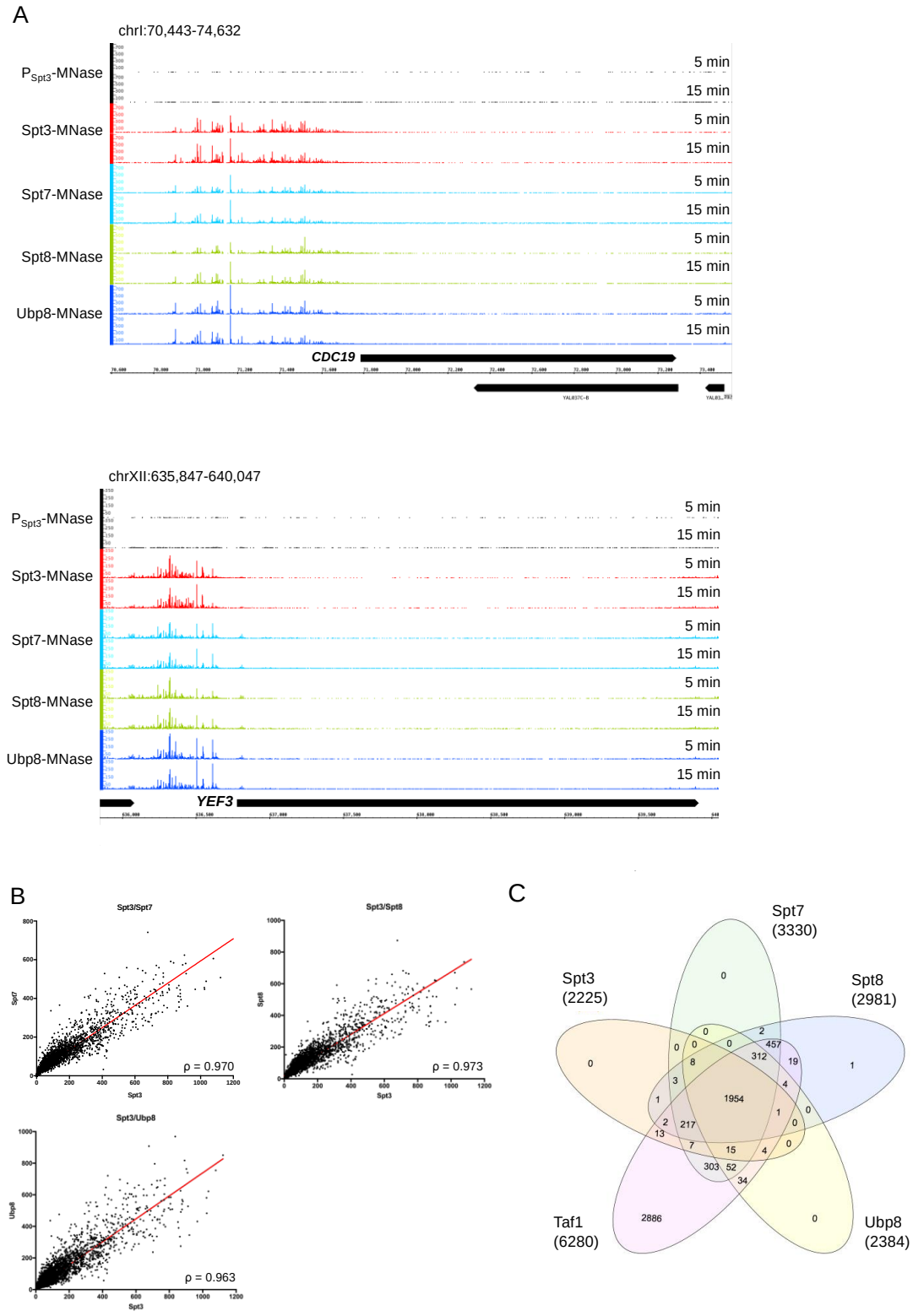
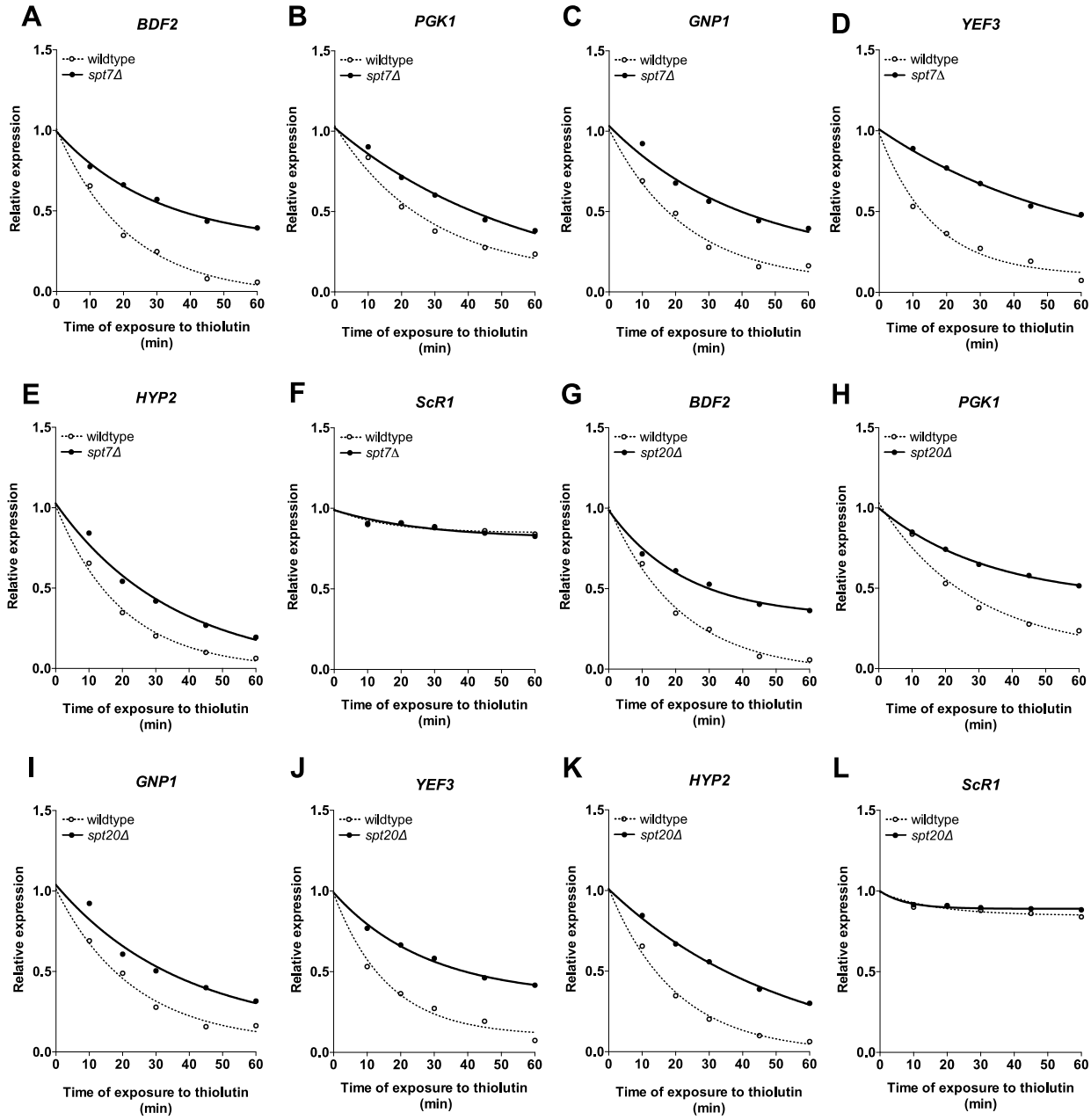


