

1067 **Supplemental Figure 1: PCH-2 does not regulate GFP::MSH-5 loading and removal through**  
1068 **HTP-3. A.** Representative images of nuclei in different stages of meiotic prophase in *htp-3<sup>H96Y</sup>* and  
1069 *pch-2; htp-3<sup>H96Y</sup>* mutants stained for DAPI (magenta) and GFP::MSH-5 (green) Scale bar in all images  
1070 is 5  $\mu$ m. **B.** Scatter plot showing average GFP::MSH-5 foci per row of germline nuclei in *htp-3<sup>H96Y</sup>*  
1071 (blue, 132 nuclei) and *pch-2; htp-3<sup>H96Y</sup>* (green, 161 nuclei) mutants from the transition zone to late  
1072 pachytene, normalized to 100. The line represents a rolling average of four rows. Similar data is  
1073 provided for a control germline (opaque yellow, 163 nuclei) for comparison  
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1075 **Supplemental Figure 2: *pch-2* meiotic nuclei with elevated numbers of GFP::*MSH-5* foci show**  
1076 **defects in crossover assurance.** Gray scale images of control and *pch-2* mutant nuclei stained for  
1077 DAPI, GFP::*MSH-5* and OLLAS::*COSA-1*. Scale bar in image is 4  $\mu$ m.

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1079 **Supplemental Figure 3: *syp-1<sup>T452A</sup>* and *pch-2;syp-1<sup>T452A</sup>* mutants display a similar defect in**  
1080 **meiotic progression. A.** Representative images of *syp-1<sup>T452A</sup>* and *pch-2;syp-1<sup>T452A</sup>* mutant germlines.  
1081 Encircled nuclei indicate transition zone nuclei. