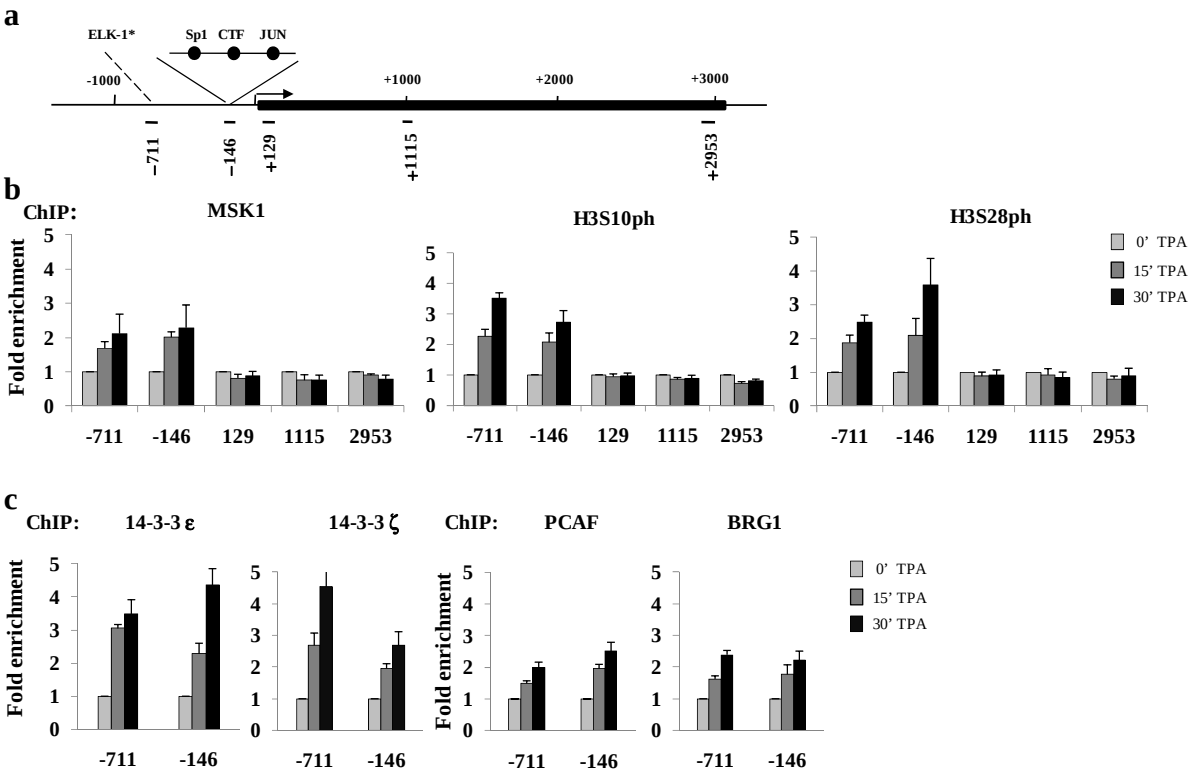
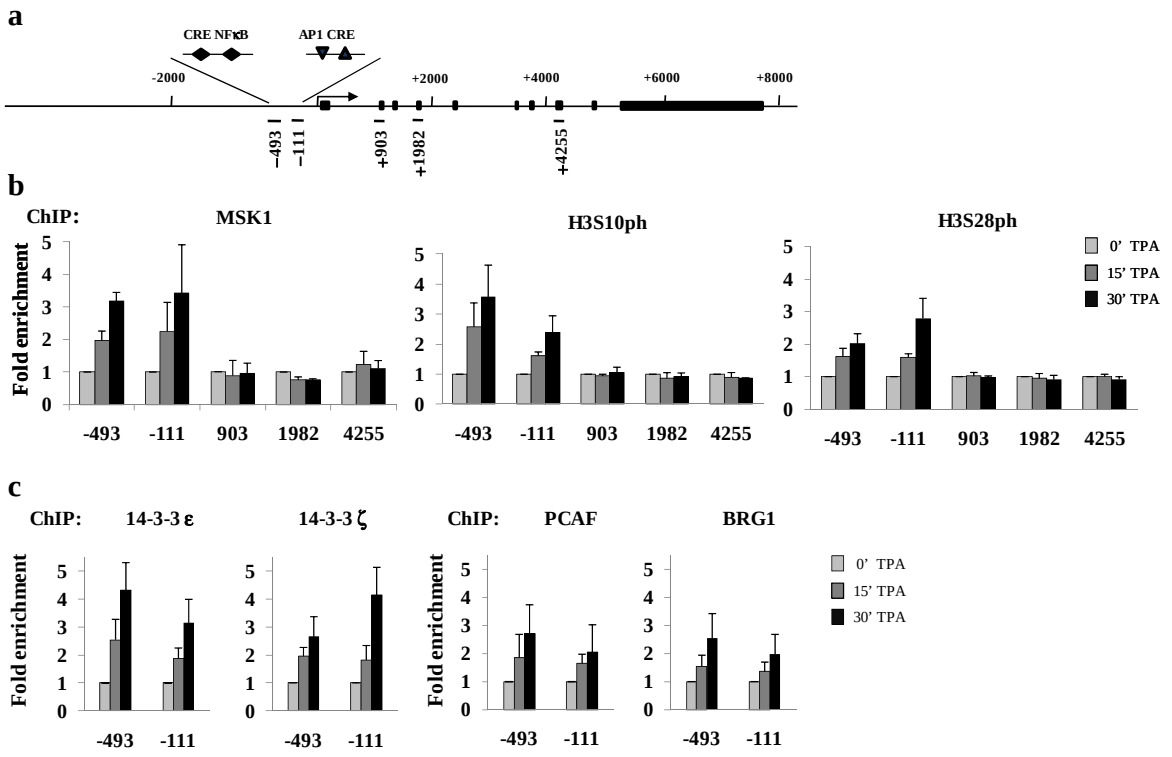
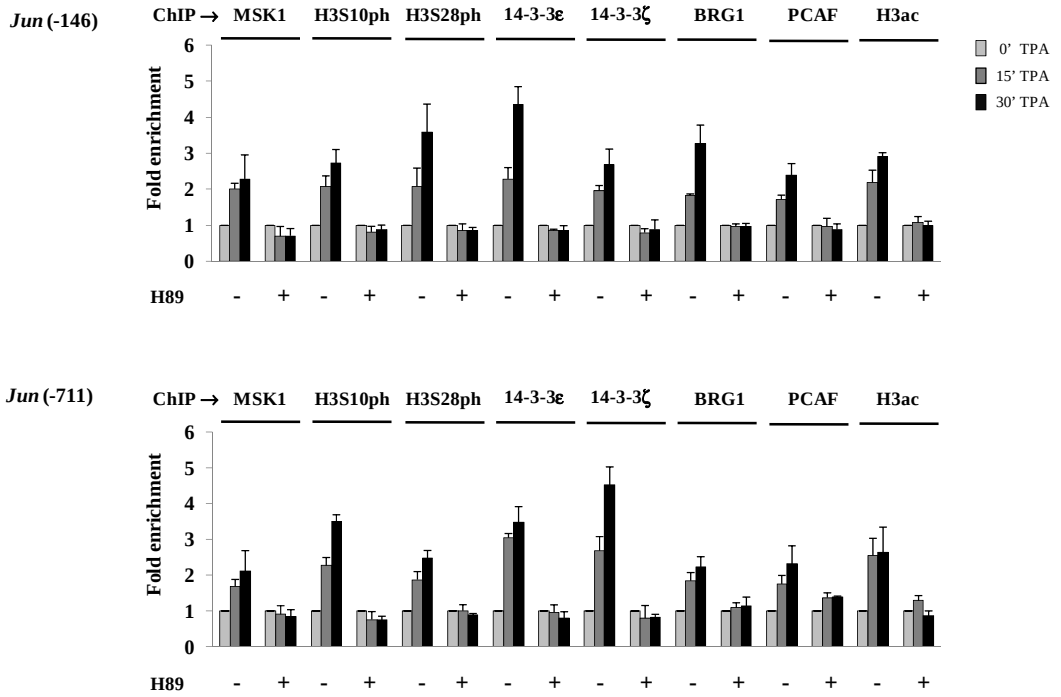


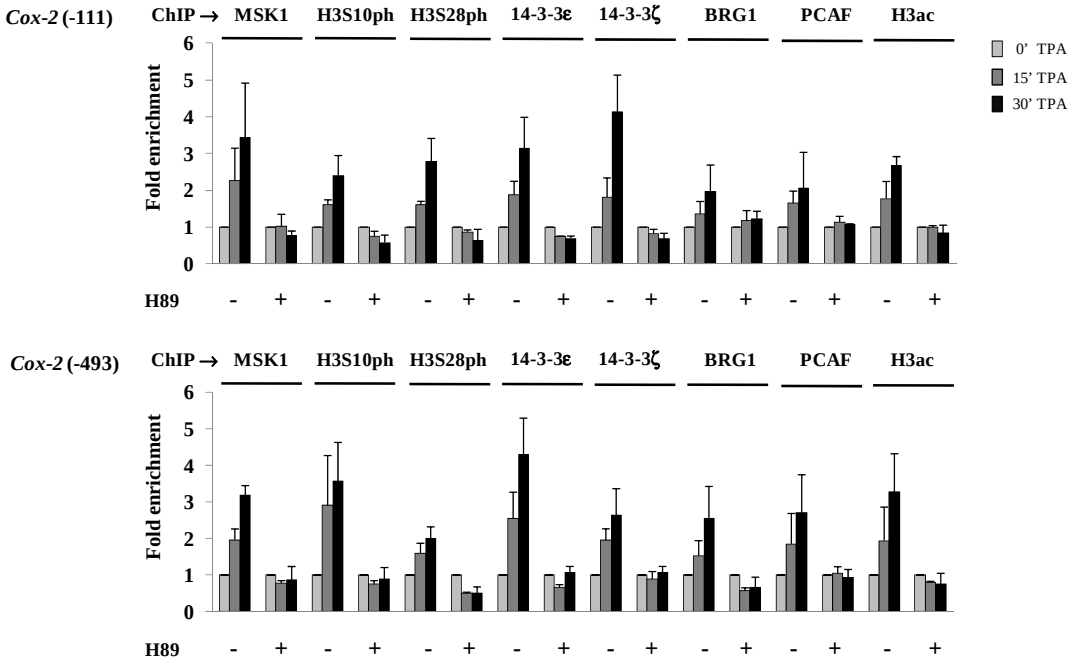
Supplementary Figure 1 TPA-induced nucleosomal response and recruitment of 14-3-3 and chromatin modifiers/remodelers at the *Jun* regulatory regions in *Hras1*-transformed mouse fibroblasts. (**a**) Schematic representation of *Jun* gene showing regions amplified in the ChIP assays. Each region is labeled according to the 5' position of the forward primer relative to the transcription start site. Exons are represented by boxes, and binding sites of relevant transcription factors located in the amplified regions are displayed. CTF, CCAAT-box-binding protein (also known as NF1, nuclear factor 1); * indicates a putative binding site. ChIP experiments were performed using antibodies against MSK1, H3S10ph, H3S28ph (**b**), 14-3-3ε/ζ, PCAF and BRG1 (**c**) on formaldehyde-crosslinked mononucleosomes prepared from serum-starved Ciras-3 cells treated with TPA for 0, 15 and 30 min. Equal amounts of input and immunoprecipitated DNA were quantified by real-time quantitative PCR. Enrichment values are the mean of three independent experiments and the error bars represent the standard deviation.