Figure S1. The majority of SAGA-bound UASs is bound by all SAGA-subunits, Related to Figures 1 and 2. (A) ChEC-seq mapping of SAGA at CDC19 (top panel) and YEF3 (bottom panel). Signal tracks showing cleavage of genomic DNA by Spt3- (red), Spt7- (cyan), Spt8- (green), Ubp8-MNase (dark blue), and a PSpt3-MNase control (black) 5 and 15 min after addition of CaCl2. **(B)** Pairwise correlations of SAGA subunits as indicated above the graphs. The Spearman's rank correlation coefficient r for each pairwise comparison is shown. **(C)** More than 99% of genes bound by SAGA are also bound by TFIID. Genes with at least 5% ChEC-seq signal compared to the gene with the highest signal for the respective SAGA- or Taf1-MNase variants were analyzed.



	Reported $t_{1/2}$ (min)	wildtype $t_{1/2}$ (min)	*spt7Δ* $t_{1/2}$ (min)	*spt20Δ* $t_{1/2}$ (min)
BDF2	15	14.8	34.6	31.2
GNP1	15	15.9	35.9	33.9
HYP2	19	19.8	30.2	37.2
PGK1	23	20.1	30.7	33.4
YEF3	12	11.1	41.5	43.2

Figure S2. Loss of SAGA leads to increased mRNA half-lives, Related to Figure 3. (**A-L**) Measurement of RNA half-life using transcription inhibition with thiolutin in *spt7*Δ **(AF)** or *spt20*Δ strains **(G-L)**. Comparison between half-lives reported elsewhere and the ones obtained in this experiments.

