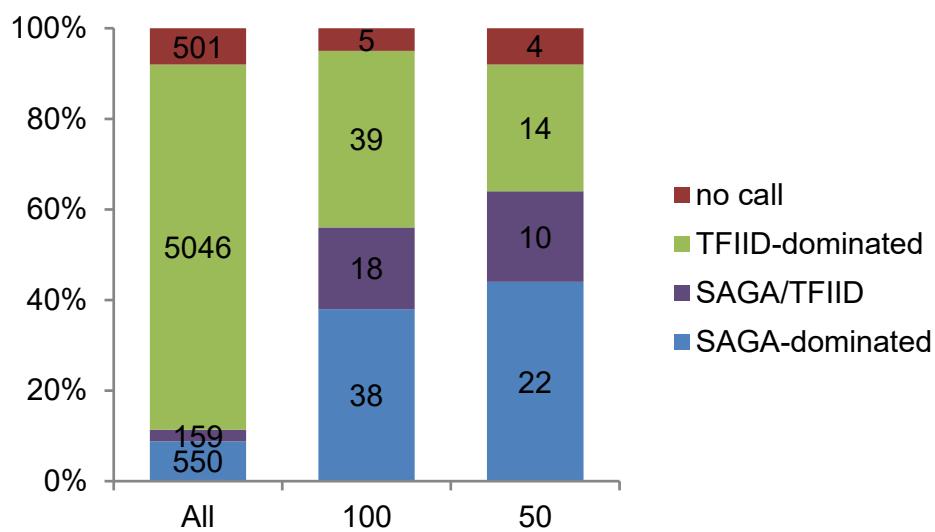


Figure S1

A**B**

Systematic name	Gene name	$[nup170\Delta]/[WT]$	SAGA/TFIID
YBR093C	PHO5	0.1168	SAGA/TFIID
YDR534C	FIT1	0.1767	no call
YOL058W	ARG1	0.1820	TFIID-dominated
YCR021C	HSP30	0.1975	TFIID-dominated
YGL255W	ZRT1	0.2014	SAGA/TFIID
YBR296C	PHO89	0.2268	no call
YOR382W	FIT2	0.2368	TFIID-dominated
YOR383C	FIT3	0.2479	TFIID-dominated
YMR120C	ADE17	0.2684	TFIID-dominated
YDR281C	PHM6	0.2756	SAGA/TFIID
YLR346C	CIS1	0.2834	TFIID-dominated
YAR071W	PHO11	0.2934	TFIID-dominated
YNR060W	FRE4	0.2947	TFIID-dominated
YLR302C	ORF:YLR302C	0.2965	TFIID-dominated
YHL047C	ARN2	0.2994	TFIID-dominated
YJL052W	TDH1	0.3093	TFIID-dominated
YJR150C	DAN1	0.3116	SAGA/TFIID
YOL014W	ORF:YOL014W	0.3171	TFIID-dominated
YOR153W	PDR5	0.3202	TFIID-dominated
YER011W	TIR1	0.3223	SAGA/TFIID
YBR145W	ADH5	0.3232	TFIID-dominated
YHR215W	PHO12	0.3287	SAGA/TFIID
YMR006C	PLB2	0.3291	SAGA/TFIID
YCL030C	HIS4	0.3315	TFIID-dominated
YMR173W-A	ORF:YMR173W-A	0.3334	TFIID-dominated
YMR173W	DDR48	0.3498	TFIID-dominated
YOR385W	ORF:YOR385W	0.3530	TFIID-dominated
YHR136C	SPL2	0.3666	TFIID-dominated
YOL064C	MET22	0.3728	TFIID-dominated
YOL016C	CMK2	0.3735	TFIID-dominated
YJL088W	ARG3	0.3749	TFIID-dominated

