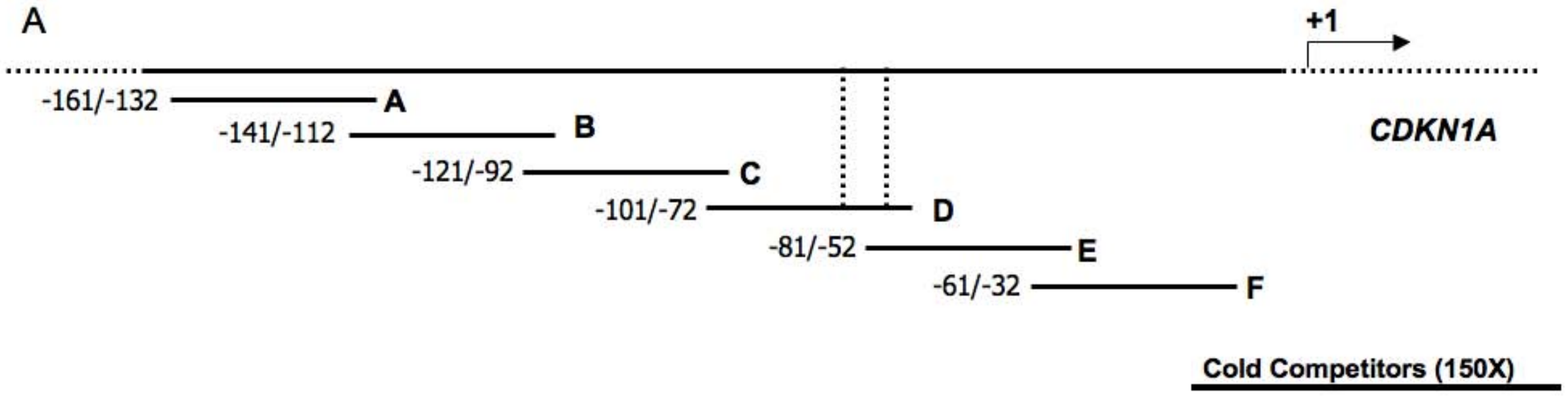
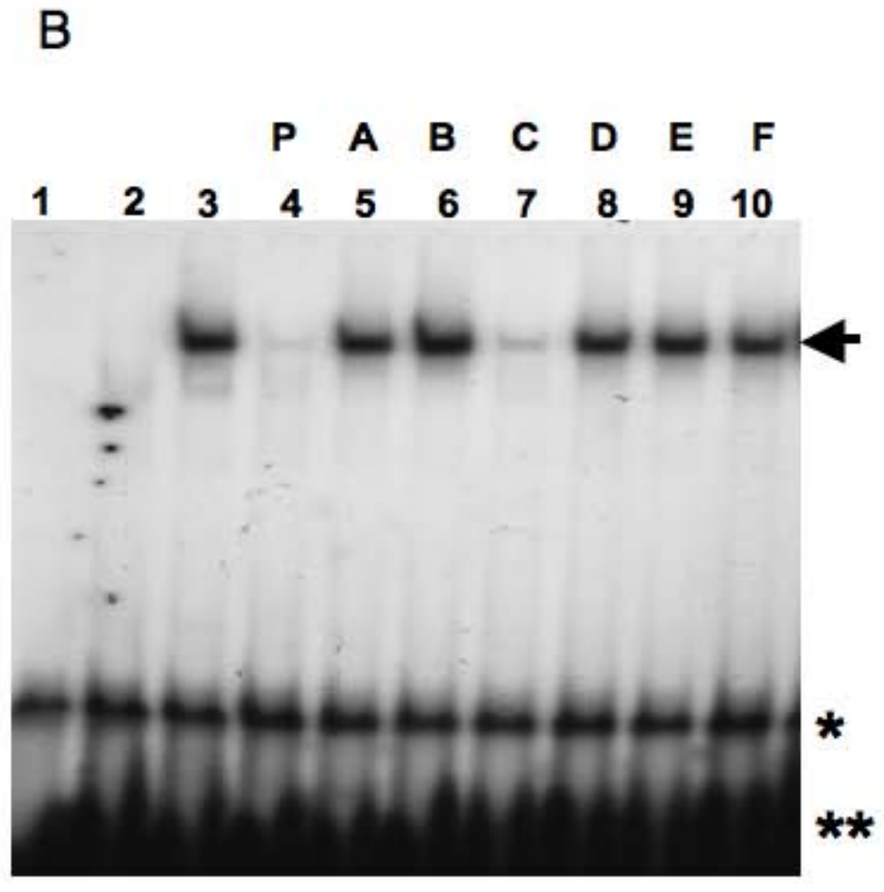
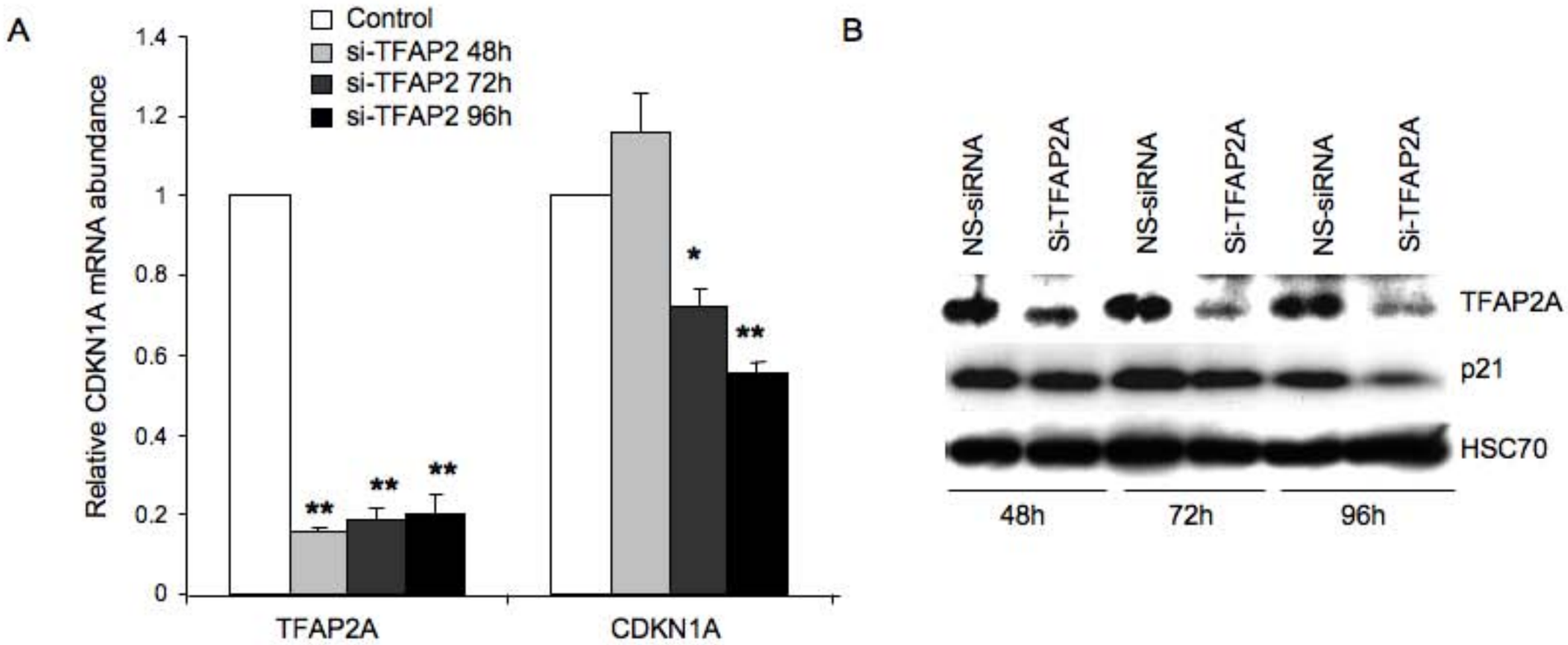




Supplementary Figure S1: TFAP2A binds to the -112/-101 region of the *CDKN1A* promoter. (**A**) Schematic representation of the series of overlapping ds oligonucleotides covering the -161/-32 region of the *CDKN1A* promoter used in the EMSA competition assay. Sequence numbering is from the start of transcription at +1 defined by RefSeq NM_078467. The binding site described by Zeng et al [10] is indicated by vertical dotted lines. (**B**) EMSAs were performed using *in vitro* translated TFAP2A protein (lanes 3 to 10), *in vitro* translated luciferase protein (lane 2) or no protein control (lane 1), incubated with an oligonucleotide probe (representing the well-characterised consensus AP-2 binding site in the metallothionein IIA promoter; [1]) with no competitor (lanes 1-3) or competed with150X molar excess of the unlabelled probe (P, lane 4) or oligonucleotides A-F, as indicated. The arrow indicates the position of the DNA/TFAP2A complex, while * and ** indicate non specific bands and free probe respectively.



Supplementary Figure S2: TFAP2A expression is efficiently silenced using siRNA. MCF10A cells were transiently transfected with a non-silensing control siRNA (NS-siRNA) or a TFAP2A targeting siRNA (see Materials & Methods) for the indicated times. (**A**) Total RNA was subjected to quantitative RT-PCR using TaqMan primers/probes for TFAP2A and *CDKN1A*. GAPDH was used as internal control and data are represented as fold change compared to the NS-siRNA transfected cells. The asterisks denote a significant difference between control cells and those transfected with TFAP2A siRNA using Student's t test: *P<0.01, ** P<0.001. (**B**) Western blot analysis of whole cell lysates (10 μg/lane) from MCF10A cells transiently transfected with NS- siRNA or TFAP2A si RNA. Hsc70 was used as a lading control.