Supplemental Fig. 1: Addition of Nsi1 to a Pol I-dependent transcription reaction causes a specific abortive transcript shortly upstream of the Nsi1- binding site

Transcription reactions were conducted with Pol I as described. Either both or one of the templates TER or reference were present. Nsi1 was used at 88nM concentration and template concentration was 10nM each. Presence (+) or absence (-) of one of the templates or Nsi1 is indicated. Cartoons of the templates visualize identity and length of the RNAs. An RNA marker demonstrates the transcript sizes. Addition of Nsi1 caused an additional transcript which ended in the proximity of the Nsi1 binding site exclusively on the template which contains the terminator element TER (lanes 1 and 2), but not on the reference template (lane 3).

Supplemental Fig. 2: Comparative iTRAQ LC MALDI TOF/TOF analysis of affinity purified RNA polymerases shows specific enrichment of Pol I, II and III, respectively.

Polymerase preparations were subjected to comparative iTRAQ analysis (1). Average iTRAQ ratios of identified proteins were plotted against a list enumerating all identified proteins. The number of allocated peptides per protein is given in brackets. Note that especially Pol specific subunits are significantly enriched in the comparative analysis (bold letters). Proteins belonging to these groups mostly had an average iTRAQ ratio of close to 1 and were often identified with only one peptide. Therefore, their abundance was generally low and comparable in the analyzed purifications.

Supplemental Fig. 3: RNA polymerase I, II and III differ in their activity in dependency of KOAc concentrations

In vitro transcription reactions were performed with Pol I, II and III. KOAc was titrated from 50mM to 400mM. The signal intensities of the full length transcripts were calculated and plotted against the KOAc concentration. The maximum signal intensity in every graph was set to 1.

Supplemental Fig. 4: Reconstitution of promoter-dependent transcription results in a single round transcription

Promoter-dependent in vitro transcription reactions were performed as described in Mat & Met. Rising amounts of heparin were added to the transcription reactions containing the template (final concentration 0.1μg/μl, 1μg/μl and 10μg/μl) either before (lanes 2 - 4) or after (lanes 6 - 8) assembly of the preinitiation complex (PIC). Transcription efficiency was not

reduced, when heparin was added after PIC assembly, suggesting a single round of transcription in the promoter dependent assay.

Table 1: Oligonucleotides

1049	GCTTAGAGAAGGGGGCAACT	RDN1 locus; fwd primer at end of 18S
2012	TCGACCCTTTGGAAGAGATG	forward primer priming in the 18S coding sequence
2865	CGACCGTACTTGCATTATACC	reverse primer priming in IGS2 of the rDNA
2105	GCGCAACGCAATTAATGTGAGTTAC	BamHI adapter for amplification of Enhancer I and II from pRS316 SIRT g-less 3' reverse
2106	GCGTCGCTGAACCATAGCAGGCTAGCAAC	EcoRI adapter for amplification of Enhancer I and II from pRS316 SIRT g-less 5' for
2107	GCTTCGGTATGATAGGAAGAGCCGACATCG	primer to amplify PolI promoter from pRS316 SIRT g-less 3' reverse
2108	CCCTTTAGGGTCTCTGAAGCGTATTTCCGT	primer to amplify PolI promoter from pRS316 SIRT g-less 5' for
2115	CGCTAGGCGCCGATATCACCTTACCCTATACTTACTCGCATTCCCTACAATTCTACTTCATACCAAACCAATTC	primer for construction of a tail for *in vitro* transcirption tailed templates; together with 3'rev_EcoRI_PolI_promoter_g-less from pRS316 SIRT g-less
2479	CTTGTCTCAAAGATTAAGCCATGC	18S
2480	ACCACAGTTATACCATGTAGTAAAGGAACT	18S
2604	TGTCTGCGTCAAGAAGAAAGA	amplification of YDR026c and introduction of BamHI/SacI sites for insertion into pFL Flag TEV
2605	TGTTTGGGAAAGTAACCCTTC	amplification of YDR026c and introduction of BamHI/SacI sites for insertion into pFL Flag TEV
3050	GAGGGAGCTCTCTCTATAAATTTTATTTG	amplification of Pol I terminator

