

Table S1. *S. cerevisiae* strains

Strain ID	Genotype	Source
BMA41 wild-type	<i>MATa ade2-1 ura3-1 leu2-3,112 his3-11,15 trp1Δ can1-100</i>	[1]
BMA41 <i>rrp6Δ</i>	BMA41 with <i>rrp6Δ::KanMX4</i>	[2]
BMA41 Rrp6-Y361A	BMA41 with <i>rrp6Y361A</i>	[3]
BMA41 <i>rrp47Δ</i>	BMA41 with <i>rrp47Δ::KanMX4</i>	[3]
BMA41 <i>trf4Δ</i>	BMA41 with <i>trf4Δ::KanMX4</i>	[3]
BMA41 <i>trf5Δ</i>	BMA41 with <i>trf5Δ::KanMX4</i>	[3]
BMA41 <i>mpp6Δ</i>	BMA41 with <i>mpp6Δ::KanMX4</i>	[3]
BMA41 <i>air1Δ</i>	BMA41 with <i>air1Δ::KanMX4</i>	[3]
BMA41 <i>air2Δ</i>	BMA41 with <i>air2Δ::KanMX4</i>	[3]
BMA41 <i>air1Δ air2Δ</i>	<i>MATa ade2-1 ura3-1 leu2-3,112 his3-11,15 trp1Δ can1-100</i> <i>air1Δ::HIS3 air2Δ::KanMX4</i>	[2]
BMA41 <i>TEF1-PHO5AS</i>	BMA41 with <i>TEF1-PHO5AS::KanMX4</i>	This work
<i>dis3Δ</i> + pDis3	<i>MATa ade2-1 ura3-1 leu2-3,112 his3-11,15 trp1-1 can1-100</i> <i>dis3Δ::KanMX4 [pBS3269-DIS3, LEU2]</i>	[3]
<i>dis3Δ</i> + pDis3-endo ⁻	<i>MATa ade2-1 ura3-1 leu2-3,112 his3-11,15 trp1-1 can1-100</i> <i>dis3Δ::KanMX4 [pBS3278-dis3D171N, LEU2]</i>	[3]
<i>dis3Δ</i> + pDis3-exo ⁻	<i>MATa ade2-1 ura3-1 leu2-3,112 his3-11,15 trp1-1 can1-100</i> <i>dis3Δ::KanMX4 [pBS3270-dis3D551N, LEU2]</i>	[3]
BY4741 wild-type	<i>MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</i>	[4]
BY4741 <i>rrp6Δ</i>	BY4741 with <i>rrp6Δ::KanMX4</i>	[5]
BY4741 <i>gcn5Δ</i>	BY4741 with <i>gcn5Δ::KanMX4</i>	EUROSCARF
BY4741 <i>gcn5Δ rrp6Δ</i>	BY4741 with <i>gcn5Δ::KanMX4 rrp6Δ::hph</i>	This work
LPY917 wild-type	<i>MATa ade2-101 his3Δ-200 leu2Δ1 trp1Δ1 lys2-801 TELadh4::URA3</i>	[6]
LPY917 <i>rrp6Δ</i>	LPY917 with <i>rrp6Δ::KanMX4</i>	This work
Nrd1-AA	<i>MATalpha tor1-1 fpr1::NAT RPL13A-2xFKB12::TRP1 Nrd1-FRB::kanMX6</i>	[7]
FSY1742 wild-type	<i>MATa ade2 his3 leu2 trp1 ura3</i>	[8]
FSY3117 <i>rrp6Δ</i>	FSY1742 with <i>rrp6Δ::KANr</i>	[8]
FSY3383 <i>rpd3Δ</i>	FSY1742 with <i>rpd3Δ::TRP1</i>	[7]
FSY3384 <i>rpd3Δ rrp6Δ</i>	FSY1742 with <i>rpd3Δ::TRP1 rrp6Δ::KANr</i>	[7]
Sth1-AA	<i>MATalpha tor1-1 fpr1::NAT RPL13A-2xFKB12::TRP1 Sth1-FRB::kanMX6</i>	[9]
Sth1-AA <i>gcn5Δ</i>	Sth1-AA with <i>gcn5Δ::SpHIS5</i>	This work
Sth1-AA <i>rrp6Δ</i>	Sth1-AA with <i>rrp6Δ::KanMX4</i>	This work
FSY6857	<i>MATa bar1Δ::hisG BrdU-Inc::HIS3</i>	This work
FSY5439	<i>MATα trp1::TRP1</i>	This work
FSY9286	<i>MATa bar1Δ::hisG BrdU-Inc::HIS3 pho5Δ::URA3</i>	This work

