

Supplementary Material

Non-Coding, RNAPII-Dependent Transcription at the Promoters of rRNA Genes Regulates Their Chromatin State in *S. cerevisiae*

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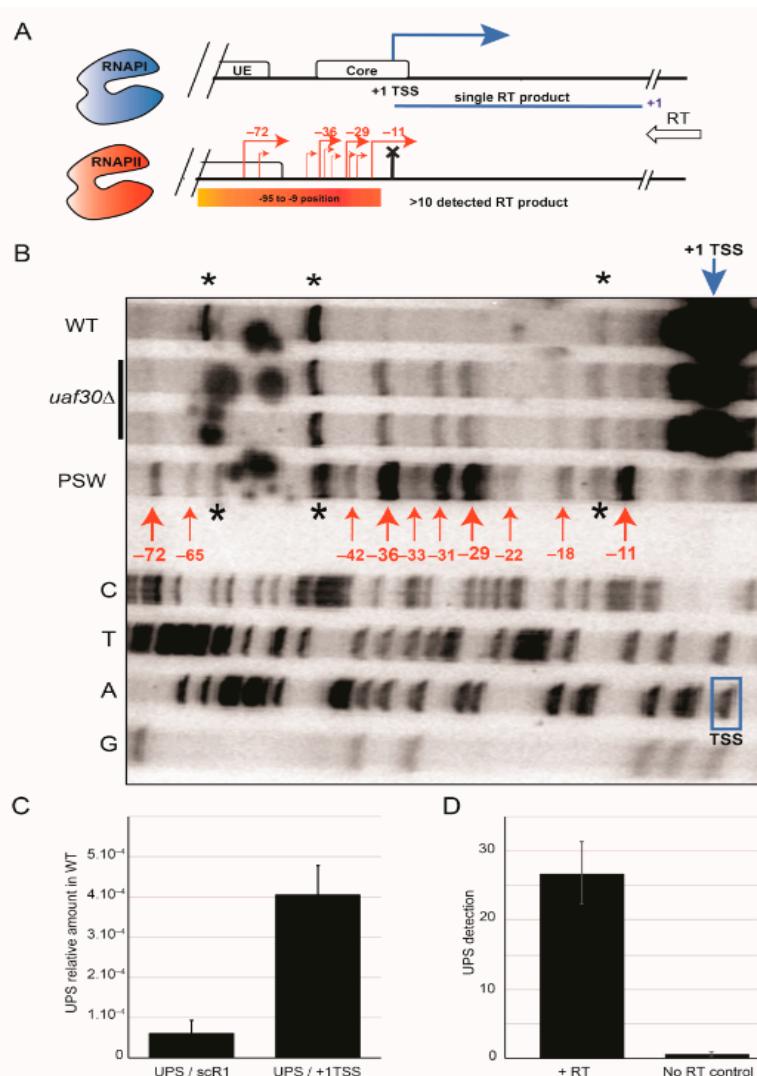


Figure S1. UPS lncRNAs are transcribed from the IGS2 region in rDNA. **A.** Schematic representation of the 35S promoter region composed of UE (Upstream Element) and Core promoter. RT forward

primer was used for reverse transcription. Blue arrows represent +1 TSS. Red arrows represent position of 5' of UPS rRNA. **B.** Primer extension reaction with radiolabelled RT primer was resolved in 10% denaturing acrylamide gel. +1 TSS is marked by blue arrows and UPS by red ones. Star (*) represents a non-specific RT product. Sequencing reaction was used as molecular weight **C.** Quantification of UPS in wild type strains. UPS were quantified using RT primer for reverse transcription (1 µg of total RNA) relative to *scR1* and +1 TSS. Error bars correspond to the standard deviation of three independent cultures. **D.** 1 µg of total RNA was used with or without reverse transcription (no RT), showing that UPS can be detected about 50-fold over background.

