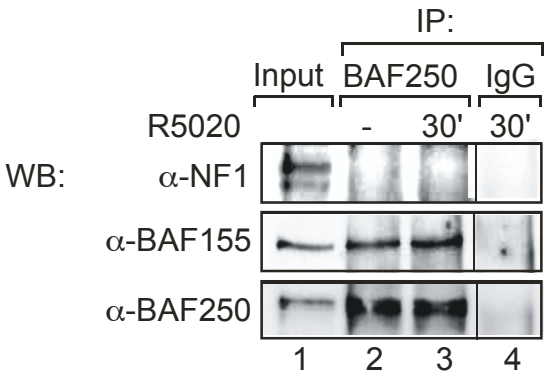


**Figure S1. NF1 fails to form a complex with BAF**
T47D-MTVL cells were untreated (-) or treated for 30 min with R5020, lysed and immunoprecipitated either with α-BAF250 antibody or with normal mouse IgG as a negative control (IgG). Inputs and IPs were analyzed by western blot using α-NF1, α-BAF155 and α-BAF250, as indicated.

Supplementary Figure 1
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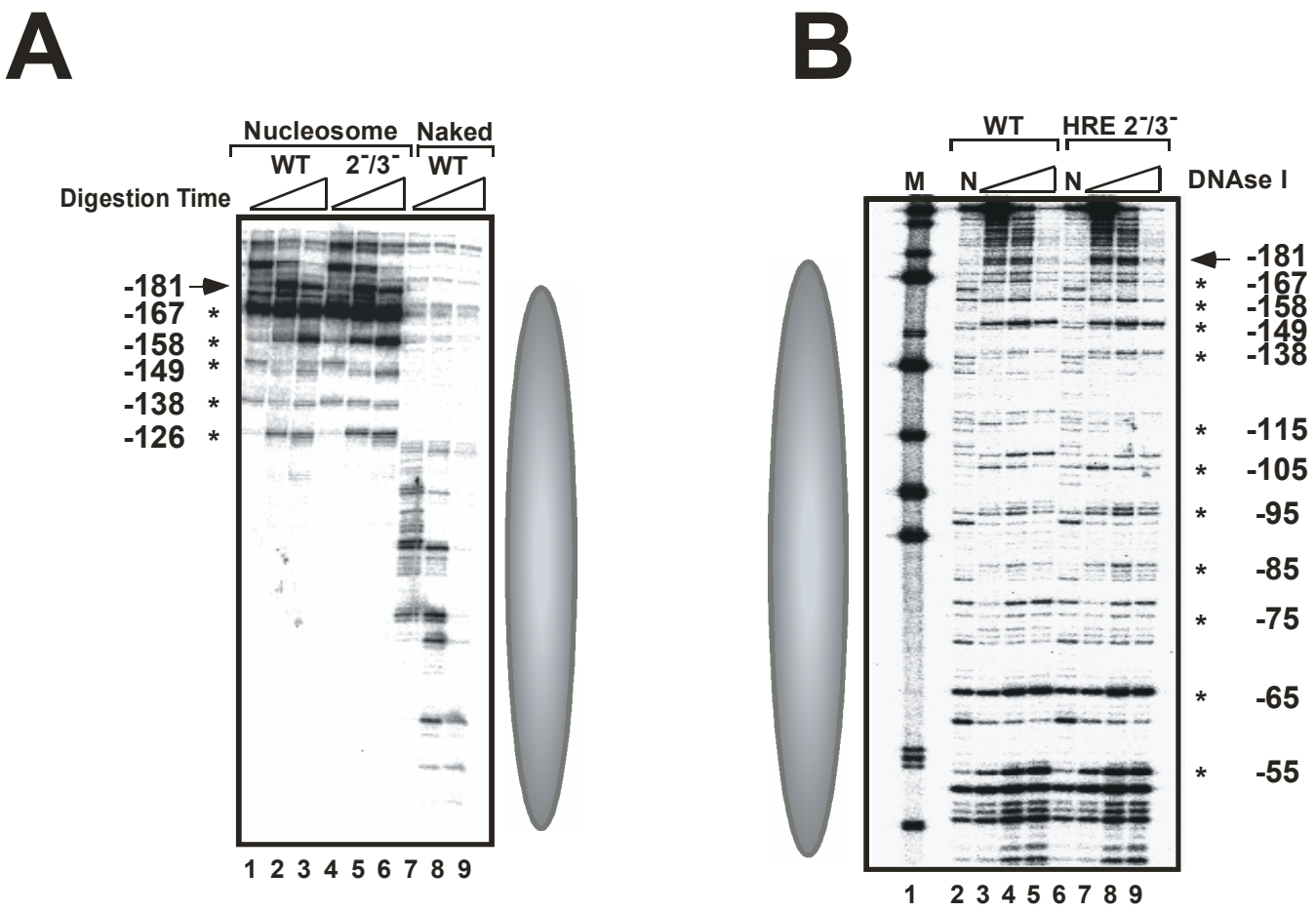