Supplementary Figure 2 TPA-induced nucleosomal response and recruitment of 14-3-3 and chromatin modifiers/remodelers at the *Cox-2* regulatory regions in *Hras1*-transformed mouse fibroblasts. (**a**) Schematic representation of *Cox-2* gene showing regions amplified in the ChIP assays. Each region is labeled according to the 5' position of the forward primer relative to the transcription start site. Exons are represented by boxes, and binding sites of relevant transcription factors located in the amplified regions are displayed. CRE is the cyclic-AMP responsive element; AP-1 constitutes a combination of dimers formed of members of the JUN, FOS and ATF families of transcription factors. ChIP experiments were performed using antibodies against MSK1, H3S10ph, H3S28ph (**b**), 14-3-3ε/ζ, PCAF and BRG1 (**c**) on formaldehyde-crosslinked mononucleosomes prepared from serum-starved Ciras-3 cells treated with TPA for 0, 15 and 30 min. Equal amounts of input and immunoprecipitated DNA were quantified by real-time quantitative PCR. Enrichment values are the mean of three independent experiments and the error bars represent the standard deviation.



Supplementary Figure 3 H89 inhibition of TPA-induced nucleosomal response and chromatin remodeler/modifier recruitment to *Jun* regulatory regions in *Hras1*-transformed mouse fibroblasts. Serum-starved Ciras-3 cells were 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 as indicated. Equal amounts of input and immunoprecipitated DNA were quantified by real-time quantitative PCR. Enrichment values are the mean of three independent experiments and the error bars represent the standard deviation.



Supplementary Figure 4 H89 inhibition of TPA-induced nucleosomal response and chromatin remodeler/modifier recruitment to *Cox-2* regulatory regions in *Hras1*-transformed mouse fibroblasts. Serum-starved Ciras-3 cells were 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 as indicated. Equal amounts of input and immunoprecipitated DNA were quantified by real-time quantitative PCR. Enrichment values are the mean of three independent experiments and the error bars represent the standard deviation.