAG1	1.69
YJL079C	PRY1	1.70
YBR092C	PHO3	1.71
YGR268C	HUA1	1.73
YNL160W	YGP1	1.76
YKR041W	YKR041W	1.76
YHR022C-A	YHR022C-A	1.77

Table S1. Cont.

ID	Name	Fold change
YDL185W	TFP1	1.77
YDR034W-B	YDR034W-B	1.85
YBR019C	GAL10	1.86
YBL013W	FMT1	1.88
YMR101C	SRT1	1.96
YNL066W	SUN4	1.98
YIL011W	TIR3	2.01
YOL047C	YOL047C	2.15
YFR035C	YFR035C	2.20
YHR079C-A	SAE3	2.26
YGR269W	YGR269W	3.19

*Forty-five Ty class transposons were decreased 0.65 ± 0.04 .

Table S2. Strains used

Strain	Genotype	Source
W303-1a	<i>MATα ade2-1; can1-100; his3-11; leu2-3,112; trp1-1; ura3-1</i> (alias JRY3009)	R. Rothstein (Columbia University)
JRY7754	<i>MATα htz1Δ::HIS3MX</i>	Kobor et al. (1)
JRY7972	<i>MATα HTZ1-FLAG::kanMX</i>	Babiarz et al. (2)
JRY8689	<i>MATα HTZ1-FLAG::kanMX YTA7-TAP::TRP1</i>	This study
JRY9199	<i>MATα HTZ1-FLAG::kanMX yta7Δ::natMX</i>	This study
JRY9200	<i>MATα yta7Δ::natMX</i>	This study
JRY9201	<i>MATα; pRS316</i>	This study
JRY9202	<i>MATα yta7Δ::natMX; YTA7/pRS316</i>	This study
JRY9203	<i>MATα yta7Δ::natMX; yta7K460A/pRS316</i>	This study
JRY9204	<i>MATα yta7Δ::natMX; yta7E519Q/pRS316</i>	This study
JRY9205 and 9206	<i>MATα (hht1-hhf1)Δ::HygMX</i>	This study
JRY9207 and 9208	<i>MATα yta7Δ::natMX (hht1-hhf1)Δ::HygMX</i>	This study
JRY9209 and 9210	<i>MATα HIS3MX-pGAL1::FMP27 RPB3-3HA::TRP1</i>	This study
JRY9211 and 9212	<i>MATα HIS3MX-pGAL1::FMP27 RPB3-3HA::TRP1 yta7Δ::natMX</i>	This study
JRY9213	<i>MATα HTZ1-FLAG::kanMX HIS3MX-pGAL1::FMP27</i>	This study
JRY9214	<i>MATα HTZ1-FLAG::kanMX HIS3MX-pGAL1::FMP27 YTA7-TAP::TRP1</i>	This study
JRY9215	<i>MATα YTA7-TAP::TRP1</i>	This study
JRY9216 and 9217	<i>MATα HIS3MX-pGAL1::YTA7-TAP::TRP1 HTZ1-FLAG::kanMX</i>	This study
JRY9218	<i>MATα HTZ1-FLAG::kanMX swr1Δ::HIS3MX</i>	This study
JRY9219 and 9220	<i>MATα HTZ1-FLAG::kanMX swr1Δ::HIS3MX yta7Δ::natMX</i>	This study
For sporulation analysis		
SK-1	<i>MATα/α ho::LYS2 lys2 ura3</i> (alias JRY2692)	N. Kleckner (Harvard University)
JRY9223	<i>MATα/α ho::LYS2 lys2 ura3 yta7Δ::natMX</i>	This study
For Fig. 2D	Derived from DDY277 and DDY282 (3); all <i>ADE2 his3 leu2 lys2Δ trp1 ura3</i>	
JRY9224	<i>MATα HMRIΔ; pRS316</i>	This study
JRY9225	<i>MATα HMRIΔ-E-Boundary-a1; pRS316</i>	This study
JRY9226	<i>MATα HMRIΔ-E-Boundary-a1 yta7Δ::kanMX; pRS316</i>	This study
JRY9227 and 9228	<i>MATα HMRIΔ-E-Boundary-a1 yta7Δ::kanMX; YTA7/pRS316</i>	This study
JRY9229	<i>MATα HMRIΔ-E-Boundary-a1 yta7Δ::kanMX; yta7K460A/pRS316</i>	This study
JRY9230	<i>MATα HMRIΔ-E-Boundary-a1 yta7Δ::kanMX; yta7E519Q/pRS316</i>	This study

1. Kobor MS, et al. (2004) A protein complex containing the conserved Swi2/Snf2-related ATPase Swr1p deposits histone variant H2A.Z into euchromatin. *PLoS Biol* 2:E131.
2. Babiarz JE, Halley JE, Rine J (2006) Telomeric heterochromatin boundaries require NuA4-dependent acetylation of histone variant H2A.Z in *Saccharomyces cerevisiae*. *Genes Dev* 20:700–710.
3. Jambunathan N, et al. (2005) Multiple bromodomain genes are involved in restricting the spread of heterochromatic silencing at the *Saccharomyces cerevisiae* HMR-tRNA boundary. *Genetics* 171:913–922.

