Table S1: Primer sequences used to amplify ChIP DNA and cDNA

***Jun* (-711)**	**Primer Sequence 5' to 3'**	***Cox-2* (-493)**	**Primer Sequence 5' to 3'**	***Fosl1* (-1113)**	**Primer Sequence 5' to 3'**
Forward	CGCAGCGGAGCATTACCTCA	Forward	AAATTAACCGGTAGCTGTGTG	Forward	TCACCAGACTCAGCCACTTAC
Reverse	CCATTGGCTTGCGTCGTTCTC	Reverse	CCGGGATCTAAGGTCCTAA	Reverse	GCCATCATAACCCCCACT
***Jun* (-146)**		***Cox-2* (-111)**		***Fosl1* (-187)**	
Forward	TTACCTCATCCCGTGAGCCTT	Forward	AAGCCTAAGCGGAAAGACAGA	Forward	CCCCCGTGGTGCAAGTGGTT
Reverse	CCATTGGCTTGCGTCGTT	Reverse	GGCTGCTAATGGGGAGAAC	Reverse	TGGCGGCTGCGGTTCTGACT
***Jun* (129)**		***Cox-2* (903)**		***Fosl1* (989)**	
Forward	GGACTGTTCATCCGTTTGTCT	Forward	AAACCGTGGGGAATGTATGAG	Forward	ACACTCGCGCTCCACATTCTC
Reverse	CAAATGCTCCCCAAAATACC	Reverse	CCAGTCCGGGTACAGTCACA	Reverse	CGCAGCTCCTTCCCTCCC
***Jun* (1115)**		***Cox-2* (1982)**		***Fosl1* (2249)**	
Forward	CCAAGAACTCGGACCTTCTCA	Forward	GCCTTCTCCAACCTCTCCTAC	Forward	CCTATCCCCAGTACAGTCCC
Reverse	GGTGATGTGCCCATTGCT	Reverse	ACTCACCCTTCACACCCA	Reverse	ATCGCTGTTTCTTACCTGCTC
***Jun* (2953)**		***Cox-2* (4255)**		***Fosl1* (7676)**	
Forward	TGGTTGAAAGCTGTATGAAGT	Forward	GACCCAGAGCTCCTTTTCAAC	Forward	CAAGGGGTAAGGGTGTC
Reverse	GGGTCCCTGCTTTGAGA	Reverse	GGGGGTGCCAGTGATAGAGT	Reverse	TCTAGAGCTGGCCTATCATAA
GAPDH	**Primer Sequence 5' to 3'**				
Forward	TTCCGTGTTCCTACCCCCAATGTGT				
Reverse	GGAGTTGCTGTTGAAGTCGCAGGAG				

