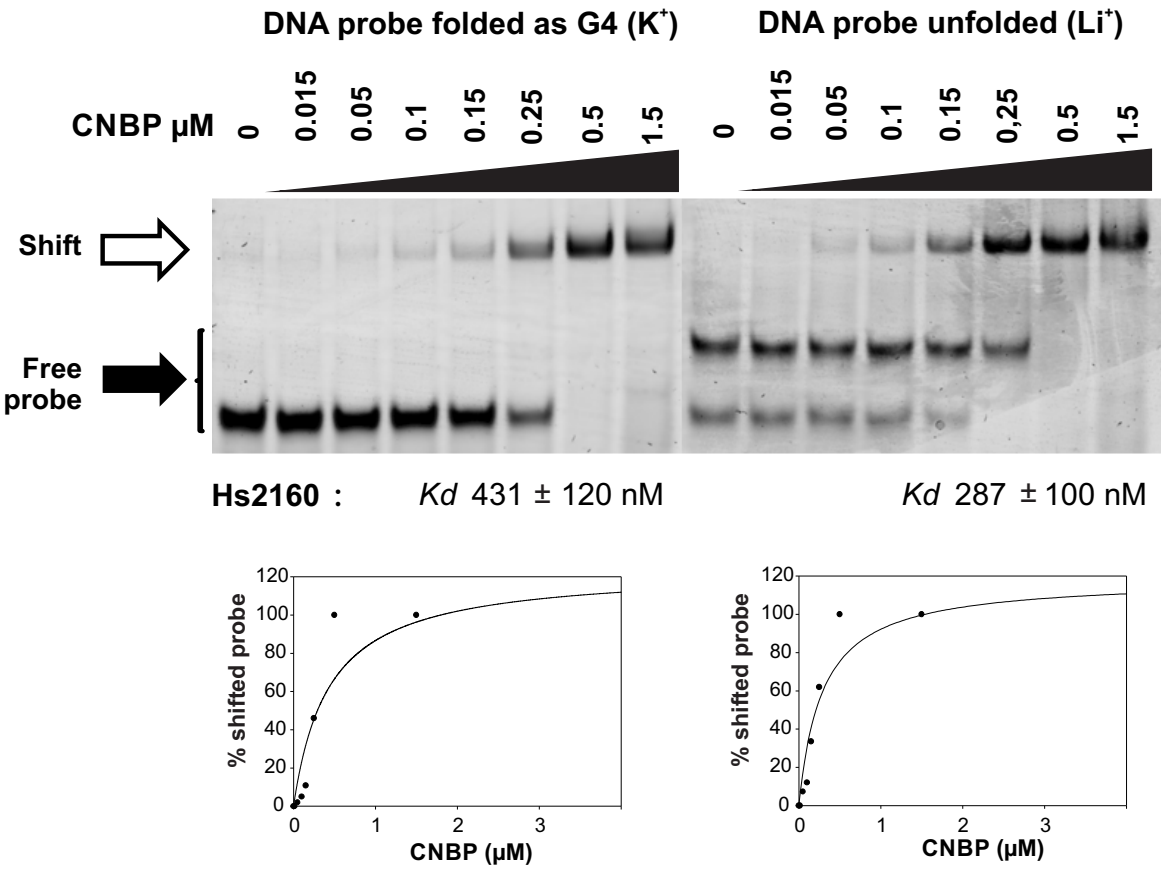

Figure S1. Analysis of CNBP binding to Hs2160 folded as G4 and unfolded. Top. Representative non-radiative EMSAs (n=3) performed using ssDNA Hs2160 incubated in the absence or presence of increasing concentrations of CNBP and folded in the presence of K^+ 100 mM (left) or Li^+ 100 mM (right) in the binding reaction. Free and shifted probes are indicated by arrows. Apparent *Kd* values for each condition are indicated below each gel. Bottom: plots of apparent *Kd* calculations.

