

Supplemental Material for

MCB

MOLECULAR AND CELLULAR BIOLOGY

The SAGA Subunit Ada2 Functions in Transcriptional Silencing

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Supplemental Figures

FIG. S1. The Ada2 silencing function acts through SAGA, not SLIK/SALSA. Diagram of C-terminal *spt7* mutant alleles (78) tested for telomeric silencing. *spt7-200* lacks amino acids (aa) 1125-1150 (-200) containing the C-terminal proteolytic cleavage site (P); *spt7-300* lacks aa 1151-1180 (-300) containing a domain mediating Spt8-association (S); *spt7-400* lacks both these regions (-400). Wild type, *spt7-200* (LPY 10057), *spt7-300* (LPY 10328), *spt7-400* (LPY 10061) strains harboring a telomeric *URA3* gene were plated on synthetic complete medium (growth) or synthetic complete medium containing 5-FOA (silencing) and assayed as in Fig. 1A. The *spt7-200* mutant fails to make the proteolytic cleavage that creates the truncated form of Spt7 and is severely depleted for SLIK/SALSA (78). The *spt7-200* strain did not have a telomeric silencing defect, indicating that SLIK/SALSA was not required for telomeric silencing. The *spt7-300* mutant has predominantly SAGA-related complexes lacking Spt8 that elute from a Mono-Q column in the same fractions as SLIK/SALSA (78). This mutant had an intermediate silencing defect. The *spt7-400* mutant lacks both regions and is depleted for SAGA (78). This strain was the most severely defective for telomeric silencing. A *gcn5Δ spt7-400* double mutant (LPY 10258) was also defective for silencing, further supporting the conclusion that the SLIK/SALSA complex was not causing this defect.

FIG. S2. Deletion of *ADA2* does not cause a significant mating defect. WT, *ada2Δ* and control strains containing the single mutants *sir2Δ*, *sir1Δ*, *sas2Δ*, *gcn5Δ*, or *spt8Δ* (upper two panels) and double mutant combinations of these genes (lower panels) are shown as mating patches in *MATa* and *MATα* strains as described in Fig. 2A. Strain numbers are listed in order of their presentation in the panels in Supplemental Table 1.

FIG. S3. Ada2 occupancy at the telomere is not dependent on Sir2 or Sir3. Fold increase in Ada2 occupancy (dark bar) as a function of distance from the end of telomere VIR (in kb) analyzed by ChIP in wild type (LPY 10885), *sir2* Δ (dark grey bar, LPY 11044) and *sir3* Δ (light gray bar, LPY 11049) cells. Occupancy of Ada2 in wild type cells for each location surveyed was assigned a value of 1.0 and fold changes in mutant cells were calculated as in Materials and Methods.

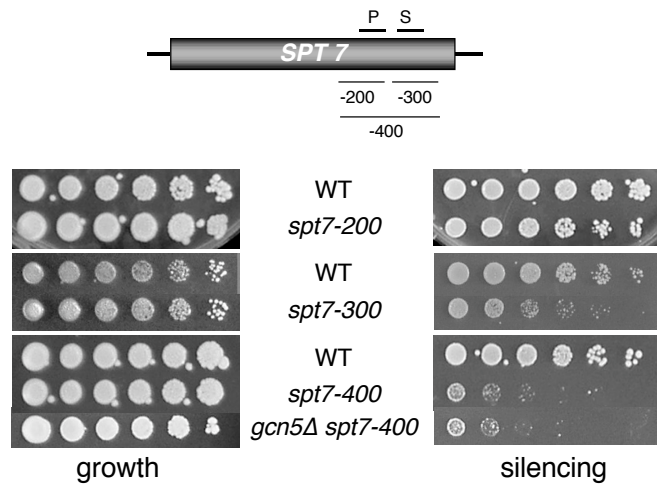
FIG. S4. Ada2 and Sas2 promote telomeric silencing by similar but distinct mechanisms (A) Increased gene dosage of Sir3 selectively rescued the *ada2* Δ telomeric silencing defect. Cells were assayed as described in Fig. 1A. An *ada2* Δ or *sas2* Δ strain was transformed with a high copy plasmid expressing the protein indicated in the middle column, and plated on selective medium (growth) or medium containing 5-FOA (silencing). (B) Sir1 targeted to the telomere rescues the *ada2* Δ and *sas2* Δ silencing defect. Top: diagram of GBD-Sir1 fusion protein targeted to the Gal4 UAS_{GAL} site adjacent to a telomeric *URA3* reporter gene (15). Cells were assayed as described in Fig. 1A. Cells were plated on selective medium (growth) or medium containing 5-FOA (silencing). Strains are labeled according to gene deletion present followed by the plasmid transformed into the strain (GBD or GBD-Sir1). GBD is a control plasmid expressing only the Gal4 DNA binding domain (aa 1-147). Strain numbers are listed in order of their presentation in the panels in Supplemental Table 1.

