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Supplementary Materials for

# Histone exchange is associated with activator function at transcribed promoters and with repression at histone loci

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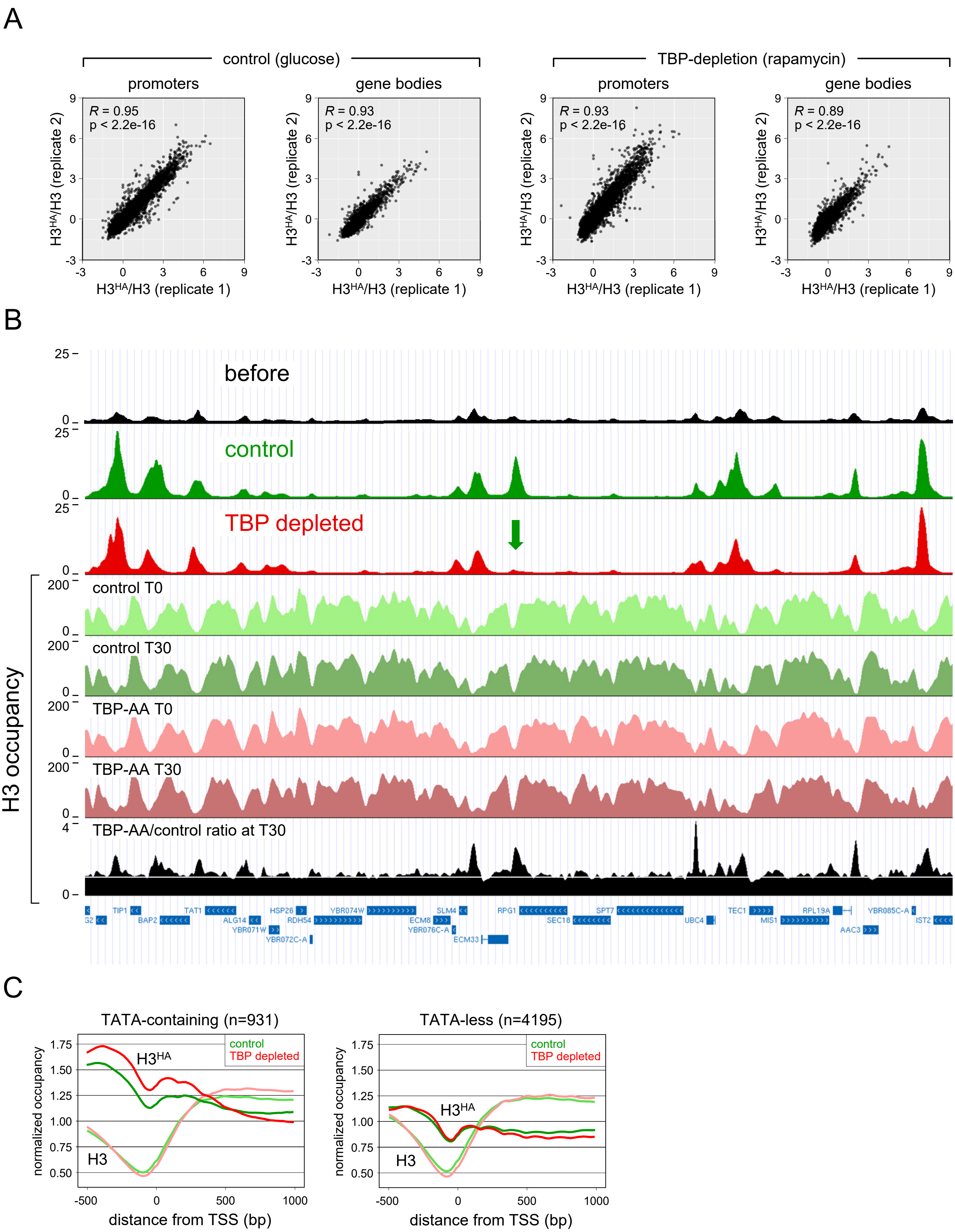
**This PDF file includes:**


A
control (glucose)
TBP-depletion (rapamycin)
promoters
gene bodies
R = 0.95
p < 2.2e-16
R = 0.93
p < 2.2e-16
R = 0.93
p < 2.2e-16
R = 0.89
p < 2.2e-16
H3HA/H3 (replicate 2)
H3HA/H3 (replicate 1)
B
before
control
TBP depleted
H3 occupancy
control T0
control T30
TBP-AA T0
TBP-AA T30
TBP-AA/control ratio at T30
TIP1
TAT1
HSP26
YBR074W
SLM4
RPG1
SPT7
TEC1
RPL19A
YBR085C-A
BAP2
ALG14
RDH54
ECM8
SEC18
UBC4
MIS1
IST2
YBR071W
YBR076C-A
AAC3
YBR072C-A
ECM33
C
TATA-containing (n=931)
TATA-less (n=4195)
control
TBP depleted
H3HA
H3
normalized occupancy
distance from TSS (bp)

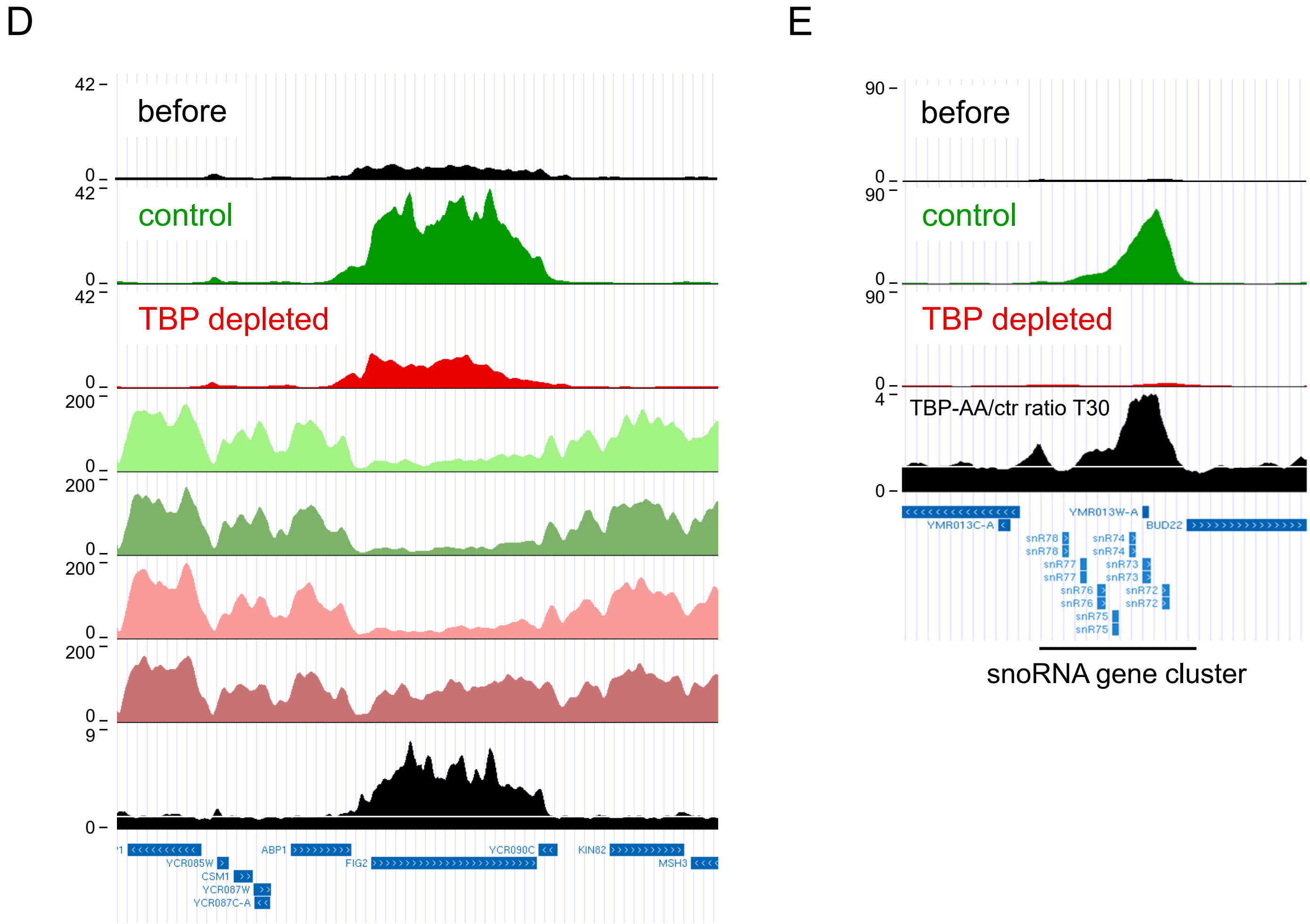



**Fig. S1. Histone exchange and nucleosome occupancy in the absence of TBP. Related to Fig. 1.**

(**A**) Comparison of the $H3^{HA}$ enrichment over promoters (-500 to TSS) and gene bodies (TSS to +1000 bp) shows good reproducibility between two independent biological ChIP-Seq replicates. R values were calculated using the stat_cor function of the ggpubr package (*57*).