**Figure S2.** Panel A. Reconstituted wild type and HRE $2^-$ /$3^-$ mutant nucleosomes labeled at the proximal end were digested at 25°C for 20, 60 and 180 minutes with 200 units/ml of exonuclease III in 20 μl reaction mixture. DNA digestion products were analyzed by electrophoresis on a 6.5% sequencing gel. M, size markers. Asterisks indicate the main stops of the exonuclease III inside the nucleosome. The grey oval indicates the main population of nucleosomes.

Panel B. Reconstituted wild type and HRE $2^-$ /$3^-$ mutant nucleosomes labeled at the proximal end, were treated with different concentrations of DNase I (1, 2, 5 ng/reaction, lanes 3-5 and lanes 7-9). The digested particles were separated on 8% sequencing gels. N, naked DNA used as control. M, size markers. Asterisks indicate the expected 10 bp periodicity produced after DNAse I digestion.

Supplementary Figure 2
Vicent et al

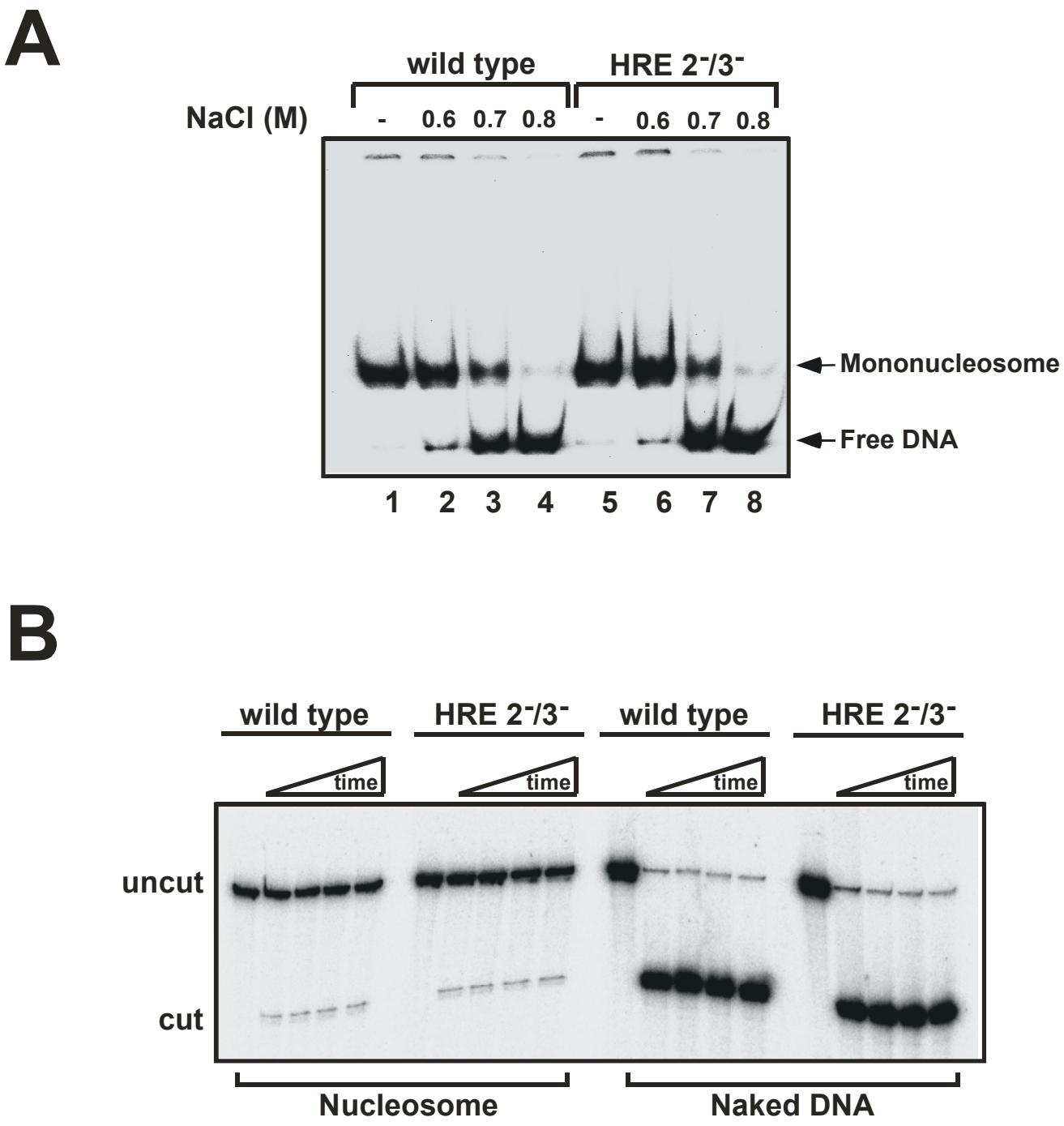


**Figure S3.** Panel A Reconstituted wild type and HRE 2$^-$ /3$^-$ mutant nucleosomes labeled at the proximal endwere subject to stability studies as previously described (21).Panel B Stability experiments