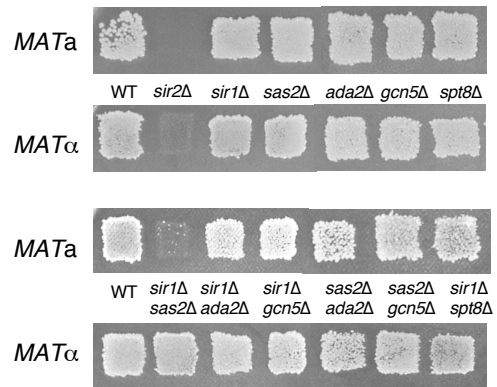
Fig S5. Quantitation of RNA expressed from the subtelomeric genes *HXK1* (15 kb from Tel VIR) and *HXK2* (25 kb from TelVILL) by RT-PCR in glucose-grown wild type (WT, light grey bar, LPY 8726), *ada2* Δ (dark grey bar, LPY 8723) or *sas2* Δ (hatched bar, LPY 8712) strains. RNA abundance in wild type cells was assigned a value of 1.0, from which fold changes in mutant cells was calculated as described in Materials and Methods.

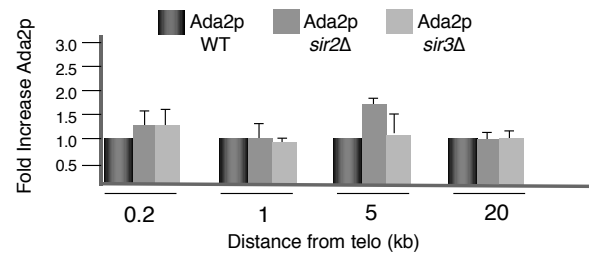
Fig S6. Ada2 telomeric occupancy at Tel IXR mimics that of VIR. Occupancy of Ada2 (dark grey bar, LPY 10885) and Gcn5 (light grey bar, LPY 12169) was calculated as fold increase over untagged samples at Tel IXR under glucose conditions (Glc; upper panel) or under inducing conditions, galactose as the sole carbon source (Gal; lower panel) and plotted as a function of distance from the end of telomere IXR. Primers used are listed in Supp. Table 2.

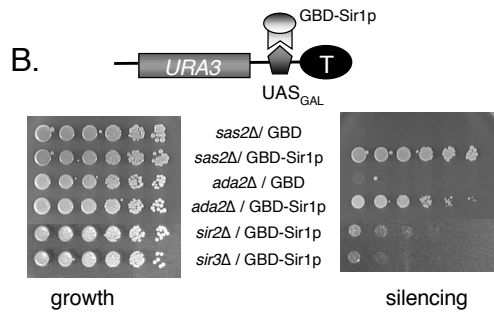
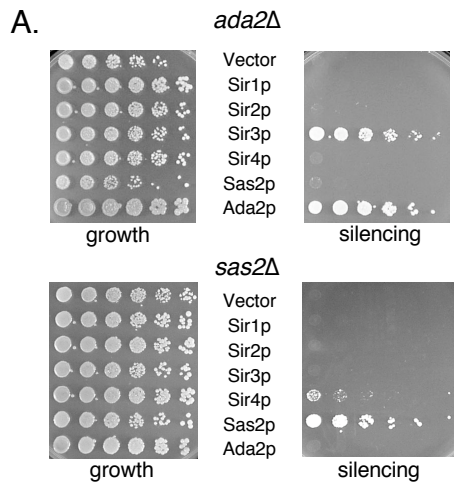
Fig. S7 (A) Telomeric H3 K14 acetylation levels are similar in wild type cells grown in glucose or galactose. Wild type (lighter boxes, LPY 8726) or *sir3Δ* (dark box, LPY 10) strains were grown in glucose (Glc, light grey box) or induced with galactose (Gal, dark grey box) and assayed by ChIP for telomeric H3 K14 acetylation levels. The level of H3 K14 acetylation in wild type cells grown in glucose was assigned a value of 1.0, from which fold changes in telomeric H3 K14 acetylation was calculated for wild type cells grown in glucose or galactose, and for *sir3Δ* cells grown in glucose. Fold changes in H3 K14 acetylation were plotted as a function of distance from the end of telomere VIR as in Fig. 5.