(**B**) Genome browser view of a region in chromosome II (365,000-425,000) showing TBP-dependent $H3^{HA}$ incorporation between two genes (*ECM33* and *RPG1*; see arrow) oriented in a tail-to-tail fashion. Shown on top is a T0 time point control (before) when $H3^{HA}$ is expressed at low levels prior to galactose induction. Shown below is H3 occupancy at T0 and T30 under control or TBP-depletion (TBP-AA) conditions as indicated. Regions of high histone exchange often show increased nucleosome occupancy upon TBP depletion (lower panel with white bar set to 1.0).

(**C**) Replicate of Fig. 1C.

(**D**) The *FIG2* gene is one of the very few RNA pol II genes showing high histone turnover over the gene body. Another example is *YHR020W*. Note that depletion of TBP results in a marked increase in nucleosome occupancy. Data are presented as in (C).

(**E**) High TBP-dependent histone turnover over a snoRNA gene cluster. Note that an increase in H3 occupancy following TBP depletion occurs in the absence of $H3^{HA}$ incorporation, thus pointing to two independent events. The increase in histone occupancy must be rapid, occurring prior to the onset of $H3^{HA}$ expression.

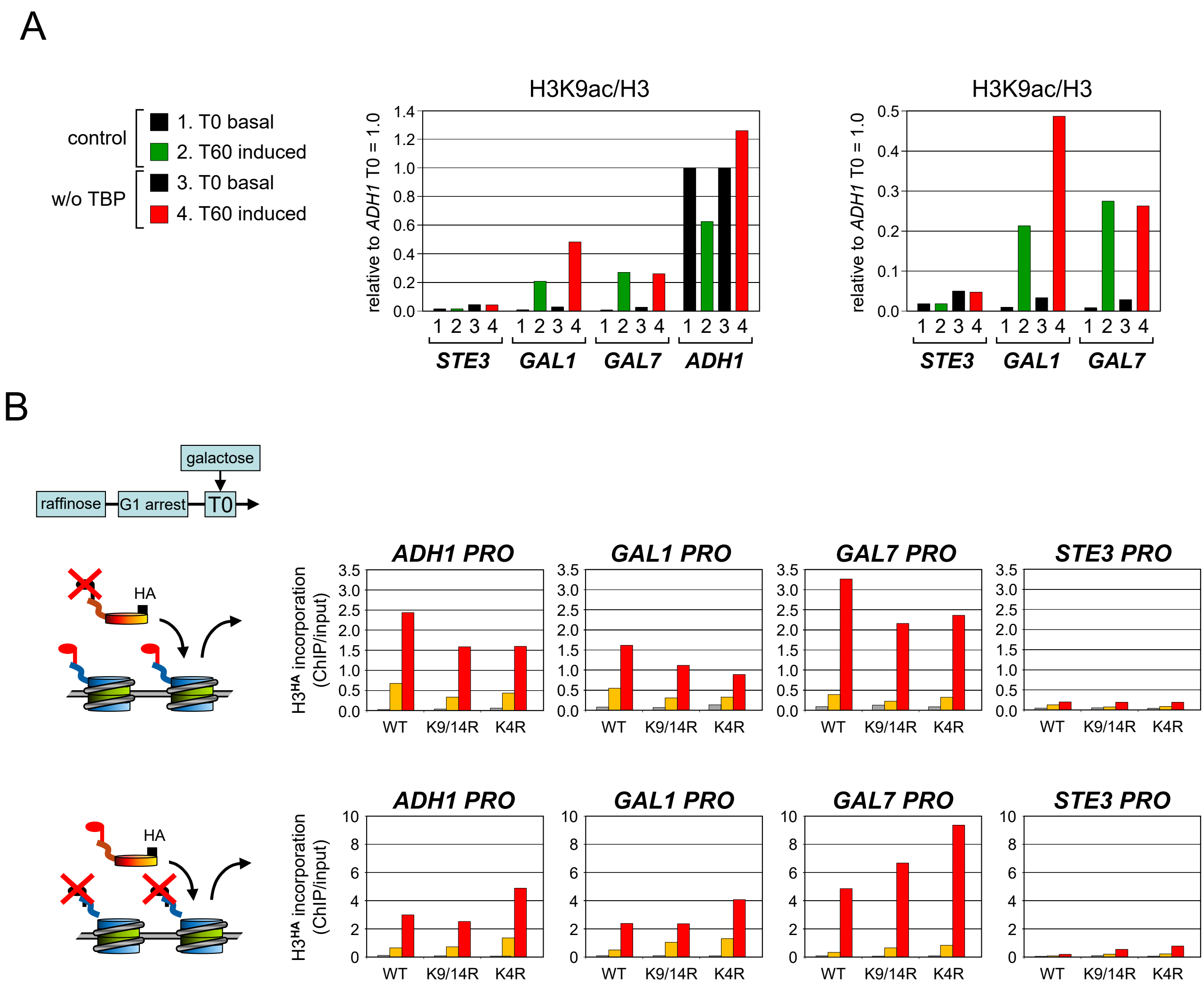



**Fig. S2. Histone exchange and modifications at *GAL* genes. Related to Fig. 2.**

(**A**) Galactose activation of the *GAL* genes is associated with increased H3K9/14ac at the promoter independently of TBP. Shown are the ChIP signals for H3K9/14ac normalized to H3 occupancy just prior to (T0) and at 60 min (T60) after galactose induction under control or TBP-depletion conditions. Right panel: without *ADH1*.

(**B**) Histone exchange at the active *GAL* promoters occurs independently of H3K4me and H3K9/14ac. Upper panels: incorporation of HA-tagged histone H3 K4R and K9/14R modification mutants in a wild-type chromatin background. Lower panel: incorporation of wild-type H3 in a chromatin containing the H3 modification mutants. Shown are the amounts of tagged histones detected just prior to (gray bars) and at 30 min (orange bars) and 60 min (red bars) after galactose induction of $H3^{HA}$. Data for the control *ADH1* and *STE3* gene promoters are from (*41*).

