

Supplemental figure legends for

Synaptonemal complex central region proteins promote localization of pro-crossover factors to recombination events during *Caenorhabditis elegans* meiosis

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Figure S1. Co-localization of pro-CO factors in *syp* null mutants. (A) Immunolocalization of GFP::COSA-1, MSH-5 and ZHP-3 from mid-late pachytene regions of wild-type, *syp-1(me17)*, and *syp-3(ok758)* germ lines. Both Jantsch *et al.* and Zhang *et al.* have also published ZHP-3 localization in *syp* null mutants (JANTSCH *et al.* 2004; ZHANG *et al.* 2018). Dashed box indicates the nucleus that is enlarged in the adjacent image and scale bar on the enlarged images represents 2 μ m. All other scale bars represent 5 μ m. (B) Unadjusted images of immunolocalization of GFP::COSA-1 from late pachytene regions of wild-type, *syp-2(ok307)*, and *syp-3(ok758)* to compare the decrease in intensity of the GFP::COSA-1 foci in the *syp* mutants relative to wild-type. Scale bar represents 5 μ m.

Figure S2. Co-localization of pro-CO factors and the SC in *him-3*, *htp-3* and *rec-8* mutants. (A) Immunolocalization of GFP::COSA-1 and MSH-5 from the late pachytene regions of wild-type, *him-3(e1256)*, *htp-3(y428)* and *rec-8(ok978)* germ lines. (B) Immunolocalization of GFP::COSA-1 and ZHP-3 from the late pachytene regions of wild-type and *rec-8(ok978)* germ lines. Scale bar represent 5 μ m.

Figure S3. Increased numbers of COSA-1 foci along SYP-1 stretches following partial depletion of SYP-1. (A) Immunolocalization of GFP::COSA-1 and SYP-1 in late pachytene nuclei from control wild-type, *him-3(e1256)*, or *rec-8(ok978)* worms and from wild-type, *him-3(e1256)*, or *rec-8(ok978)* worms treated with *syp-1* partial RNAi. Arrowheads point to nuclei that are enlarged in panels on the right. As SYP-1 immunofluorescence intensities following *syp-1* partial RNAi often appeared weaker relative to controls, SYP-1 signal intensities were boosted for the *syp-1* partial RNAi panels to facilitate visualization of SYP-1 tracks (LIBUDA *et al.* 2013). Whereas SYP-1 is localized along most sister chromatid pairs in *rec-8* control nuclei, SYP-1 is detected along only a subset of sister chromatid pairs in the *rec-8; syp-1* partial RNAi nuclei. Further, in contrast to controls, nuclei from either *him-3(e1256)* or *rec-8(ok978)* mutants treated with *syp-1* partial RNAi often contained SYP-1 stretches harboring more than one GFP::COSA-1. Scale bars represent 5 μ m. (B) Graph showing quantitation of the percentage of contiguous SYP-1 stretches in control *him-3(e1256)* nuclei (n=103) or *him-3(e1256)* nuclei treated with *syp-1* partial RNAi (n=100) that had the indicated numbers of GFP::COSA-1 foci in late pachytene. Only continuous stretches of SYP-1 were counted, therefore if a single chromosome had two discontinuous stretches of SYP-1, then it was counted as two separated stretches of SYP-1. Quantitation of COSA-1 foci along entire individual chromosomes was not possible as the unsynapsed chromosomes in *him-3(e1256)* made resolving individual chromosomes difficult. Thus, we are likely under-estimating of the actual number of COSA-1 foci along a single chromosome in *him-3(e1256)*.

Figure S4. Connection of sister chromatids in *rec-8* mutants during diakinesis is dependent on pro-CO factors and SYP proteins. (A) Representative image of DAPI stained nuclei from the diakinesis region of wild-type, *rec-8*, *cosa-1*, *cosa-1; rec-8*, and *rec-8; syp-2* germ lines. Both *rec-8* and *cosa-1* mutant are defective in maintaining connected pairs of

homologs, while the *cosa-1; rec-8* double mutant is also unable to maintain connected pairs of sister chromatids. In *rec-8; syp-2* double mutant, 90% of the nuclei display severe chromosome fragmentation with 10% displaying 9-15 DAPI staining bodies at diakinesis. Both Colaiacovo *et al.* 2003 and Crawley *et al.* 2016 have also published these same diakinesis results for *rec-8; syp-2* and *cosa-1; rec-8* mutants respectively. Scale bars represent 5 μ m. (B) Box plot depicting the quantification of the DAPI bodies in panel A. Number of diakinesis nuclei scored for DAPI bodies: wild-type, n=213; *rec-8*, n=193; *cosa-1*, n=226; *cosa-1; rec-8*, n=162; *syp-2; rec-8*, n=85 (due to the degree of chromosome fragmentation in *rec-8; syp-2* a majority of these nuclei could not be accurately scored for DAPI bodies). Number of asterisks represent degree of statistical significance from a Mann Whitney test (***)= $P<0.0001$).

Figure S5. Persistence of RAD-51 foci into late pachytene and diakinesis nuclei of *syp-2; rec-8* mutants. Immunofluorescence of RAD-51 (green) and DAPI (blue) from late pachytene (A) and diakinesis (B) in *rec-8; syp-2* double mutants, *syp-2 (ok307)* single mutant, and wild-type. Colaiacovo *et al.* 2003 has also published these same results for *syp-2* in late pachytene. Scale bars represent 5 μ m.

References for supplemental figure legends

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