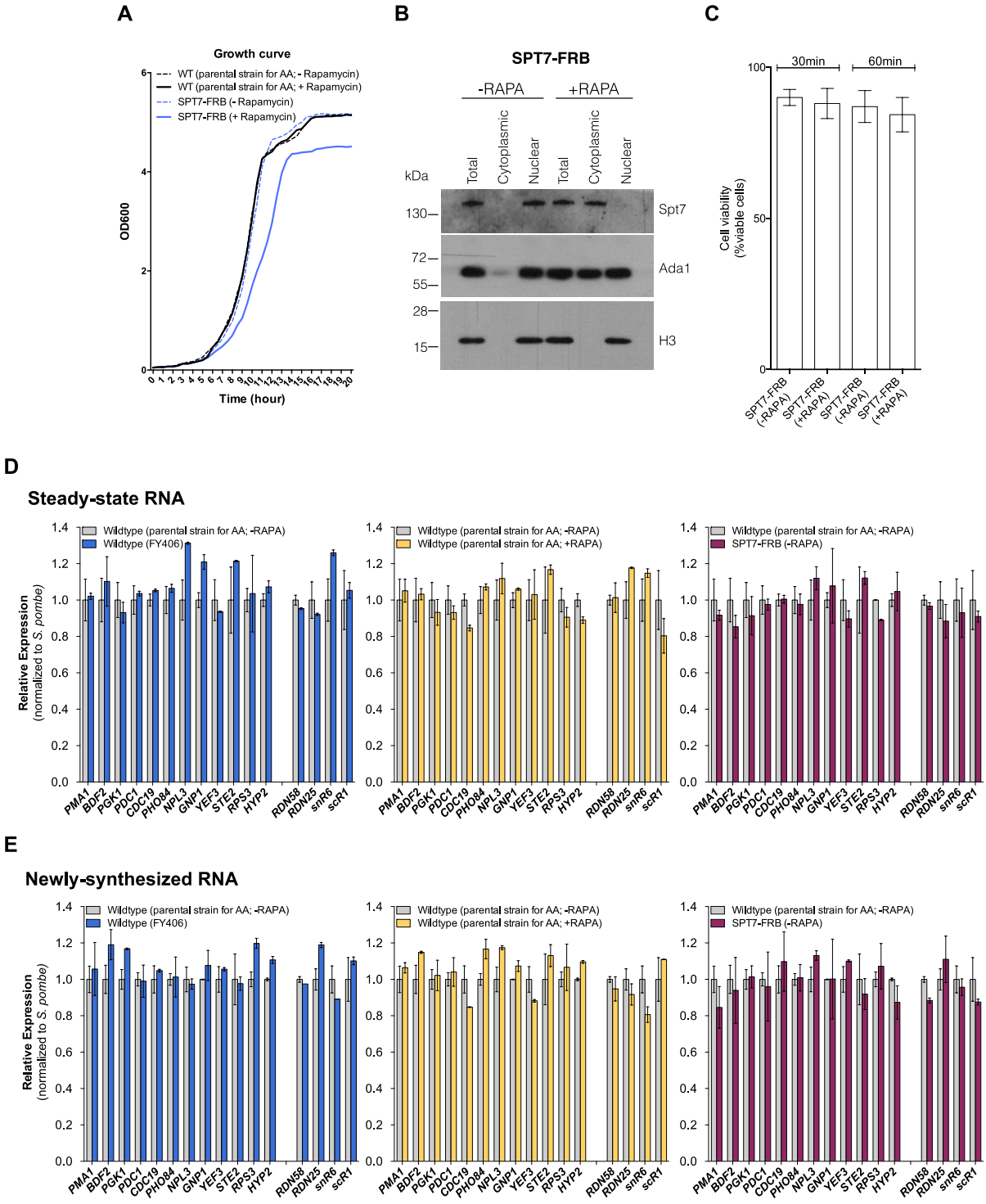


Figure S3. FRB strain characterization and validation of Spt7 nuclear depletion, Related to Figure 5. (A) SPT7-FRB strain does not present a growth phenotype in comparison to the parental strain. Exposure to rapamycin eventually promotes a slower growth phenotype, as observed for the corresponding constitutive deletion strain. **(B)** Cell fraction depicting efficient nuclear depletion of Spt7 upon exposure to rapamycin. **(C)** Upon 30 min of exposure to rapamycin viability of cells in log-phase is not affected, in comparison to its counterpart with vehicle only. **(D-E)** Fusion of FRB domain to Spt7 does not affect RNA Pol II transcription by itself, both at the steady-state **(D)** or newly-synthesized RNA **(E)** levels. Expression values (mean ± SD of three independent experiments) were normalized to spiked-in *S. pombe* signal.