	T	introducing SacI site
3051	GATGGATCCACTATAGGAAATGAGCTTTTC	amplification of Pol I terminator introducing BamHI site
3792	ATTTGTCTTAAGAATTCTATGAATTTTTACCCGGCATGTATTGTATATATCTATTATAATATAC	PCR primer for introduction of an inverted Nsi1 BS in pUC19 tail g- TER elong with 2105
3793	ATTTGTCTTAAGAATTCTATGATCATGTATTGTATATATCTATTAT	PCR primer for deletion of the Nsi1 BS in pUC19 tail g- TER elong with 2105
3796	TGAGGATGATAGTGTGTAAGAGTGTACC	PCR primer for amplification of pUC19 tail g- TER elong and introduction of a PsiI site in the Abf1 binding site via introduction of a point mutation with #3797
3797	TCGTATATTATAATAGATATATACAATACATGTTTTTAC	PCR primer for amplification of pUC19 tail g- TER elong and introduction of a PsiI site in the Abf1 binding site via introduction of a point mutation with #3796
3658	TTAAGTATGATCCGGGTAAAAACATGTATC	Oligonucleotide for cloning a Reb1 binding site into K773 after annealing with oligonucleotide 3659
3659	TTAAGATACATGTTTTTACCCGGATCATAC	Oligonucleotide for cloning a Reb1 binding site into K773 after annealing with oligonucleotide 3658
3660	TTAAGGTCTCTATAAATTTTATTTGTCTTAAGAATTCTATGATCCGGGTAAAAACATGTATC	Oligonucleotide for cloning a the combination of T-rich element and Reb1 binding site into K773 after annealing with oligonucleotide 3661
3661	TTAAGATACATGTTTTTACCCGGATCATAGAATTCTTAAGACAAATAAAATTTATAGAGACC	Oligonucleotide for cloning a the combination of T-rich element and Reb1 binding site into K773 after annealing with oligonucleotide 3660
3371	TTGAATTCGAGTCATTGGACTGTCTCGC	PCR primer for Nsi1 cloning in Ycplac33
3372	TTAAGCTTGTCTCCACCAAGATGCACCG	PCR primer for Nsi1 cloning in YCplac33

3374	TTTGGATCCATGGACAGCGGTGTCAAACCTTAAG	PCR primer for Nsi1 cloning in YCplac111GAL
3375	TTTGGTACCTTAATTGATTTGTTCCAACAATGAATTC	PCR primer for Nsi1 cloning in YCplac111GAL
3833	5'-BIOTIN-GATGGATCCACTATAGGAAATGAGCTTTTC	primer used together with primer 3834 to amplify cassettes for in vitro transcription with a 5' biotinylated template strand
3834	CGAGGACTGGGTTACCGGGGCACCTGTCAC	primer used together with primer 3833 to amplify cassettes for in vitro transcription with a 5' biotinylated template strand

Templates for *in vitro* transcription

We followed a systematical approach to obtain a defined and comparable plasmid-based set of templates for *in vitro* transcription. They are made up of two main DNA modules. The first module contains sequences for transcription initiation. This is either the RNA Pol I promoter (PIP) from *S. cerevisiae* or a single stranded 3' extension (tail) to the template strand. The second module is variable and contains different cis-element combinations of the 35S rDNA terminator.

A plasmid library was established based on the common cloning vector pUC19. Following a general strategy, we first inserted modules containing transcription initiation elements (PIP or tail). Afterwards, the elongation cassettes were cloned into the respective vectors. The PIP was obtained from the plasmid pRS316 SIRT G-less (#1245) via PCR with primers #2107 and #2108 making use of existing 5' EcoRV and 3' EcoRI restriction sites flanking the promoter. The vector pUC19 was first linearized with KasI and the resulting sticky end blunted, followed by an EcoRI digest. The PIP fragment was cloned into the vector via these restriction sites, which resulted in pUC19 PIP G- (#1247).

To generate tailed templates the site specific nicking endonuclease Nb. BsmI (NEB) was used. The DNA permitting 3' tailing of a template was created via PCR from pRS316 SIRT G-less to produce an amplicon containing an Nb. BsmI nicking site in the coding strand with PCR primer #2115 and #2107. The PCR product was cloned into pUC19 via the KasI/EcoRI restriction sites resulting in the vector pUC 19 tail G- (#1253).

35S rDNA terminator cis-element containing cassettes were amplified from plasmid pRS316SIRT G-less (#1245) with primers #2105 and #2106 (Nsi1 BS RFB) or #3050 and

#3051 (TER). In this context, “TER” refers to a sequence in the rDNA terminator region between +70 and +414bp downstream of the end of the 25S rRNA gene, covering the first T-rich stretch (T-rich 1), the Nsi1 binding site (Nsi1 BS), the second T-rich stretch (T-rich 2) and the replication fork barrier (RFB). In contrast, the “Nsi1 BS RFB” template contains a truncated version of the TER DNA sequence starting at +96bp and thus missing T-rich 1. To study the *cis* element dependency of elongation roadblocks or termination events, templates were constructed lacking the Nsi1 BS, carrying an inverted version of the Nsi1 BS, missing the RFB or missing the T-rich 1 element (TER Nsi1 inv, TER no Nsi1 BS, Nsi1 BS RFB, Nsi1 BS, T-rich 1)(see also Fig. 2A).

Tailed templates were generated in two steps via restriction enzyme and nicking enzyme cleavage. First, the templates were cut out of the respective vectors with blunt-end cutting restriction enzymes. After heat inactivation of the restriction enzymes, the DNA was precipitated, resuspended and incubated with the nicking endonuclease Nb. BsmI (NEB) for 1.5h at 65°C. Nb.BsmI was heat inactivated at 80°C for 20min. After 10min, a competitor oligo (#2207) with the same sequence as the 24 nt tail overhang was added in excess to anneal with the 5' single strand DNA released upon the nicking reaction. DNA was then precipitated and resuspended in RNase free water.