Figure S1. The SAGA-dominated genes are overrepresented in genes showing the greatest downregulation in the *nup170Δ* strain. A) Yeast protein encoding genes have been previously categorized based on their regulation by the transcriptional complexes TFIID and SAGA (Huisinga and Pugh, 2004). Plotted here are the percentage of genes in the indicated groups regulated primarily by the SAGA complex (SAGA-dominated, blue), TFIID (TFIID-dominated, green), or both complexes (SAGA/TFIID, purple), or were uncharacterized (no call, red). Three groups of genes are shown: all yeast protein-encoding genes (All) and the top 50 and 100 genes showing the greatest proportional decrease in mRNA levels in the *nup170Δ* strain relative to WT cells (based on data from Van De Vosse et al., 2013). B) The genes whose expression was most repressed in the *nup170Δ* mutant are listed, and their calculated mRNA ratios ($[nup170\Delta] / [WT]$) are shown. Genes are colored in a same way as in (A) except for uncharacterized genes (no call), which are left uncolored.

Figure S2

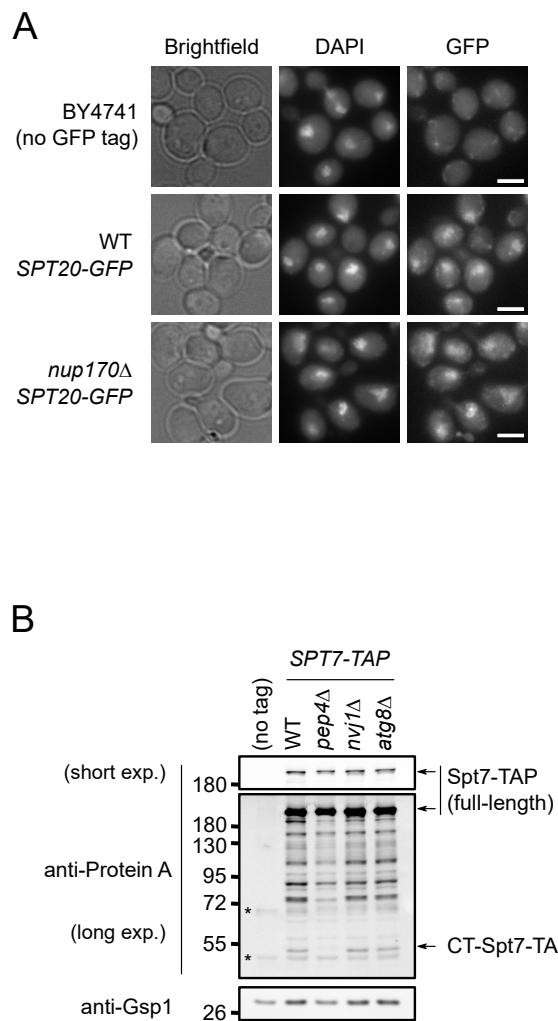


Figure S2. Localization of Spt20-GFP and autophagy-independent Spt7-TAP cleavage. A) The localization of the SAGA/SLIK component SPT20-GFP was examined in WT and the *nup170Δ* mutant. The position of the nucleus was determined by DAPI staining. Cells lacking GFP fusion proteins (BY4741) were also examined to assess autofluorescence signal. Bars: 5 μ m. B) The whole cell extracts were prepared from the indicated strains producing Spt7-TAP, and extracts were analyzed by western blot using anti-Protein A and anti-Gsp1 (loading control) antibodies. The protein extracts from a WT, untagged (no tag) were also analyzed to reveal background signals (asterisks). The position of full-length Spt7-TAP (two exposures are shown) and CT-Spt7-TAP (C-terminal fragment) are indicated. The positions of mass markers are shown in kD.