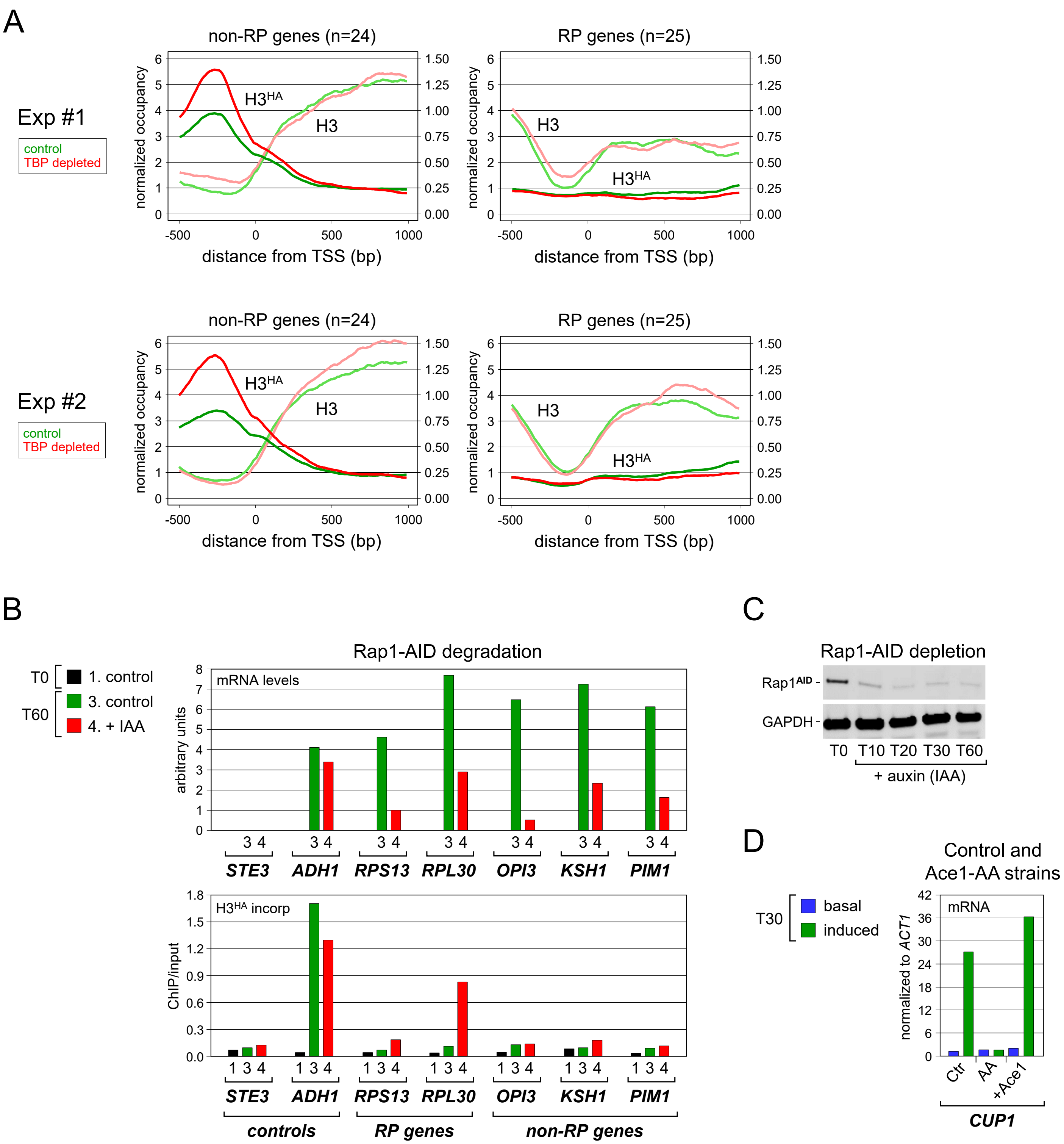



**Fig. S3. Lack of histone exchange at Rap1-dependent RP and non-RP gene promoters. Related to Fig. 5.**

(**A**) Low histone exchange at RP gene promoters in the presence or absence of TBP. Metagene analysis of the average $H3^{HA}$ incorporation and H3 occupancy under control (green) or TBP-depletion (red) conditions; left panels show a selected set of non-RP genes with high turnover at their promoters, right panels show RP genes (gene lists can be found in Table S4). The results are presented as in Fig. 1C. The scale for H3 occupancy is on the right axis. Note that H3 levels are similar at both sets of promoters, indicating that the difference in $HA^{H3}$ incorporation between these gene sets is not simply a result of H3 occupancy differences. Also see Fig. 1C.

(**B**) Same experiment as in Fig. 5C but including three Rap1-regulated non-RP genes. The genes were selected based on ChIP-Seq (*58*) and RNA-Seq (*59*) studies. The OPI3 mRNA signal, and the KSH1 and PIM1 mRNA signals were multiplied, respectively, by 8 and 100 to facilitate comparison.

(**C**) Time course analysis of auxin-mediated degradation of Rap1 fused to AID. Rap1-AID was detected using anti-Rap1 antibodies.

(**D**) Control experiment for Fig. 5E showing that anchor-away of Ace1 (AA) in the parental strain abrogates copper-mediated activation of *CUP1* and that normal activation is restored upon ectopic expression of Ace1 (+Ace1).

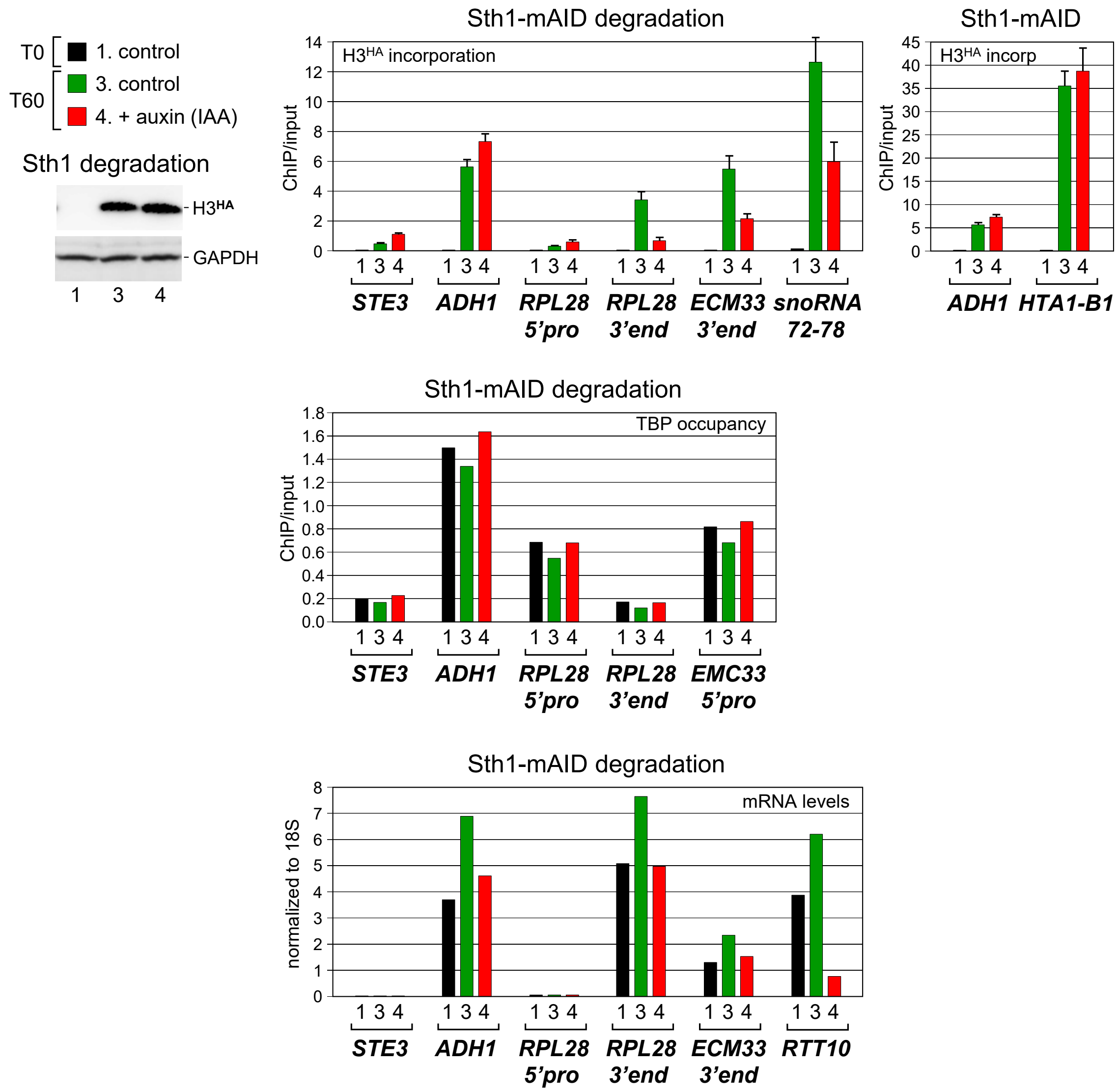



**Fig. S4. Histone exchange in the absence of RSC. Related to Fig. 6.**

Upper panels: Yeast cells expressing the essential RSC complex subunit Sth1 fused to mini-AID (mAID) were arrested in G1 by alpha factor. Auxin (IAA) was added or not 30 min prior to galactose activation of $H3^{HA}$ to induce degradation of Sth1-mAID. $H3^{HA}$ incorporation was measured at the indicated gene promoters and 3' ends as before. Shown are the mean and SD of triplicate cultures. On the left is the sample color code and a Western blot analysis for $H3^{HA}$ expression. See fig. S5 for experimental details. *RPL28* (Fig. 1A) and *ECM33* (fig. S1B) are two genes showing TBP-dependent histone exchange at their 3' ends.

