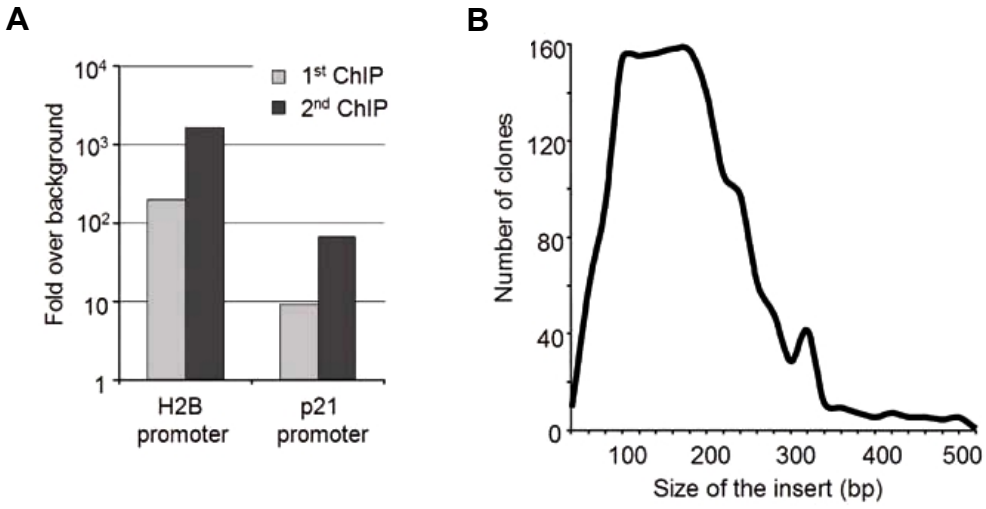
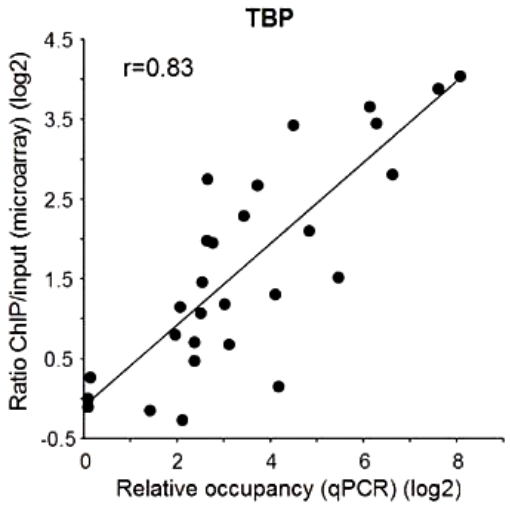
Supplementary figures.



Supplementary Figure 1.