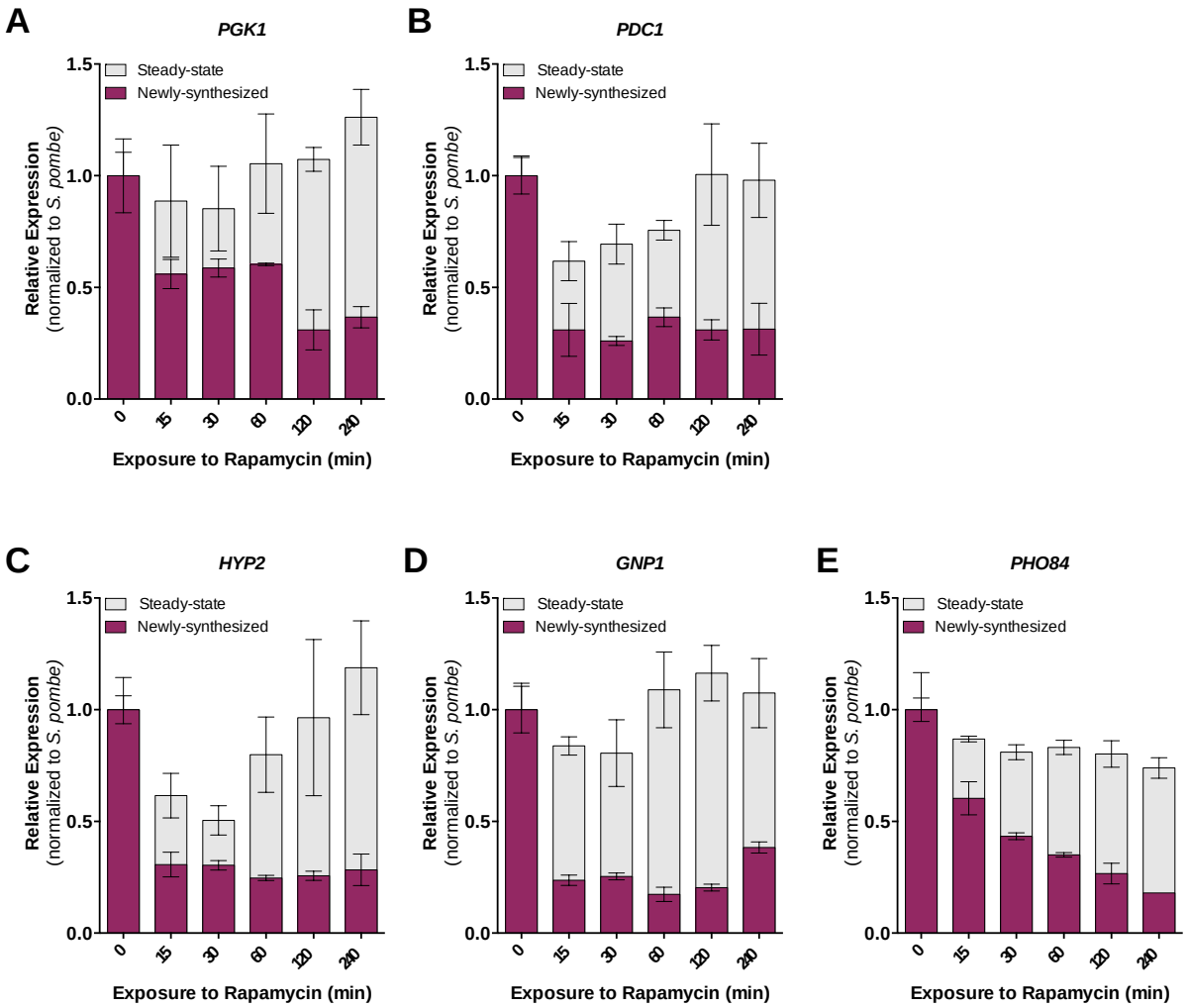


Figure S4. Nuclear depletion of Spt7 decreased transcription of both SAGA- and TFIID-dominated genes, Related to Figure 5. (**A-E**) Time course analysis of changes in steady-state and newly- synthesized RNA for SAGA-dominated genes **(A, B)**, TFIID-dominated genes **(C, D)** and a SAGA- and TFIID-dominated gene **(E)** upon Spt7 nuclear depletion. Expression values (mean ± SD of three independent experiments) were normalized to spiked-in *S. pombe* signal and set to 1 in the untreated sample.