Figure S3

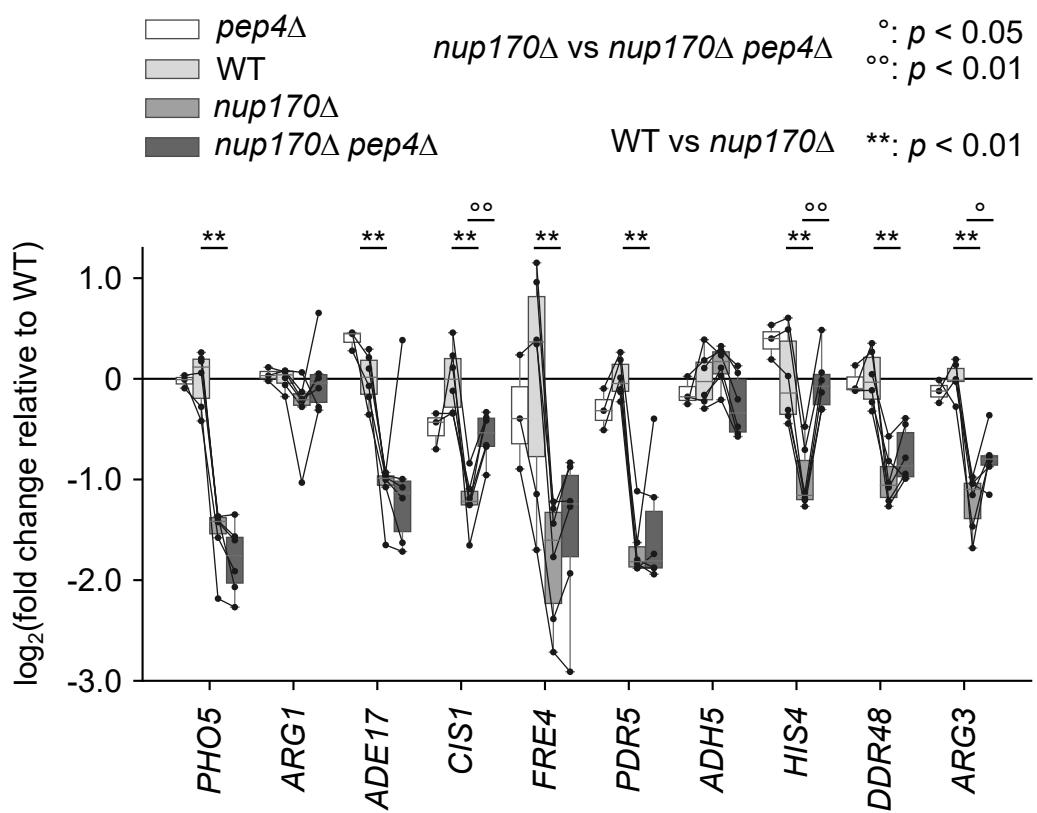


Figure S3. Reduced expression of several genes in the *nup170Δ* mutant is Pep4-dependent.

The same data are presented as in Fig. 6, except that all the observed data points are plotted in this figure. Total RNA was isolated from WT, *nup170Δ*, *pep4Δ* and *nup170Δ pep4Δ* mutant strains, and the mRNA levels of the indicated genes were examined by the RT-qPCR. Levels of mRNA encoded by the indicated genes in each mutant were normalized to amounts in the WT strain. Fold changes in amounts detected in the mutants relative to WT cells were plotted on a log₂ scale. The individual observations are plotted as filled circles ($n = 3$ for *pep4Δ*, $n = 6$ for WT, *nup170Δ*, and *nup170Δ pep4Δ*), and the data points from each of repeated experiments are connected with lines. Boxes represent the first and third quartiles of the data points. Significant differences in mRNA levels between WT and the *nup170Δ* strain, as determined by a two-tailed paired *t*-test, are indicated by asterisks (*). For the genes exhibiting reduced mRNA levels in the *nup170Δ* strain, we further tested their mRNA levels between the *nup170Δ* and the *nup170Δ pep4Δ* strains. Significant differences (two-tailed paired *t*-test) in mRNA levels between the *nup170Δ* and the *nup170Δ pep4Δ* strains are indicated by open circles (°).