For insertion of the different 35S rDNA termination site cis element cassettes, EcoRI/BamHI (Nsi1 RFB) or SacI/BamHI (TER) restriction sites were used. The procedure was identical for PIP and tailed templates and resulted in vectors #1960 (pUC19 tail G- TER), #1961 (pUC19 PIP G- TER), #1251 (pUC19 PIP G-Nsi1 BS RFB) and #1257 (pUC19 tail G- Nsi1 BS RFB). Reeder and co-workers showed that Reb1 is involved in the termination of Pol I transcription *in vitro* and *in vivo* (Morrow et al. 1993; Reeder et al. 1999) and stated, that a fraction of Pol I is terminated at T-rich 1. In our *in vitro* transcription system this results in short RNAs (<100nt) whose detection is at the technical limit of the gel system. Therefore, 125bp of the 18S rDNA amplified with primers #2479 and #2480 were inserted into EcoRI cut and blunted vectors #1251 and #1257 and SacI cut and blunted vectors #1961 and #1960. This resulted in plasmids #2148 (pUC19 PIP G- TER elong), #2145 (pUC19 tail G- TER elong), #2147 (pUC19 PIP G- ENH elong) and #2144 (pUC19 tail G- ENH elong) carrying additional 125bp upstream of the rDNA terminator cis-elements. To study the cis-element dependency of elongation roadblocks or termination events, templates were constructed lacking or carrying an inverted version of the Nsi1 BS (#2246 [pUC19 tail G- TER noReb elong] and #2245 [pUC19 tail G- TER Nsi1inv elong]). Deletion (inversion) of the Nsi1 BS was achieved by insertion of the AflII/ BamHI digested PCR amplicons obtained with primers #3793 (#3792) and #2105 on plasmid #1960 into equally cut vector #2145, respectively. This also involved the creation of a blunt-end PsiI cutting site in the Abf1 binding site by introduction of a point mutation. Thus, from these vectors templates with or without the RFB can be prepared. The

PsiI site was also introduced in plasmid #2247 (pUC19 tail G- TER elong PsiI) and #2248 (pUC19 tail G- Nsi1BS RFB elong PsiI) by amplification and re-ligation of the complete plasmid #2145 / #2144 with primers #3796 and #3797.

Vectors #1573 (pUC19 tail G- w/o BS) and #1959 (pUC19 PIP G- w/o BS) were constructed by re-ligation of the EcoRI/HindIII fragment of vectors #1243 and #1247, respectively. The resulting templates do not contain binding sites for one of the investigated DNA-binding proteins.

To produce biotinylated transcription templates, PCR from plasmid K2147 or K2148 using oligos 3833 and 3834 was performed to generate templates carrying biotin at the 5´end of the template strand. Biotinylated PCR fragments were incubated for 30 min at room temperature with streptavidine-coupled magnetic beads (10 ug DNA/1 mg beads) in 5 mM Tris pH 7.5, 0.5 mM EDTA and 1 M NaCl, washed 3 times with the same buffer and and 3 times with 20 mM HEPES pH 7.8 before being used to analyse transcript release in the promoter specific transcription assay. 50 – 100 ng template were used for transcription reactions.

Plasmid construction for genetic modification of the rDNA locus in *S. cerevisiae*

5‘ phosphorylated oligonucleotides 3658/3659 or 3661/3662 were annealed and cloned into AflII digested plasmid K773. Plasmids carrying the respective insert in the two possible orientations were named K2281 and K2282, or K2283 and K2284, respectively (pT28-Reb1BS and pT28-Reb1BSinv, or pT28-T-rich-Reb1BS and pT28-T-rich-Reb1BSinv). Plasmids K2281, K2282, K2283 and K2284 were digested with DraII and SacII and the 18S rDNA fragments (1.5kbp) were cloned into plasmid K366 digested with DraII and SacII yielding plasmids pT2-Reb1BS, pT2-Reb1BSinv, pT2-T-rich-Reb1BS and pT2-T-rich-Reb1BSinv. Those plasmids were digested with SacII and MluI and the respective 18S-25S containing fragments (2.6kbp) were cloned into the 11.7kbp fragment of plasmid K775 yielding plasmids K2285, K2286, K2287, K2288 (pNOY373ura-Reb1BS, pNOY373ura -Reb1BSinv, pNOY373ura -T-rich-Reb1BS and pNOY373ura -T-rich-Reb1BSinv). Finally, plasmids K2285, K2286, K2287, K2288 were digested with PstI and MluI and the respective fragments (4.3kbp) were cloned into the PstI/MluI fragment of K375 (9.6kbp) yielding plasmids K2289, K2290, K2291, K2292. A SpeI fragment of plasmids K2289, K2290, K2291, and K2292 was transformed into yeast strain NOY989 and mutant clones containing a modified rDNA locus were selected as described (2). Strain identity was verified by PCR with primer pair 2012/2865 flanking the AflII insertion site within ITS1 and sequencing of the PCR product using oligonucleotide 1049.