were done as previously reported (21).Wild type and mutant MMTV mononucleosomes and naked DNA were digested at 37°C with 500 U/ml of Sac I in a total volume of 160 μl. At different time points, aliquots of 19 μl were removed and added to 181 μl of stop buffer to give a final concentration of 12.5 mM EDTA and 0.5% SDS. The samples were then extracted with phenol, phenol/chloroform, and chloroform/isoamylic alcohol and precipitated with three volumes of ethanol. After washing with 80% ethanol and drying, the samples were analyzed on 8% denaturing polyacrylamide gels.

Supplementary Figure 3
Vicent et al

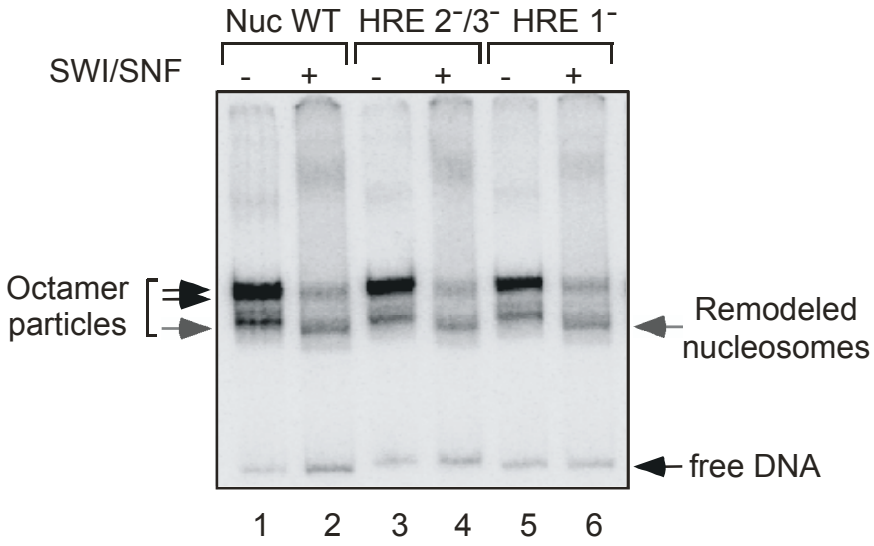


**Figure S4: SWI/SNF remodeling of wild type, HRE2$^{-}$/3$^{-}$ and HRE1$^{-}$ mutant nucleosomes**

Wild type (WT), HRE 2$^{-}$/3$^{-}$ and HRE 1$^{-}$ MMTV nucleosomes were incubated with SWI/SNF in the presence of ATP. The nucleosome positions were then analyzed on native 5% polyacrylamide gels. The migration of the three main populations of MMTV nucleosomes are indicated on the left, the new population generated after SWI/SNF remodeling and the free DNA are indicated on the right.