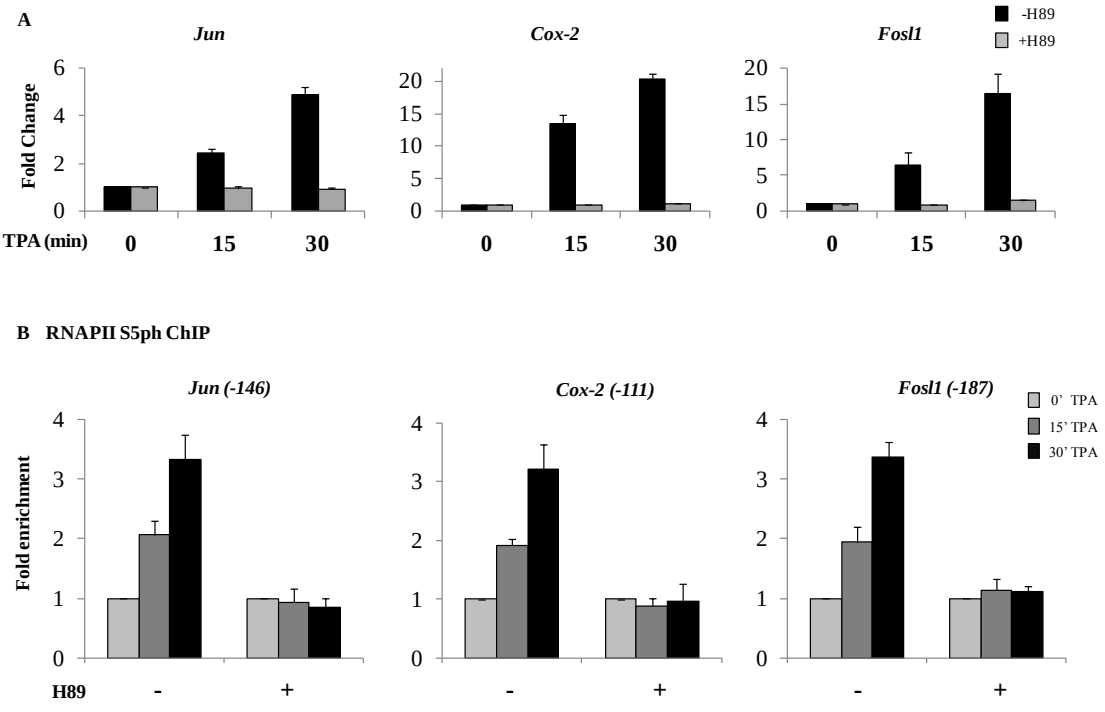

Figure S1. Inhibition of TPA-induced transcription initiation of the *Jun*, *Cox-2* and *Fosl1* genes by H89. Serum-starved 10T1/2 cells were pre-treated or not with H89 prior to TPA stimulation for 0, 15 or 30 min. (A) Total RNA was isolated and quantified by real time RT-PCR. Fold change values, normalized to GAPDH levels in untreated and treated samples and to time 0 values, are the mean of three independent experiments, and the error bars represent the standard deviation. (B) Formaldehyde crosslinked mononucleosomes were prepared and used in ChIP assays with anti-RNAPII S5ph antibodies. Equal amounts of input and immunoprecipitated DNAs were quantified by real-time quantitative PCR. The enrichment values of the 5' proximal sequences of *Jun* (-146), *Cox-2* (-111) and *Fosl1* (-187) genes are the mean of three independent experiments, and the error bars represent the standard deviation.

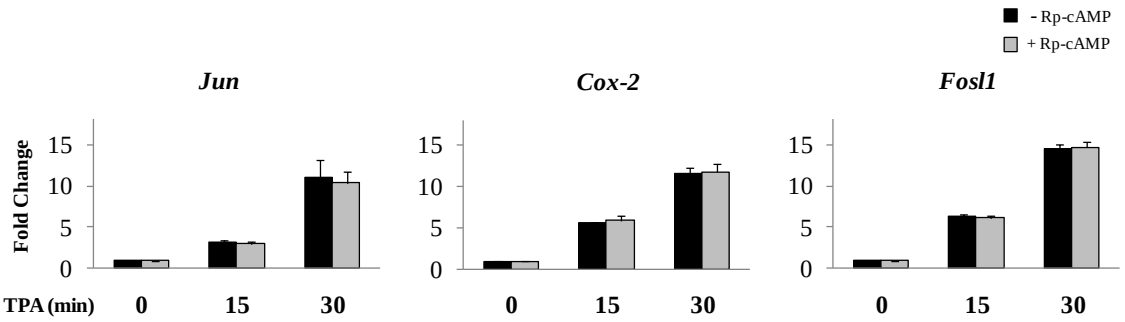

Figure S2. No inhibition of TPA-induced transcription initiation of the *Jun*, *Cox-2* and *Fosl1* genes by Rp-cAMP. Serum-starved 10T1/2 cells were pre-treated or not with Rp-cAMP prior to TPA stimulation for 0, 15 or 30 min. Total RNA was isolated and quantified by real time RT-PCR. Fold change values, normalized to time 0 values, are the mean of three independent experiments, and the error bars represent the standard deviation.

