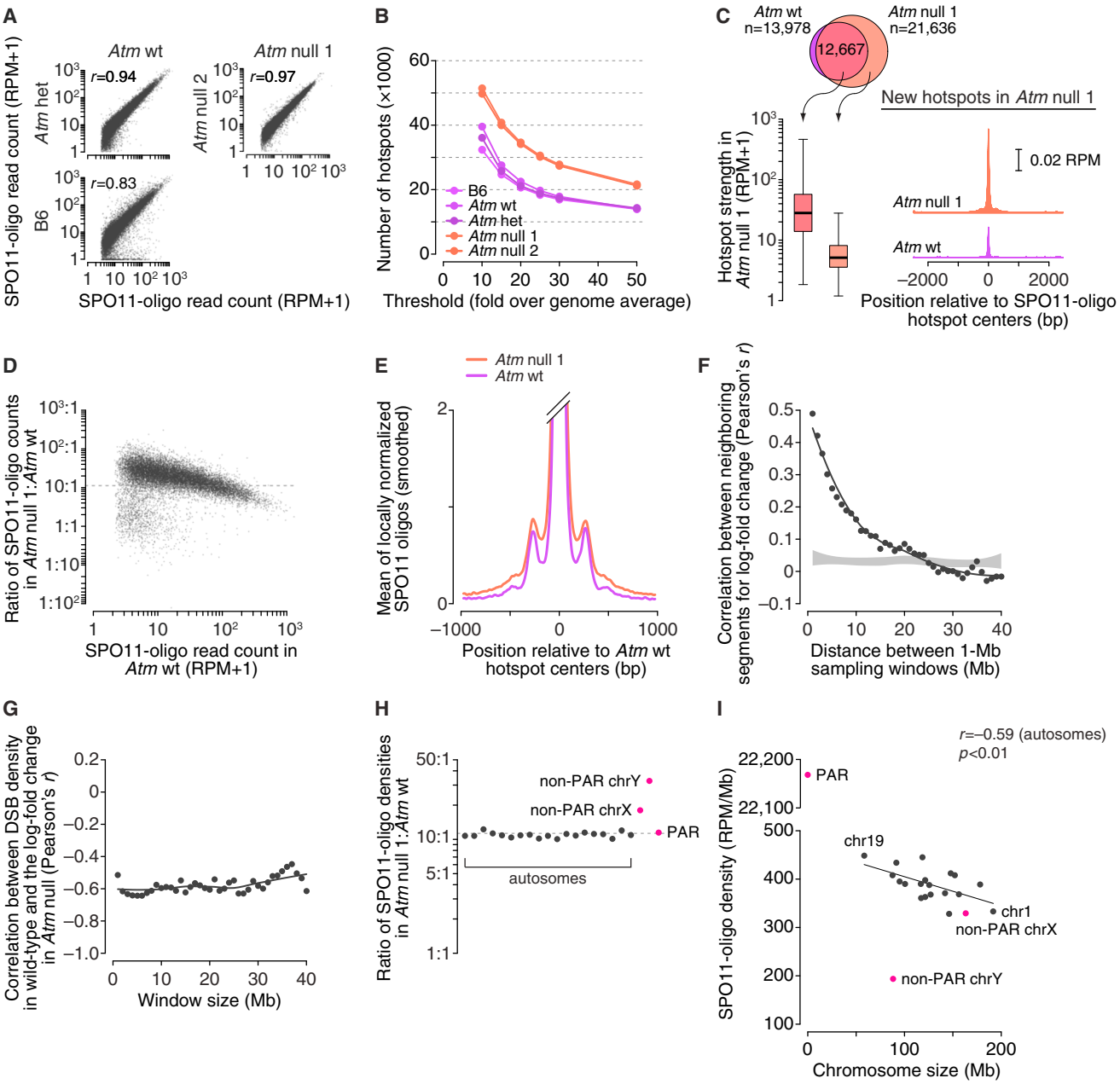

Figure 7. DSB Patterns in the Absence of ATM

(A) Reproducibility of SPO11-oligo maps. SPO11-oligo read counts were summed in 1,001-bp windows.

(B) *Atm* null spermatocytes display more hotspots than ATM-proficient spermatocytes. Data for B6 are reproduced from Figure 2A.

(C) New hotspots in *Atm* null are weak hotspots that also yield small numbers of DSBs in wild-type. Boxplot is as defined in Figure S2A legend; SPO11-oligo profiles were smoothed with a 51-bp Hann filter.

(D) In ATM-deficient spermatocytes, weaker hotspots increase more than stronger hotspots. Each point represents a 1,001-bp window around a hotspot called in the *Atm* wt map (one outlier is not shown). The dashed horizontal line marks the 11.3-fold increase in whole-testis SPO11-oligo levels in *Atm* null mice (Lange et al., 2011).

(E) Wider average SPO11-oligo distribution around hotspots in the absence of ATM. SPO11-oligo profiles were smoothed with a 51-bp Hann filter.

(F) Local domains of correlated behavior. Each point compares the log-fold change in SPO11-oligo density in 1-Mb segments on autosomes to the log-fold change in neighboring segments the indicated distance away. Shaded area denotes estimated 95% confidence intervals for data randomized within-chromosome.

(G) Domains that are relatively DSB-poor in wild-type tend to be more strongly suppressed by ATM. Each point compares the log-fold change in SPO11-oligo density in *Atm* null to the SPO11-oligo density in *Atm* wt when autosomes are segmented into non-overlapping windows of the indicated size.

(legend continued on next page)

(H) In the absence of ATM, DSB densities increase more on the non-PAR segments of the sex chromosomes than on autosomes or the PAR.
(I) In *Atm* null spermatocytes, SPO11-oligo density remains negatively correlated with chromosome size, and the X chromosome more closely matches expectation from its size.
See also Figure S7.