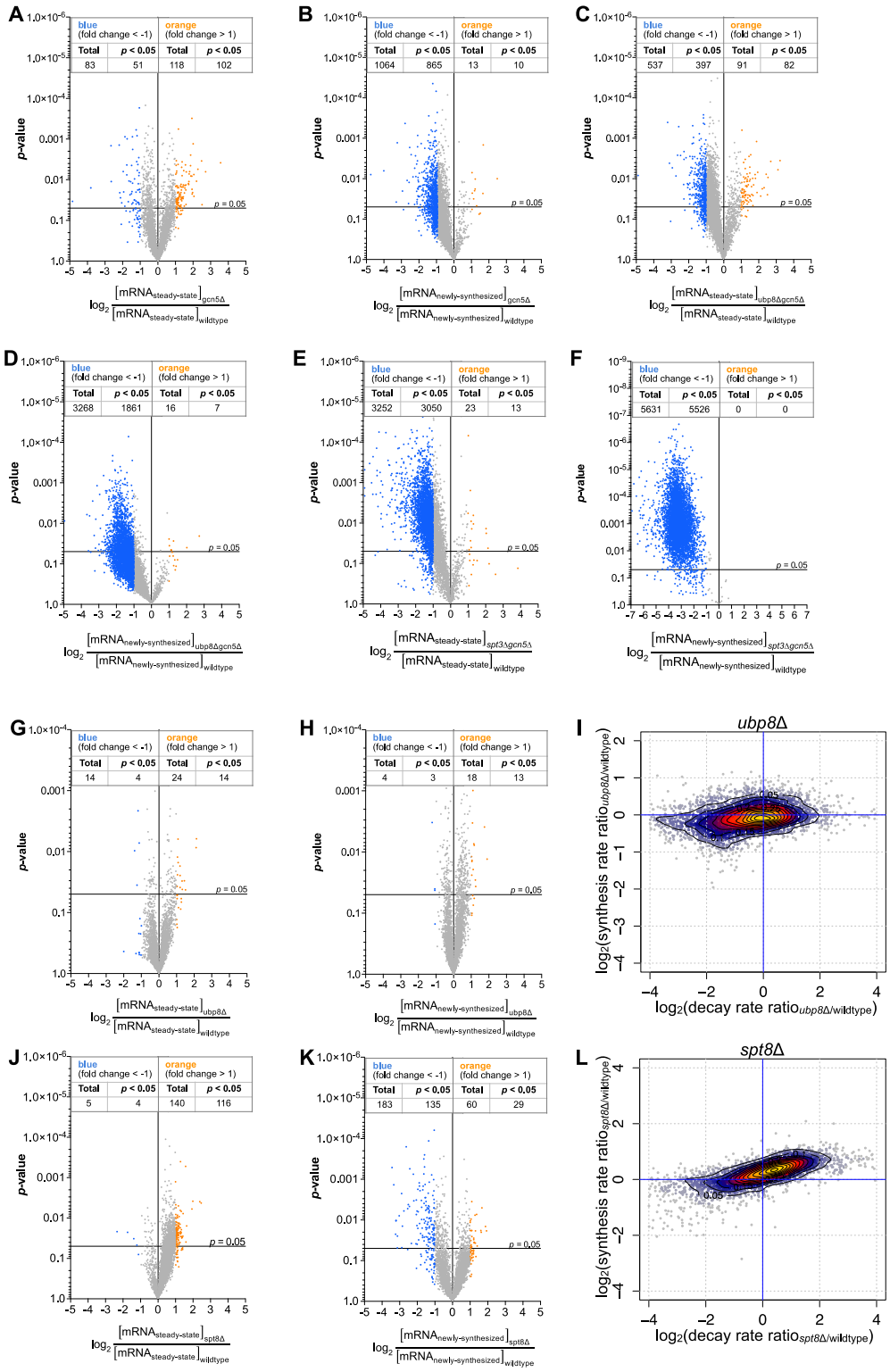


Figure S5. cDTA analysis for several SAGA mutants, Related to Figure 6. (**A-F, G-H, J-K**) Volcano plots showing changes in steady-state (A, C, E, G and J) and newly-synthesized mRNA levels **(B, D, F, H and I)** between mutant and wild-type *S. cerevisiae* cells relative to their significance (*p*-value). Fold changes (FC) were calculated as the log2 of the ratio of the expression value of each gene after normalization to *S. pombe* signal in the *gcn5*Δ **(A, B)**, *ubp8*Δ*gcn5*Δ **(C, D)**, *spt3*Δ*gcn5*Δ **(E, F)**, *ubp8*Δ **(G, H)** and *spt8*Δ **(J, K)** strains versus the expression value of the same gene in wild-type *S. cerevisiae*. **(I and L)** For all analyzed genes, changes in synthesis rates were plotted against the changes in mRNA decay rates. Changes were calculated as the Log2 of the ratio between *ubp8*Δ **(I)** or *spt8*Δ **(L)** and wild-type. 90% of genes are contained within the outer contour. Yellow and red dots correspond to 60% of genes. For each strain, results were obtained from at least two independent biological replicates.

