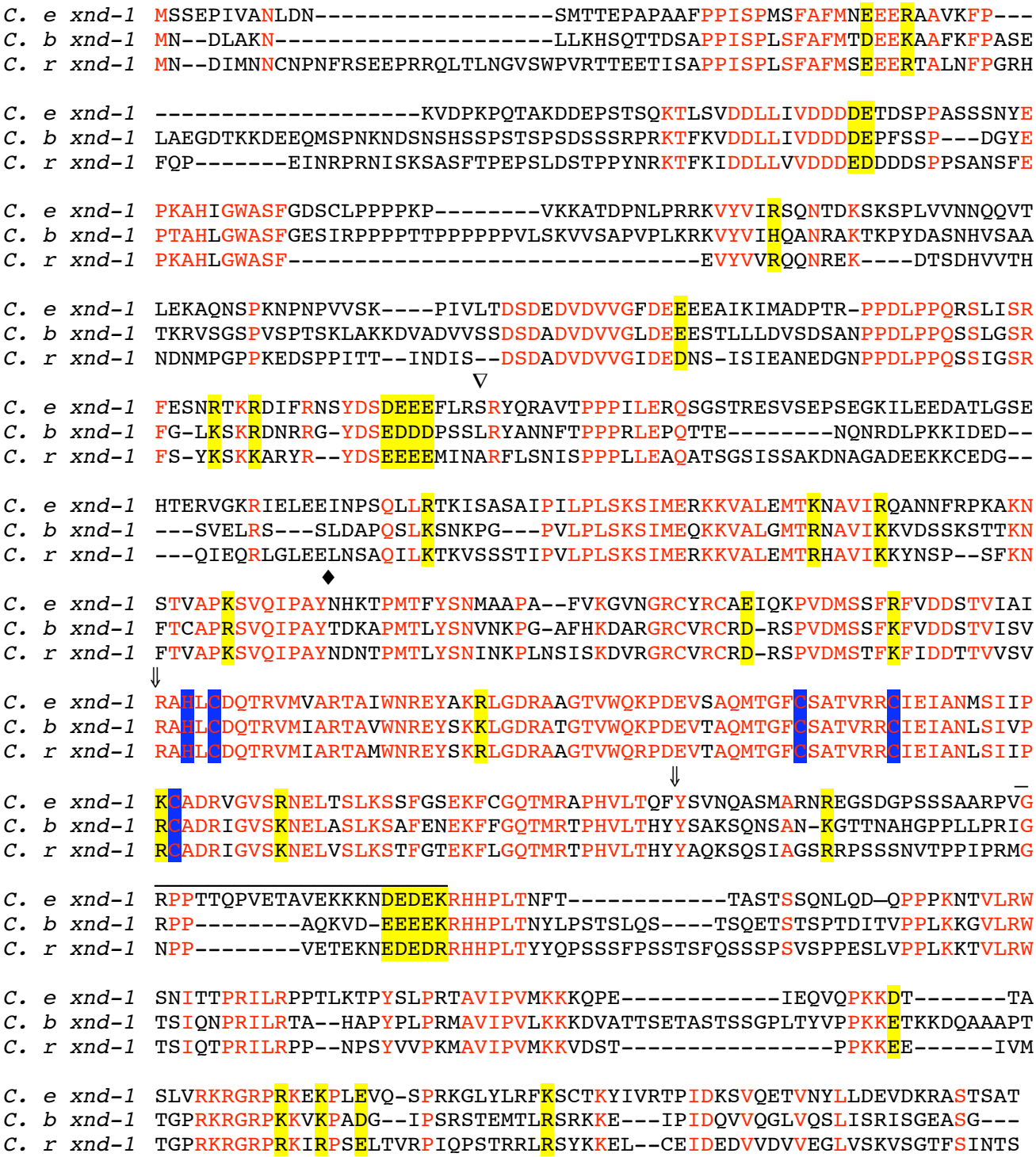
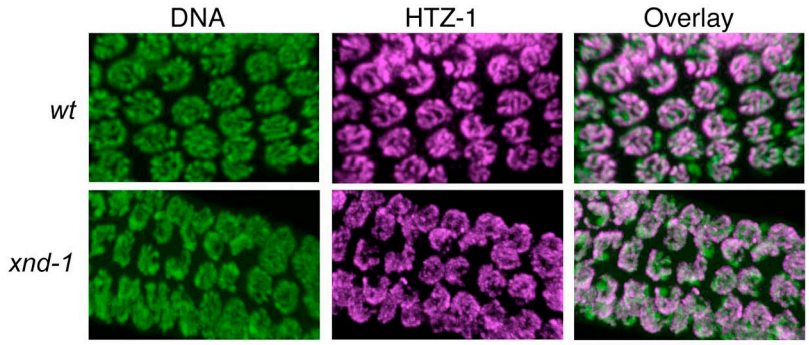
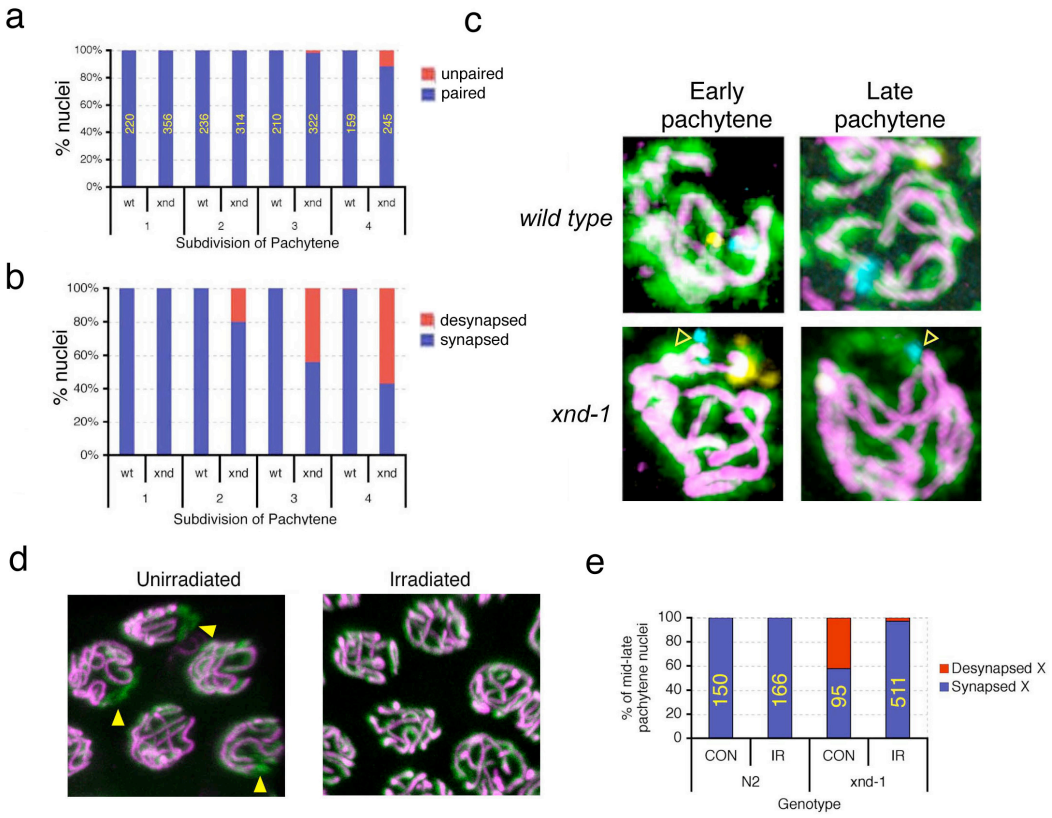
Supplementary Figure 1