Table 2: Plasmids

1245	pRS316 SIRT g-less	SIRT fragment containing PIP and 35S rDNA terminator sequences	(3)
1247	pUC19 PIP g-	contains Pol I promoter dependent template for *in vitro* transcription	this study
1253	pUC19 tail g-	contains tailed template for *in vitro* transcription	this study
1251	pUC19 PIP g- Nsi1 BS RFB	contains Pol I promoter dependent Nsi1 BS RFB template for in vitro transcription	this study
1257	pUC19 tail g- Nsi1 BS RFB	contains tailed template Nsi1 BS RFB for in vitro transcription	this study
1573	pUC19 tail g- w/o BS	contains tailed template without protein binding site for in vitro transcription	this study
1959	pUC19 PIP g- w/o BS	contains Pol I promoter template without protein binding site for in vitro transcription	this study
1960	pUC19 tail g- TER	contains tailed template with rDNA terminator including T1 T-rich element for in vitro transcription	this study
1961	pUC19 PIP g- TER	contains Pol I promoter template with rDNA terminator including T1 T-rich element for in vitro transcription	this study
2144	pUC 19 tail g- Nsi1 BS RFB elongated	an 18S sequence was inserted to give a longer transcription product /better detection	this study
2145	pUC 19 tail g- TER elongated	an 18S sequence was inserted to give a longer transcription product /better detection	this study
2147	pUC 19 PIP g- Nsi1 BS RFB elongated	an 18S sequence was inserted to give a longer transcription product /better detection	this study
2148	pUC 19 PIP g- TER elongated	An 18S sequence was inserted to give a longer transcription product /better	this study

		detection	
2245	pUC 19 tail g- TER Nsi1 inv elongated	contains tailed template with rDNA terminator including T1 T-rich element for in vitro transcription, Nsi1 BS is inverted	this study
2246	pUC 19 tail g- TER noNsi1 BS elongated	contains tailed template with rDNA terminator including T1 T-rich element for in vitro transcription, Nsi1 BS is deleted	this study
2247	pUC 19 tail g- TER PsiI elongated	contains tailed template with rDNA terminator including T1 T-rich element for in vitro transcription, introduction of a PsiI site in the Abf1 BS via a point mutation	this study
2248	pUC 19 tail g- Nsi1 BS RFB PsiI elongated	contains tailed template with rDNA terminator including T1 T-rich element for in vitro transcription, introduction of a PsiI site in the Abf1 BS via a point mutation	this study
1129	pSPL	MultiBac Vector	(4)
1130	pFL	MultiBac Vector	(4)
1321	pFL-Rrn11/pSPL-Rrn6-6xHis-3xHA/Rrn7FLAG	MultiBac vector for CF expression	this study
729	YCplac111 GAL-Rrn3-ProtA	Genomic Rrn3-ProtA (5) cloned into SphI and HindIII in Ycplac111GAL	this study
773	pT28real	Cloning vector to modify rDNA	(6)
2172	pNsi::NSI1 (Ycplac33::Nsi1)	pCAL1: expression of Nsi1 under its own promoter; EcoRI-HindIII fragment of PCR with oligos 3371-3372 from genomic DNA cloned in YCplac33	this study
2174	pGAL::NSI1 (Ycplac181::Nsi1)	pCAL3: expression of Nsi1 under GAL1/10 promoter; BamHI-HindIII fragment of modified PCR product from oligos 3374-3375 cloned in YCplac111GAL	this study

Table 3: Strains

Strain	Name	Parental strain	Genotype	Reference

y2423	BY4741 A135-TEV-ProtA	BY4741	MATa, *his3-1 leuy2-0 met15-0 ura3-0 rpa135::RPA135-TEV-ProtA-kanMX6*	(7)
y2424	BY4741 Rpb2-TEV-ProtA	BY4741	MATa, *his3-1 leu2-0 met15-0 ura3-0 rpb2::RPB2-TEV-ProtA-kanMX6*	(7)
y2425	BY4741 C128-TEV-ProtA	BY4741	MATa, *his3-1 leu2-0 met15-0 ura3-0 c128::C128-TEV-ProtA-kanMX6*	this study
Y950	NOY989		Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdnΔ::URA3/pNOY353*	(2)
Y2276	NOY989 no-BS *Δnsi1*	Y1599	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-WT nsi1Δ::TRP1*	(6)
y2281	NOY989 TERM-BS *Δnsi1*	Y2042	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-TERM nsi1Δ::TRP1*	(6)
y2806	NOY989 Nsi1-BS	NOY989	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-Nsi1BS*	this study
y2807	NOY989 Nsi1-BSinv	NOY989	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-Nsi1BSinv*	this study
y2808	NOY989 T-rich-Nsi1-BS	NOY989	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-T-rich-Nsi1BS*	this study
y2809	NOY989 T-rich-Nsi1-BSinv	NOY989	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-T-rich-Nsi1BSinv*	this study
y3097	NOY989 Nsi1-BS *Δnsi1*	Y2806	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-Nsi1BS nsi1Δ::TRP1*	this study
y3098	NOY989 Nsi1-BSinv *Δnsi1*	Y2807	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-Nsi1BSinv nsi1Δ::TRP1*	this study
y3099	NOY989 T-rich-Nsi1-BS *Δnsi1*	Y2808	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-T-rich-Nsi1BS nsi1Δ::TRP1*	this study

y3100	NOY989 T-rich-Nsi1-BSinv *Δnsi1*	Y2809	Mat a, *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-11 can1-100 rdn-ITS1-T-rich-Nsi1BSinv nsi1Δ::TRP1*	this study
Y2183	BSY420-Rrn3-TEV-ProtA-His7-Tag	BSY420	MATα, , *ade2-1 ura3-1 trp1-1 leu2-3,112 his3-200 RRN3-TEV-ProtA-7HIS*	this study