Table S3. Primers used

Strain construction	
<i>yta7</i> KO	TCTCTTCTCGCTATTTATTCACAATTGGTGCAGAAAGAACC GGATCCCCGGGTTAATTA AACTACATTTAAGAATTATATAAACATTATGGACTCCTGCCGATGAATTCGAGCTCGTTT
<i>YTA7</i> cloning	TGGCGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAG TGCTGAGTTTGAGATGTTTT CTGGGTACCGGGCCCCCTCGAGGTGACGGTATCGATCGGCTATTGATGGTACGGATC
<i>yta7K460A</i>	CCTCCTGGTACGGGTGCAACACTTATGGCAAG CTTGCCATAAGTGTGACCCGTACCAGGAGG
<i>yta7E519Q</i>	CTTCATCATTTTTTTGATCAAATCGACGGATTAGCGCC GGCGTAATCCGTCGATTTGATCAAAAAAATGATGGAAG
<i>YTA7-TAP</i>	AACAGGAACTGTCGATGAAATAATAAAATTTTTATCTGAATCCATGAAAAAGAGAAG AACTACATTTAAGAATTATATAAACATTATGGACTCCTGCTACGACTCACTATAGGG
(<i>hht1-hhf1</i>) KO	ATATTTGCTTGTGTTACCGTTTTCTAGAATTAGCTAAACGGATCCCCGGGTTAATTA TTTTGTTGTTTTTACTAAAACCTGATGACAATCAACAAACGATGAATTCGAGCTCGTTT
<i>pGAL1::FMP27</i>	AAGAACGGTAGCTATTACAAAGGACAGTAAAAGCAAACAGGAATTCGAGCTCGTTAAAC ATATAAGCCACTTGTACAGTAGAACATTAATCGGAAACATCATTTTGAGATCCGGGTTTT
<i>RPB3-HA</i>	AATGGGTAATACTGGATCAGGAGGGTATGATAATGCTTGGCGGATCCCCGGGTTAATTA GTTCACTTGTTTTTTCTCTATTACGCCCACTTGAGAAGAATTCGAGCTCGTTAAAC
<i>pGAL1::YTA7</i>	CCCATTGTTGTTTTCGACAGTCATAAAAAAGGTTACCACGAATTCGAGCTCGTTAAAC CTTCAACGTCGCTACCGCTCTATTCTTAAATTCGTGCCATTTTGAGATCCGGGTTTT
qPCR, listed in order of use	
<i>SPO1</i>	GAC AAC TAT CCA AAC GGC TCC AAG CCA GTG GGT AAC ATA CTG CTA ACT
<i>ZIP1</i>	AAGTGTCTAAGGTGGATCATATAAG GAA GGG TTG GTT AAC TCT AGG TC
<i>GIP1</i>	CAC ATT TCG CGG CCT TAC TAA TA TGAGTACTCCGATCCTTTATACA
<i>PXA1</i>	TTGGCTAACTTACCTAGATGCCAT CGT TGT CAA TCG ACG TGA TTG C
<i>FOX2</i>	ATA TCG ATC CCA CGC TAG CCA A TAC AGC GGC GTT ATC CAA TAC A
<i>ACT1</i>	TGTCCTGTACTCTCCGGT CCGGCAAATCGATTCTCAA [described by Babiarz et al. (1)]
<i>SPO11</i>	CCT ATG GGA TTA GCA TAG CCC TA TGTTGGCAGTCAGAGATGCTATC
<i>YSW1</i>	ACCTGCTGTAGTGCCTAAACA GGC AGA TCT CTC GTA GAA CCT
<i>GAL1 +1,400</i>	TGGATCATATGGTCCCGTTTGAC GGT ACT TGA CCT TGT AGA ACT CAT TG
<i>GAL10 +1,865</i>	CTACAAA GCCAACGGTC TTAGGC CTTGCTTCGTAACCAGCAGACAA
<i>PRP8</i>	GAGTGTGGCTAAATTTCTAAGAGG TCGAATACTCTCAGGCATATTTCT [described by Babiarz et al. (1)]
<i>GAL10 +535</i>	CCT TAG GGC CTA CTA ATC CGT A AGAGGGATGTGCGCAATTG
<i>GAL10 +114</i>	GGT TAC AGG TGG TGC TGG ATA C GAT GCT TGG TCA AGA CCT CTA A
<i>GAL1 Prom</i>	AAGTACGGATTAGAAGCCGCC GGCCAGGTTACTGCCAATTT
<i>GAL1 +97</i>	CTGAGTTCAATTCTAGCGCAAAGG CTCTACCAGGCGATCTAGCAACAA
<i>GAL1 +756</i>	CTCTGTTTGCAGTGGAGGAAGATCA CAGCTGTAGTACTTCTACCCTC
<i>GAL7 -326</i>	AGCAGGAGCC GCGGAGTTCA T GATCACGGTCAACAGTTGTCCGAG
<i>GAL7 +217</i>	GGTTAGG TCAACAGGAG GCTG AGATTGCACTTTAAGCAGCCTATT
<i>SUC2 -317</i>	ATACG CGTAGCGTTA ATCGACC TAC TAT AGA GCC CTT AGG CAA CAT
<i>SUC2 +69</i>	CACTAACGTATATGATGCTTTTGCA TTT CAT CGT ACC ACA ACC CAT T
<i>SUC2 +564</i>	AGCTGCCAACTCCACTCAATTC TTG GCA AAT GCA GAT TCT AGC TT
<i>ADY3</i>	AAT TAC TGA CGA GTT AGC TGG AAA TGCGATTGCACATAGGTAAGGTC