Figure S4

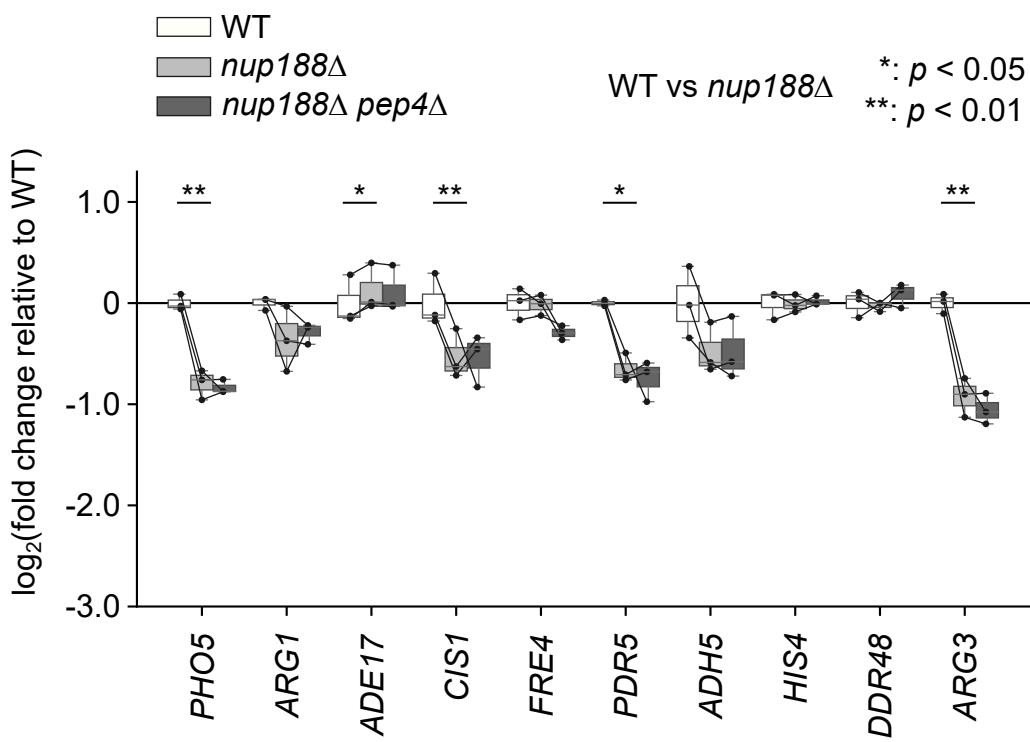


Figure S4. Changes in mRNA levels in the *nup188* Δ and *nup188* Δ *pep4* Δ mutants. Total RNA was isolated from WT, *nup188* Δ , and *nup188* Δ *pep4* Δ strains, and the mRNA levels of the indicated genes were examined by the RT-qPCR. Levels of mRNA encoded by the indicated genes in each mutant were normalized to amounts in the WT strain. Changes in mRNA level detected in the mutants relative to WT cells were plotted. Individual biological replicates are plotted as filled circles ($n = 3$), and the data points from samples analyzed in parallel are connected with lines. Boxes represent the first and third quartiles of the data points. Significant differences in mRNA levels between the WT and the *nup188* Δ strain, as determined by a two-tailed paired *t*-test, are indicated by asterisks.

Table S1. The members of SAGA/SLIK complexes.

SAGA	SLIK	Calculated mass (kD)
Tra1	Tra1	433
Spt7		153
	Spt7ΔC	132
Taf5	Taf5	89
Ngg1	Ngg1	79
Sgf73	Sgf73	73
Spt20	Spt20	68
Spt8		66
	Rtg2	66
Taf12	Taf12	61
Taf6	Taf6	58
Hfi1	Hfi1	54
Ubp8	Ubp8	54
Gcn5	Gcn5	51
Ada2	Ada2	51
Spt3	Spt3	39
Sgf29	Sgf29	29
Taf10	Taf10	23
Taf9	Taf9	17
Sgf11	Sgf11	11
Sus1	Sus1	11

All proposed SAGA/SLIK components and their calculated molecular masses, approximated in kilodaltons, are summarized (Pray-Grant et al., 2002; Spedale et al., 2010).

Table S2. Yeast proteins identified by the mass spectrometry analysis of the protein species highlighted in Figure 3A.