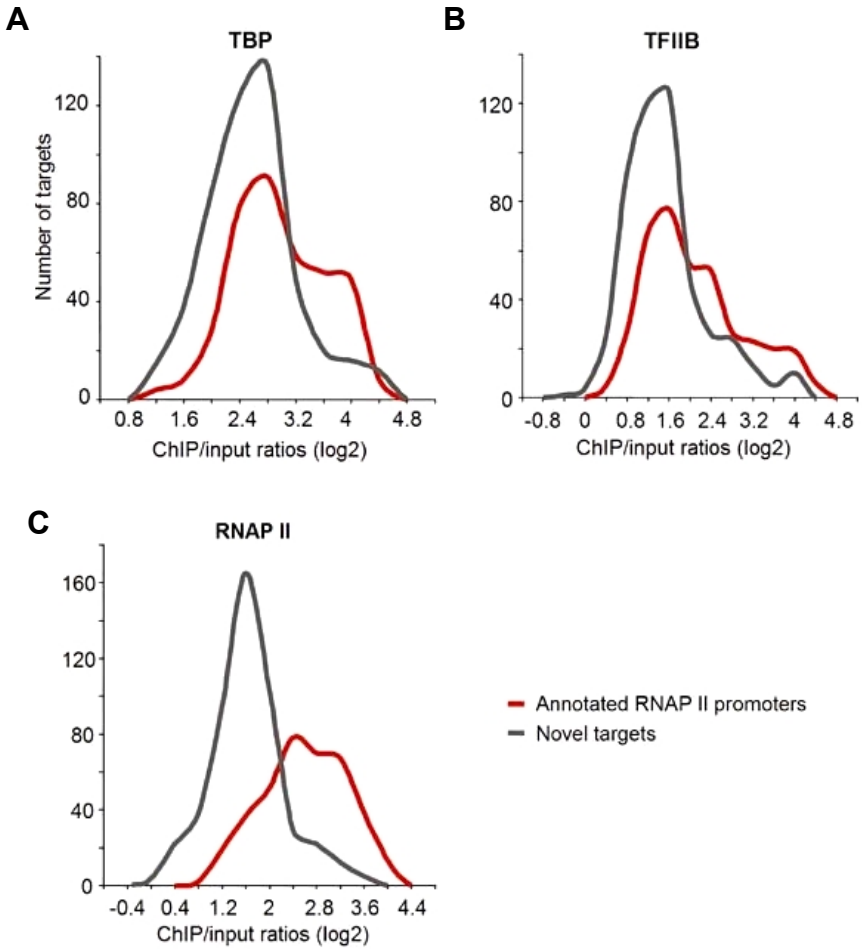
(A) Sequential chromatin immunoprecipitation (ChIP) was performed with anti-TBP antibody to achieve a high enrichment of TBP binding sites. Enrichment of genomic promoters was measured by qPCR and plotted as fold over background probe (exon 2 of the myoglobin gene).

(B) Size distribution of the cloned DNA fragments. Weighted average length is about 160 bp.

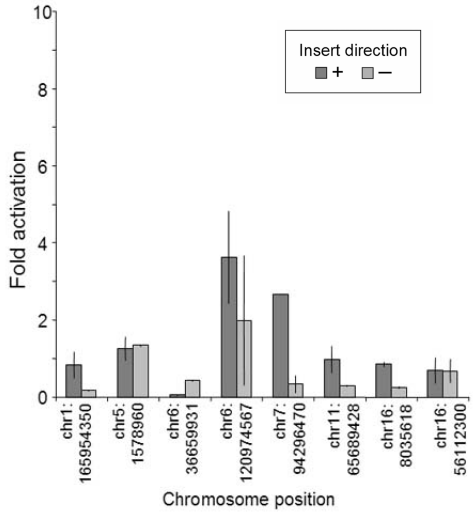


Supplementary Figure 2. Correlations as visualized by scatter plot.

ChIP/input ratios from microarray and occupancy values from single gene qPCR were obtained for a set of printed control targets and plotted against each other.

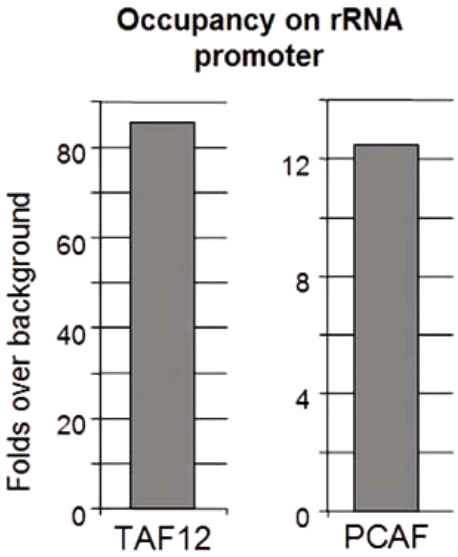


Supplementary Figure 3. Transcription factor profiling with TBP binding site microarray. Percentile plots were calculated separately on novel TBP binding sites and annotated RNAP II promoters.

