SUPPLEMENT

Table 1. siRNA targets

Targets	Sequences
Mismatch	sense 5'UUC UCC GAA CGU GUC ACG Utt 3' antisense 5'ACG UGA CAC GUU CGG AGA Att 3'
Mouse Brf1 siRNA:	**A:** sense 5' ACC UUG AGA UUG ACA GAU A dTdT 3' antisense 5' UAU CUG UCA AUC UCA AGG UdTdT 3'; **B:** sense 5' AAG CAC UGC CCC ACU UAU UUG dTdT 3' antisense 5' CAA AUA AGU GGG GCA GUG CUU dTdT 3' **C**: sense: 5' AAG CAC UGC CCC ACU UAU UUG dTdT 3'(1) antisense: 5' CAA AUA AGU GGG GCA GUG CUU dTdT3'

Table 2. Primer Sets for Quantitative RT-PCR

Target	Primers	Annealing Temperature
Pre-tRNA^{Leu} (2)	(F) 5'-GTC AGG ATG GCC GAG TGG TCT AAG-3' (R) 5'-CCA CGC CTC CAT ACG GAG AAC CAG AAG ACC C-3'	61º
5S rRNA (3)	(F) 5′ GGC CAT ACC ACC CTG AAC GC 3′ (R) 5′ CAG CAC CCG GTA TTC CCA GG 3′	61º
7SL (3)	(F) 5' GTG TCC GCA CTA AGT TCG G-3' (R) 5' TAT TCA CAG GCG CGA TCC-3'	55º
Mouse TBP	F) 5' GCT AGG TTT CTG CGG TCG CGT C -3' (R) 5' CTG TAC TGA GGC TGC TGC AGT TGC TAC -3'	60º
Mouse Brf1	(F) 5' GGA GCA GAG CCA ATC AAG CCA -3' (R) 5' CAT CAC CAT CAC AGC CGT AAT C -3'	62º
Mouse Bdp1	(F) 5'GCGTGAAGCCAAATGTCAGG3' (R)5'CAATGTGCTGGACTCTGCAGC 3'	64°
TFIIIC$_{63}$ (3)	(F) 5′ CGG CAG ATG TTC TAC CAG TTA TGC G 3' (R) 5′ ATG GCT TGA AGT CCT CCT CC 3′	64º
GAPDH (3)	(F) 5′-TCC ACC ACC CTG TTG CTG TA-3′ (R) 5′-ACC ACA GTC CAT GCC ATC AC-3′	61º

Abbreviations: (F) = forward, (R) = reverse.

Table 3 Primer Sets for ChIP

Target	Primers	Annealing Temperature
Brf1 promoter –71/+98	(F) 5' CAG TCC CGC CCC GTT GTT G 3' (R) 5' TGC GGG CCG CGC TGC CTG CAA 3'	64º

Brf1 promoter –507/–346	(F) 5’ GGC AGT CCT TGA TCC TGC C 3’ (R) 5’ GTA GTG GGA TGG GTT TGT GG 3’	63º
$tRNA^{Leu}$ gene (2)	(F) 5'-GTC AGG ATG GCC GAG TGG TCT AAG-3' (R) 5'-CCA CGC CTC CAT ACG GAG AAC CAG AAG ACC C-3'	61º
5S rRNA (3)	(F) 5′ GGC CAT ACC ACC CTG AAC GC 3′ (R) 5′ CAG CAC CCG GTA TTC CCA GG 3′	61º

ChIP assay. Chromatin immunoprecipitation (ChIP) assays were performed as described previously (4). Cells were treated with 20ng/ml EGF prior to cross-linking with formaldehyde. Briefly, chromatin was precleared with protein A/G plus agarose beads for 30 min at 4°C prior to adding antibodies or control antibody overnight. Protein A/G plus agarose beads were added for 3 h, and the immunocomplex was isolated. The cross-links were reversed by incubating the mixture with 0.3 M NaCl at 65°C overnight. DNAs were extracted with phenol/chloroform. Real-time PCR was performed using the isolated DNA and SYBR green supermix (Bio-Rad) on an MX3000P system (Strategene). The primer sequences that were used are shown in Table 3 in Supplementary Data. The fold change in promoter occupancy was calculated by setting the level of promoter occupancy in the cells without EGF treatment at 1.

Supplemental References

1. Johnson SA, Dubeau L, Johnson DL. (2008b). Enhanced RNA polymerase III-dependent transcription is required for oncogenic transformation. *J Biol Chem*. **283**:19184-19191.

2. Crighton, D., Woiwode, A., Zhang, C., Mandavia, N., Morton, J.P., Warnock, L.J. *et al*, (2003). p53 represses RNA polymerase III transcription by targeting TBP and inhibiting promoter occupancy by TFIIIB. *EMBO J*. **22**, 2810–2820.

3. Winter AG, Sourvinos G, Allison SJ, Tosh K, Scott PH, Spandidos DA, et al (2000). RNA polymerase III transcription factor TFIIIC2 is overexpressed in ovarian tumors. *Proc Natl Acad Sci U S A*. **97**:12619-24,

4. Zhong, S., D.L. Johnson. **(**2009) The JNKs differentially regulate RNA polymerase III transcription by coordinately modulating the expression of all TFIIIB subunits. *Proc Natl Acad Sci U S A*. **106:**12682-12687.