The Synaptonemal Complex Shapes the Crossover Landscape Through Cooperative Assembly, Crossover Promotion and Crossover Inhibition During Caenorhabditis elegans Meiosis

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FIGURE S1.—SYP-1 localization following partial depletion by RNAi. Images show SYP-1 localization in regions of germ lines from empty vector control (top) and syp-1 RNAi worms, extending from the beginning of the transition zone (containing nuclei in the zygotene stage, when SYP-1 loading begins) through the early pachytene region (in which all chromosome pairs are fully synapsed in control germ lines). In the syp-1 RNAi germ lines, robust SYP-1 stretches are detected on a subset of chromosomes; this pattern becomes apparent early in the transition zone, soon after loading of SYP-1 onto chromosomes begins. The two syp-1 RNAi germ lines shown differ in the fraction of chromosomes that are associated with SYP-1 stretches, presumably reflecting variation in the degree of SYP-1 depletion. Scale bar = 5 μm.
Figure S2.—Quantitation of peak levels of RAD-51 foci. For each germ line evaluated, RAD-51 foci were quantified in 8 contiguous rows of nuclei from the region where foci were most abundant. Images were acquired using a DeltaVision deconvolution microscope (Applied Precision) and quantitation was carried out on Z-stacks of images using Priism software; for all nuclei scored, the entire nucleus was represented in the Z-stack and there was no overlap with adjacent nuclei. Data are depicted using a box-and-whisker plot to display the numbers of RAD-51 foci in nuclei from each individual germ line scored; the horizontal line corresponds to the median, the top and bottom of the box correspond to the 75th and 25th percentile, and the top and bottom extent of the whiskers correspond to the highest and lowest values for the data set. All four syp-1 RNAi germ lines exhibited extremely significant differences (p < 0.0001, two-sided Mann Whitney test) from all three controls (N2 wild type and empty vector), while no significant differences were detected among the controls. Significant differences were also observed between different syp-1 RNAi germ lines, presumably reflecting variability in the extent of SYP-1 depletion. Numbers of nuclei scored were: N2_1 (n=36), N2_2 (n=24), empty vector (n=47), SYP-1 RNAi_1 (n=36), SYP-1 RNAi_2 (n=38), SYP-1 RNAi_3 (n=36), SYP-1 RNAi_4 (n=36). The peak levels of RAD-51 foci detected in these syp-1 RNAi germ lines clearly exceeded a recently published estimate of the number of DSBs formed during normal C. elegans meiosis (mean of 12.6 per nucleus; METS and MEYER 2009). The most straightforward explanation is that partial depletion of SYP-1 results in formation of an increased number of DSBs. However, we cannot exclude several possible alternative explanations, e.g. that DSB ends might become uncoupled or that RAD-51 might load promiscuously in the context of SYP-1 depletion, or that a hidden class of DSBs not normally detectable as RAD-51 foci could become exposed to resecting enzymes following SYP-1 depletion, leading to an increase in visible RAD-51 foci without increasing DSB number.