Table 4: Buffers

TAP 100	NaCl Tris/HCl pH 7.5 $MgCl_2$ NP40 DTT (PIs)	100mM 50mM 5mM 0.15% 1mM (1x)
TAP 300	NaCl Tris/HCl pH 7.5 $MgCl_2$ NP40 DTT (PIs)	300mM 50mM 5mM 0.15% 1mM (1x)
P1	KCl Tris/HCl pH 8 MgAc glycerol PIs	200/300/500mM 20mM 5mM 20% 1x
P2	KOAc Hepes pH 7.8 $MgCl_2$ glycerol NP40 (PIs)	200mM 20mM 1mM 20% 0.1% (1x)
10x transcription buffer	Hepes pH 8 $MgCl_2$ EDTA EGTA DTT	200mM 100mM 50mM 0.5mM 25mM
P600	Hepes pH 7.8, glycerol	20mM 20%

	KoAc $MgCl_2$ imidazole NP40 ß-mercaptoethanol	600mM 5mM 5mM 0.1% 5mM
buffer B	Hepes pH 7.8, glycerol KoAc $MgCl_2$ imidazole NP40 ß-mercaptoethanol	20mM 20% 1500mM 5mM 5mM 0.1% 5mM
buffer C	buffer B, but 600mM KoAc	
buffer TE1000	Tris-HCl pH 7.5 EDTA 1M NaCl	5mM 0.5mM 1000mM