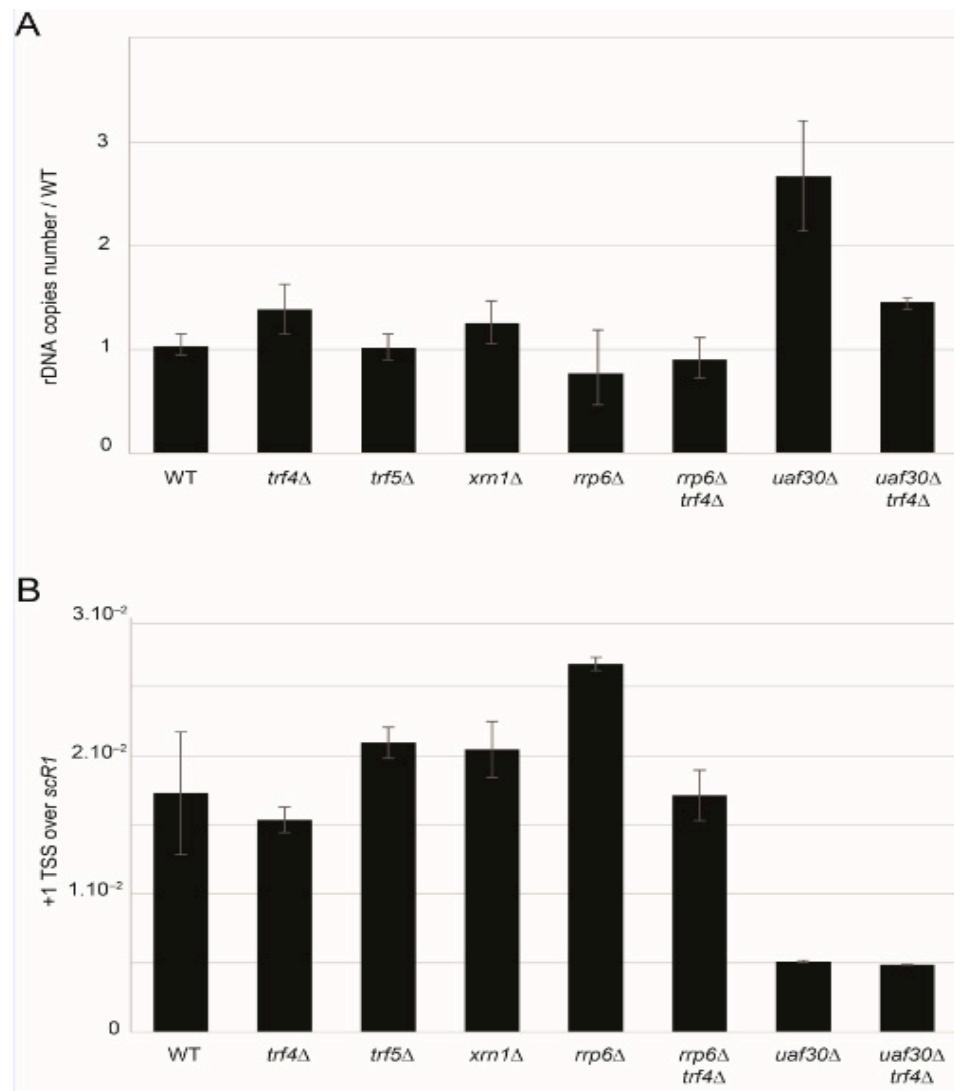


Figure S2. rDNA copy number and +1 TSS rRNA accumulation in various mutants. **A.** Quantification of rDNA copy number was performed using qPCR and are shown relative to WT control (BY4741). **B.** Quantification of +1 TSS in various mutants relative to *scR1* accumulation. Error bars correspond to the standard deviation of three independent cultures.

Table S1. Strains used in this study.

