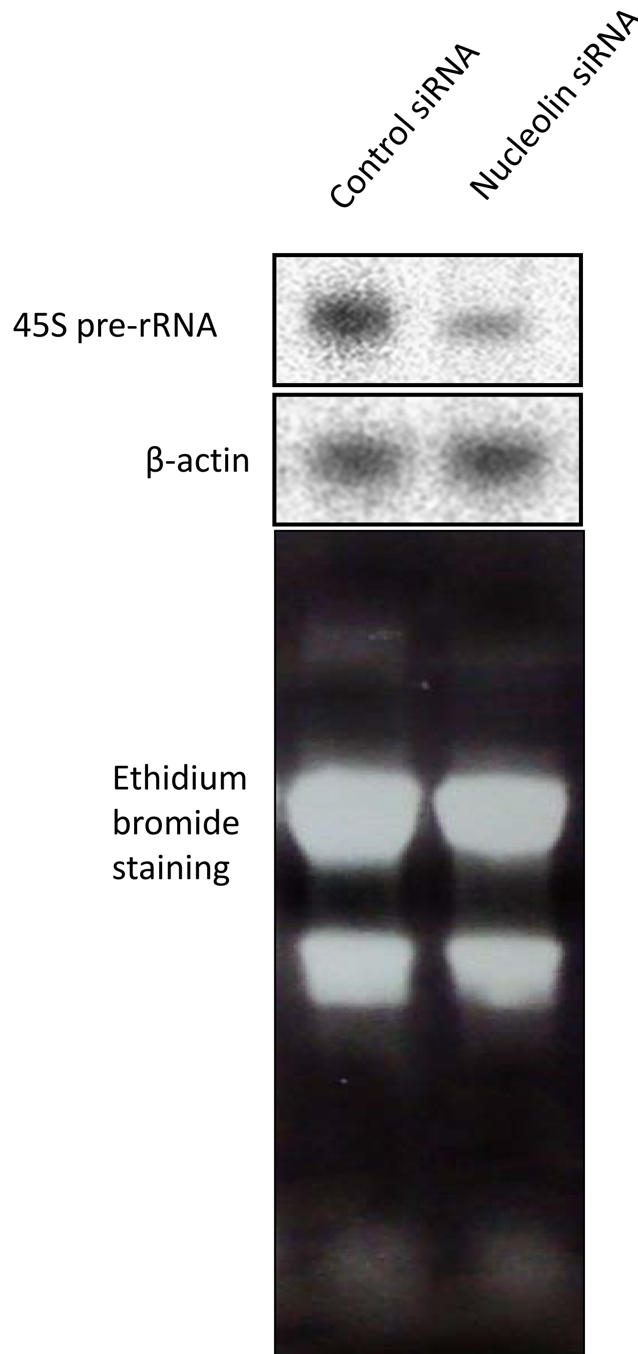
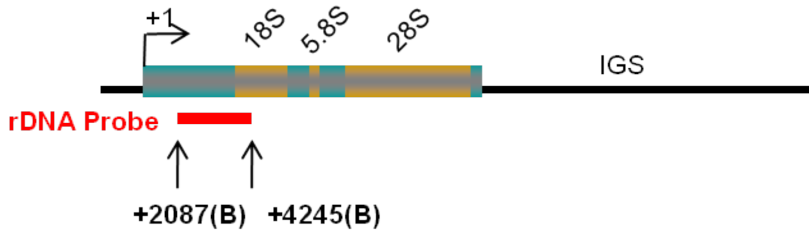
Supplementary Figure 1



Supplementary Figure 1. Effect of nucleolin depletion on pre-rRNA accumulation.
Northern blot for detection of 45S pre-rRNA in HeLa cells transfected with control or nucleolin siRNA. An oligo-nucleotide complementary to the 5′ ETS was used as a probe. For data normalisation, the membrane was also hybridised with a probe specific for β-actin. The same samples of RNA were separated on a denaturing agarose gel and stained with ethidium bromide to check the integrity and equal loading of RNA.