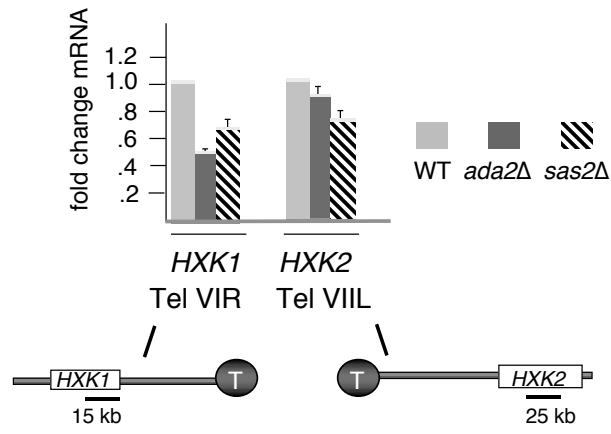
(B) Deletion of *GCN5* does not suppress the galactose induced telomeric silencing defect. Cells were assayed as described in Fig. 1A. Cells were plated on synthetic complete medium containing 2% galactose (growth) or synthetic complete medium containing 2% galactose and 5-FOA (silencing). Note that there is a range of severity in the telomeric silencing defect in wild type cells grown on galactose. The silencing assay shown here illustrates a more severe silencing defect than in Fig. 7E. Although more severe, loss of *GCN5* does not relieve the telomeric silencing defect upon growth in galactose, either as the sole mutation or in combination with an *ada2* null mutation. An *ada2Δ gcn5Δ* control strain (LPY 8833) that is *ura3-* was included as a control for growth on 5FOA medium. Other strains plated to assess telomeric silencing that contain a telomeric *URA3* reporter gene (labeled Tel *URA3* at left) are: wild type (LPY 8037), *ada2Δ* (LPY 8039), *gcn5Δ* (LPY 8719), and *ada2Δ gcn5Δ* (LPY 8805).

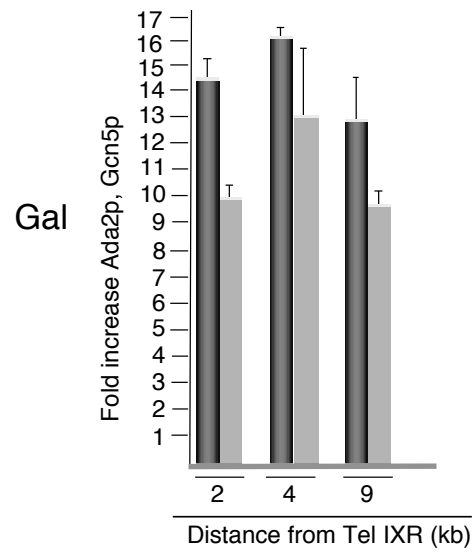
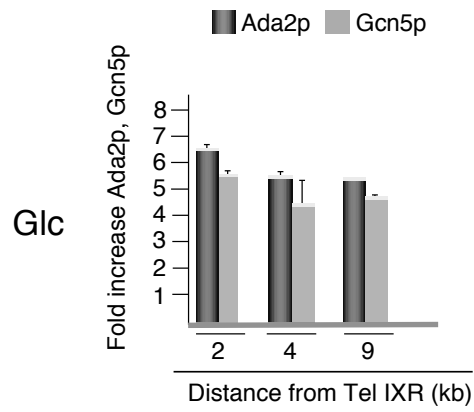