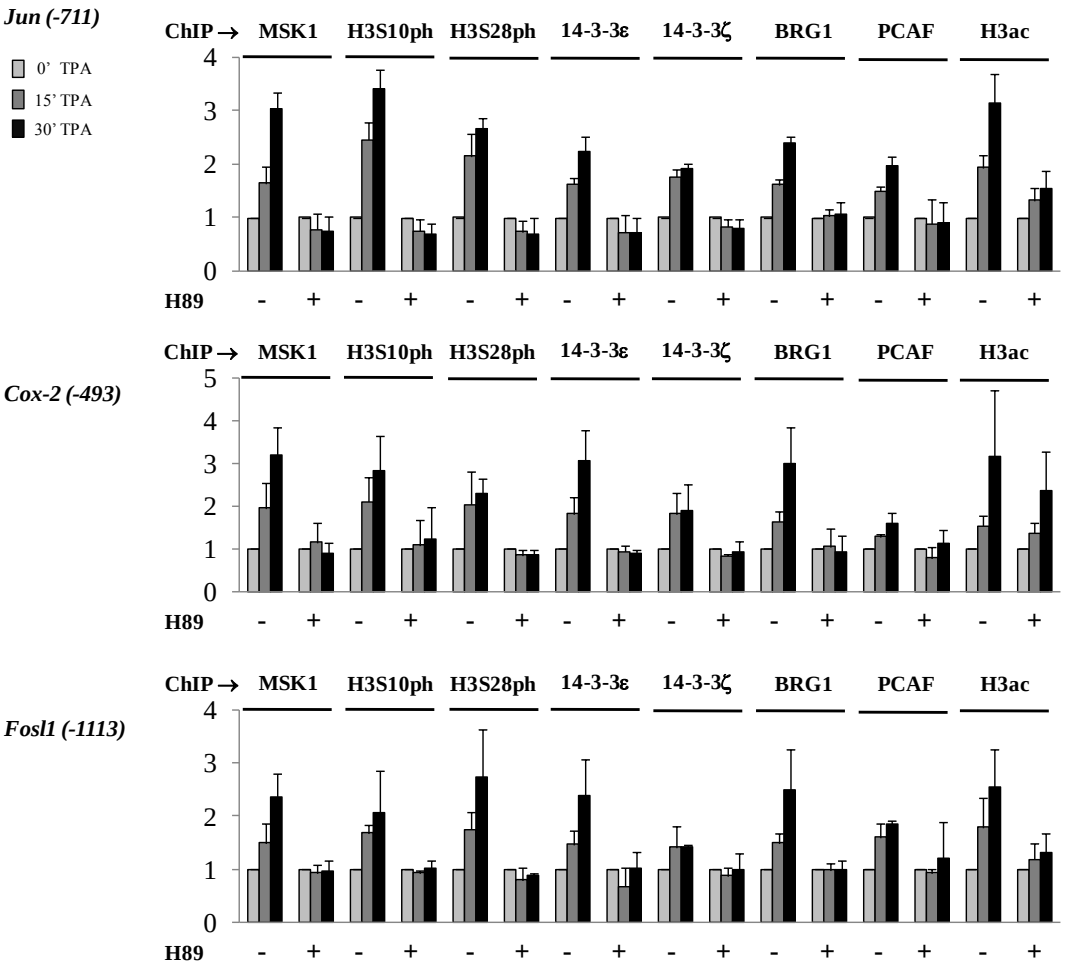

Figure S3. Inhibition by H89 of TPA-induced nucleosomal response and chromatin remodeler/modifier recruitment to the *Jun*, *Cox-2* and *Fosl1* 5' distal regulatory regions. Serum-starved 10T1/2 cells were pre-treated or not with H89 prior to TPA stimulation for 0, 15 or 30 min. Formaldehyde crosslinked mononucleosomes were prepared and used in ChIP assays with antibodies against MSK1, H3S10ph, H3S28ph, 14-3-3ε, 14-3-3ζ, BRG1, PCAF or H3K9acK14ac. Equal amounts of input and immunoprecipitated DNAs were quantified by real-time quantitative PCR. The enrichment values of the 5'distal sequences of *Jun* (-711), *Cox-2* (-493) and *Fosl1* (-1113) genes are the mean of three independent experiments, and the error bars represent the standard deviation.