FSY9287	<i>MATα trp1::TRP1 pho5Δ::URA3</i>	This work
FSY9288	<i>MATα bar1Δ::hisG BrdU-Inc::HIS3 PHO5-Sense-Terminator</i>	This work
FSY9291	<i>MATα trp1::TRP1 PHO5-Antisense-Terminator</i>	This work

REFERENCES

1. Baudin-Baillieu A, Tollervey D, Cullin C, Lacroute F. Functional analysis of Rrp7p, an essential yeast protein involved in pre-rRNA processing and ribosome assembly. *Mol Cell Biol.* 1997;17: 5023–5032. doi:10.1128/mcb.17.9.5023
2. Mosrin-Huaman C, Honorine R, Rahmouni AR. Expression of bacterial Rho factor in yeast identifies new factors involved in the functional interplay between transcription and mRNP biogenesis. *Mol Cell Biol.* 2009;29: 4033–4044. doi:10.1128/MCB.00272-09
3. Stuparevic I, Mosrin-Huaman C, Hervouet-Coste N, Remenaric M, Rahmouni AR. Cotranscriptional recruitment of RNA exosome cofactors Rrp47p and Mpp6p and two distinct Trf-Air-Mtr4 polyadenylation (TRAMP) complexes assists the exonuclease Rrp6p in the targeting and degradation of an aberrant messenger ribonucleoprotein particle (mRNP) in yeast. *J Biol Chem.* 2013;288: 31816–31829. doi:10.1074/jbc.M113.491290
4. Brachmann CB, Davies A, Cost GJ, Caputo E, Li J, Hieter P, et al. Designer deletion strains derived from *Saccharomyces cerevisiae* S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast.* 1998;14: 115–132. doi:10.1002/(SICI)1097-0061(19980130)14:2<115::AID-YEA204>3.0.CO;2-2
5. Novačić A, Beauvais V, Oskomić M, Štrbac L, Dantec A Le, Rahmouni AR, et al. Yeast RNA exosome activity is necessary for maintaining cell wall stability through proper protein glycosylation. *Mol Biol Cell.* 2021;32: 363–375. doi:10.1091/mbc.e20-08-0544-t
6. Nislow C, Ray E, Pillus L. SET1, a yeast member of the Trithorax family, functions in transcriptional silencing and diverse cellular processes. *Mol Biol Cell.* 1997;8: 2421–2436. doi:10.1091/mbc.8.12.2421
7. Castelnovo M, Zaugg JB, Guffanti E, Maffioletti A, Camblong J, Xu Z, et al. Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast. *Nucleic Acids Res.* 2014;42: 4348–4362. doi:10.1093/nar/gku100
8. Camblong J, Iglesias N, Fickentscher C, Dieppois G, Stutz F. Antisense RNA Stabilization Induces Transcriptional Gene Silencing via Histone Deacetylation in *S. cerevisiae*. *Cell.* 2007;131: 706–717. doi:10.1016/j.cell.2007.09.014
9. Gill JK, Maffioletti A, García-Molinero V, Stutz F, Soudet J. Fine Chromatin-Driven Mechanism of Transcription Interference by Antisense Noncoding Transcription. *Cell Rep.* 2020;31. doi:10.1016/j.celrep.2020.107612