Middle and lower panels: TBP occupancy and mRNA levels for the indicated genes were monitored by RT-qPCR and quantitative ChIP under the same experimental conditions as above. Expression of *RTT10* is dependent on RSC (*35*) and serves as a control for auxin-induced degradation of Sth1. Note that HIR-mediated $H3^{HA}$ incorporation at the histone *HTA1-HTB1* locus is unaffected by inactivation of RSC.

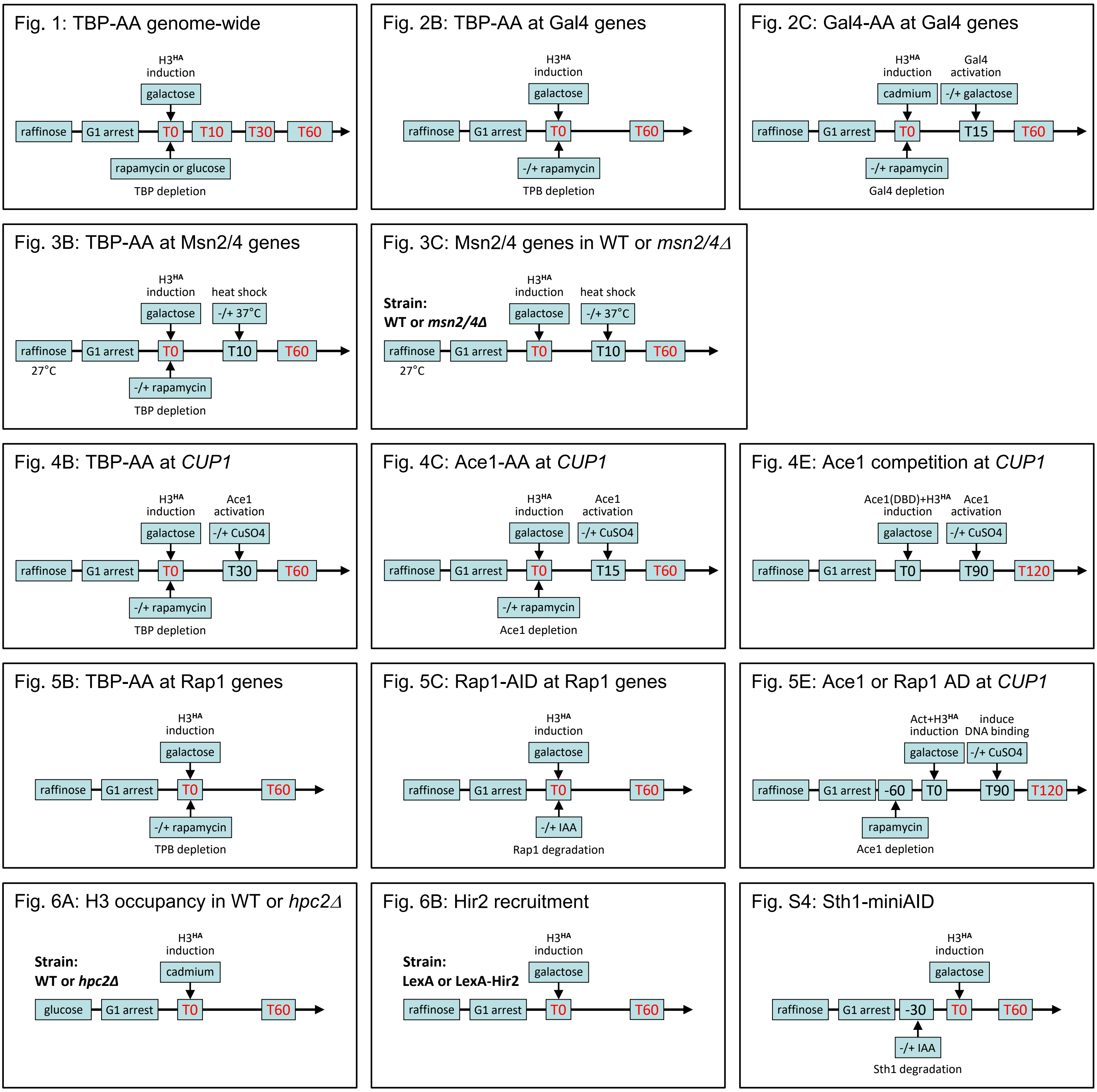



**Fig. S5. Experimental schemes.**

Schematic diagram illustrating the experiments presented in the indicated figures. Measurements were made at the time points indicated in red.

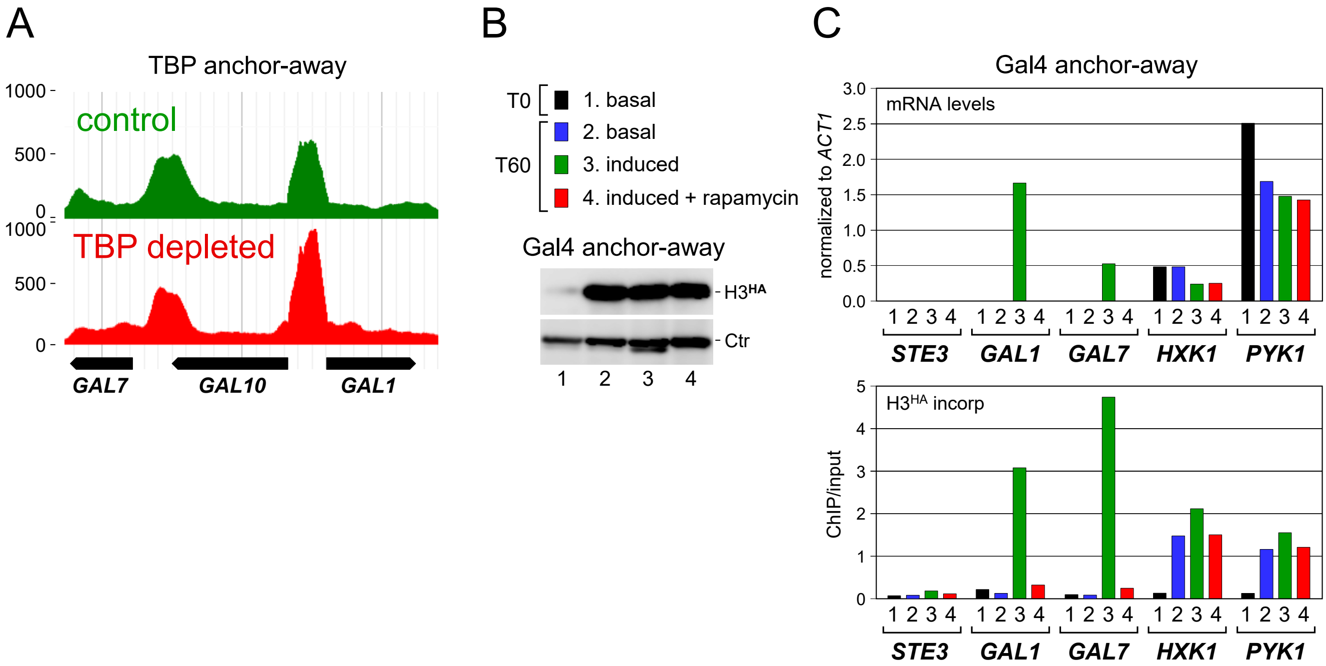



**Fig. S6. Independent biological replicate of Fig. 2.**

Same experiments as in Fig. 2 except that (A) shows a genome browser view of $H3^{HA}$ incorporation at the *GAL* gene cluster. The data are presented as in Fig. 1B but without normalization to H3 occupancy. Shown in (B) is the sample color code and a Western blot analysis for $H3^{HA}$ expression in the Gal4 anchor-away experiment presented in (C). Ctr: cross-reactive band that serves as loading control.