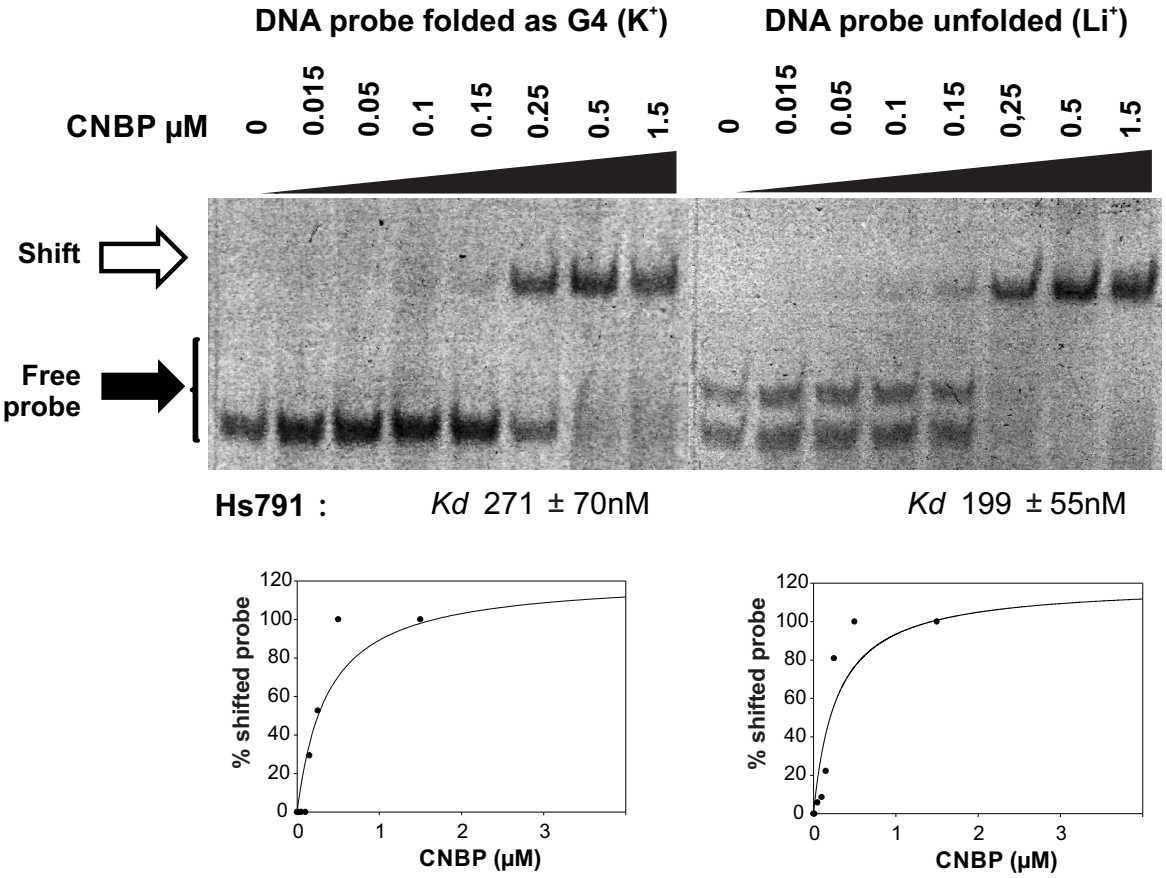

Figure S2. Analysis of CNBP binding to Hs791 folded as G4 and unfolded. Top. Representative non-radiative EMSAs (n=3) performed using ssDNA Hs791 incubated in the absence or presence of increasing concentrations of CNBP and in the presence of K^+ 100 mM (left) or Li^+100 mM (right) in the binding reaction. Free and shifted probes are indicated by arrows. Apparent *Kd* values for each condition are indicated below each gel. Bottom: plots of apparent *Kd* calculations.