Sample No.	Gene Name	Score	Coverage	# PSMs	~MM [kD]
1	SPT7	35.5	12.3	13	153
2	TRA1	8.9	1.3	4	433
	SPT7	7.6	2.9	3	153
3	SPT7	15.9	6.2	6	153
	TRA1	4.6	0.7	2	433
4	SPT7	51.4	16.1	23	153
	TRA1	13.3	1.8	6	433
5	SGF73	26.9	18.3	16	73
	SPT8	20.7	14.6	7	66
	SPT20	5.7	5.0	2	68
6	SGF73	14.5	6.9	7	73
7	SSA2	22.0	16.1	9	70
	SSB1	8.4	7.8	4	67
8	SGF73	7.8	4.6	3	73

Protein samples derived from the numbered species in Fig. 3A were analyzed by mass spectrometry, and the identified gene products in each sample are summarized. From analysis using the software Proteome Discoverer, the score, the percentage of protein sequence coverage by the identified peptides (Coverage), the total number of peptide spectral matches (PSM), and the calculated molecular mass (MM), approximated in kilodaltons, for each gene product are shown.

Table S3. Peptides derived from Spt7 identified in the mass spectrometry analysis.

Peptide Sequences	position	Sample 1	Sample 2	Sample 3	Sample 4
GNIALNVEK	65-73	N/D	N/D	N/D	1
SDDVSSQTIK	95-104	N/D	N/D	N/D	2
FAEDEDYDDEDENYDEDSTDVK	232-253	2	N/D	1	2
NLDSSISSNIEIDDER	261-276	1	N/D	N/D	1
TNNVEEImGNWNK	294-306	1	N/D	N/D	1
SDLEAATDEQDRENTNDEPDTNQK	341-364	N/D	N/D	1	1
HLLSSIQQK	401-409	N/D	N/D	N/D	1
KSQLGISDYELK	410-421	N/D	N/D	N/D	1
SQLGISDYELK	411-421	1	N/D	N/D	1
IGQEELYEAcEK	440-451	1	1	1	1
NYTEHSTPFLNK	458-469	1	N/D	N/D	1
SmDLNTVLK	485-493	N/D	N/D	N/D	1
SMDLNTVLK	485-493	N/D	N/D	N/D	1
TASSTVTVHENVNKNEIK	634-651	1	N/D	N/D	N/D
LNSDSEAFLK	761-770	N/D	N/D	N/D	1
LNSDSEAFLKNPQR	761-774	N/D	N/D	N/D	1
FDQLFLEYK	778-786	1	N/D	N/D	1
QPNDIELDDTR	837-847	N/D	N/D	N/D	1
MLQNGINK	882-889	N/D	N/D	N/D	1
mNQNITLIQQIR	905-916	1	N/D	1	1
MLQSPLSAQNSR	927-938	1	1	1	1
mLQSPLSAQNSR	927-938	1	1	1	1
KIQPEESDSIVYK	1159-1171	1	N/D	N/D	N/D
VGAENDGDSSLFLR	1285-1298	1	1	N/D	N/D

Peptides derived from Spt7 identified by mass spectrometry analysis are summarized. The identified peptide sequences derived from Spt7 and their amino-acid residue positions in Spt7 are shown in columns 1 and 2. Peptide sequences are shown in the single letter code. The letters with lower case ('c' and 'm') indicate residues modified during the sample preparation for the mass spectrometry analysis. c: carbamidomethyl cysteine, m: oxidized methionine. The numbers of peptide spectrum matches (PSMs) for each sample indicated in Table S2 are shown in columns 3 to 6. N/D: not detected.

Table S4. Yeast strains used in this study.