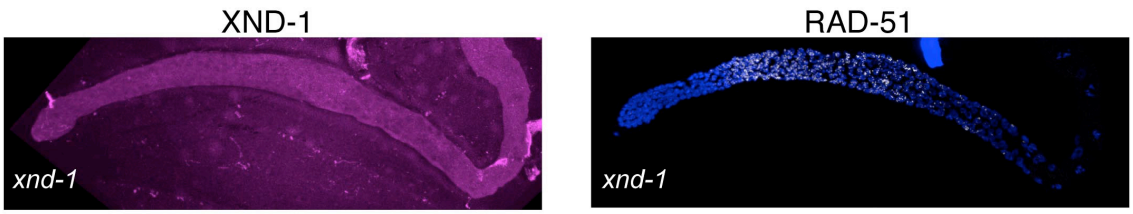
Supplementary Figure 1. XND-1 protein sequences from *C.elegans*, *C. briggsae*, and *C. remaneii* are compared. Identical amino acids between the three proteins are red, and conserved charge amino acids are highlighted in yellow. The out-of-frame *ok709* allele begins at the open arrowhead; *ok709* encodes an additional 64 amino acids followed by a termination codon. The diamond indicates the amino acid at which the out-of-frame *ok708* deletion begins; *ok708* encodes an additional 20 amino acids followed by a termination codon. The line above the sequences indicates the amino acids that are absent in alternatively spliced transcripts of the *xnd-1* gene. The amino acids between the arrows contain a potential metal-binding (relevant amino acids shaded in blue) domain that may mediate chromatin-binding and/or protein-protein interactions (personal communication, E. Koonin).