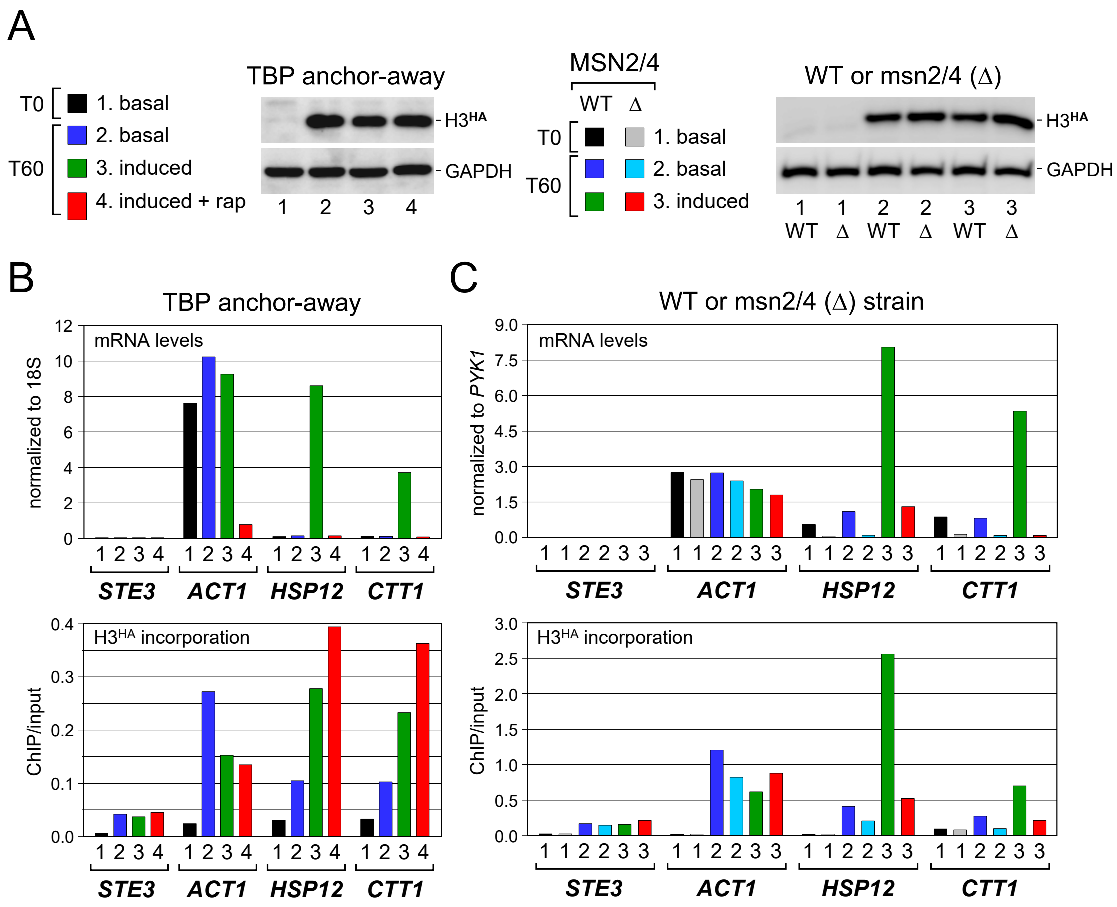



**Fig. S7. Independent biological replicate of Fig. 3.**

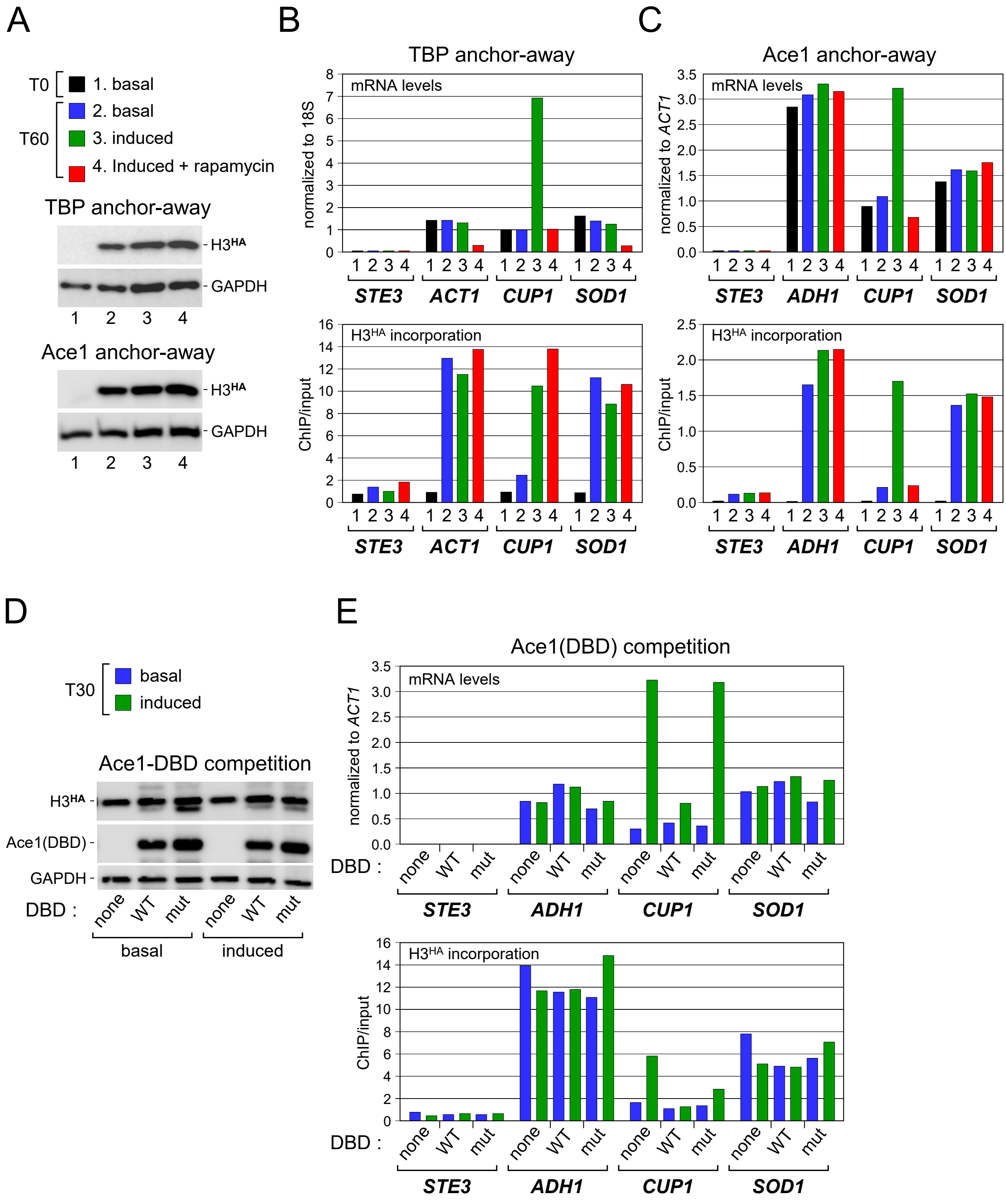



**Fig. S8. Independent biological replicate of Fig. 4.**

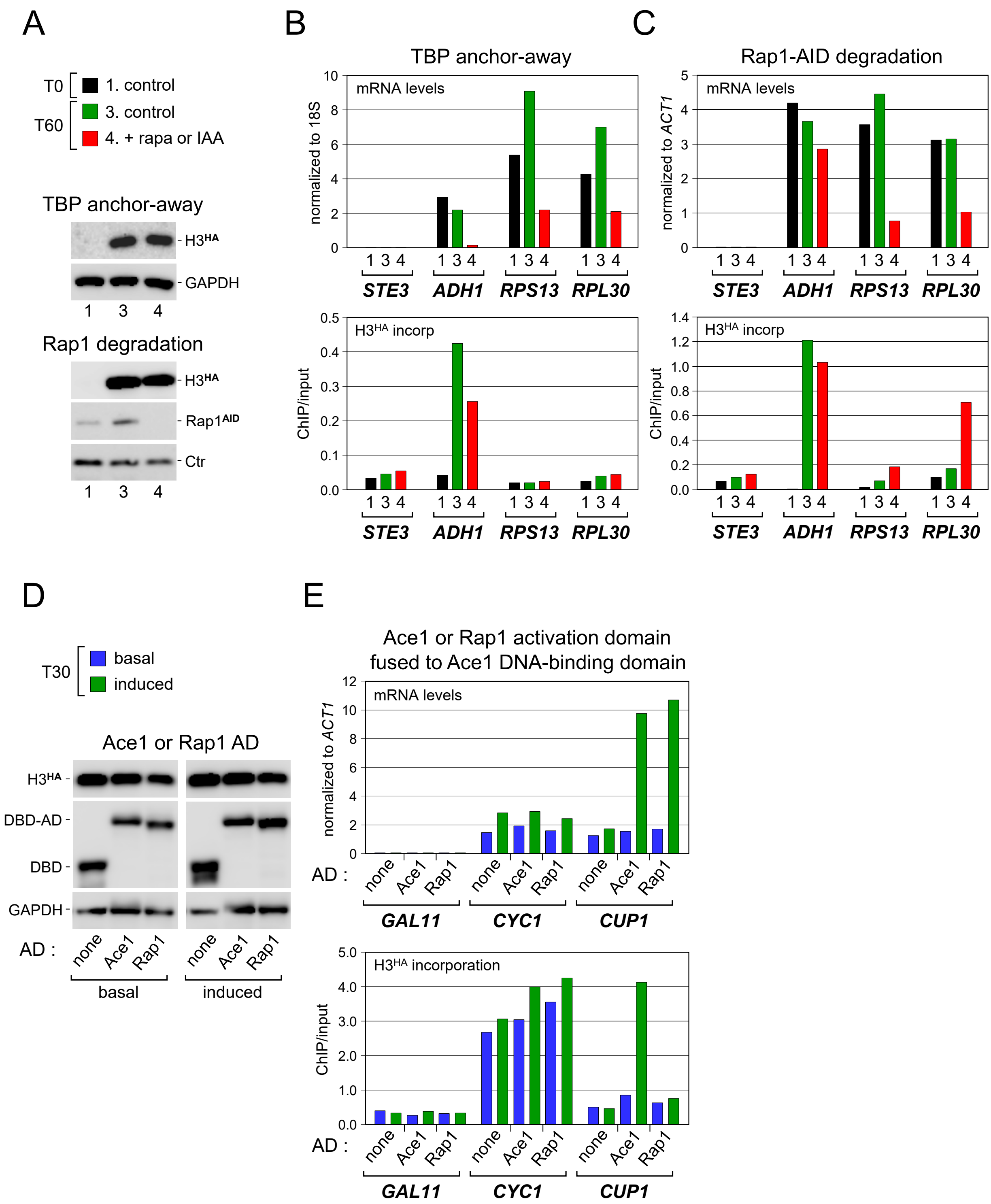



**Fig. S9. Independent biological replicate of Fig. 5.**

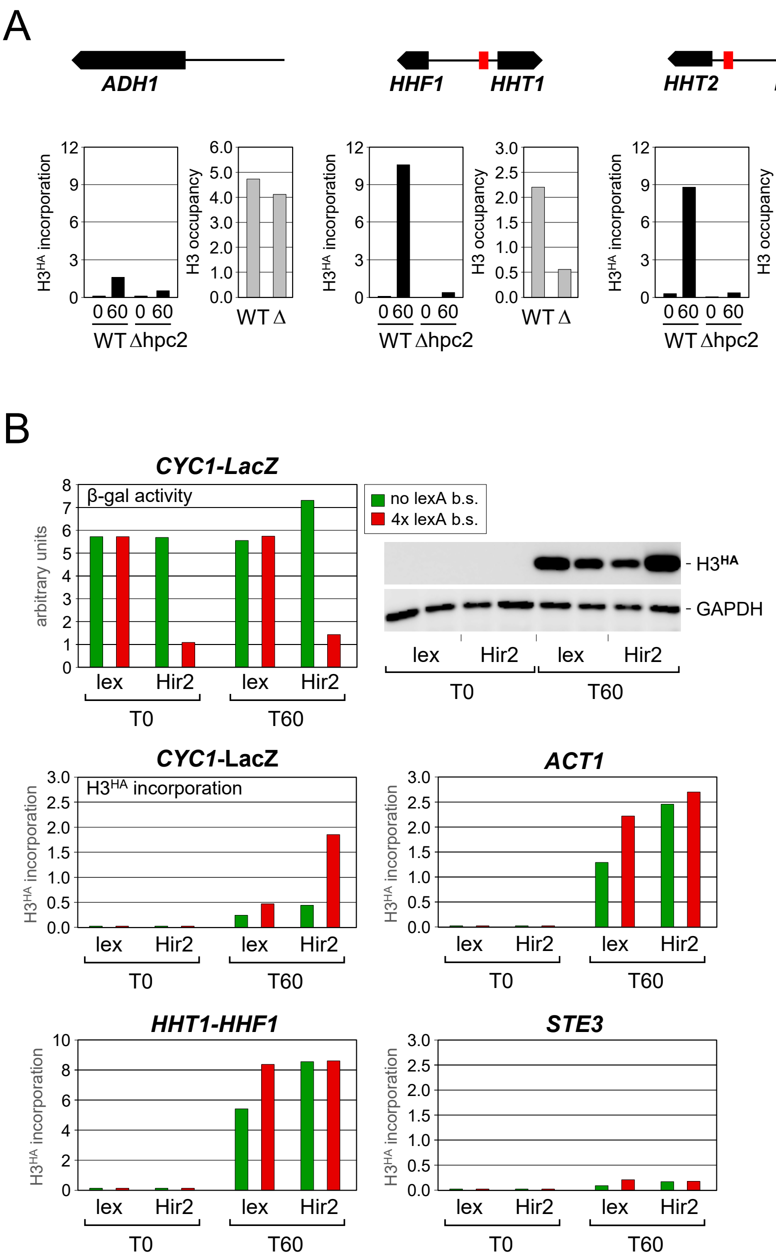



**Fig. S10. Independent biological replicate of Fig. 6.**

## Supplementary Table S1

### Yeast strains

| Strain | Relevant genotype | Figure | Source |
|---|---|---|---|
| HHY221 | *MAT***a***, tor1-1, fpr1::loxP-LEU2-loxP, RPL13A-2×FKBP12::loxP, ade2-1, trp1-1, his3-11, ura3* | | (*17*) |
| HH4 | HHY221; *bar1::URA3* | | (*10*) |
| SKY50 | HH4; *GAL4-FRB-HISMX3, pRS314-GAL1pro-H3.HA* | 2C | This study |
| SKY15 | HH4; *ACE1-FRB-HISMX3* | | This study |