Table S3. Cont.

<i>HHT</i>	GGT GGT GTT AAG AAG CCT CA CTT GAG CGA TTT CTC TGA CC
<i>HHF</i>	AGC TAG AAG AGG TGG TGT CA TCTTTCTCTGGCGTGTTTCG
<i>HTA1</i>	ACGTTACCATTGCCCAAGG GTTTAGTTCCTTCCGCCTTC [described by Fillingham et al. (2)]
<i>GAL10 +1,092</i>	CAG ACC GAG TTG CAG GTT GAA GAC CAACAATGCTGGCGCCCAAATTG
ORF-free Chr I	GTT TAT AGC GGG CAT TAT GCG TAG ATC AG GTT CCT CTA GAA TTT TTC CAC TCG CAC ATT C [described by Mason and Struhl (3)]
<i>pGAL1::FMP27</i>	CTGGGGTAATTAATCAGCGAAGCGATG CAGTTGTACAGTAGAACATTAATCGGAAAC [described by Mason and Struhl (3)]
<i>FMP27, 0.5 kb</i>	CGCAATTAGTCAACAACGATATCACGATTG CCTACTTGAAGTCCATCCTTCAGAGG [described by Mason and Struhl (3)]
<i>FMP27, 2 kb</i>	CATATCATCCACCCTAGGTGCTAGGTCGG GAGCTGACCAGACCTAACCATAGTAGCGTG [described by Mason and Struhl (3)]
<i>FMP27, 4 kb</i>	AGATATTACTCGTTGTTTCGTGCCAG TCCCAAACCCTAGTTTAACAGAAGG [described by Jimeno-Gonzalez et al. (4)]
<i>FMP27, 6 kb</i>	CGTACTGTTGAAATGGAACGAGGACGC ATCGCTTCCATACTCGTTGTATCATCAGTC [described by Mason and Struhl (3)]
<i>FMP27, 8 kb</i>	GAGGGTCACA GATCTATTAC TTGCC GTTGTGAGTTGCTTCAGTGGTGAAGTG [described by Mason and Struhl (3)]

Chr, chromosome; Prom, promoter.

1. Babiarz JE, Halley JE, Rine J (2006) Telomeric heterochromatin boundaries require NuA4-dependent acetylation of histone variant H2A.Z in *Saccharomyces cerevisiae*. *Genes Dev* 20: 700–710.
2. Fillingham J, et al. (2009) Two-color cell array screen reveals interdependent roles for histone chaperones and a chromatin boundary regulator in histone gene repression. *Mol Cell* 35: 340–351.
3. Mason PB, Struhl K (2005) Distinction and relationship between elongation rate and processivity of RNA polymerase II in vivo. *Mol Cell* 17:831–840.
4. Jimeno-Gonzalez S, Haaning LL, Malagon F, Jensen TH (2010) The yeast 5'-3' exonuclease Rat1p functions during transcription elongation by RNA polymerase II. *Mol Cell* 37:580–587.