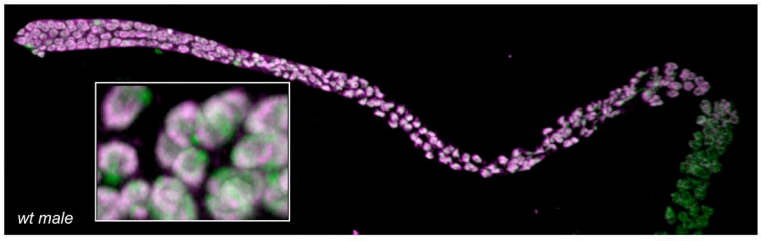
Supplementary Figure 2. HTZ-1 staining is unaffected in *xnd-1* mutant germline nuclei. *wt* (top), *xnd-1* (bottom) germlines co-stained with anti-HTZ-1 antibodies (magenta) and DAPI (green). In both *wt* and *xnd-1*, HTZ-1 appears excluded from one chromosome (the X) as it is preferentially localized to the autosomes.



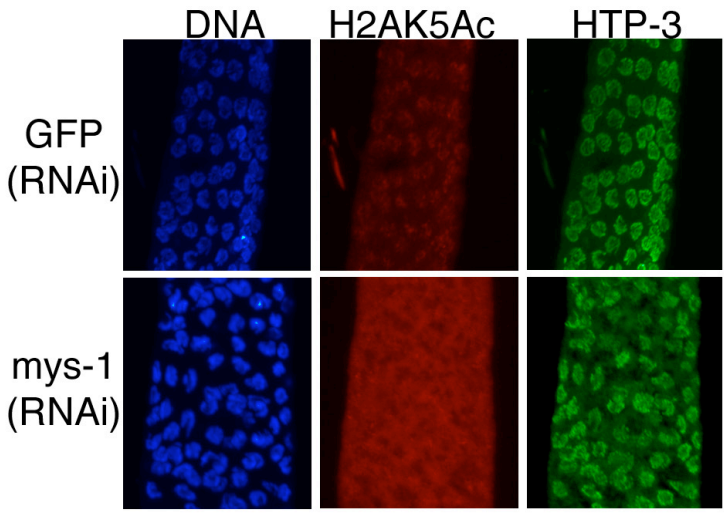
Supplementary Figure 3. The SC disassembles on X chromosomes that do not receive a DSB in *xnd-1* mutants. (a) Quantification of pairing and (b) synapsis during pachytene in wild type and *xnd-1* (pairing and synapsis were quantified simultaneously: regions 1-4, *wt*, N=220, 236, 210, 159 nuclei; *xnd-1*, N=356, 314, 322, 245 nuclei). The X chromosome desynapses in ~50% of *xnd-1* late pachytene nuclei. (c) Images of early pachytene and late pachytene nuclei in *wild type* (top) and *xnd-1* (bottom) reveal the loss of the SC on the X. DAPI (green), FISH probes to the 5S locus on Chromosome V (yellow) and the right end of the X chromosome (cyan, yellow arrows) and anti-SYP-1 antibody (magenta). (d, e) Desynapsis is rescued by ionizing radiation (IR) which provides exogenous DSBs. (d) Unirradiated *xnd-1* and irradiated *xnd-1* germlines stained for DNA (green) and anti-SYP-1 antibodies (magenta) demonstrate that the desynapsis defect in *xnd-1* is rescued by exogenous break formation. Yellow arrowheads mark the X chromosome in the unirradiated samples. (e) Quantification of SC status on the X chromosome in control and irradiated animals 16 hrs post-IR (*wt* -/+ IR, N= 150, 166; *xnd-1* -/+ IR, N= 95, 511).