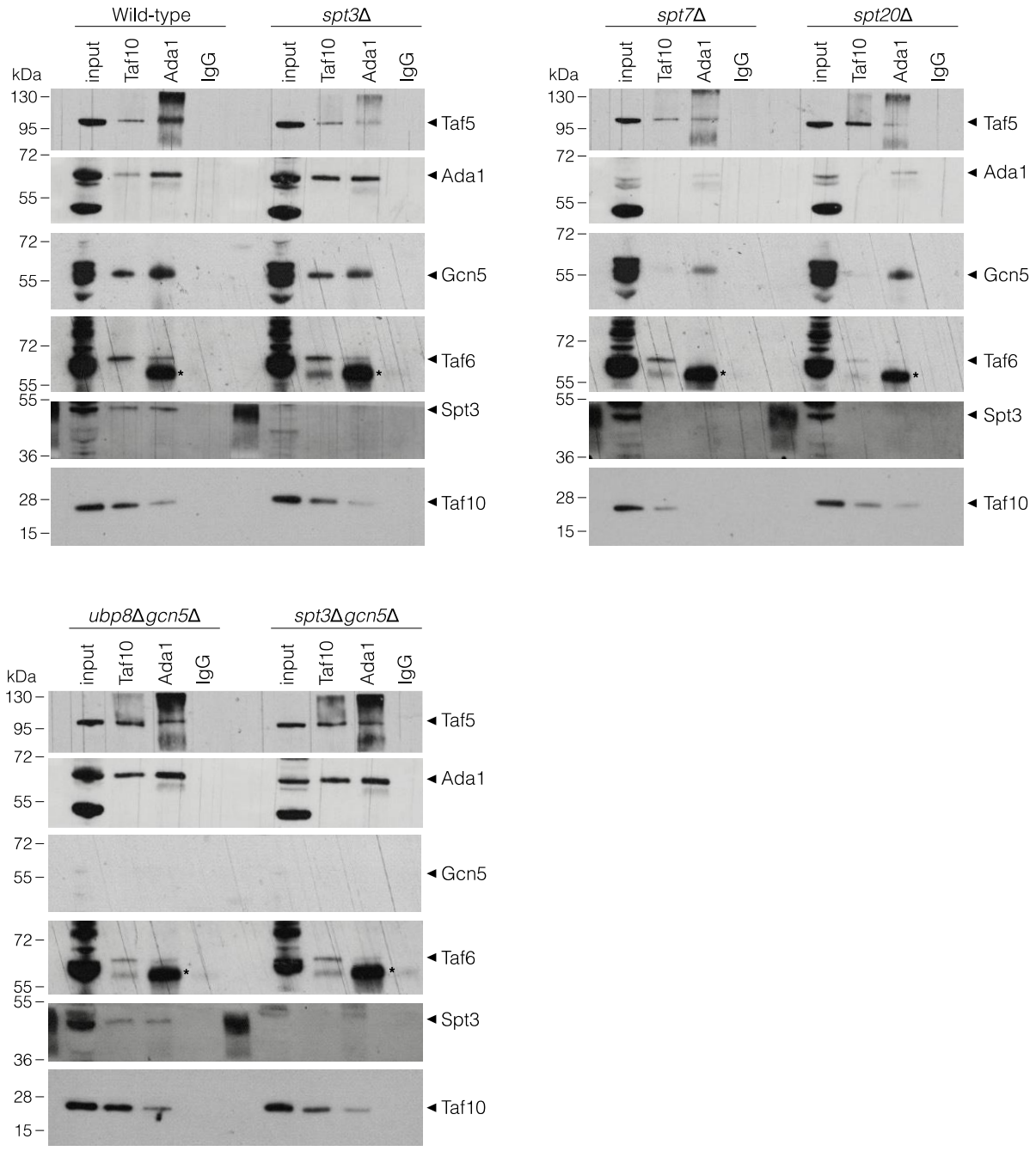
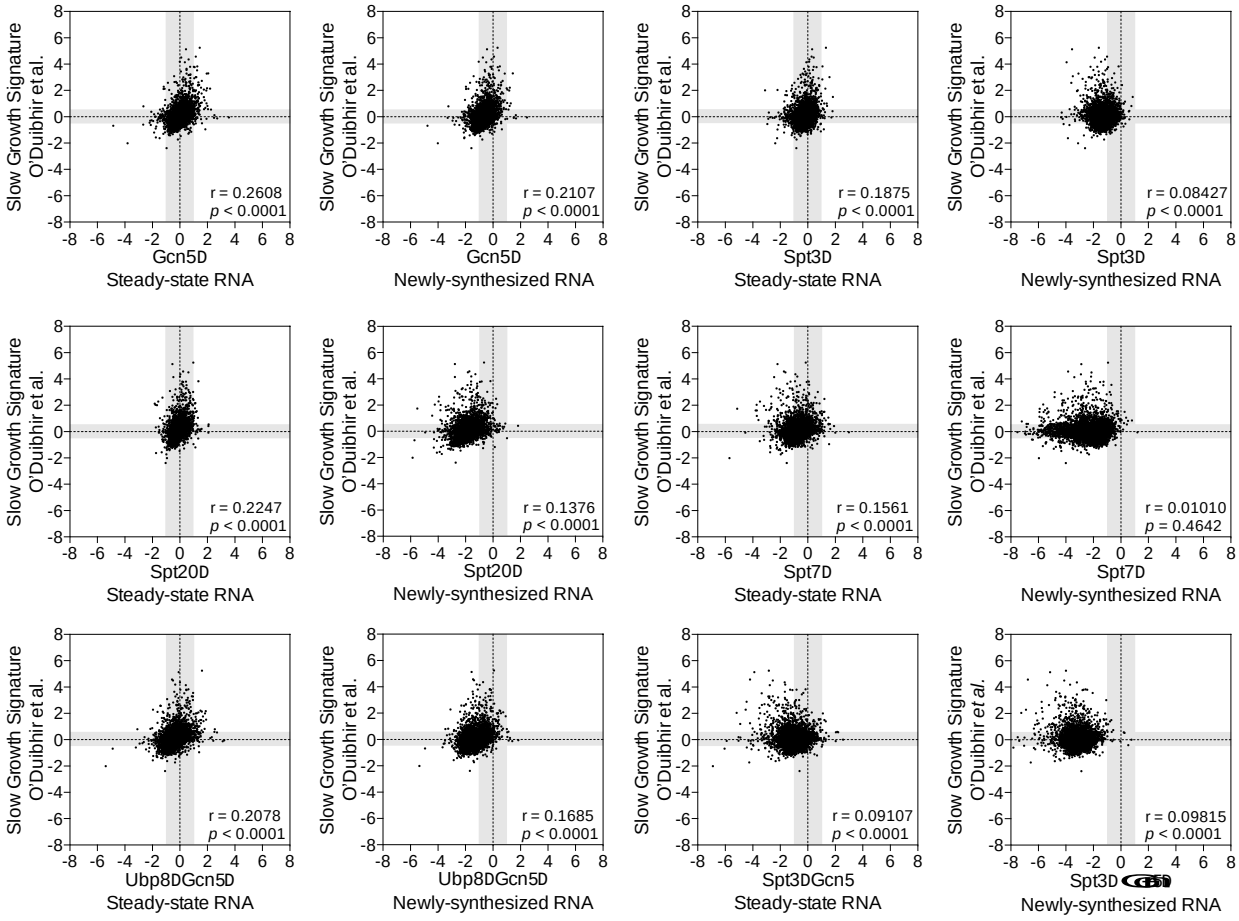


Figure S6. SAGA complex characterization upon deletion of one or more subunits, Related to Figure 6. Upon deletion of *spt3*Δ, *spt7*Δ, *spt20*Δ, *ubp8*Δ*gcn5*Δ and *spt3*Δ*gcn5*Δ SAGA purification was performed by immunoprecipitation of two subunits (Taf10 and Ada1). Eluates were separated by SDS-PAGE and shown are quantitative Western blot analyses of the IP blotted against Taf5, Taf6, Taf10, Ada1, Spt3 and Gcn5.



Steady-state

Wildtype	*gcn5*Δ	*spt3*Δ	*spt7*Δ	*spt20*Δ	*ubp8*Δ*gcn5*Δ	*spt3*Δ*gcn5*Δ
-0.1728	0.2608	0.1875	0.1561	0.2247	0.2078	0.09107

Newly-synthesized

Wildtype	*gcn5*Δ	*spt3*Δ	*spt7*Δ	*spt20*Δ	*ubp8*Δ*gcn5*Δ	*spt3*Δ*gcn5*Δ
-0.1107	0.2107	0.08427	0.0101	0.1376	0.1685	0.09815

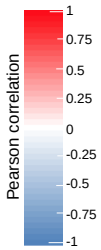


Figure S7. Transcriptional changes observed in SAGA mutants do not correlate with the slow growth phenotype gene expression signature, Related to Figure 6. Transcriptional profiles for SAGA mutants were compared with the slow-growth transcriptional signature obtained elsewhere. The shaded regions on the scatter plots correspond to the threshold applied for each of the studies as a cut-off for either up- or down-regulation. The color code of the tables indicates the degree of correlation between the results obtained in this work and the slow-growth signature (red indicates positive correlation and blue indicates negative correlation).