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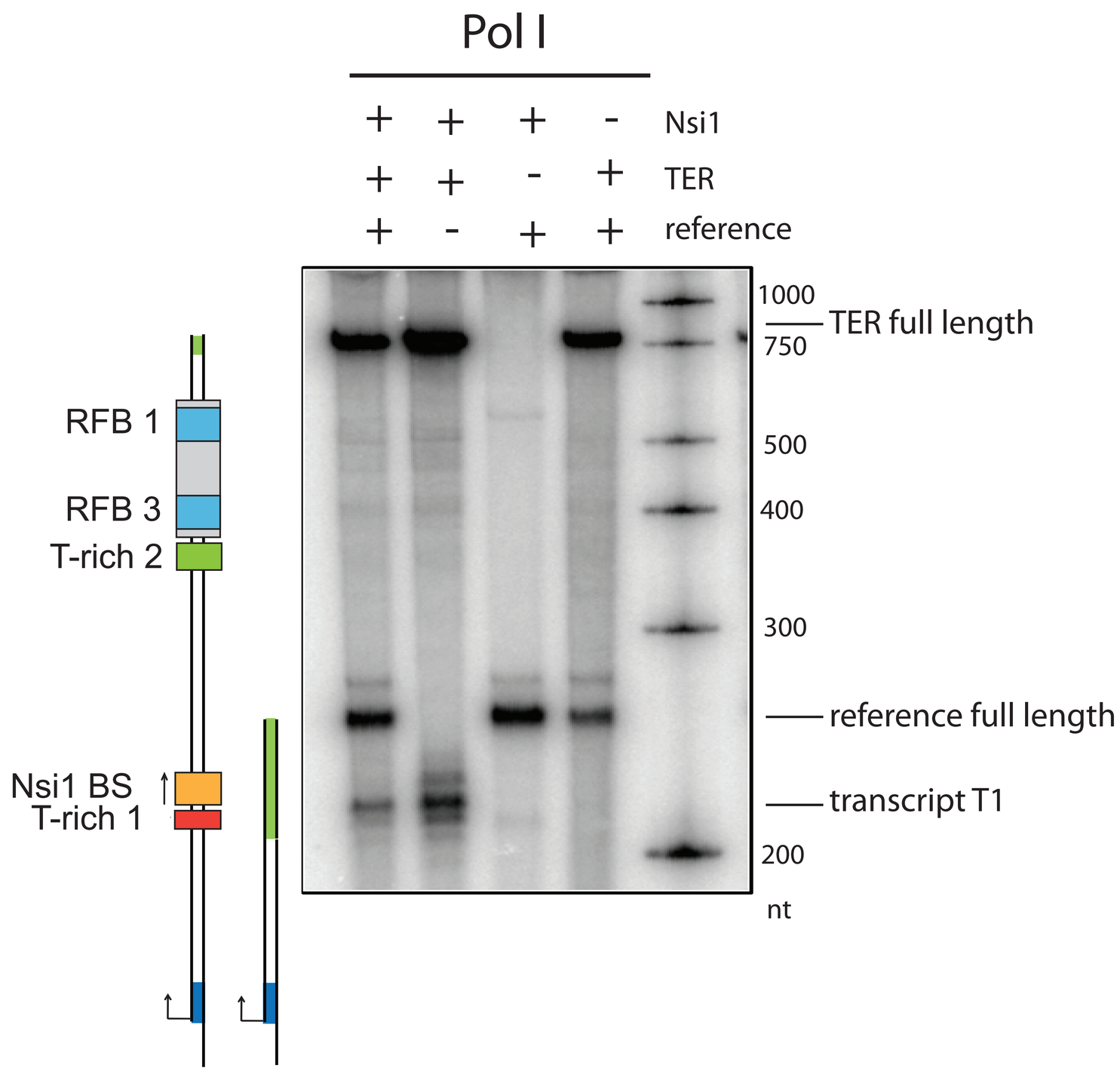
Suppl. Fig. 1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+ + - + TER
+ - + + reference
RFB 1
RFB 3
T-rich 2
Nsi1 BS
T-rich 1
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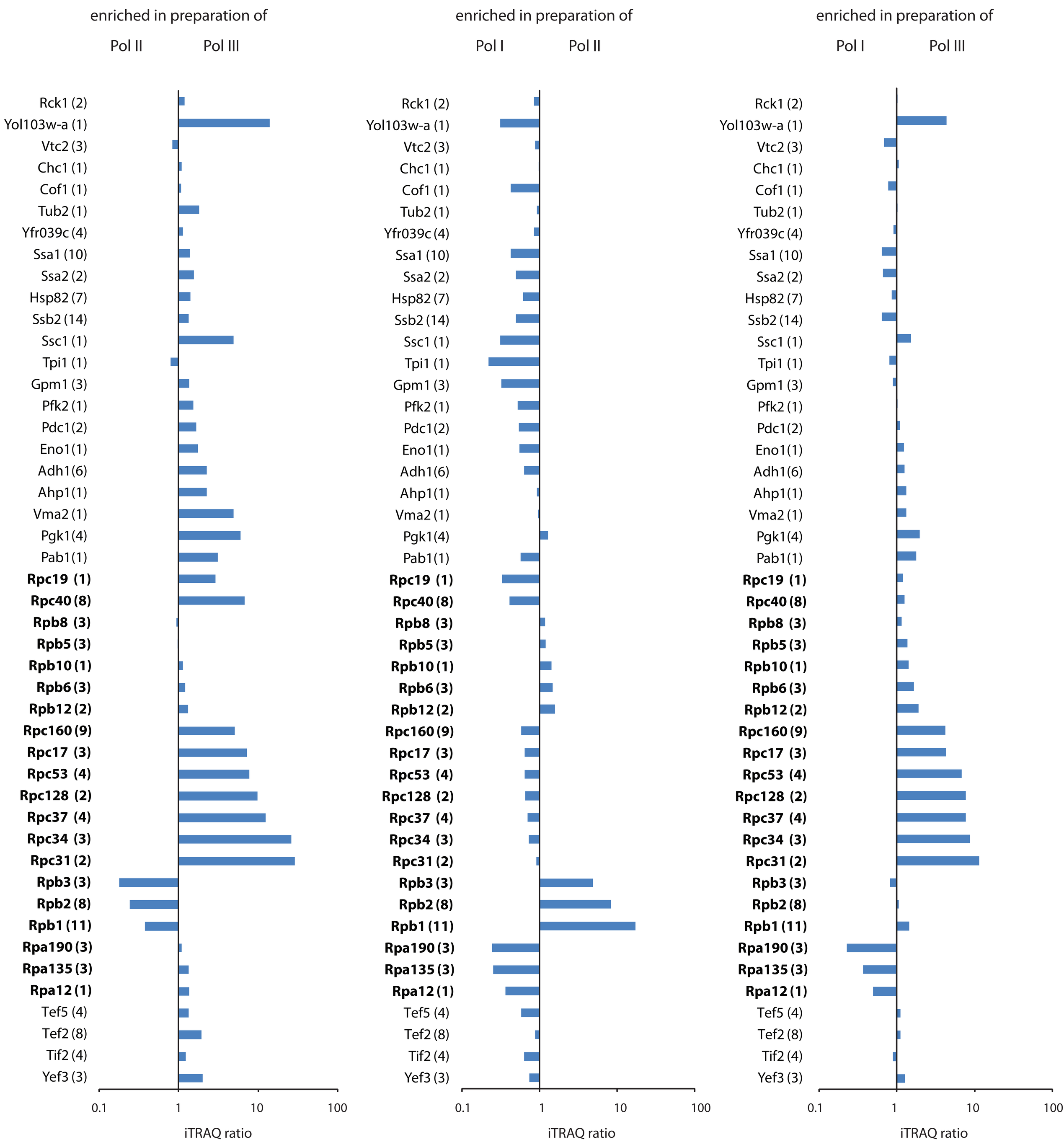
750
500
400
300
200
nt
TER full length
reference full length
transcript T1

