



Supplemental Figure S1. The frog sperm genome is organized without TADs and corner peaks.

- (A) Confocal microscopy of frog sperm and de-membrated frog sperm as used for Hi-C analysis. Nuclei were stained with Hoechst to visualize DNA and Nile red to visualize the nuclear membrane
- (B) TAD size distribution for frog sperm and frog XL-177 cells
- (C) 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)
- (D) Corner peak size distribution for the same samples as in (B)
- (E) 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)