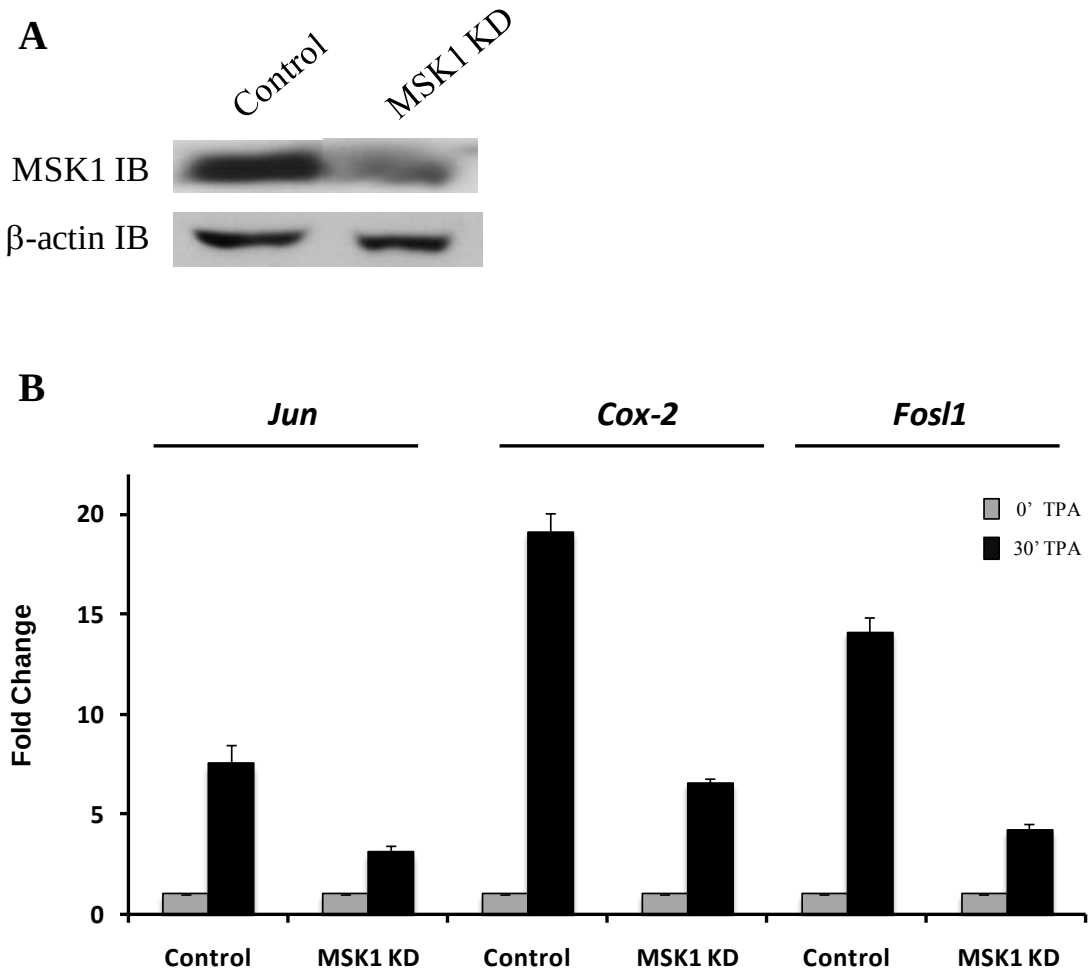

Figure S4. Reduced TPA-induced transcription initiation of the *Jun*, *Cox-2* and *Fosl1* genes in MSK1 knockdown 10T1/2 cells. (A) Aliquots of 1 mg total cell extracts from control and MSK1 knockdown 10T1/2 cells were incubated with anti-MSK1 antibodies. Immunoprecipitated proteins were resolved on SDS-10%-PAGE and immunoblotted with indicated antibodies (IB). (B) Quiescent control and MSK1 knockdown 10T1/2 cells were TPA-stimulated for 0 or 30 min. Total RNA was isolated and quantified by real time RT-PCR. Fold change values, normalized to GAPDH levels and to time 0 values, are the mean of three independent experiments, and the error bars represent the standard deviation.