Suppl. Fig. 2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Pol II
Pol III
enriched in preparation of
Pol I
Pol II
enriched in preparation of
Pol I
Pol III
Rck1 (2)
Yol103w-a (1)
Vtc2 (3)
Chc1 (1)
Cof1 (1)
Tub2 (1)
Yfr039c (4)
Ssa1 (10)
Ssa2 (2)
Hsp82 (7)
Ssb2 (14)
Ssc1 (1)
Tpi1 (1)
Gpm1 (3)
Pfk2 (1)
Pdc1(2)
Eno1(1)
Adh1(6)
Ahp1(1)
Vma2 (1)
Pgk1(4)
Pab1(1)
Rpc19 (1)
Rpc40 (8)
Rpb8 (3)
Rpb5 (3)
Rpb10 (1)
Rpb6 (3)
Rpb12 (2)
Rpc160 (9)
Rpc17 (3)
Rpc53 (4)
Rpc128 (2)
Rpc37 (4)
Rpc34 (3)
Rpc31 (2)
Rpb3 (3)
Rpb2 (8)
Rpb1 (11)
Rpa190 (3)
Rpa135 (3)
Rpa12 (1)
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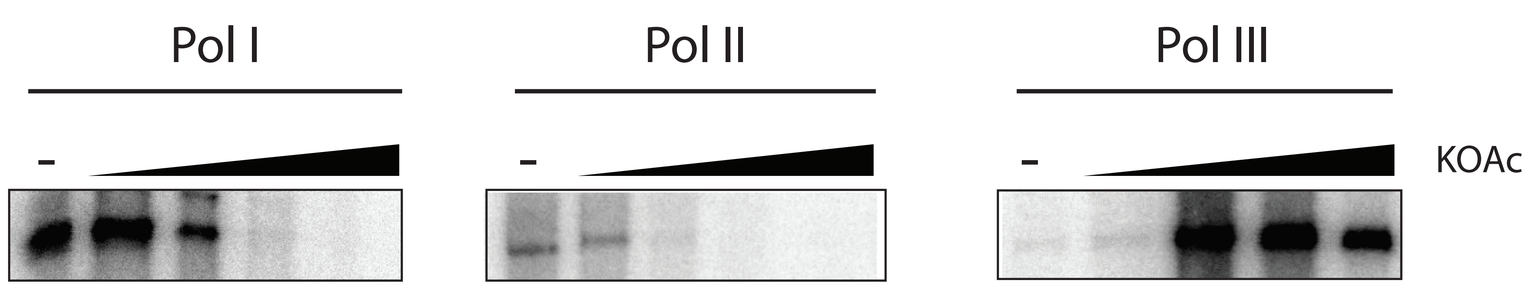
1
10
100
iTRAQ ratio