| SKY23 | HH4; *ACE1-FRB-HISMX3, pRS314-GAL1pro-H3.HA* | 4A, 4C | This study |
| HHY154 | *MAT***α***, ade2-1, ura3-1, tor1-1, fpr1::NAT, TBP1-FRB::KAN, RPL13A-2×FKBP12::TRP1* | | (*17*) |
| YG19 | HHY154; *MAT***a**, *bar1::URA3* | | (*10*) |
| SKY12 | YG19; *pRSADE-GAL1pro-H3.HA* | 1A-1C, 2A, 2B, 3A, 3B, 4A, 4B, 5A, 5B, 6A, S1, S2A, S2B, S3A | This study |
| YG31 | YG19; *hpc2::LEU2* | | This study |
| SKY54 | YG31; *pRSADE-MET3pro-H3.HA* | 6A | This study |
| W303-1A | *MAT***a***, leu2-3,112, his3-11,15 ura3-1, ade2-1, trp1-1, can1-100* | | (*25*) |
| Wmsn2-msn4 | W303-1A; *msn2-Δ3::HIS3, msn4–1::TRP1* | | (*25*) |
| SKY65 | W303-1A; *bar1::KANMX3, pRSADE-GAL1pro-H3.HA* | 3A, 3C | This study |
| SKY66 | Wmsn2-msn4; *bar1::KANMX3, pRSADE-GAL1pro-H3.HA* | 3A, 3C | This study |

