



Supplemental Figure S4. Somatic contamination of around 50% could explain the somatic-like genome organization observed in mouse sperm.

- (A) Compartment tracks from principal component analysis for *in silico* mixtures of, as indicated, varying percentages of mouse sperm enriched by FACS by Vara et al. 2019 and mouse CH12.LX cells by Rao et al. 2014
- (B) The autocorrelation of the PC1 value as a function of genomic distance, for the same samples as in (A)