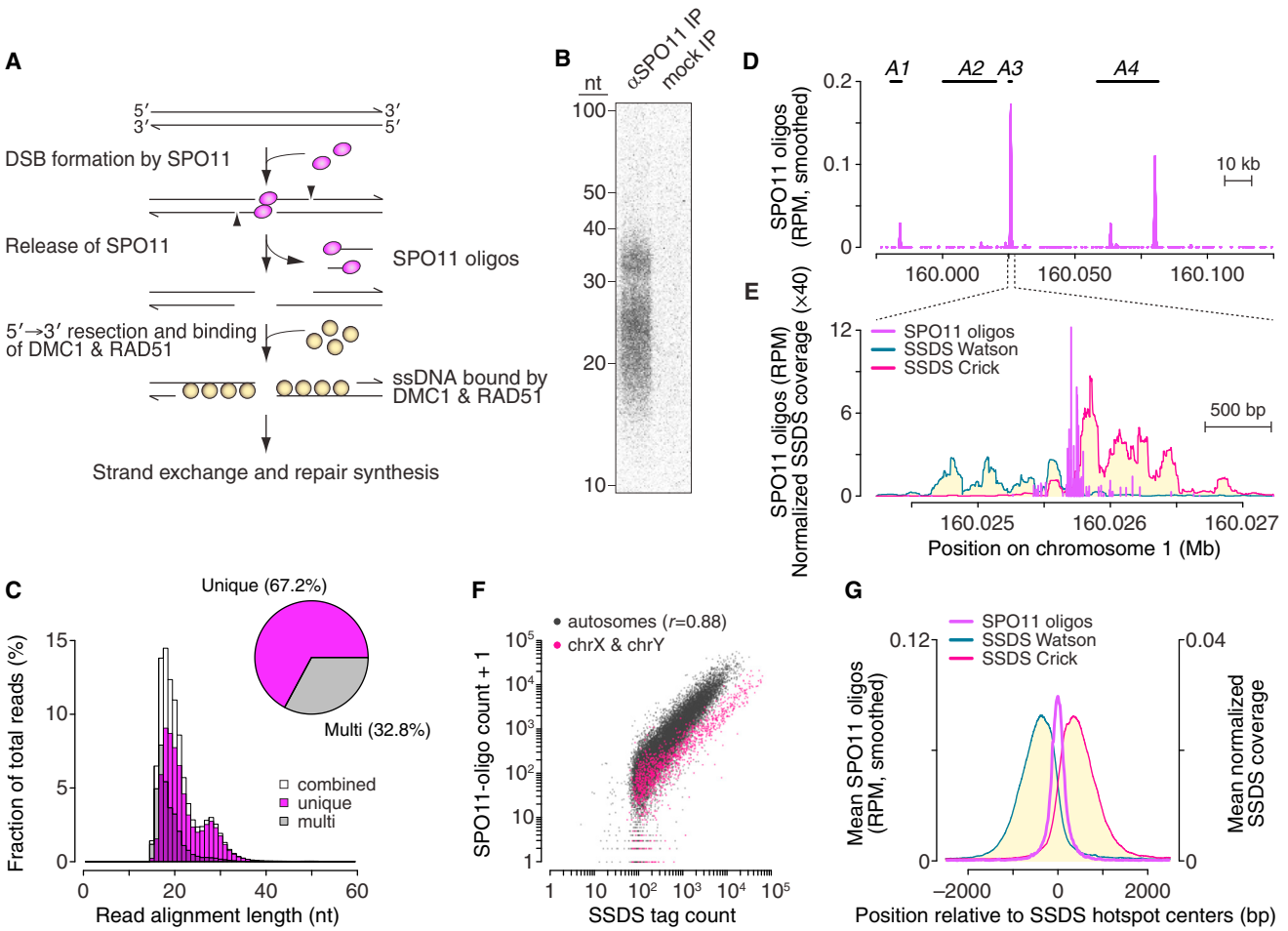

Figure 1. Nucleotide-Resolution Map of Meiotic DSBs in Wild-Type Mice

(A) Early steps in recombination and the protein-DNA complexes (SPO11 oligos and ssDNA bound by DMC1 and RAD51) used to generate genome-wide recombination initiation maps.

(B) SPO11 oligos immunoprecipitated (IP) from B6 mouse spermatocytes, deproteinized, 3′-end-labeled, and resolved in a denaturing 15% polyacrylamide gel. Anti-SPO11 antibody was omitted from the mock IP processed in parallel.

(C) Length distribution of SPO11 oligos that map uniquely or to multiple sites. Oligos appear longer on gels (B) because of nucleotides added for labeling and amino acid(s) left after SPO11 proteolysis.

(D) SPO11-oligo map (smoothed with a 1,001-bp Hann filter) compared to positions of four known crossover hotspots (*A1–A4*) (Table S2A).

(E) SPO11 oligos and SSDS coverage (Brick et al., 2012) in a 3,001-bp window around hotspot *A3*. SSDS coverage at each position was normalized to the total strand-specific coverage in the genome and multiplied by 10^6. See also Figure S1C.

(F) In SSDS hotspots (n = 18,294), SPO11-oligo counts correlated strongly (Pearson's *r*) with SSDS tag counts. One SPO11-oligo read was added to permit plotting of hotspots with no oligos.

(G) Distribution of SPO11 oligos (51-bp Hann filter) and SSDS coverage around centers of SSDS hotspots.

See also Figure S1.