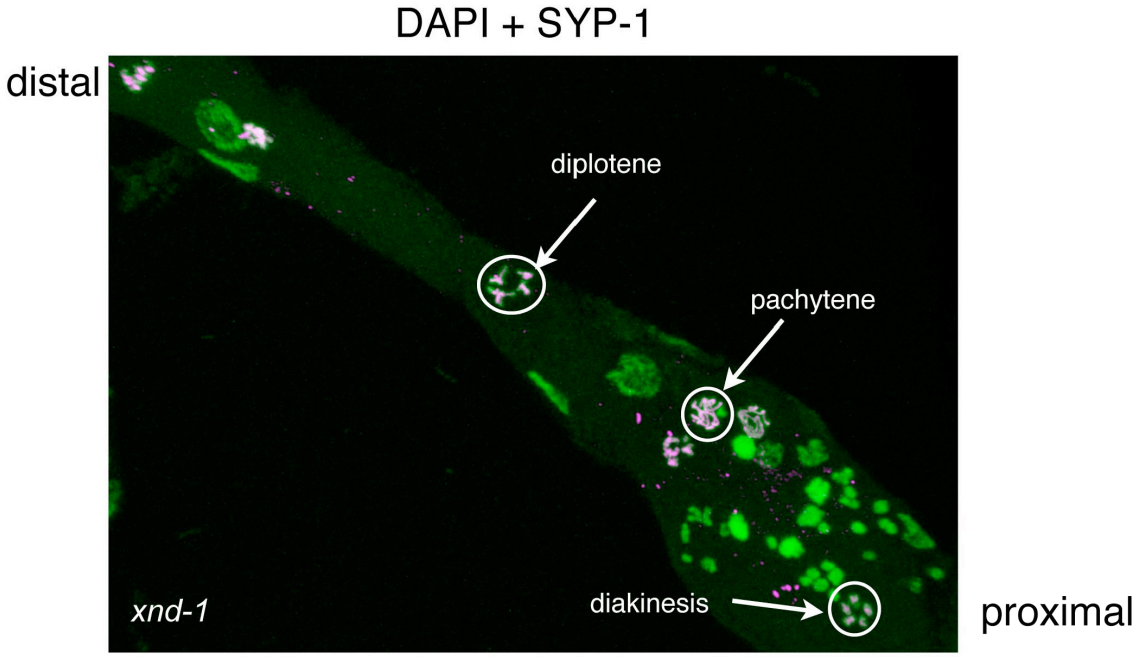
Supplementary Figure 4. XND-1 antibodies are specific. anti-XND-1 antibodies do not stain *xnd-1* mutant germlines. *xnd-1* mutant germlines were dissected and co-stained with anti-XND-1 antibodies (left panel, magenta) and anti-RAD-51 antibodies (right panel, white; DAPI, blue).



Supplementary Figure 5. XND-1 is enriched on autosomes in *wild type* males. Germlines from *wild type* males were dissected and stained with DAPI (green) and anti-XND-1 antibodies (magenta). As in *wild type* hermaphrodites, XND-1 is preferentially localized to the autosomes (inset).



Supplementary Figure 6. *mys-1* treated animals have decreased levels of H2AK5Ac. *GFP(RNAi)* or *mys-1(RNAi)* treated *xnd-1* mutant gonads were dissected, fixed, and stained on the same slides and imaged with identical settings on a Nikon A1 confocal microscope. The 1:2500 dilution of the anti-H2AK5Ac was used in these experiments so that small perturbations in signal could be seen. Anti-Htp-3 immunolocalization shows that the *mys-1(RNAi)* treated samples are not impervious to antibody and that the diffuse red signal with the anti-H2AK5Ac antibody corresponds to background staining.