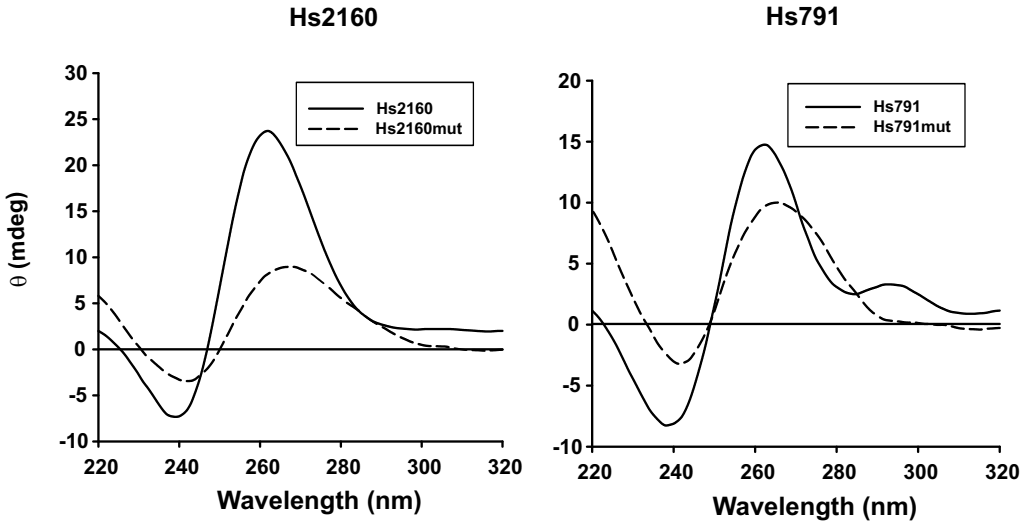

Figure S3. CD spectra of PQSs and their mutated versions. Oligonucleotides representing Hs2160 and Hs791 (solid lines), and their mutated versions (dashed lines were folded as G4 in the presence of stabilizing cation (100 mM KCl) and the CD spectra were obtained.

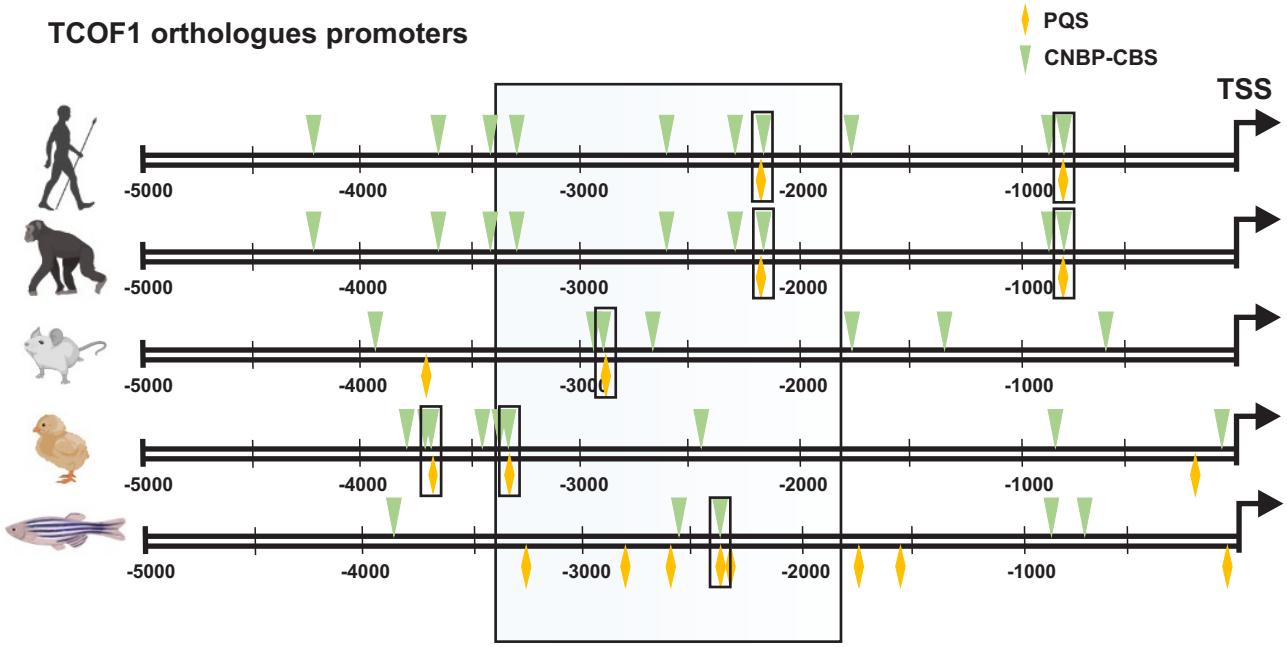

Figure S4. Scheme of the different *TCOF1* orthologues promoter regions showing CNBP binding sites and PQSs. The extended promoter regions (between the transcription start sites (TSS, indicated by an arrow and +1) and 5000 bp upstream) of *TCOF1* genes from different species (indicated by the pictures on the left) were downloaded from Ensembl and analyzed according Mat. & Methods. Included sequences are: *Homo sapiens* (ENSG00000070814), *Pan troglodytes* (ENSPTRG00000017416) *Mus musculus* (ENSMUSG00000024613), *Gallus gallus* (ENSGALG00000005535), *Danio rerio* (ENSDARG00000024561). The scheme details the CNBP consensus sites (green arrowheads) and PQSs (yellow diamonds). The rectangle shadowed indicates the -2000 to -3500 region where all the sequences present a PQS overlapping with a CNBP binding site.