Supplementary Figure 2

A



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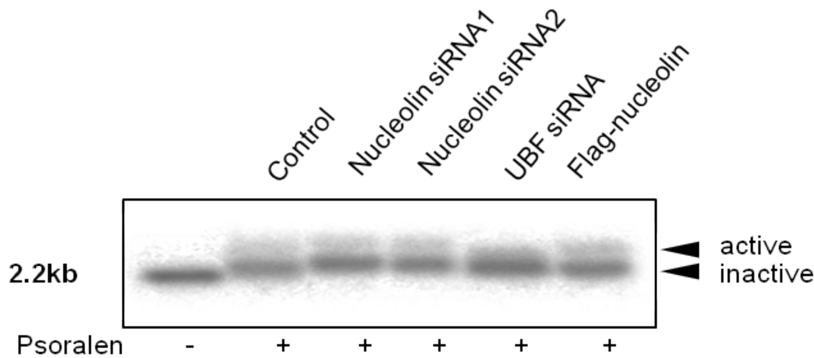
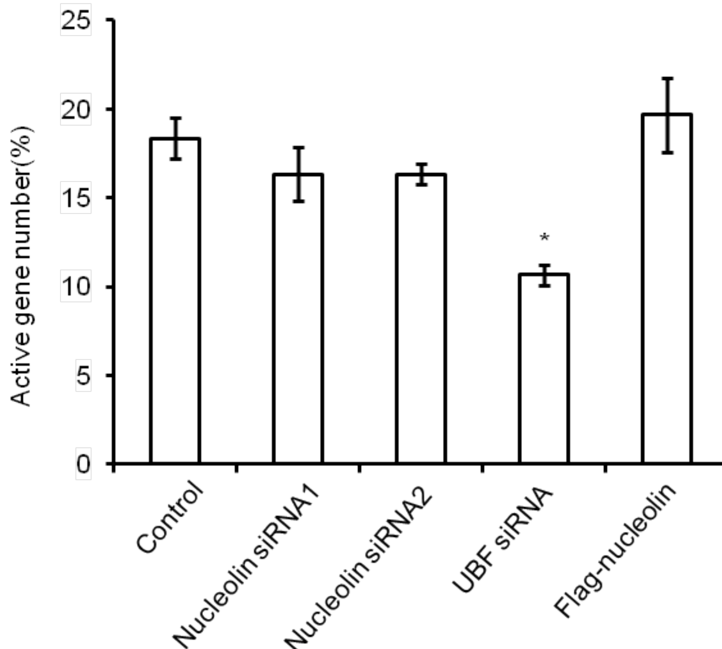
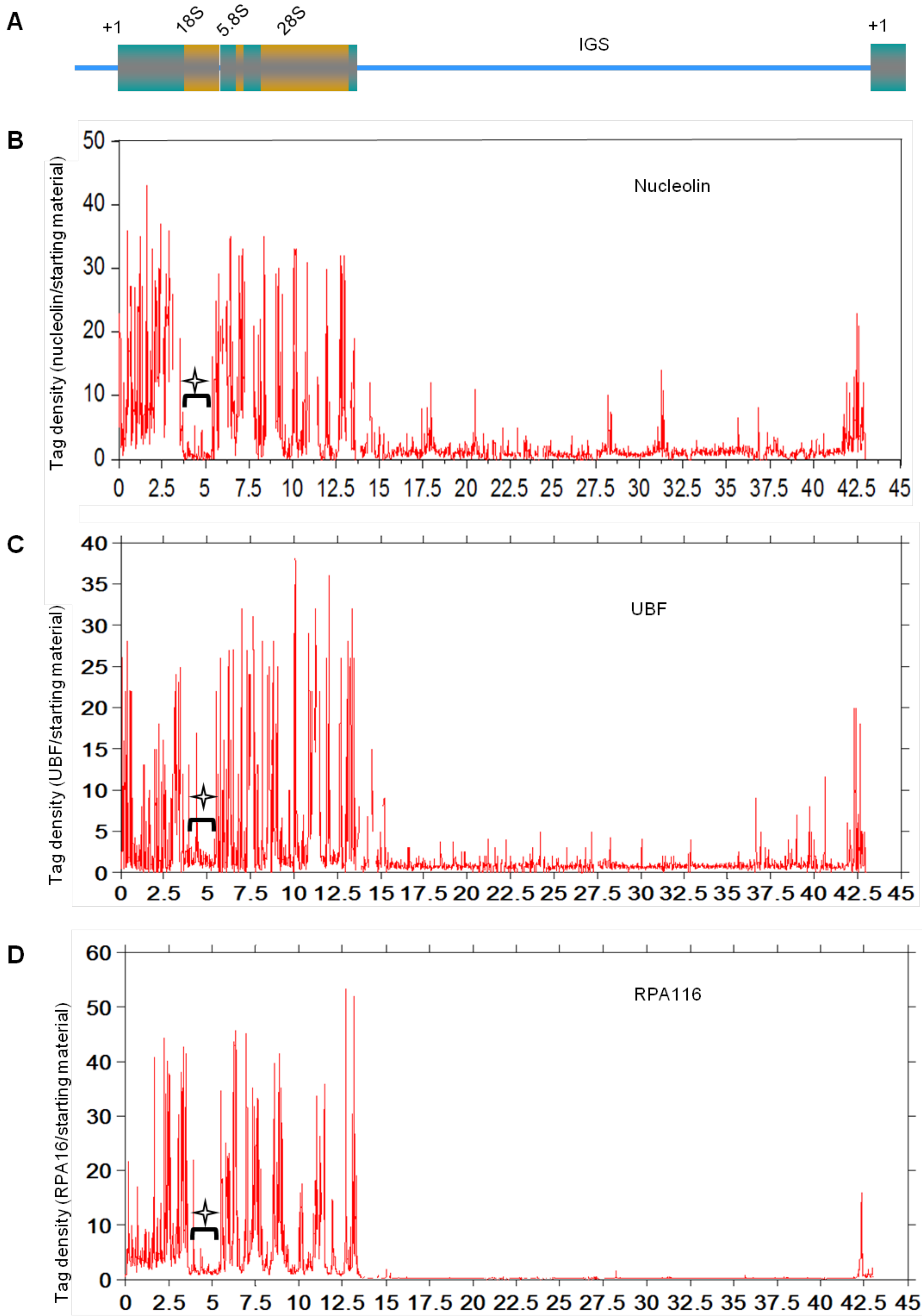