Supplementary Figure 7. Sterile *xnd-1* mutant germlines display meiotic packaging defects. Dissected *xnd-1* germlines were stained with anti-SYP-1 antibody (magenta) and DAPI (green). As shown by the white circles, meiotic progression is aberrant with defects in the temporal and spatial organization of late meiotic events.

Supplementary Table 1. Crossover distribution on chromosome I from oocytes

Interval (Mb)		0.17 -1.91	1.91-4.59	4.59-10.72	10.72-12.05	12.05-14.68	*N*
oocytes	***wt***	8.9 (21)	10.6 (25)	0.0 (0)	5.5 (13)	26.3 (62)	236
	xnd-1	6.5 (15)	16.9 (39)	21.2** (49)	2.2 (5)	1.3** (3)	231

Values are map units for each interval (number of COs per interval)
The change in crossover distribution between *N2* and *xnd-1* is statistically significant:
$\chi^2(5,N=111)=24{,}000$, $p< .001$
*, **Significant difference in map size of the interval between *wild type* and *xnd-1* (*p<0.05; **p<0.001)

Supplementary Table 2. Crossover distribution on the X chromosome

Interval (Mb)		0.06 - 2.34	2.34 - 4.13	4.13 - 6.88	6.88 - 10.64	10.64 - 14.26	14.26 - 17.22	*N*
oocytes	***wt*[1]**	7.3 (27)	9.5 (35)	6.5 (24)	7.6 (28)	9.8 (36)	10.3 (38)	--
	xnd-1	1.5* (6)	2.5* (10)	4.5 (18)	8.7** (35)	6.5 (26)	1.7** (7)	402

Values are map units for each interval (number of COs per interval)
The change in crossover distribution between *N2* and *xnd-1* is statistically significant:
$\chi^2(6,N=102)=50.2$, $p< .001$
[1]Data from Lim et al.[1]
*, **Significant difference in map size of the interval between *wild type* and *xnd-1* (*p<0.05; **p<0.001)

Supplementary Table 3. Crossover distribution on chromosome I from sperm

Interval (Mb)		0.17 -1.91	1.91-4.59	4.59-10.72	10.72-12.05	12.05-14.68	*N*
sperm	***wt***	14.0 (46)	12.8 (42)	6.1 (20)	4.3 (14)	13.4 (44)	328
	xnd-1	5.7** (20)	17.5* (61)	22.6** (79)	0.9* (3)	3.4** (12)	349

Values are map units for each interval (number of COs per interval)
The change in crossover distribution between *N2* and *xnd-1* is statistically significant: χ^2 (5, N=166)=207, $p< .001$
*, **Significant difference in map size of the interval between *wild type* and *xnd-1* (*p<0.05; **p<0.001)

Supplementary Table 4. *xnd-1* viability and % HIM

genotype	#embryos	%hatched	%males
N2	3347	99.9	0.06
ok708 **M^+Z^-**	2502	87.4	13.8
ok708 **M^-Z^-**	3263	75.5	23.2
ok709 **M^+Z^-**	2132	69.4	12.3
ok709 **M^-Z^-**	2288	65.5	19.9
+/+;sEx826	1502	ND	24.7
rde-2;sEx826	2047	ND	0.49

Supplementary Table 5. Number of RAD-51 foci in *wt* and *xnd-1* meiotic germline nuclei.

REGION:	TZ	1	2	3	4	5	6
N2#1							
0	86	6	1	1	38	44	21
1-2	30	53	9	24	16	5	1
3-4	0	23	51	30	7	0	0
5-7	0	1	17	16	4	0	0
N2#2							
0	33	2	0	0	2	29	20
1-2	8	27	6	6	11	4	0
3-4	0	8	31	23	9	0	0
5-7	0	0	10	14	13	0	0
N2#3							
0	43	7	0	0	0	34	0
1-2	8	26	26	12	11	3	0
3-4	0	1	29	25	21	0	0
5-7	0	0	1	12	4	0	0
xnd-1#1							
0	32	1	1	0	2	17	25
1-2	2	2	19	9	20	25	12
3-4	0	17	29	12	17	5	1
5-7	0	22	12	16	4	0	0
xnd-1#2							
0	34	0	0	0	2	10	8
1-2	14	15	0	16	12	8	1
3-4	0	8	7	11	7	0	0
5-7	0	5	14	2	0	0	0
xnd-1#3							
0	35	1	0	4	12	21	10
1-2	10	10	2	19	14	7	3
3-4	1	22	12	9	5	1	0
5-7	0	14	14	1	0	0	0
xnd-1#4							
0	37	1	0	3	7	22	17
1-2	16	0	1	29	30	16	1
3-4	7	36	19	34	6	3	0
5-7	2	47	46	22	1	1	0
xnd-1#5							
0	25	2	0	0	2	8	28
1-2	13	7	7	9	8	27	15
3-4	2	17	18	17	24	8	2
5-7	1	16	15	4	4	1	0