Strain name	Genotype
BY4741	<i>MATa his3Δ0 leu2Δ0 ura3Δ0 met15Δ0</i>
CPL33	<i>MATa nup170Δ::KanMX</i>
TMY2837	<i>MATa pep4Δ::HphMX</i>
TMY2838	<i>MATa nup170Δ::KanMX pep4Δ::HphMX</i>
nup188D	<i>MATα nup188Δ::KanMX</i>
TMY3186	<i>MATα nup188Δ::KanMX pep4Δ::HphMX</i>
TMY2674-2B	<i>MATa PDR1-V5-HphMX HFI1-HA-HIS3MX</i>
TMY2674-14B	<i>MATa nup170Δ::KanMX PDR1-V5-HphMX HFI1-HA-HIS3MX</i>
TMY2716-6C	<i>MATa BAS2-V5-HphMX HFI1-HA-HIS3MX</i>
TMY2716-5B	<i>MATa nup170Δ::KanMX BAS2-V5-HphMX HFI1-HA-HIS3MX</i>
TMY2836	<i>MATa SPT20-TAP-HIS3MX</i>
TMY2863	<i>MATa nup170Δ::KanMX SPT20-TAP-HIS3MX</i>
TMY2854	<i>MATa SPT7-TAP-HIS3MX</i>
TMY2821	<i>MATa nup170Δ::KanMX SPT7-TAP-HIS3MX</i>
TMY2849	<i>MATa pep4Δ::HphMX SPT7-TAP-HIS3MX</i>
TMY2846	<i>MATa nup170Δ::KanMX pep4Δ::HphMX SPT7-TAP-HIS3MX</i>
TMY3168	<i>MATa SPT20-TAP-HIS3MX SPT8-myc-KanMX RTG2-HA-HphMX</i>
TMY3170	<i>MATa nup170Δ::NatMX SPT20-TAP-HIS3MX SPT8-V5-KanMX RTG2-HA-HphMX</i>
TMY3132	<i>MATa his3::HIS3-P_{GAL1}-GFP-NLS-spt7(1088-1180)-GST-TCYC1</i>
TMY3134	<i>MATa his3::HIS3-P_{GAL1}-GFP-NES-spt7(1088-1180)-GST-TCYC1</i>
TMY3136	<i>MATa nup170Δ::KanMX his3::HIS3-P_{GAL1}-GFP-NLS-spt7(1088-1180)-GST-TCYC1</i>
TMY3138	<i>MATa nup170Δ::KanMX his3::HIS3-P_{GAL1}-GFP-NES-spt7(1088-1180)-GST-TCYC1</i>
TMY3139	<i>MATa pep4Δ::HphMX his3::HIS3-P_{GAL1}-GFP-NLS-spt7(1088-1180)-GST-TCYC1</i>
TMY3140	<i>MATa pep4Δ::HphMX his3::HIS3-P_{GAL1}-GFP-NES-spt7(1088-1180)-GST-TCYC1</i>
TMY2995	<i>MATa nup157Δ::URA3MX SPT20-TAP-HIS3MX</i>
TMY2996	<i>MATa nup188Δ::URA3MX SPT20-TAP-HIS3MX</i>
TMY2997	<i>MATa pom152Δ::URA3MX SPT20-TAP-HIS3MX</i>
TMY2862	<i>MATa pep4Δ::HphMX SPT20-TAP-HIS3MX</i>
TMY3184	<i>MATa nvj1Δ::KanMX SPT7-TAP-HIS3MX</i>
TMY3185	<i>MATa atg8Δ::KanMX SPT7-TAP-HIS3MX</i>
TMY3187	<i>MATa SPT20-GFP-HIS3MX</i>
TMY3190	<i>MATa SPT20-GFP-HIS3MX nup170D::KanMX</i>