C



Supplementary Figure 2. Psoralen cross-linking analysis. (A) Schematic of the human rRNA indicating the analysed fragment and the probe used in (B). The numbers indicate the restriction sites for BamHI (B) relative to the 45S rRNA initiation site. (B) Determination of the active gene fraction by psoralen cross-linking. (C) Quantitative analysis of psoralen cross-linking. "*" indicates that the difference is significant ($0.01<P<0.05$) compared to the control group analysed by Student's t-test.

Supplementary Figure 3



Supplementary Figure 3. Comparison of the nucleolin ChIP-seq data with ChIP-seq for the RNAPI subunit (RPA116) and UBF.

(A) Schematic representation of a human rRNA repeat.

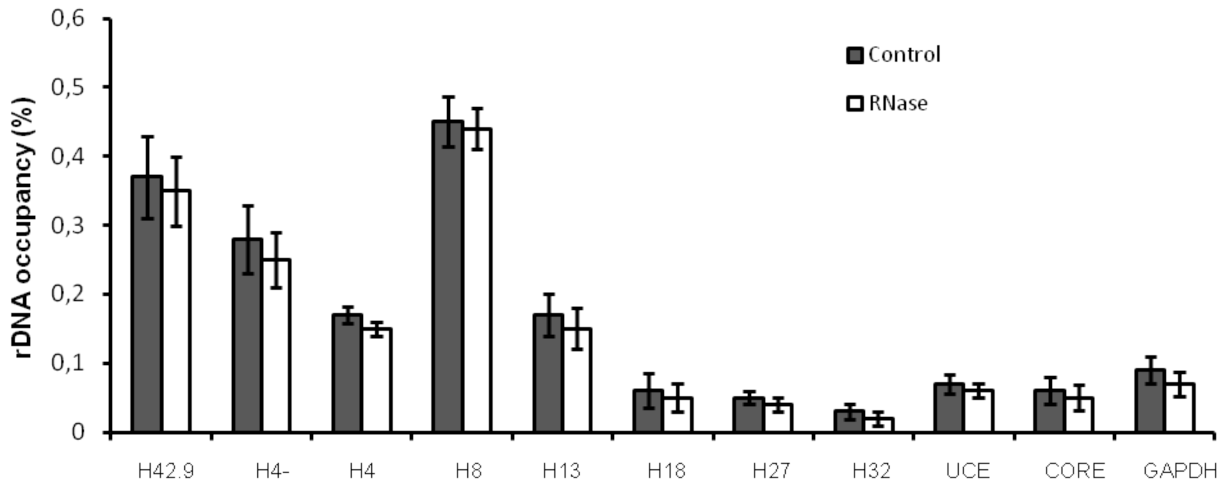
(B) ChIP-seq mapping of nucleolin binding sites throughout the rRNA locus in HeLa cells as shown in 3A.