Supplementary Table 6. XND-1 localization in meiotic mutants.

Genotype	Function	XND-1 temporal staining pattern*	XND-1 exclusion from X chromosome	Reference
chk-2(me64)	pairing	wild type	yes	[2]
him-8(e1489, me4, tm611)		wild type	yes	[3]
prom-1(ok1140)		wild type	yes	[4]
sun-1(jf18)		wild type	yes	[5]
him-3(e1147, e1256)	Axial element/SC formation	wild type	yes	[6]
htp-1(gk150)		wild type	yes	[7,8]
rec-8(ok978)		wild type	yes	[9]
syp-1(me17)		wild type	yes	[10]
syp-2(ok307)		wild type	yes	[11]
him-6(e1104, e1423)	DSB formation and break repair	wild type	yes	[12]
him-14(it44)		wild type	yes	[13]
him-17(ok424)		wild type	yes	[14]
mre-11(ok179)		wild type	yes	[15]
msh-2(ok2486)		wild type	yes	[16]
msh-5(me23)		wild type	yes	[17]
rad-51(lg8701)		wild type	yes	[18]
spo-11(me44)		wild type	yes	[19]
dpy-28(y1)	Crossover Control	wild type	yes	[20]
dpy-27(y56)	Dosage compensation	wild type	yes	[21]
dpy-30(y228)		wild type	yes	[22]
him-1(e879)	Chromatin structure	wild type	yes	[23]
his-72(tm2066)		wild type	yes	[24]
hpl-1(tm1621)		wild type	yes	[25]
hpl-2(tm1489)		wild type	yes	[25]
htz-1(tm2469)		wild type	yes	[26]
met-2(n4256)		wild type	yes	[27]
mrg-1(qa6200)		wild type	yes	[28]
rbr-2(ok2544)		wild type	yes	[29]
set-2(tm1630)		wild type	yes	[30]
him-5(e1467, ok1896)	Unknown	wild type	yes	[23]

*Nuclear staining pattern is consistent with particular substage of prophase I, rather than position in germline.

Supplementary Table 7. *xnd-1* mutants do not desilence transgene arrays.

	let-868.1::GFP[31] **expression**
wild type	-
xnd-1	-
mes-4 **(RNAi)**	++

Supplementary Movie 1. RAD-51 foci are detected on X chromosomes in wild type nuclei. 3D reconstructions of confocal stacks showing accumulation of RAD-51 foci (magenta) in wild type animals treated with *rad-54(RNAi)*. Autosomes are labeled with anti-HTZ-1 antibodies (cyan), all chromosomes are labeled with DAPI (green), therefore the X chromosome is revealed by the absence of colocalization.

Supplementary Movie 2. RAD-51 foci cannot be detected on a subset of X chromosomes in *xnd-1* nuclei. 3D reconstructions of confocal stacks showing accumulation of RAD-51 foci (magenta) in *xnd-1* mutant animals treated with *rad-54(RNAi)*. Autosomes are labeled with anti-HTZ-1 antibodies (cyan), all chromosomes are labeled with DAPI (green), therefore the X chromosome is revealed by the absence of colocalization. Yellow arrows indicate X chromosomes that do not have RAD-51 foci; blue arrows indicate X chromosomes with RAD-51 foci.

Supplementary Movie 3. XND-1 is enriched on autosomes. 3D reconstructions of confocal stacks from the mid-pachytene region of wild type animals labeled with anti-Histone H4K12Ac (magenta), anti-XND-1 antibody (cyan); and DAPI (green). Note the complete colocalization of the antibodies and the absence of staining on the X chromosome (yellow arrows).

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