Table S1. Genotypes of the yeast strains used in this study, Related to STAR Methods.

Name	Genotype	Approach	Source
SGY95	ade2Δ::hisG his3Δ200 leu2Δ0 lys2Δ0 met15Δ0 trp1Δ63 ura3Δ0 SPT3-3FLAGMNase(83-231)-kanMX6	ChEC-seq	This study
SGY96	ade2Δ::hisG his3Δ200 leu2Δ0 lys2Δ0 met15Δ0 trp1Δ63 ura3Δ0 SPT7-3FLAGMNase(83-231)-kanMX6	ChEC-seq	This study
SGY98	ade2Δ::hisG his3Δ200 leu2Δ0 lys2Δ0 met15Δ0 trp1Δ63 ura3Δ0 SPT8-3FLAGMNase(83-231)-kanMX6	ChEC-seq	This study
SGY99	ade2Δ::hisG his3Δ200 leu2Δ0 lys2Δ0 met15Δ0 trp1Δ63 ura3Δ0 UBP8-3FLAGMNase(83-231)-kanMX6	ChEC-seq	This study
FY406	MATa (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pSAB6-(HTA1-HTB1, URA3)]	cDTA	Hirschhorn et.al., 1995
WT yH2B	MATa (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA, mRNA half-life	Bonnet *et al*., 2014
FY406 ubp8Δ- hH2B	MATa ubp8Δ::KANMX4 (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2 128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	Bonnet *et al*., 2014
FY406 gcn5Δ	MATa gcn5Δ::HPH (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	Bonnet *et al*., 2014
FY406 spt7Δ	MATa spt7Δ::KAN MX4(hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA, mRNA half-life	Bonnet *et al*., 2014
FY406 spt20Δ	MATa spt20Δ::HPH (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA, mRNA half-life	Bonnet *et al*., 2014
FY406 ubp8Δgcn5Δ	MATa ubp8Δ::KANMX6;gcn5Δ::HPH (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	This study
FY406 spt3Δ	MATa spt3Δ::KANMX6 (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	This study

FY406 spt8Δ	MATa spt8Δ::KANMX6 (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	This study
FY406 spt3Δgcn5Δ	MATa spt3Δ::KANMX6;gcn5Δ::HPH (hta1-htb1)Δ::LEU2 (hta2-htb2)Δ::TRP1 leu2Δ1 ura3-52 lys2Δ1 lys2-128δ his3Δ200 trp1Δ63 [pRS413-(HTA1-Flag-HTB1,CEN, HIS)]	cDTA	This study
BY4742 SPT7-FRB	MATα; tor1-1; fpr1del; RPL13A-FKBP12-NAT; MET15; his3-1; leu2; lys2; ura3; SPT7-FRB::Hygro	Ancho-away	This study
BY4742	MATα; his3D1; leu2D0; lys2D0; ura3D0	Parental strain, ChIP	Euroscarf
BY4742 3HA-TBP	BY4742; MATα; ura3Δ0; leu2Δ0; his3Δ1; lys2Δ0; URA3::3HA::SPT15	ChIP	This study
BY4742 spt3Δ	BY4742; MATα; ura3Δ0; leu2Δ0; his3Δ1; lys2Δ0; URA3::3HA::SPT15 spt3::KanMX6	ChIP	This study
BY4742 spt3Δ; 3HA-TBP	BY4742; MATα; ura3Δ0; leu2Δ0; his3Δ1; lys2Δ0; URA3::3HA::SPT15 spt3::KanMX6	ChIP	This study

Table S2. List of plasmids used in this study, Related to STAR Methods.

Plasmid	Description	Source
pGZ108	pFA6a-based vector for C-terminal tagging with 3FLAG-MNase; kanMX6 marker	(Zentner et al., 2015)
pFA6a–hphNT1	Gene deletion cassette: marker pAgTEF-hph-tScCYC1, selectable phenotype: hygromycin resistance.	Janke et al., 2004
pFA6a-kanMX6	Plasmid for yeast gene deletion using the kanMX selectable marker conferring kanamycin resistance.	Bähler et al., 1998
YIplac211-3HA-TBP	Yeast integrative plasmide containing 3HA-TBPΔC for N-terminal tagging of TBP; URA3 marker	Eyboulet et al., 2015

Table S3. List of primers used for RT-qPCR and ChIP-qPCR, Related to STAR Methods.