(C) ChIP-seq mapping of UBF binding sites throughout the rDNA locus.

Data were analysed as explained in the Materials and Methods, and the UBF tag density normalised to the starting material was plotted.

(D) ChIP-seq mapping of RPA116 subunit of RNAPI. Data were analysed as explained in the Materials and Methods, and the RPA116 tag density normalised to the starting material was plotted.

Supplementary Figure 4



Supplementary Figure 4. QPCR analysis of the enrichment of nucleolin on rDNA treated with RNase.

Permeabilised HeLa cells were treated with 1 mg/ml RNase A for 5 minutes, cross-linked with formaldehyde and subjected to ChIP with anti-nucleolin antibody. Immuno-precipitated DNA was analysed by QPCR using sets of primers indicated in Figure 3B. The percentage of DNA immuno-precipitated with anti-nucleolin antibody was calculated relative to the ChIP input DNA. Student's t-test was done between HeLa cells treated with or without RNase, no significant difference was detected.

Table 1. List of siRNA sequences

siRNA target name	Sequence 5' → 3'
human nucleolin	UCCAAGGUAACUUUAUUUCUU UUCUUUGACAGGCUCUUCCUU
human UBF	AUCUCACUCAGCUCUCUCUCAUAUC
human TTF-1	GGCCCUGGAAACUUAUAUA

Table 2. List of primers

Primer name	**5'→3'**	
	Forward	**Reverse**
human rDNA -ETS	CCTGCTGTTCTCTCGCGCGTCCGAG	AACGCCTGACACGCACGGCACGGAG
human nucleolin	ACCCAGGGGATCACCTAATG	CCTTTGGAGGACCCAGTTTC
human TTF-1	CTCCTTGGGAATGACTGGAA	CCAAGCACCACGATTTCTTT
human UBF	GTCGGCCATGTTCATCTTCT	CTCAGACAGGTCGTTCCACA
H4	CGACGACCCATTCGAACGTCT	CTCTCCGGAATCGAACCCTGA
H4-	GGATGCGTGCATTTATCAGA	GATCGGCCCGAGGTTATCTA
H8	AGTCGGGTTGCTTGGGAATGC	CCCTTACGGTACTTGTTGACT
H13	ACCTGGCGCTAAACCATTCGT	GGACAAACCCTTGTGTCGAGG
H18	GTTGACGTACAGGGTGGACTG	GGAAGTTGTCTTCACGCCTGA
H27	CCTTCCACGAGAGTGAGAAGCG	CTCGACCTCCCGAAATCGTACA
H32	GGAGTGCGATGGTGTGATCT	TAAAGATTAGCTGGGCGTGG
UCE	CTCCCGCTCTGGAGACAC	GGACACCTGTCCCCAAAAAC
CORE	AGGTGTCCGTGTCCGTGT	GCCCAAAATTGCCGACTC
H42.9	CCCGGGGGAGGTATATCTTT	CCAACCTCTCCGACGACA
T0	GCTCCCCGGCCCGGCGCT	CCATCGCAGCCACACACG
GAPDH	TCCACCACCCTGTTGCTGTA	ACCACAGTCCATGCCATCAC