| Name | Genotype | Source / reference |
|-------------------------|---|--------------------|
| WT BY4741 | <i>MATa, his3Δ, leu2Δ0, met15Δ0, ura3Δ0</i> | Euroscarf |
| WT BY4742 | <i>MATa, his3Δ1, leu2Δ0, lys2Δ0, ura3Δ0</i> | Euroscarf |
| WT BY4743 | <i>MATa/α, his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 LYS2/lys2Δ0 met15Δ0/MET15 ura3Δ0/ura3Δ0</i> | Euroscarf |
| <i>rrp6Δ</i> | <i>MATα, lys2, ura3, his3, leu2, rrp6::KAN-MX4</i> | Euroscarf |
| <i>trf4Δ</i> | <i>MATα, ura3, his3, leu2, trf4::KAN-MX4</i> | Euroscarf |
| <i>trf5Δ</i> | <i>MATα, lys2, ura3, his3, leu2, trf5::KAN-MX4</i> | Euroscarf |
| <i>rrp6Δ trf4Δ</i> | <i>MATα, met15, lys2, rrp6::NAT-MX, trf4::KAN-MX4</i> | This study |
| <i>uaf30Δ</i> | <i>MATa, his3Δ1, leu2Δ0, lys2Δ0, ura3Δ0, met15Δ0, uaf30::KAN-MX4</i> | This study |
| <i>xrn1Δ</i> | <i>MATa, his3Δ1, leu2Δ1, ura3Δ0 met15Δ0, xrn1::KAN-MX4</i> | Euroscarf |
| <i>rat1-1</i> | <i>MATa, his3Δ1, leu2Δ1, ura3Δ0 met15Δ0, rat1-1::NAT-MX</i> | [1] |
| <i>rpb4Δ</i> | <i>MATa, his3Δ1, leu2Δ1, ura3Δ0 met15Δ0, rpb4::KAN-MX4</i> | Euroscarf |
| <i>uaf30Δ trf4Δ</i> | <i>MATa, his3Δ1, leu2Δ0, lys2Δ0, ura3Δ0, met15Δ0, uaf30::KAN-MX4 trf4::NAT-MX</i> | This study |
| <i>rpa49Δ</i> | <i>MATα, his3Δ1, leu2Δ0, ura3Δ0, met15Δ0, lys2Δ0 rpa49::alpha NAT-MX</i> | This study |
| <i>pMET3-RAT1</i> | <i>MATa, ade2-1 (ochre), can1-100 (ochre), his3-11,15, leu2-3,112, trp1-1 (ambre), ura3-1 HIS3::pMET3-RAT1</i> | [2] |
| <i>pMET3-RAT1 rrp6Δ</i> | <i>MATa, ade2-1 (ochre), can1-100 (ochre), his3-11,15, leu2-3,112, trp1-1 (ambre), ura3-1 HIS3::pMET3-RAT1, rrp6::KAN-MX4</i> | This study |
| WT YPH499 | <i>MATa, ura3-52, lys2-801_amber, ade2-101_ochre, trp1-Δ63, his3-Δ200, leu2-Δ1</i> | [3] |
| <i>rpb1-1</i> | <i>MATa, leu2-Δ1, ura3-52, trp1-Δ63, lys2-801, his3-Δ200, rpb1-1 (rpb1-G1437D)</i> | [4] |
| <i>rDNA 190C</i> | <i>MATa, leu 2-3, 112 ura3-1, his3-11, trp1-1, ade2-1, can1-100, fob1::HIS3 rDNA copy number 190</i> | [5] |
| <i>rDNA 25C</i> | <i>MATa, leu 2-3, 112 ura3-1, his3-11, trp1-1, ade2-1, can1-100, fob1::HIS3 rDNA copy number 25</i> | [5] |
| PSW | <i>MATa, rpa135::LEU2, rrn9::HIS3, ade2-1, ura3-1, trp1-1, leu2-3, 112, his3-11, can1-100</i> | [6] |

Table S2. Primers used in this study.

| Name | Sequence 5'-3' |
|-------------------|-------------------------------|
| RT (35S rRNA) - R | ACACGCTGTATAAGAGACTAGGC |
| A (35S rRNA) - R | GACTCTCTCCACCGTTGACG |
| B (35S rRNA) - F | AAAGCAGTTGAAGACAAGTCGAA |
| C (UPS) - R | ACGACAAGCCTACTCGAATTCTG |
| D (UPS) - F | GAGGAAAAGTAGTGGGAGGTAC |
| sCR1 - F | GGCTGTAATGGCTTCTGG |
| sCR1 - R | GTGCGGAATAGAGAACTATCC |
| pGAL7 - F | CGAACAGTAGCTGATCTCAG |
| pGAL7 - R | ATTTAACCAATGGTGAAGGAGGACCTCGC |
| PMA1 - F | CCTCTTCATCATCCTCTTCAGC |
| PMA1 - R | AGCGTCATCGTAAGCTTAGCAG |
| PCR rDNA - F | CTTGTCTCAAAGATTAAGCCATGC |
| PCR rDNA - R | ACCACAGTTATACCATGTAGTAAAGGAAC |

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