Supplementary Figure 4
Vicent et al

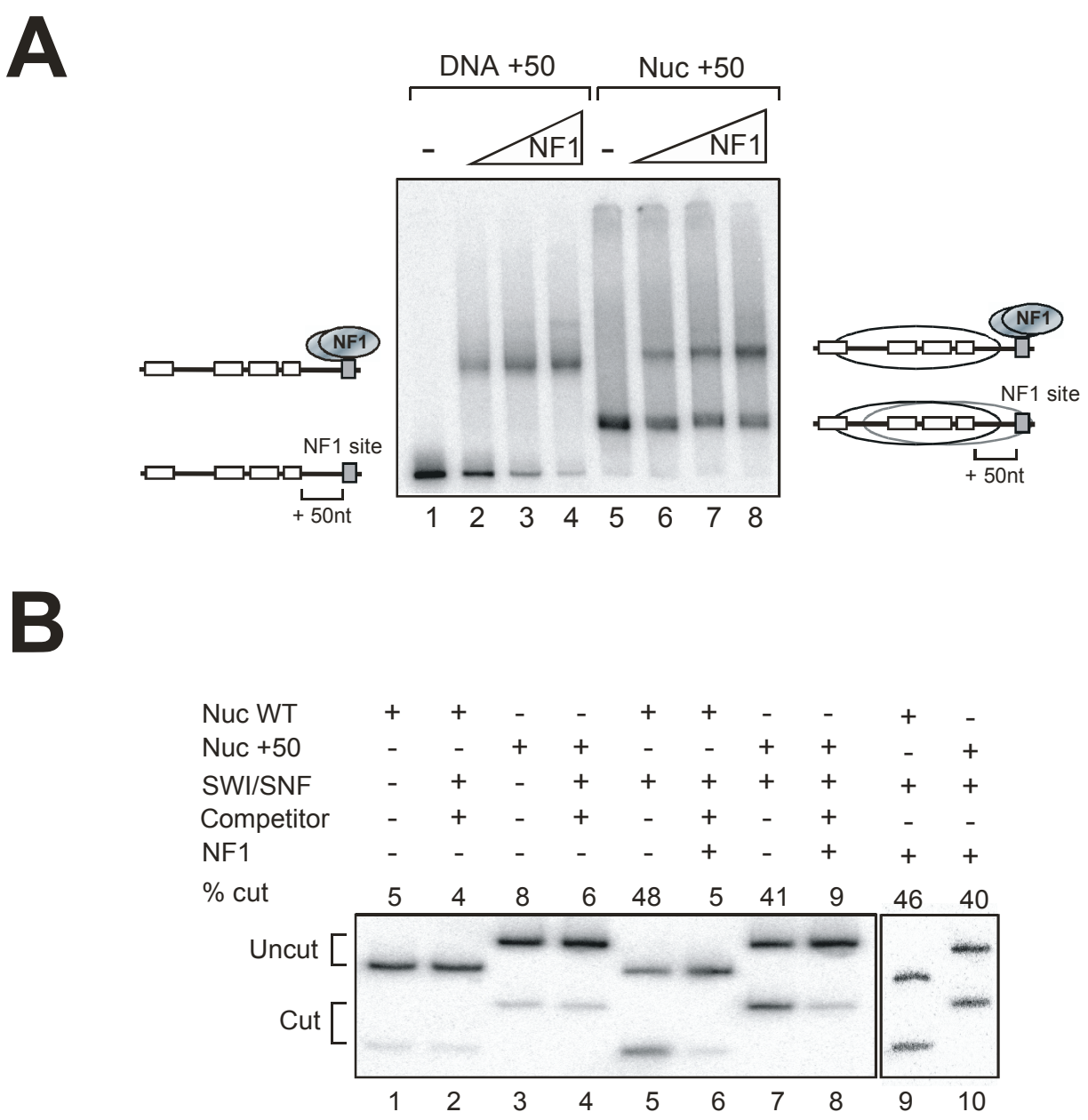


**Figure S5. NF1 cannot recruit SWI/SNF to MMTV nucleosomes**

Panel A. Reconstituted +50 MMTV nucleosomes and +50 naked DNA were incubated at room temperature for 20 minutes with increasing amounts of recombinant NF1 in 20 μl reactions. The samples were electrophoresed on a 3.5% acrylamide/0.5% agarose/20% glycerol/0.3 x TBE gel. The interpretation of the bands is shown on the left for naked DNA and on the right for nucleosomes.