Suppl. Fig. 3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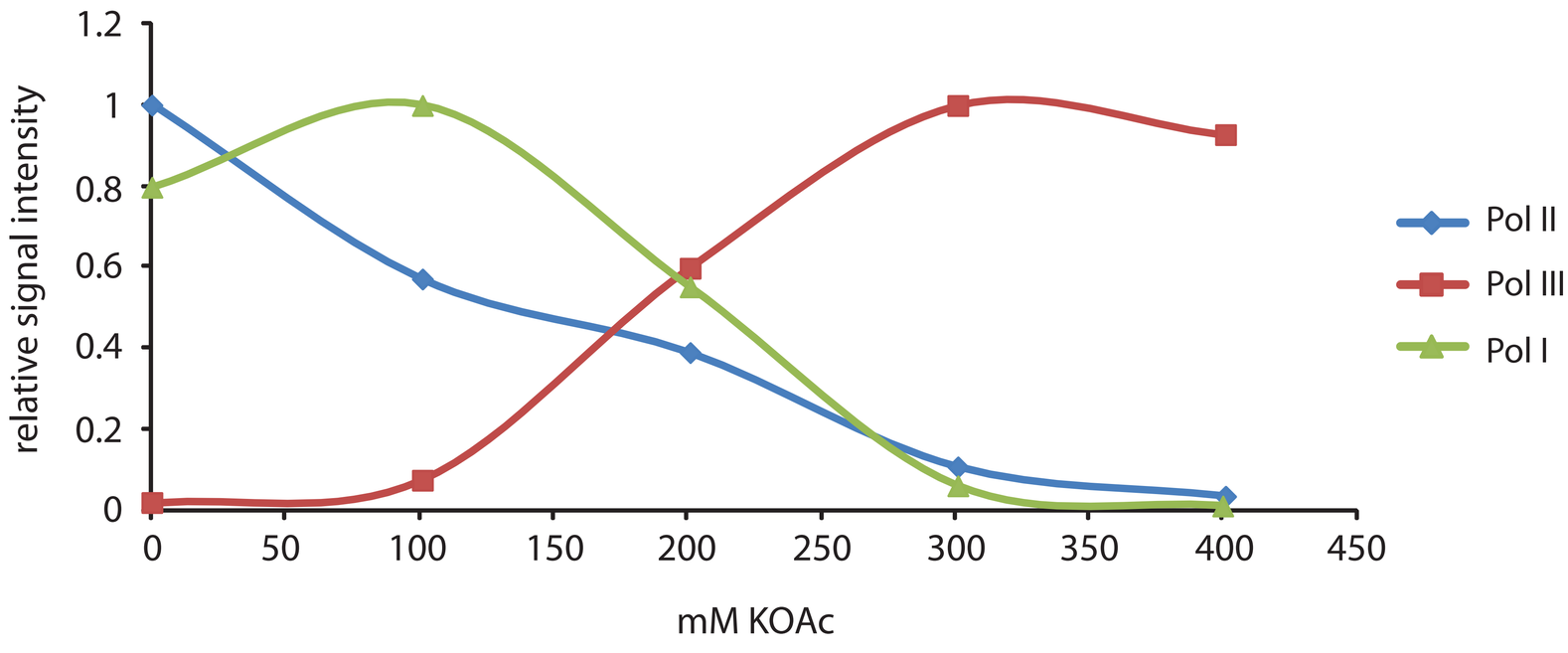
Pol II
Pol III
-
-
-
KOAc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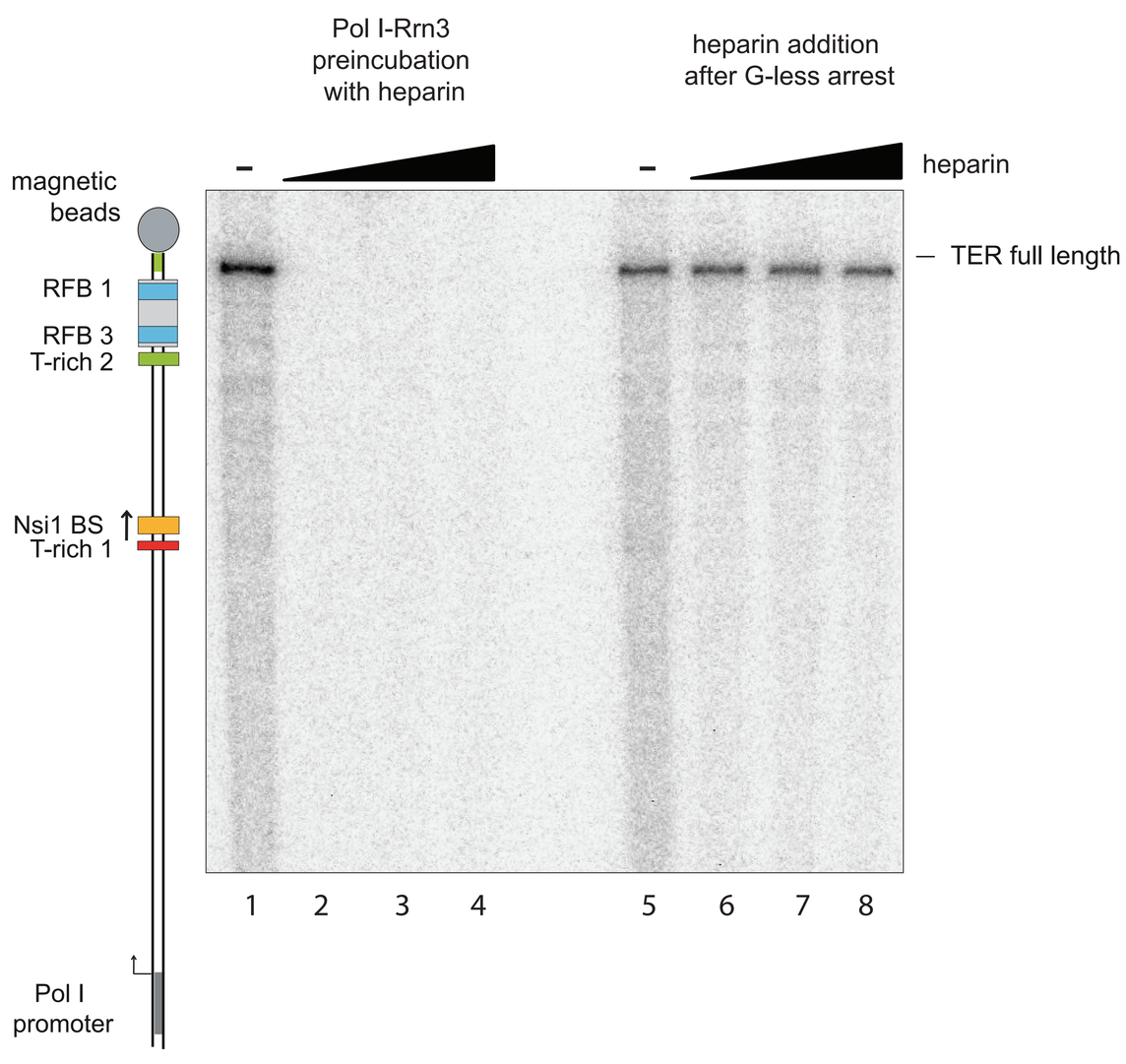
1.2
1
0.8
0.6
0.4
0.2
0
0
50
100
150
200
250
300
350
400
450
mM KOAc
Pol II
Pol III
Pol I

Suppl. Fig. 4


Pol I-Rrn3
preincubation
with heparin
heparin addition
after G-less arrest
–
–
heparin
magnetic
beads
RFB 1
RFB 3
T-rich 2
Nsi1 BS
T-rich 1
Pol I
promoter
TER full length
1
2
3
4
5
6
7
8