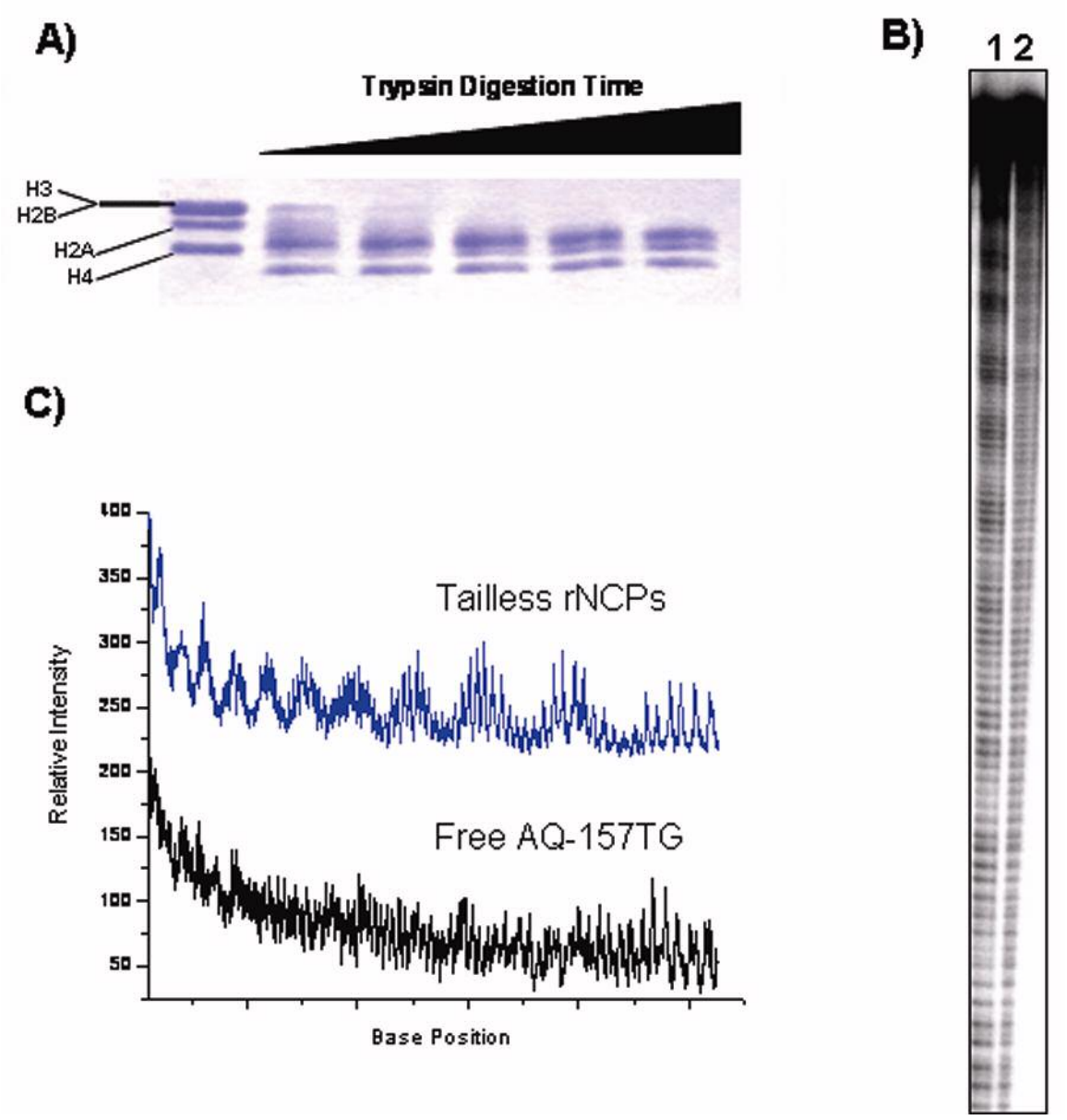
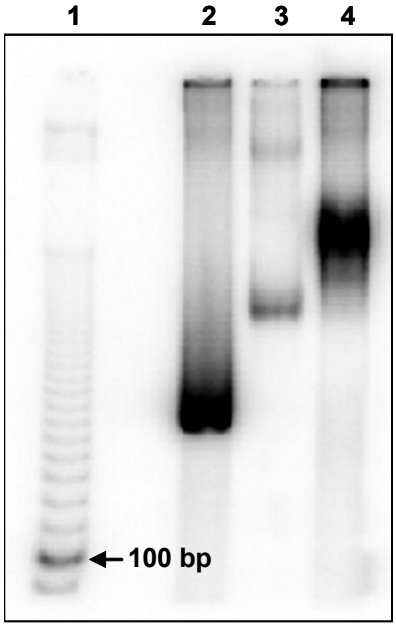
Supplementary Figure 1



Supplementary Figure 1: Structural analysis of limited trypsin digestion of AQ-157TG rNCPs. **A)** 18% SDS PAGE showing undigested histones (left lane) with increasing trypsin digestion time from left to right. **B)** Autoradiogram of hydroxyl radical footprinting on tailless AQ-157TG rNCPs (lanes 1) and free AQ-157TG (lane 2). **C**) Partial scan of the footprint in Part **B)** of both free AQ-157TG (bottom) and tailless AQ-157TG rNCPs (top). The 10 bp periodic cutting in the tailless rNCPs is apparent.

Supplementary Figure 2



Supplementary Figure 2: Result of an EMSA conducted to evaluate the effect of mixing AQ-157TG and native chicken erythrocyte NCPs together in a 1:50 molar ratio in a 10 mM sodium phosphate buffer without proper reconstitution into rNCPs. Lane 1 is a 10 bp DNA ladder, Lane 2 is free AQ-157TG, Lane 3 shows the results of a proper reconstitution of a 1:50 molar ratio of AQ-157TG and native NCPs carried out according to the materials and methods, and Lane 4 is the non-reconstituted 1:50 molar ratio mixture of AQ-157TG and native NCPs. It is apparent from a comparison of Lanes 2-4 that mixing together AQ-157TG and native NCPs results in almost 100% formation of DNA-protein aggregates of uncharacterized structure, and that these aggregates are distinct from the AQ-157TG rNCPs.