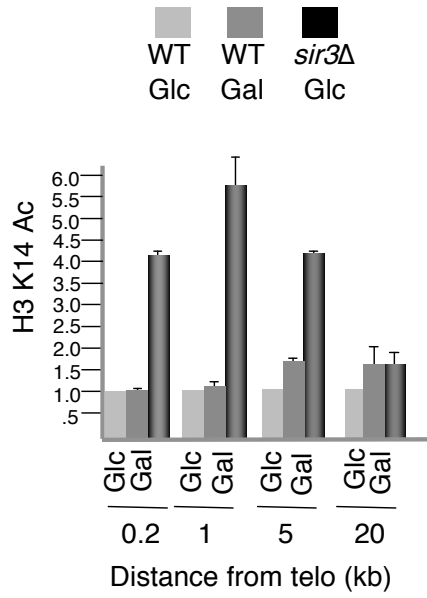




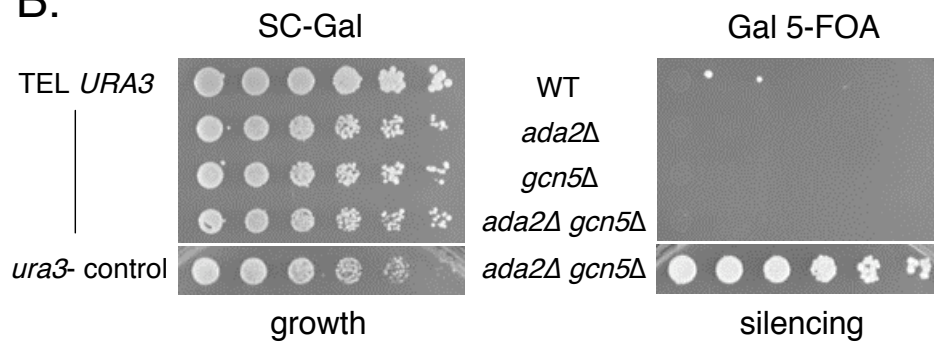




A.



B.



Supplemental Table 1

Strain	Genotype	
LPY 8037	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS GAL -1elo VII-L</i>	this study
LPY 8719	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5::HIS3 adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 8039	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX HML::TRP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	Jacobson and Pillus, 2003
LPY 9957	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS-GAL -Telo VII-L ADE2 Tel V-R</i>	this study
LPY 9966	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX adh4::URA3-UAS-GAL -Telo VII-L ADE2- Tel V-R</i>	this study
LPY 9961	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2 Δ::LEU2 ADE2 Tel V-R</i>	this study
LPY 11806	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5 Δ::HIS3 ADE2 Tel V-R</i>	this study
LPY 10910	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada3 Δ::KANMX adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 5843	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt8 Δ::KANMX adh4::URA3-UAS-GAL -1elo VII-L</i>	Jacobson and Pillus, 2003
LPY 9865	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt3 Δ::KANMX adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 9111	MAT <i>ade2 his3 leu2, trp1 ura3 spt7 Δ::LEU2 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 7880	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2Δ::IHP1 adh4::URA3 -1elo VII-L</i>	this study
LPY 7888	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir3Δ::IHP1 adh4::URA3 -1elo VII-L</i>	this study
LPY 8036	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 4624	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2 Δ::TRP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	Garcia and Pillus, 2002
LPY 8038	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 9122	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::HIS3</i>	this study
LPY 8044	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 ada2 Δ::KANMX</i>	this study
LPY 4638	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::IHP1 adh4::URA3-UAS-GAL -1elo VII-L</i>	Garcia and Pillus, 2002
LPY 8708	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::HIS3</i>	this study
LPY 9123	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 ada2 Δ::KANMX HML::IHP1</i>	this study
LPY 11678	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 rDNA ::ADE2-CAN1</i>	this study
LPY 6926	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 rDNA ::HIS3 rDNA ::ADE2-CAN1</i>	this study
LPY 8282	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5Δ::HIS3 rDNA ::ADE2-CAN1</i>	Ruault and Pillus (unpub)
LPY 11673	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2Δ::KANMX rDNA ::ADE2-CAN1</i>	this study
LPY 8712	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8726	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1</i>	this study
MPC8135/LPY10885	MATα <i>ADA2-18Myc::TRP1</i> from M.P. Cosma (refrozen as LPY 10885) W303 background	Cosma et al, 1999
LPY 9831	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3</i> w/ pLP1536 (HA control vector; 2u, <i>TRP1</i>)	this study
LPY 9832	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3</i> w/ pLP1872 (3XHA-SAS2)CEN, <i>URA3</i>)	this study
LPY 9323	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::TRP1</i> pLP126 (<i>CEN, URA3</i> vector)	this study
LPY 9326	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::TRP1</i> pLP1872(3XHA-SAS2)	this study
LPY 11	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2 Δ::HIS3</i>	this study
LPY 8723	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX</i>	this study
LPY 10	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir3 Δ::TRP1</i>	this study
LPY 11509	MATα <i>hht1 hht1::KANMX hht2 hht2::KANMX hta2 htb2::HPH</i> pLP 1990 (<i>CEN, TRP1</i> plasmid <i>HHT2 hht2 K16A</i>)	Ruault and Pillus (unpub)
Z1466/LPY12169	MATα <i>GCN5-9Myc::TRP1</i> from F. Robert (refrozen as LPY 12169) W303 background	Robert et al, 2004
LPY 4621	MATα <i>9Myc-NET1::LEU2</i> from A. Straight WY53 (refrozen as LPY 4621) W303 background	Garcia and Pillus, 2002
LPY 10274	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas3Δ::HIS3</i>	this study
LPY 12321	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir3Δ::TRP1 gcn5Δ::HIS3</i>	this study
LPY 12323	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir3Δ::IHP1 sas3Δ::HIS3</i>	this study