Table S5. Oligo nucleotides used in this study.**Oligos for RT-qPCR**

Oligo name	Sequence
TUB2F	TACTAGTGAAGGTATGGACGAATTG
TUB2R	TTCTTCATCATCTTCTACAGTAGCC
ACT1F	CATCCCATTAACTGTAAGAAGAAT
ACT1R	GATCAGTCAATATAGGAGGTTATGG
SUR4-F	TGTTATGGTACTCAGGCTGC
SUR4-R	ACACCAGTAGAAGAACCGGA
ERG11-F	CAGATGATCTGGCTGGACC
ERG11-R	CTTCGGTGGTAGACAC
DPS1-F	ATGGTCGTGGATACGTTGTG
DPS1-R	CGACAAATACGACACCGACT
DED81-F	TACCGATAACCGTAACCACCA
DED81-R	GAATCGACGACATGGACGAA
RPL3-F	CTACCAGCTTCGACAGAAC
RPL3-R	GCTGACTTCTCCAAGCCT
PHO5-F	TCAAATGCACACCACGAGAA
PHO5-R	CATGTCCTGCTTGGACTAC
HIS4-F	TCTAGACCCTCCTTCTTGGC
HIS4-R	TGCGGTGACTATTCAAGTGG
PDR5-F	TATGCGAATCATTGGCGGA
PDR5-R	ACTTCAGCAATGGAGACACG
SNQ2-F	AAGTTGAAGTGTGCGAGGT
SNQ2-R	TGAAGACGATGGATGCAGTG
ARG1-F	CACCATGGAGAATGCCTGAA
ARG1-R	GGGCTTGGTTTCGTAGTA
ADE17-F	ACATGCCAGGGGAGATAAGT
ADE17-R	TGAATTACCAGCAGCAGCA
CIS1-F	ACTCCTGCATTCCGCTTCC
CIS1-R	CAGAGTGGTAGCATGTCCA
FRE4-F	CAAAGGCCACCCAGTAAA
FRE4-R	ATAGCGGACCCATTGAACCC
ADH5-F	CGAAGGTGCTGGTGTGTTG
ADH5-R	GTGTGAAGCCAGTACCATCCA
DDR48-F	TTCTGGCAATAACAATCAAGGCG
DDR48-R	TCTGCTCTCCGATTTGCT
ARG3-F	GGTGCCCAACCGATGTTTT
ARG3-R	TCATGTTGTTCACACGGGC

Oligos for ChIP-qPCR

Oligo name	Sequence
RPL3-2F	TGTCTCTTCGTGCTTCCGT
RPL3-2R	CTAAATGACCGTGACGTGGT
RPL3-3F	CTACCAGCTTCGACAGAACCC
RPL3-3R	GCTGACTTCTTCAAAGCCT
DPS1-2F	CAGGTTCTGCGGATTCTCA
DPS1-2R	GGATGAAGCAAGACAACCGA
DPS1-3F	ATGGTCGTGGATACGTTGTG
DPS1-3R	CGACAAATACGACACCGACT
HIS4-1F	AGAATGCCCATCACAATC
HIS4-1R	GAGTCACTGTGCATGGGTTT
HIS4-2F	GCTCGAGCCATCCAAAAGTA
HIS4-2R	TTCACCTCCGATGTGTGTTG
HIS4-3F	TAGAACAAATCGGCAGCCTC
HIS4-3R	GGTTTGGTGGGGCTAGAACATC
HIS4-4F	TCTAGACCCTCCTTCTTGGC
HIS4-4R	TGCGGTGACTATTCAAGTGG
PDR5-1F	GATCACGATTCAGCACCCCT
PDR5-1R	TACCACGGCGTAGAACAGAGTT
PDR5-2F	TCTACGCCGTGGTACGATA
PDR5-2R	GTTTGCAACTTGCCTGACT
PDR5-3F	TATGCGAATCATTGGCGGA
PDR5-3R	ACTTCAGCAATGGAGACACG
PDR5-4F	TATGACTACCCCAAGTGCCA
PDR5-4R	CGTCTACGTTAGCAACACCA
SNQ2-1F	ACCTTCACGCCAGACTATGT
SNQ2-1R	ATGGGCGGACATTTAGTCAT
SNQ2-2F	ATTGTATTCCCTGCAACCCCC
SNQ2-2R	GCATAAAAAGTGGTGAGGCG
ChrV-1F	TACTGACCTCCGAAGCTAGG
ChrV-1R	CAGGACTTTAGTCAGGACCG
ChrV-2F	TCTGCATTGTTCCAACGAA
ChrV-2R	AAGGGACAGGGCACTAAAACG
ChrII-1F	AATTACGGAAGCGCCAATGA
ChrII-1R	AACAAAAACGCGGAAGCTCT

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