Gene	Name	Sequence	Approach
PMA1	PMA1_Forward	CTCATCAGCCAACTCAAGAAA	RT-qPCR
	PMA1_Reverse	CGTCATCGTCAGAAGATTCA	
BDF2	BDF2_Forward	CTGAAGAAAATGGAGGTTGAAT	RT-qPCR
	BDF2_Reverse	CTTCCTCTTCCTTTCCTTCG	
PGK1	PGK1_Forward	AGCGTGTCTTCATCAGAG	RT-qPCR
	PGK1_Reverse	TGGCAAAGCAGCAACAA	
PDC1	PDC1_Forward	ATTCACCGACACCGAAG	RT-qPCR
	PDC1_Reverse	TTACGCCGCTGATGGTT	
CDC19	CDC19_Forward	CCAAAGACCAACAACCC	RT-qPCR
	CDC19_Reverse	ATTCGTAAGAACCGTGAGAG	
PHO84	PHO84_Forward	GTGTTGGTTTCTTGACAGATTC	RT-qPCR
	PHO84_Reverse	GCATACTACCGTGCCAG	
NPL3	NPL3_Forward	CACCACCGTCAAGAAGGA	RT-qPCR
	NPL3_Reverse	CAAAGATTTCATTCAACTCGGAT	
GNP1	GNP1_Forward	CGTAATGGGAAACATCGTC	RT-qPCR
	GNP1_Reverse	TGGGCGGAATAATGAGGG	
YEF3	YEF3_Forward	AGAAGTTATCTGTTGCCACTG	RT-qPCR
	YEF3_Reverse	TACCATTCAAGAAAGAAGCGAC	
STE2	STE2_Forward	GACTTACGCTCTCACCG	RT-qPCR
	STE2_Reverse	AGAAGCCACAAGAAGGAC	
RPS3	RPS3_Forward	ATTGTTGAACGGTTTGGC	RT-qPCR
	RPS3_Reverse	CCCTTAGCACCAGATTCCATA	
HYP2	HYP2_Forward	TTGAAACTGCTGACGCT	RT-qPCR
	HYP2_Reverse	TCTTGATGACAACGAAACCG	
RDN58	RDN58_Forward	AACGGATCTCTTGGTTCTCG	RT-qPCR
	RDN58_Reverse	GTGCGTTCAAAGATTCGATG	
RDN25	RDN25_Forward	TGGCAGTCAAGCGTTCATAG	RT-qPCR
	RDN25_Reverse	CGCTTACCGAATTCTGCTTC	
snR6	snR6_Forward	CGAAGTAACCCTTCGTGGAC	RT-qPCR
	SNR6_Reverse	TCATCCTTATGCAGGGGAAC	
scR1	scR1_Forward	CCTTTGGGCAAGGGATAGTT	RT-qPCR
	scR1_Reverse	TTTACGACGGAGGAAAGACG	
S. pombe Tubulin	Sp_Tubulin_F	CCGCTGGTGGAAAGTATGTT	RT-qPCR
	Sp_Tubulin_R	GCCAATTCAGCACCTTCAGT	
PMA1	PMA1_P1_Forward	GATGGTGGGTACCGCTTATG	ChIP-qPCR
	PMA1_P1_Reverse	TTGGTGTTATAGGAAAGAAAGAG	
CDC19	CDC19_P1_Forward	CCTTTCCTTCCCATATGATGC	ChIP-qPCR
	CDC19_P1_Reverse	ACTTTGAAAGGGGACCATGA	
PDC1	PDC1_P1_Forward	CAGCTTATGGTGATGGCACA	ChIP-qPCR
	PDC1_P1_Reverse	ACCCAAATCTGATTGCAAGG	
PGK1	PGK1_P1_Forward	GTTCGTTCGATCGTACTGTT	ChIP-qPCR
	PGK1_P1_Reverse	AAACTAAACCACCCCCTTGG	

ILV5	ILV5_P1_Forward	CACCCAGTATTTTCCCTTTCC	ChIP-qPCR
	ILV5_P1_Reverse	GCGGCTTGAGTTCTCAACAT	
STI1	STI1_P1_Forward	CCAAAAGTCTGCTCCCAAAT	ChIP-qPCR
	STI1_P1_Reverse	TGCAGCGTTACCTTGTTGTT	
RPS3	RPS3_P1_Forward	TCCGTAACATCCATACCTTTCC	ChIP-qPCR
	RPS3_P1_Reverse	TACCACTGCCCATGGGAGAAA	
NPL3	NPL3_P1_Forward	TTTTCTAACGGCCTGTGCTT	ChIP-qPCR
	NPL3_P1_Reverse	GCCACCAATTAGAAGGCTACTC	
EFB1	EFB1_P1_Forward	TCAGCACTGAAGAGTCCAACC	ChIP-qPCR
	EFB1_P1_Reverse	TGACTTGTCAGCCAAAGAAGC	
RPS5	RPS5_P1_Forward	CCAAGAAAAGAGACTAGAAAT	ChIP-qPCR
	RPS5_P1_Reverse	TGGAGTAGCCAAGACGACTG	
YEF3	YEF3_P1_Forward	CTTACGCTCTCTTTCTTTCCT	ChIP-qPCR
	YEF3_P1_Reverse	TTCTAGAACCTTAATGGA	
GAL1	GAL1_P1_Forward	ACATTTCCACACCCTGGAAC	ChIP-qPCR
	GAL1_P1_Reverse	TTCTTCGCGAGAACAATTCA	
HMR	HMR_P1_Forward	ACGATCCCCGTCCAAGTTATG	ChIP-qPCR
	HMR_P1_Reverse	CTTCAAAAGGAGTCTTAATTTCCCTG	
HSP42	HSP42_P1_Forward	GGGAGGCCTCTGTGAAGTTA	ChIP-qPCR
	HSP42_P1_Reverse	GCCTGAACGTGTCCCTATGT	