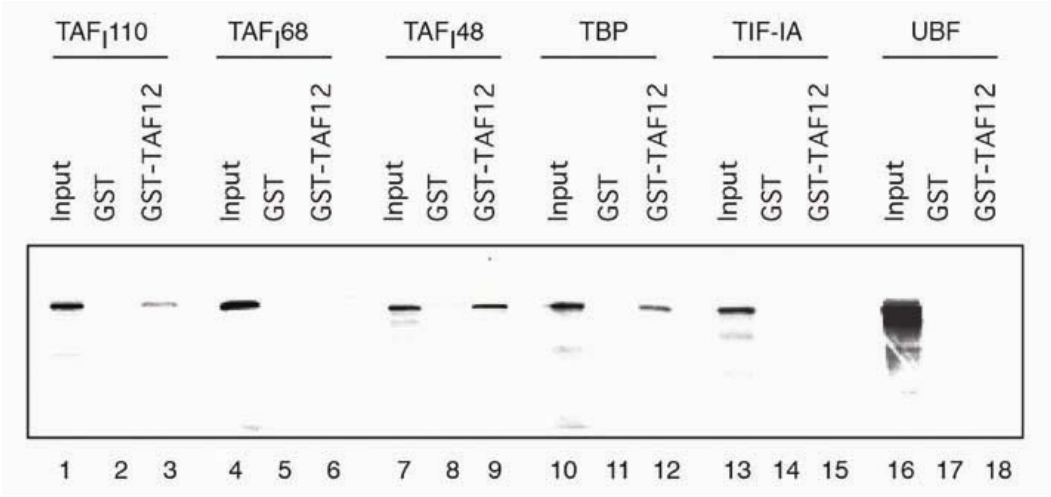


Supplementary Figure 4. Gene-reporter assay with randomly selected regions.

Eight genomic DNA fragments of about 1kb from randomly selected regions lacking gene annotation were cloned in 2 orientations in front of gene-reporter in promoter-less vector pGL3-basic. These DNA constructs were transfected in U2OS cells; ratios of transcription activity of the reporter gene over empty vector are shown. The "+" and "–" refers to the direction of the sequence (UCSC genome browser definition) with respect to the reporter gene. Genomic positions of centers of the cloned fragments are indicated.



Supplementary Figure 5. Occupancy of rRNA promoter with TAF12 and PCAF.
The ChIP occupancy is presented as enrichment recovery over negative control (exon 2 of the myoglobin gene).



Supplementary Figure 6. TAF12 interacts with TBP, TAF$_I$48 and TAF$_I$110.

The indicated proteins were synthesized by in vitro translation in the presence of ^{35}S-methionine, captured by GST-TAF12 (lane 3, 6, 9, 12, 15, 18) or GST alone (lane 2, 5, 8, 11, 14, 17), and analyzed by SDS-PAGE and autoradiography. The Input lanes (1, 4, 7, 10, 13, 16) contain 10% of the material used in the pull-down assays.

Supplementary Table I. The E2F1 / E2F4 target genes from the TBP binding sites microarray.

Gene name	Descripiton	Biological function
CDCA1	cell division cycle associated 1	cell cycle
DRF1	Dbf4-related factor 1	cell cycle
BRCA2	breast cancer 2	cell cycle, DNA repair, transcription
CDKN2D	cyclin-dependent kinase inhibitor 2D	cell cycle
ADPRTL2	ADP-ribosyltransferase-like 2	transcription, DNA repair
HMG2L1	high-mobility group protein 2-like 1	transcription
ZNF443	zinc finger protein 443	transcription
ZNF143	zinc finger protein 143	transcription
ZFP36L2	zinc finger protein 36, C3H type-like 2	transcription
H2BK, H2AH	Histone	chromatin
H2BJ, H2AG	Histone	chromatin
H4	Histone	chromatin
PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	nucleotide biosynthesis
RPS16	ribosomal protein S16	protein biosynthesis
TK1	thymidine kinase 1	DNA metabolism
SLC3A2	solute carrier family 3	carbohydrate metabolism
LYK5	breast cancer antigen NY-BR-96.	protein kinase
CCT5	chaperonin containing TCP1, subunit 5	protein folding
bA33E24.2		Vega predicted gene
dJ564F22.2		Vega predicted gene
MGC13170		Predicted protein
CRAMP1L		Predicted protein

Supplementary Table II. Quantitative PCR primers targeting the novel TBP binding sites.