| | | | |
|---|---|---|---|
| RH932.5A | *MAT***a***, trp1, bar1-1* | | Howard Riezman |
| SKY84 | RH932.5A; *pBTM116-HIR2 + pAJ1+ pRSADE-GAL1pro-H3.HA* | 6B | This study |
| SKY86 | RH932.5A; *pBTM116-HIR2 + pJK1621+ pRSADE-GAL1pro-H3.HA* | 6B | This study |
| SKY88 | RH932.5A; *pBTM116 + pAJ1+ pRSADE-GAL1pro-H3.HA* | 6B | This study |
| SKY89 | RH932.5A; *pBTM116 + pJK1621+ pRSADE-GAL1pro-H3.HA* | 6B | This study |
| SKY56 | RH932.5A; *pRS314-GAL1pro-H3.HA + p793* | 4D, 4E | This study |
| SKY57 | RH932.5A; *pRS314-GAL1pro-H3.HA + p1883* | 4D, 4E | This study |
| SKY58 | RH932.5A; *pRS314-GAL1pro-H3.HA + p1885* | 4D, 4E | This study |
| YJB25 | *MAT***a***, HIS3, ADE2, pRS306Padh1.OsTIR1, pRAP1-AID-LEU2* | | (*58*) |
| SKY44 | YJB25; *bar1::KANMX3, pRS314-GAL1pro-H3.HA* | 5A, 5C, S3B | This study |
| SKY113 | SKY15; ura3*::KANMX3* | | This study |
| SKY114 | SKY113; *pRS314-GAL1pro-H3.HA + p793* | 5D, 5E, S3C | This study |
| SKY115 | SKY113; *pRS314-GAL1pro-H3.HA + p1883* | 5D, 5E | This study |
| SKY116 | SKY113; *pRS314-GAL1pro-H3.HA + p1883-ACE1(AD)* | 5D, 5E, S3C | This study |
| SKY117 | SKY113; *pRS314-GAL1pro-H3.HA + p1883-RAP1(AD)* | 5D, 5E | This study |
| SKY164 | *MAT***a**, *HIS3, ADE2, pRS306Padh1.OsTIR1, STH1-miniAID-KANMX3*, *bar1::HYGB* | | gift from David Shore |
| SKY165 | SKY164; *pRSADE-GAL1pro-H3.HA* | S4 | This study |

## Supplementary Table S2

### Plasmids

| Plasmid name | Description | Marker | Source |
|---|---|---|---|
| | pRS314-GAL1pro-H3.HA | TRP1 | (*10*) |
| | pRSADE-GAL1pro-H3.HA | ADE2 | (*10*) |
| | pRSADE-MET3pro-H3.HA | ADE2 | This study |
| p793 (GFP-pYeF2) | pYeF2-GAL1pro-GFP | URA3 | (*28*) |
| p1883 | pYeF2-GAL1pro-Ace1(DBD:WT).GFP | URA3 | (*28*) |
| p1885 | pYeF2-GAL1pro-Ace1(DBD:G37Q).GFP | URA3 | (*28*) |
| p1883-ACE1(AD) | pYeF2-GAL1pro-Ace1(DBD:WT).Ace1(AD).GFP | URA3 | This study |
| p1883-RAP1(AD) | pYeF2-GAL1pro-Ace1(DBD:WT).Rap1(AD).GFP | URA3 | This study |
| pBTM116 | pBTM116-ADH1pro-LexA | TRP1 | (*36*) |
| pBTM116-HIR2 | pBTM116-ADH1pro-LexA.HIR2 | TRP1 | (*36*) |
| pAJ1 | pAJ1-CYC1pro-LACZ reporter without LexA-binding sites | URA3 | (*36*, *60*) |
| pJK1621 | pAJ1-CYC1pro-LACZ reporter carrying four LexA-binding sites upstream of the *CYC1* UAS elements | URA3 | (*36*, *60*) |

## Supplemental Table S3

### Cloning PCR amplification primers

| Name | Description | Sequence | Comments |
|---|---|---|---|
| MS2293 | ClaI RAP1 AD Fw | CCATCGATgcAATTATAGTTCTCAAAGAAATGTTCAGCC | Cla1 site underlined; used to generate p1883-RAP1(AD). The bases in lower case have been added to keep the reading frame open |
| MS2294 | ClaI RAP1 AD Rev | CCATCGATtTGGTGGAAAGCTTATGGTATCAGG | Cla1 site underlined; same |
| MS2295 | ClaI ACE1 AD Fw | CCATCGATgcCTGGACGTTCTTTTGGGCC | Cla1 site underlined; used to generate p1883-ACE1(AD). The bases in lower case have been added to keep the reading frame open |
| MS2296 | ClaI ACE1 AD Rev | CCATCGATtTTGTGAATGTGAGTTATGCGAAG | Cla1 site underlined; same |
| MS1730 | KpnI MET3pro Fw | CGCGGTACCAATGAAAACACAGAAGTA | Kpn1 site underlined; used to generate pRSADE-MET3pro-H3.HA |
| MS1734 | MscI MET3pro Rev | GCGTGGCCATACTTTATTCTTGTTATTA | Msc1 site underlined; same |

### ChIP qPCR primers

| Name | Description | Sequence | Comments |
|---|---|---|---|
| MS819 | ACT1 PRO Fw | GCGCTAGAACATACCAGAATC | |
| MS820 | ACT1 PRO Rev | TCTTCCTTCCCCTTTCTACTC | |
| MS291 | ADH1 PRO Fw | CACGCACACTACTCTCTAATGAG | |
| MS290 | ADH1 PRO Rev | CTGGGATAGACATTGTATATGAG | |
| MS2056 | CTT1 PRO Fw | ATGAGTACGTCGCCGATC | |
| MS2057 | CTT1 PRO Rev | GTCCAGGCTACGTCGAAT | |
| MS1922 | CUP1 PRO Fw | ACTTCACCACCCTTTATTTC | |

| | | | |
|---|---|---|---|
| MS1923 | CUP1 PRO Rev | CTGACAATCCATATTGCGTT | |
| MS1141 | CYC1 PRO Fw | GATGGCCAGGCAACTTTA | |
| MS1142 | CYC1 PRO Rev | ATGCTGCAAAGGTCCTAA | |
| MS2054 | CYC1-LACZ PRO Fw | TGTGCGACGACACATGATC | Hybridizes to the CYC1 core promoter |
| MS2055 | CYC1-LACZ PRO Rev | GTGAGACGGGCAACAGCCAA | Hybridizes at the junction between CYC1 and the LacZ ORF |
| MS2698 | EMC33 PRO Fw | CGTTCATTCGCTTCTACAC | |
| MS2699 | EMC33 PRO Rev | GCAGTAGCAGTCAAAGCG | |
| MS2694 | EMC33 3'-end Fw | GAACGGTGCCACATCTAC | |
| MS2695 | EMC33 3'-end Rev | GAGCAGCACCCTTAGACT | |
| MS699 | GAL1 PRO Fw | GCTGCATAACCACTTTAAC | |
| MS700 | GAL1 PRO Rev | CTTTGCGCTAGAATTGAAC | |
| MS705 | GAL7 PRO Fw | CTTGGACCCGTAAGTTTCAC | |
| MS706 | GAL7 PRO Rev | TGCTGGTTACGAAGCAAGAC | |
| MS1041 | GAL11 PRO Fw | GCTGGTTCCACAAAGAAG | |
| MS1042 | GAL11 PRO Rev | ACGGCACTATACGAAACG | |
| MS1599 | HHF1-HHT1 URR Fw | ACCGTATTCGCGGGCATTTGC | To amplify the regulatory region between HHF1 and HHT1 |
| MS1600 | HHF1-HHT1 URR Rev | ATAATGTATGGGACAATGCG | Same |
| MS1601 | HHF2-HHT2 URR Fw | ACATTGGGCGATAATGAACGC | To amplify the regulatory region between HHF2 and HHT2 |
| MS1602 | HHF2-HHT2 URR Rev | TCTGGTCTGGTCTGCATTTCG | Same |
| MS1595 | HTA1-HTB1 URR Fw | TCTTGATTTTAAATCCATCG | To amplify the regulatory region between HTA1 and HTB1 |
| MS1596 | HTA1-HTB1 URR Rev | ATAGCTTCGCACAGTGAGGC | Same |
| MS1905 | HTA2-HTB2 URR Fw | CACCGCTTTATTAGGCGAAG | To amplify the regulatory region between HTA2 and HTB2 |
| MS1906 | HTA2-HTB2 URR Rev | TTATGGCCCCCAGGTTAATG | Same |
| MS2596 | HSP12 PRO Fw | TGCGTTCTACTTCCTCAATTGC | |
| MS2597 | HSP12 PRO Rev | GCGTCAGACATTGTTGTATTTAGTTTTT | |
| MS1344 | HXK1 PRO Fw | TGAGTATTGCAAGCCACA | |
| MS1345 | HXK1 PRO Rev | CTTCTGTTTCCTCCTTTTC | |