Supplemental Figures Strain List

LPY 10057	MATα <i>his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt7-200 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 10328	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt7-300 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 10061	MATα <i>his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt7-400 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 10258	MATα <i>ADE2 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5Δ::HIS3 spt7-400 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8036	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 4624	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2 Δ::TRP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	Garcia and Pillus, 2002
LPY 8042	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 HML::TRP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8050	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3</i>	this study
LPY 8038	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8979	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5 Δ::HIS3 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8718	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt8 Δ::KANMX adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8037	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS GAL -Telo VII-L</i>	this study
LPY 4638	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::TRP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	Garcia and Pillus, 2002
LPY 8043	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 HML::IHP1 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 8712	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3 adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 8039	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX HML::IHP1 adh4::URA3-UAS-GAL -1elo VII-L</i>	Jacobson and Pillus, 2003
LPY 8719	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5::HIS3 adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 5843	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 spt8 Δ::KANMX adh4::URA3-UAS-GAL -1elo VII-L</i>	Jacobson and Pillus, 2003
LPY 8036	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 adh4::URA3-UAS-GAL -Telo VII-L</i>	this study
LPY 9122	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::HIS3</i>	this study
LPY 8044	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 ada2 Δ::KANMX</i>	this study
LPY 8809	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 gcn5 Δ::HIS3</i>	this study
LPY 8713	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 ada2 Δ::KANMX sas2 Δ::HIS3</i>	this study
LPY 8981	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5 Δ::HIS3 sas2 Δ::HIS3 HML::TRP1</i>	this study
LPY 8983	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 spt8 Δ::KANMX HML::TRP1 adh4::URA3-UAS-GAL -Tel VII-L</i>	this study
LPY 8708	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 sas2 Δ::HIS3</i>	this study
LPY 9123	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 ada2 Δ::KANMX HML::IHP1</i>	this study
LPY 8810	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 gcn5 Δ::HIS3</i>	this study
LPY 8714	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::HIS3 ada2 Δ::KANMX</i>	this study
LPY 8982	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 gcn5 Δ::HIS3 sas2 Δ::HIS3 adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 8984	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir1 Δ::LEU2 spt8 Δ::KANMX adh4::URA3-UAS-GAL -1elo VII-L</i>	this study
LPY 11044	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir2 Δ::HIS3 ADA2-18Myc::TRP1</i>	this study
LPY 11049	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sir3 Δ::LEU2 ADA2-18Myc::IHP1</i>	this study
LPY 10964	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2Δ::HIS3 ADA2-18Myc::TRP1</i>	this study
LPY 11878	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 271 (2u. <i>TRP1</i> Vector)</i>	this study
LPY 11880	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 118 (2u. <i>IHP1 SIR1</i>)</i>	this study
LPY 11882	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 983 (2u. <i>IHP1 SIR2</i>)</i>	this study
LPY 11884	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 764 (2u. <i>IHP1 SIR3</i>)</i>	this study
LPY 11886	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 762 (2u. <i>IHP1 SIR4</i>)</i>	this study
LPY 11888	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 290 (2u. <i>IHP1 SAS2</i>)</i>	this study
LPY 11890	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1Δ0 ura3-1 ada2 Δ::KANMX adh4::URA3- Telo VII-L pLP 1425 (2u. <i>IHP1 LexAADA2</i>)</i>	this study
LPY 9742	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 271 (2u. <i>IHP1</i> Vect) this study</i>	this study
LPY 9744	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 118 (2u. <i>IHP1 SIR1</i>) this study</i>	this study
LPY 9746	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 983 (2u. <i>IHP1 SIR2</i>) this study</i>	this study
LPY 9748	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 764 (2u. <i>IHP1 SIR3</i>) this study</i>	this study
LPY 9750	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 762 (2u. <i>TRP1 SIR4</i>) this study</i>	this study
LPY 10010	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 290 (2u. <i>TRP1 SAS2</i>) this study</i>	this study
LPY 9754	MATα <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::KANMX adh4::URA3-UAS-GAL Telo VII-L pLP 1425 (2u. <i>TRP1 Lex</i>) this study</i>	this study
LPY 7792	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::IHP1 adh4::URA3-UAS-GAL -1elo VII-L pLP493 (GBD)</i>	this study
LPY 7794	MA1α <i>ade2-1 his3-11, 15 leu2,3-112 trp1-1 ura3-1 sas2 Δ::IHP1 adh4::URA3-UAS-GAL -1elo VII-L pLP409 (GBD-Sir1)</i>	this study