Panel B. Reconstituted wild type (WT) and +50 MMTV nucleosomes were treated with SWI/SNF in the presence of ATP, competitor DNA and NF1 as indicated. Following incubation at room temperature for 20 min, the nucleosomes were digested with Sac I. The DNA fragments were electrophoresed in 8% denaturing polyacrylamide gels. The % of cut DNA is shown on top of each lane.

Supplementary Figure 5
Vicent et al

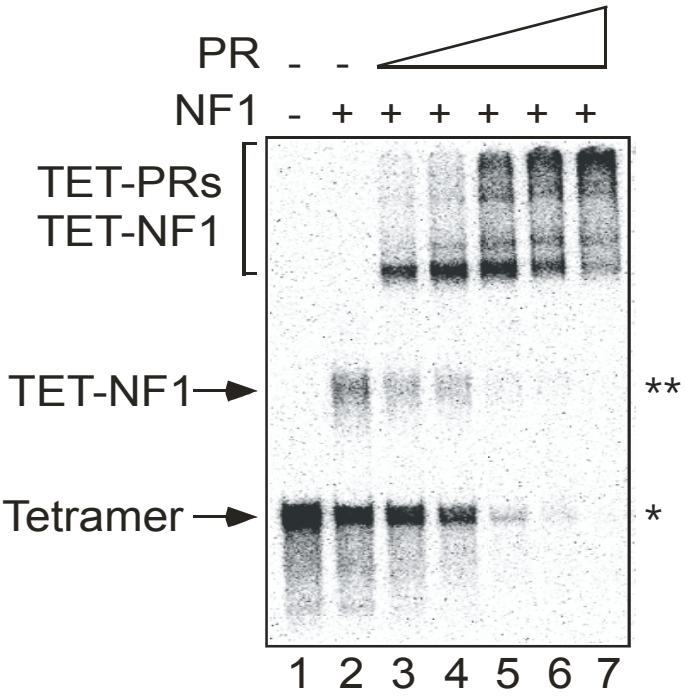


**Figure S6. NF1 facilitates binding of PR to the HREs 2 and 3.** Reconstituted MMTV tetramer particles were incubated with a fixed amount of NF1 (*lane 2*) and increasing amounts of PR (*lanes 3-7*). Samples were analyzed in a 5% acrylamide gel. * and ** from lane 2 to 7 indicate the bands used to quantify the relative affinity of PR to TET and to TET-NF1, respectively.

Supplementary Figure 6
Vicent et al

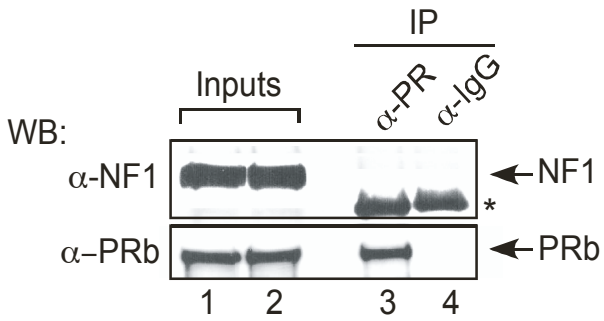


**Figure S7: Interaction of PR with NF1 *in vitro*.** For binding of the factors, recombinant PR and NF1 were incubated for 2 hs at 4ºC. For precipitation of the complexes, binding reactions were incubated 2 hs at 4ºC with 20 μl glutathione sepharose beads coupled with the corresponding antibodies and eluted by boiling in SDS sample buffer. Input and IPs were analyzed for NF1 and PR by western blot using specific antibodies. The band labeled with an asterisk corresponds to IgG (50 kD).

Supplementary Figure 7
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