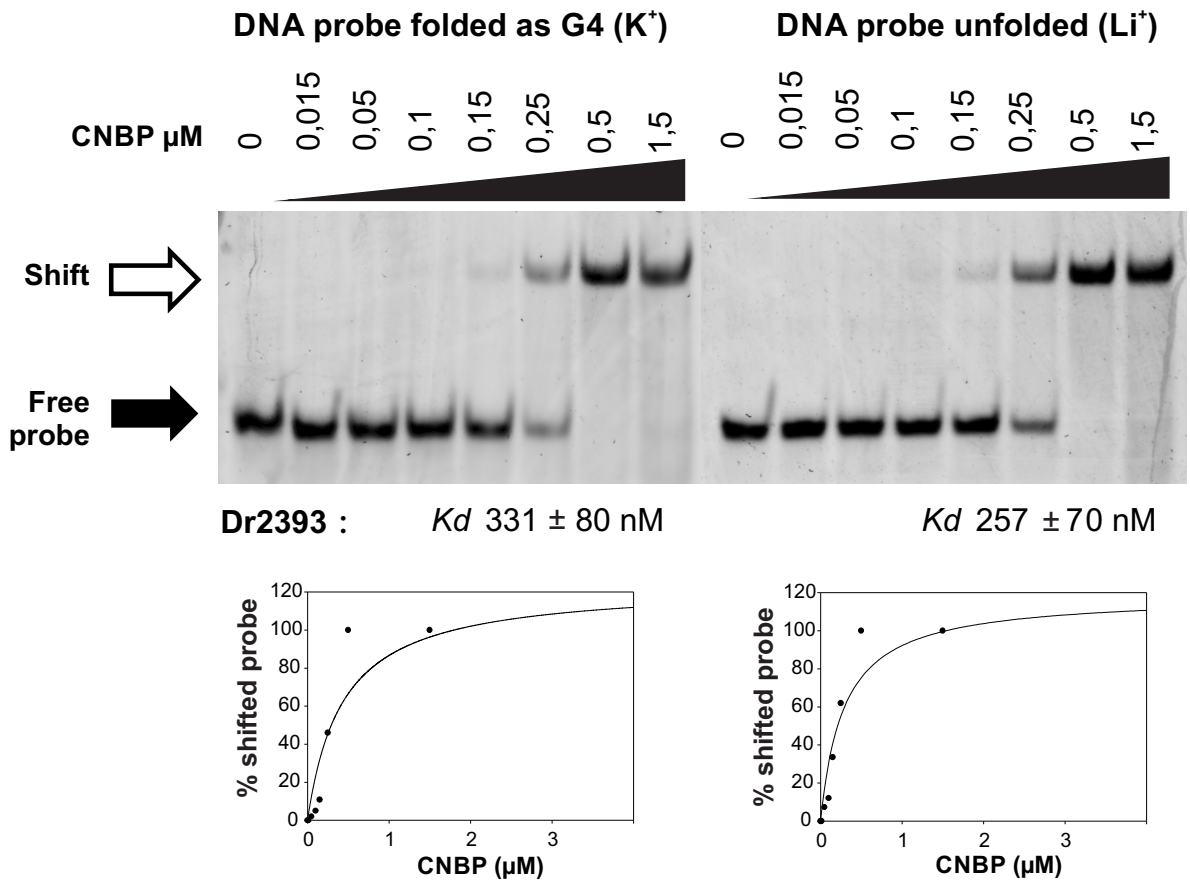

Figure S5. Analysis of CNBP binding to Dr2393 folded as G4 and unfolded. Top. Representative nonradiative EMSAs (n=3) performed using ssDNA Dr2393 incubated in the absence or presence of increasing concentrations of CNBP and folded in the presence of K^+ 100 mM (left) or Li^+ 100 mM (right) in the binding reaction. Free and shifted probes are indicated by arrows. Apparent *Kd* values for each condition are indicated below each gel. Bottom: plots of apparent *Kd* calculations.