Name	Position (hg17)	Forward primer	Reverse primer
A2_3_39	chr6:65450495	CCACTAGGGTTGGGACCATG	CGGTTAGGCCTGGGACTTGT
A5_8_39	chr16:83280487	AGTCTGATTCAGCTCTGGAGGAA	CACGCCATAAAACCAGCACA
A9_9_39	chr16:85520562.5	GAGGATGGCTAGCAACGAGC	AATGCAGTCCAGGGATTTGG
B10_10_39	chr14:19137583, 18575885	AGCAGCACACCAGCACTGAA	AGCACGGTGAGAGCAACCTC
B7_8_46	chr4:169927436	AGTGCGATAAGAGCATGGAGTG	AGGAATGCTGCTAAACTCCAGAA
B8_1_46	chr1:24308606	TTACCCATGAGGACGACACG	GGCATGGAACTTGGACGAGT
C10_1_39	chr7:1326447	TGCCTCATGCACACTGGAAG	ACTCACGGCTTTGACACTCGT
C10_10_39	chr9:33151138.5	ACTGCCAAAGAATTCAGCAACA	TGCACAAATGAAGGCCAGG
C4_5_46	chr8:67597684.5	CCAAGAGGCACTCCCCTGTA	TCCCAGCCTGCTTCTCAACT
C6_5_39	chr8:65832131	ATTGTGGAGACCAGCCAGGT	AGGCTTGTCAACATCCTCCAA
C8_0_46	chr14:23634665.5	CTCCCACCAACACCAAAGCT	GCTTCCCCTGGCTCTTCTTC
C8_10_39	chr1:195382748	GGCTGATTATGCTGGTGCTATG	CACACAGGCGCTACCAAATG
D10_6_46	chr5:34753810	ACCACATCCTTCCAACCCTG	AAACATTCTGCTTCCCTCTGAAA
D3_2_46	chr8:104266344.5	GACCAGGATGCAGGCTCAAG	AACGACAGCTCTCTGCGGTT
D5_1_46	chr4:41261444.5	AAGGTTTCAGGTGGTTGGGC	GCAGCCTGTCTGACGGAGA
D5_10_39	chr17:42638140	GTCACCAGGCCTTCAACACC	CCTGCTTCTCTCGGCACAG
D9_7_39	chr17:73338135.5	TGGACACACAAGTTAGGGTTCTGA	TTGGAGGCTGCAGAGACTCA
E1_3_39	chr16:2013230	GGATCGAGTGGAAGGAAGCC	ATCGTGCGAGGAGTTGCC
F11_3_46	chr7:54974791.5	CAGAGCAGGGTGGAGTGAGC	TGGAGTCAGCCACAGAGGTTG
F12_7_39	chr2:26858648.5	ACGTCAGCAGGTCCTCACACT	GCCTGTCCCATTGTCACTGG
F5_4_46	chr14:80755508	TAAATGGAGAGGCGGTGACG	GACTCTGCCAGGATGGGAAG
G11_0_46	chr16:22160131	AAAAAATTGAGATCACTAAATAAAGCACA	TTACAGAAGAGTGGGTCAATGGG
G2_5_46	chr17:76629358	GGCTCTTGGTGTTGGTCCTG	CACTCTTGCTCCCTGGGCT
G9_5_46	chr4:49157967	GCCCGAGGCTATTTAAACCC	CGCGAAGATCTGAGTACAGGC
H9_1_39	chr20:55221364.5	GCTCCCCCACCTCAGCTT	CTGTTCTATGATTTGGCAGGAAAG
H9_10_39	chr17:61966655	ATGCAGTTGGTGCCTCTCCT	GCAACAAACACAACAGCCTCC
GADD45A enhancer	chr1:67864614	TTCCTTTAGCAGGGCAGATTAGA	GGGTGAGCCAGGAATTCATTT
H2BR promoter	chr6:27208560	TTGCATAAGCGATTCTATATAAAAGCG	ATAAAGCGCCAACGAAAAGG
myoglobin exon2	chr22:34331584.5	AAGTTTGACAAGTTCAAGCACCTG	TGGCACCATGCTTCTTTAAGTC
p21 promoter	chr6:36754172	TGCTGTGTCCTCCTGGAGAGT	CACGAAGTGAGCCACAAATCTG