| | | | |
|---|---|---|---|
| MS2682 | KSH1 PRO Fw | GTCGGCAGATTTCTCACC | |
| MS2683 | KSH1 PRO Rev | CAGGTGGGTTTATGCAGTG | |
| MS2678 | OPI3 PRO Fw | TGATGACCAGGGTAGGTG | |
| MS2679 | OPI3 PRO Rev | CAGTGGTCATTGCAGTGG | |
| MS2700 | PIM1 PRO Fw | ATTGCAGCAACGACAAGC | |
| MS2701 | PIM1 PRO Rev | AGACCCTTAGCACAGTGG | |
| MS835 | PYK1 PRO Fw | CCCCTTTCAAAGTTATTCTCTACTC | |
| MS836 | PYK1 PRO Rev | GAACCAGCAACAACGTTTAATG | |
| MS2208 | RPL28 PRO Fw | CAGGGACCCACACATTAC | |
| MS2209 | RPL28 PRO Rev | GGAGAAAGCAAACGCCAT | |
| MS2210 | RPL28 3'-end Fw | TGGACATTGATCCCAGAAG | Used to amplify the 3' end of the RPL28 open reading frame |
| MS2211 | RPL28 3'-end Rev | CTTCAGCCAACTTGGAGA | Same |
| MS2236 | RPL30 PRO Fw | TTCTGGATAGGACGCCAAC | |
| MS2237 | RPL30 PRO Rev | GATCCTTACTGCGGTGCTA | |
| MS2228 | RPS13 PRO Fw | ACCACCCATAAACCATAAAGT | |
| MS2229 | RPS13 PRO Rev | GTACAGAAGTGGAAATCTCATTC | |
| MS1924 | SOD1 PRO Fw | GCCGCTTACTGGAAGTAC | |
| MS1925 | SOD1 PRO Rev | ACAGCTAAACATTTGCCC | |
| MS588 | STE3 PRO Fw | CAAAGCCCTATTATTGCTGAC | |
| MS589 | STE3 PRO Rev | TCTCCACAATTTGGGCAGAAG | |
| MS2646 | snoRNA72-78 Fw | TTCACGACGGTCAACTGC | |
| MS2647 | snoRNA72-78 Rev | GAGTCGTCCAAATAGTCAGC | |

## Expression analysis qPCR primers

| Name | Description | Sequence | Comments |
|---|---|---|---|
| MS825 | ACT1 ORF Fw | GTCCAAGGCGACGTAACATAG | |
| MS826 | ACT1 ORF Rev | GCCGGTAGAGATTTGACTGAC | |

| | | | |
|---|---|---|---|
| MS315 | ADH1 ORF Fw | TAGGTTCTTTGGCTGTTCAATACG | |
| MS316 | ADH1 ORF Rev | CGGAAACGGAAACGTTGATGACACCG | |
| MS2151 | CTT1 ORF Fw | TGCCACGCTTGTAAGATC | |
| MS2152 | CTT1 ORF Rev | CAAGGAACTCCCAAGCATT | |
| MS1898 | CUP1 ORF Fw | GAAGGTCATGAGTGCCAATG | |
| MS1899 | CUP1 ORF Rev | CATTTGTCGTCGCTGTTACAC | |
| MS2076 | CYC1 ORF Fw | CTCTGGTCAAGCTGAAGG | |
| MS2077 | CYC1 ORF Rev | CACCAAAGGCCATCTTGG | |
| MS701 | GAL1 ORF Fw | GGGCCCAAATGGCAACATAG | |
| MS702 | GAL1 ORF Rev | GCCCAATGCTGGTTTAGAGAC | |
| MS737 | GAL7 ORF Fw | CTCTTTGAGGCTCACCTAAC | |
| MS738 | GAL7 ORF Rev | GCTCCTTTGAATGCGACTG | |
| MS1043 | GAL11 ORF Fw | GAAAGTGGCACCTATTCC | |
| MS1044 | GAL11 ORF Rev | CTTCGCAGCTTCCATATC | |
| MS2002 | HSP12 ORF Fw | AGCTTTGAAGCCAGACTCTCA | |
| MS406 | HSP12 ORF Rev | CAGAGTCGTGGACACCTTGGA | |
| MS903 | HXK1 ORF Fw | TGTAGCAATGGGACGACATC | |
| MS904 | HXK1 ORF Rev | AACACCAAGGACACCTTACC | |
| MS2666 | KSH1 ORF Fw | TTCGTTCTCTTCTGCAAGTG | |
| MS2667 | KSH1 ORF Rev | GACTGGCCCTTTCACCAA | |
| MS2600 | OPI3 ORF Fw | TGGGTGTGGCTCTCTTTG | |
| MS2601 | OPI3 ORF Rev | GACAAAGTGGAACCCTGG | |
| MS2702 | PIM1 ORF Fw | AGGCGTCTATCCACTTGC | |
| MS2703 | PIM1 ORF Rev | CTCAACCCACCGATACGT | |
| MS839 | PYK1 ORF Fw | CCAAGGGTCCAGAAATCAG | |
| MS840 | PYK1 ORF Rev | CTTGTCATCGGTGGTGAAG | |
| MS2238 | RPL30 ORF Fw | TTGCCGCTAACACTCCAG | |
| MS2239 | RPL30 ORF Rev | CAGAGTCACCAGCTTCCA | |
| MS2230 | RPS13 ORF Fw | GGTTTGGCTCCAGAAATCC | |
| MS2231 | RPS13 ORF Rev | GGTGGTAAGACAGCAACAG | |

| | | | |
|---|---|---|---|
| MS2692 | RTT10 ORF Fw | CGCGCTTGGGAAATTACC | |
| MS2693 | RTT10 ORF Rev | CCAACACCTCCGATCAGT | |
| MS1902 | SOD1 ORF Fw | ACCTCCGTTGTAGGCAGAAG | |
| MS1903 | SOD1 ORF Rev | CGGCATTACCAGTCTTCAAA | |
| MS591 | STE3 ORF Fw | CGTCAAGGACCTTGTGATTAGC | |
| MS590 | STE3 ORF Rev | GCGCCCACAAATGACCATATAAGC | |
| MS1237 | 18S RNA Fw | CCTGAGAAACGGCTACCACATC | |
| MS1238 | 18S RNA Rev | ATTGTCACTACCTCCCTGAATTAGGA | |

## Supplemental Table S4

### List of non-RP and RP genes used for fig. S3A

| | non-RP genes | RP genes | | non-RP genes | RP genes |
|---|---|---|---|---|---|
| 1 | YAL040C | YBL087C | 14 | YKL189W | YKL180W |
| 2 | YBL029W | YBR181C | 15 | YLR023C | YKR057W |
| 3 | YBL042C | YBR189W | 16 | YLR354C | YKR094C |
| 4 | YBR114W | YDR012W | 17 | YML008C | YLR029C |
| 5 | YDR085C | YDR064W | 18 | YMR017W | YLR287C-A |
| 6 | YEL036C | YDR500C | 19 | YMR065W | YLR441C |
| 7 | YER045C | YER056C-A | 20 | YMR205C | YML026C |
| 8 | YER056C | YER102W | 21 | YOR274W | YMR194W |
| 9 | YER132C | YFL034C-A | 22 | YOR303W | YMR230W |
| 10 | YHR007C | YGL147C | 23 | YPL048W | YOL120C |
| 11 | YHR162W | YGR085C | 24 | YPL137C | YOR167C |
| 12 | YIL099W | YHL033C | 25 | | YPL198W |
| 13 | YJR104C | YJR094W-A | | | |

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