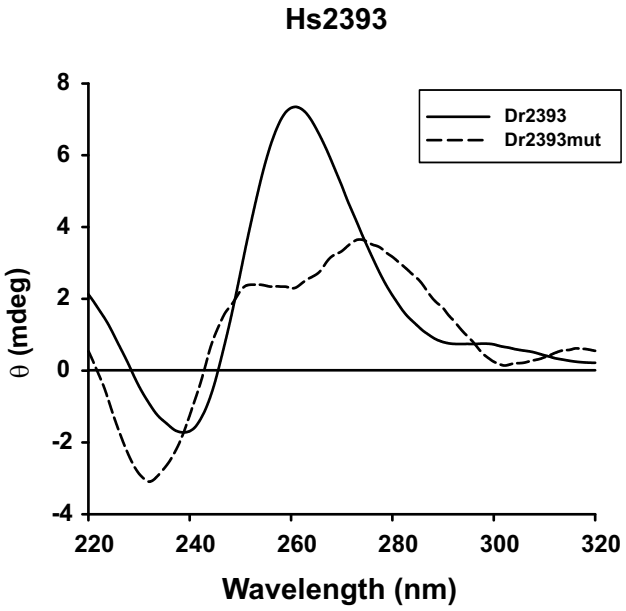

Figure S6. CD spectra of PQS Dr2393 and its mutated version. Oligonucleotide representing Dr2393 (solid lines), and its mutated version (dashed lines) were folded in the presence of stabilizing cation (100 mM KCl) and the CD spectra were obtained.

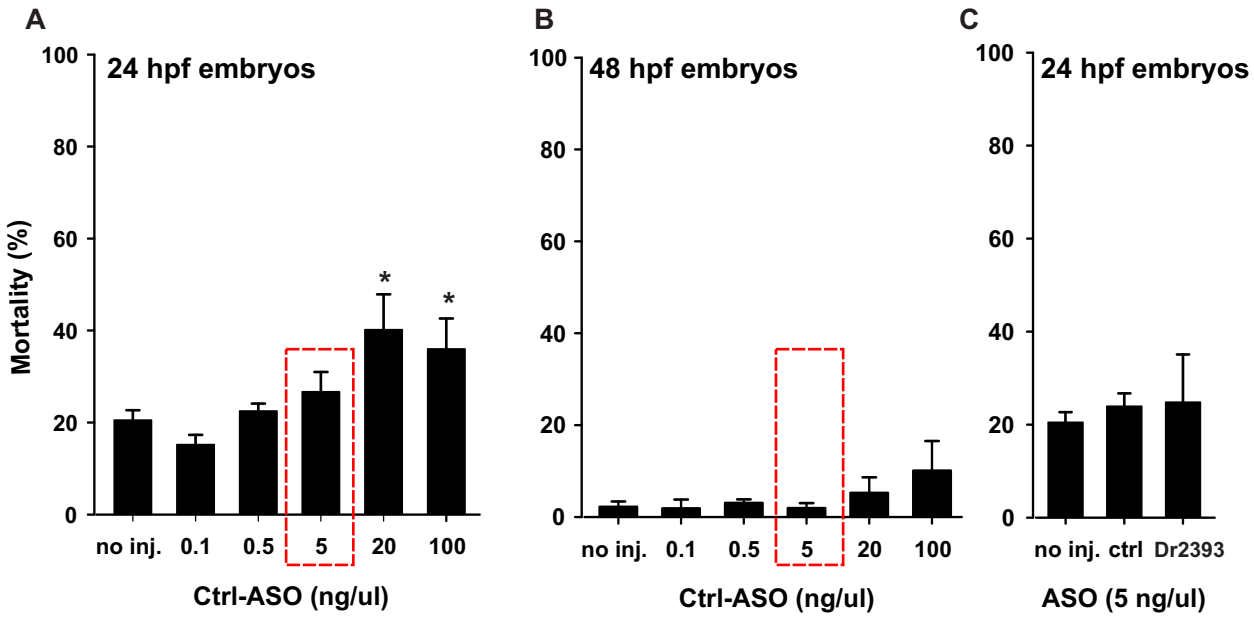

Figure S7. Determination of the highest sub-toxic dose of ASO for embryo microinjection. Control oligonucleotide (Ctrl-ASO) was injected in several dilutions in KCl 0.1 M ranging from 0.001 to 100 ng/µl in order to determine the highest sub-toxic dose that did not produced mortality, or evident phenotypes compared to control embryos (no inj). Percentages of dead embryos were determined at 24-hpf (A) and 48-hpf (B) to define 5 ng/µl as the highest sub-toxic dose of ASO. The selected dose is indicated by the red dashed rectangle. Finally, at 5 ng/µl the specific ASO (Dr2393-ASO) was injected and mortality was not different from controls.