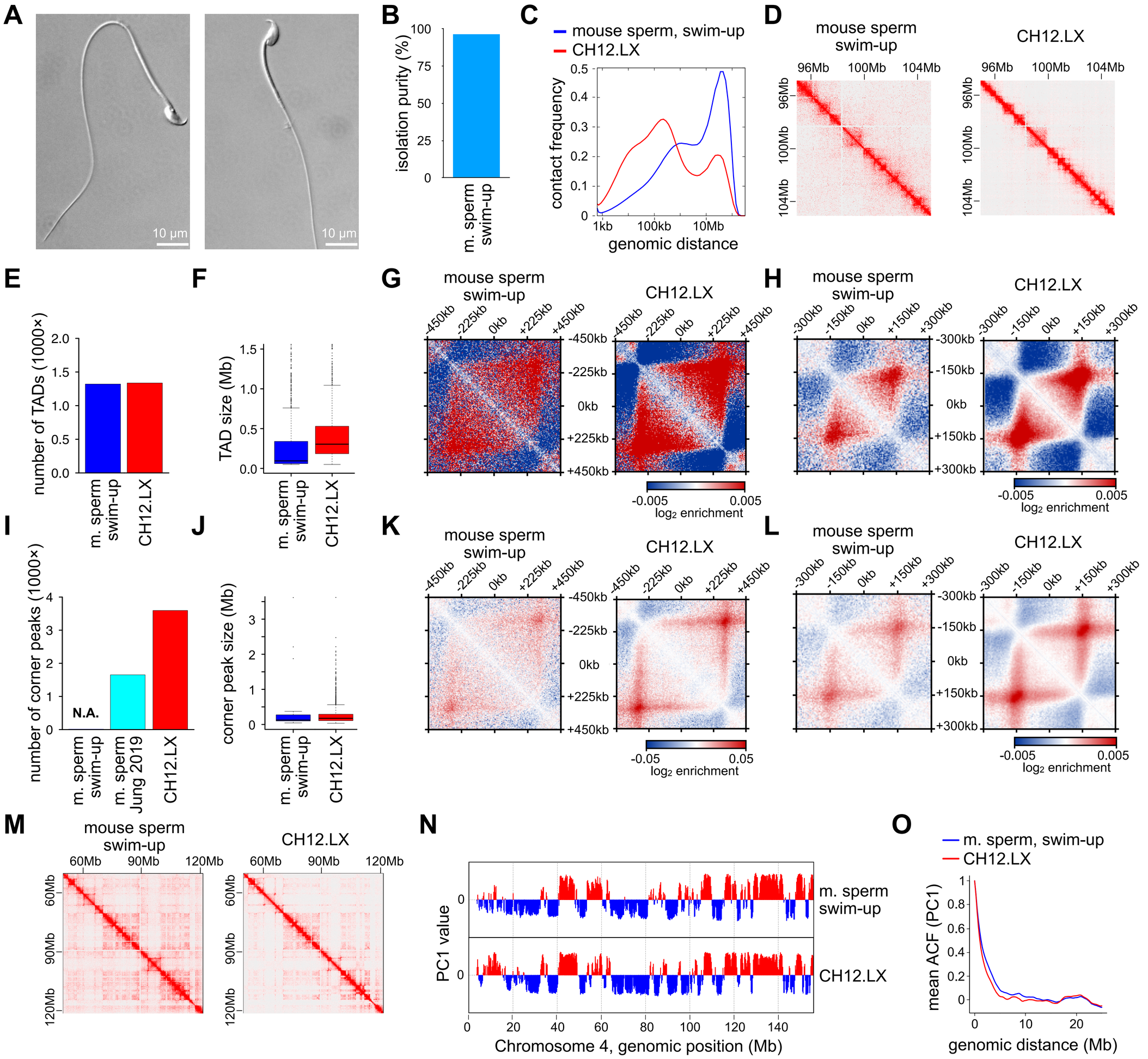

Supplemental Figure S3. TADs and corner peaks can be detected in mouse sperm datasets.
(A) Exemplary DIC microscopy of *Mus musculus* (mouse) sperm as enriched for Hi-C analysis by swim-up
(B) Purity of mouse sperm enriched for Hi-C analysis as determined by DIC microscopy, n=1,242
(C) Contact frequency as a function of genomic distance for mouse sperm enriched by swim-up compared to mouse CH12.LX cells by Rao et al. 2014
(D) Normalized Hi-C matrices for the same samples as in (C) in the region of Chr3:95-105Mb at 25 kb resolution
(E) Number of TADs called for the same samples as in (C)
(F) TAD size distribution for the same samples as in (C)
(G) Aggregate contact frequencies (coverage and distance corrected) around the 70 550-650 kb long TADs called in CH12.LX cells, for the same samples as in (C)
(H) Aggregate contact frequencies (coverage and distance corrected) around the 203 250-350 kb long TADs called in CH12.LX cells, for the same samples as in (C)
(I) Number of corner peaks called for mouse sperm enriched by swim-up from this study, mouse sperm enriched by swim-up from Jung et al. 2019 and for CH12.LX cells by Rao et al. 2014. N.A. indicates artifacts in corner peak calling due to low sequencing depth
(J) Corner peak size distribution for the same samples as in (C)
(K) Aggregate contact frequencies (coverage and distance corrected) around the 55 550-650 kb long corner peaks called in CH12.LX cells, for the same samples as in (C)
(L) Aggregate contact frequencies (coverage and distance corrected) around the 362 250-350 kb long corner peaks called in CH12.LX cells, for the same samples as in (C)
(M) Normalized Hi-C matrices for the same samples as in (C) in the region of Chr12:50-120Mb at 100 kb resolution
(N) Compartment tracks from principal component analysis for the same samples as in (C)
(O) The autocorrelation of the PC1 value as a function of genomic distance, for the same samples as in (C)