LPY 7797	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 ada2</i> Δ :: <i>KANMX adh4::UHA3-UAS-GAL</i> -1elo VII-L pLP493 (GBD)	this study
LPY 7799	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 ada2</i> Δ :: <i>KANMX adh4::UHA3-UAS-GAL</i> -1elo VII-L pLP409 (GBD-Sir1)	this study
LPY 7886	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 sir2</i> Δ :: <i>IHP1 adh4::UHA3-UAS-GAL</i> -1elo VII-L pLP409 (GBD-Sir1)	this study
LPY 7894	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 sir3</i> Δ :: <i>IHP1 adh4::UHA3-UAS-GAL</i> -1elo VII-L pLP409 (GBD-Sir1)	this study
LPY 1029	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 adh4::UHA3-GAL</i> -1elo VII-L	this study
LPY 5833	MA1 α <i>ade2-1 his3-11,15 leu2,3-112 trp1-1 ura3-1 ada2</i> Δ :: <i>KANMX adh4::UHA3-GAL</i> -1elo VII-L	this study

Supplemental Table 2

Oligonucleotides used in ChIP and RT-PCR analysis:

Tel VIR:

200 bp:

5' AAATGGCAAGGGTAAAAACCAG 3'

5' TCGGATCACTACACACGGAAAT 3'

1 kb AND *YFR057W*:

5' GGACCTACTAGTGTCTATAGTAAGTG 3'

5' CTCTAACATAACTTTGATCCTTACTCG 3'

5 kb:

5' GGCTAGAAAAGCTTCAACATGGCCTTAC 3'

5' CTCCAGCCTGCCTAAGACAAGCTATAG 3'

20 kb:

5' GAATGTAACGTACTATTGGACAAGATATTC 3'

5' GAACCTCCATTAAGATTAGCAAAATTGC 3'

GAL1 core promoter region:

5' ATAGGATATAATGCGATTAGTTTTTTAGCCTT 3'

5' GAAAATGTTTGAAAGTATTAGTTAAAGTGGTTATGCA 3'

rDNA array (25S):

5' TGCGACGTAAGTCAAGGATG 3'

5' CTGGCTTCACCCTATTCAGG 3'

rDNA array (5S):

5' CATGGAGCAGTTTTTTCCGC 3'

5' TACAAGCACTCATGTTTGCCG 3'

ACT1:

5' GGTGGTTCTATCTTGGCTTC 3'

5' ATGGACCACTTTCGTCGTAT 3'

HXK1:

5' GACCTCCGGTTACTACTTGGG 3'

5' CCTCGATTCTTGCTGGGTAGG 3'

HXK2:

5' GCTAGAGCTGCTAGATTGTCCG 3'

5' GTGAGGTTTGAGTCCAGCCG 3'

TEL IXR:

2 kb:

5' GCGGGTACTTTGAGAGCGTGTC 3'

5' GTTTTCTCACAGGCAATCTACGC 3'

4 kb:

5' TACGCCACTCGCTGAATTTG 3'

5' TTGTAAGCCCAGTAAACAGCTTC 3'

9 kb:

5' ATTTGCTACCCTGTCGCTCA 3'

5' GAAGAGTACTGCTTGCATGAGG 3'