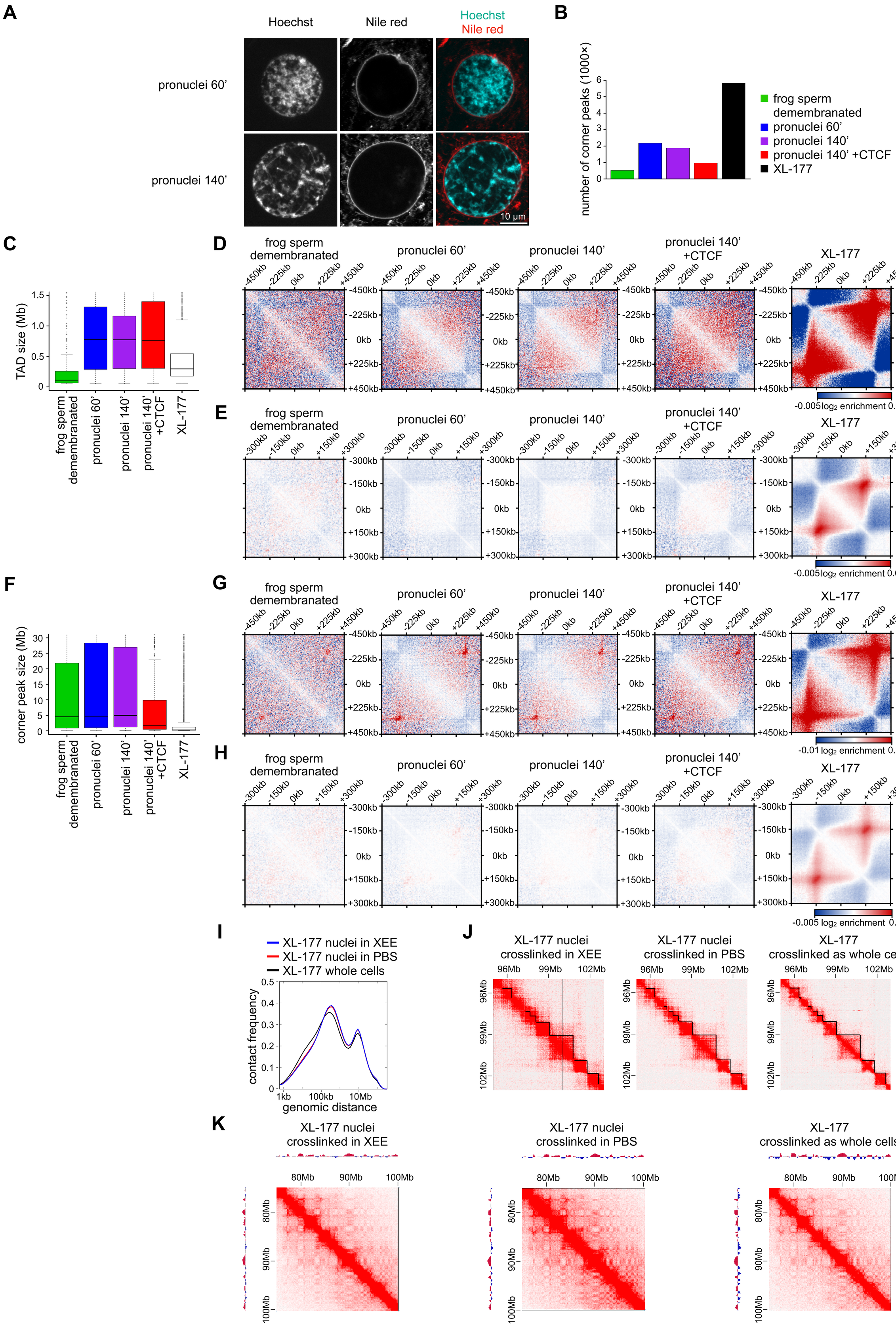

Supplemental Figure S5. Demembranated frog sperm is remodeled upon incubation in egg extract.

Supplemental Figure S5. Demembranated frog sperm is remodeled upon incubation in egg extract.
(A) Confocal microscopy of demembranated frog sperm in *Xenopus* egg extract after 60' (pronuclei 60') or 140' (pronuclei 140') used for Hi-C analysis. Nuclei were stained with Hoechst to visualize DNA and Nile red to visualize the nuclear membrane
(B) Number of corner peaks called for demembranated frog sperm, pronuclei 60', pronuclei 140', pronuclei 140' with addition of 50 nM CTCF protein and frog XL-177 cells
(C) TAD size distribution for the same samples as in (B)
(D) Aggregate contact frequencies (coverage and distance corrected) around the 135 550-650 kb long TADs called in XL-177 cells, for the same samples as in (B)
(E) Aggregate contact frequencies (coverage and distance corrected) around the 372 250-350 kb long TADs called in XL-177 cells, for the same samples as in (B)
(F) Corner peak size distribution for the same samples as in (B)
(G) Aggregate contact frequencies (coverage and distance corrected) around the 109 550-650 kb long corner peaks called in XL-177 cells, for the same samples as in (B)
(H) Aggregate contact frequencies (coverage and distance corrected) around the 479 250-350 kb long corner peaks called in XL-177 cells, for the same samples as in (B)
(I) Contact frequency as a function of genomic distance for isolated XL-177 nuclei crosslinked in *Xenopus* egg extract (XEE) or PBS and XL-177 cells crosslinked as whole cells
(J) Normalized Hi-C matrices for the same samples as in (I) in the region of Chr1S:95-103Mb at 25 kb resolution with TAD calling indicated using black lines
(K) Normalized Hi-C matrices for the same samples as in (I) in the region of Chr2S:75-100Mb at 100 kb resolution with compartment tracks from principal component analysis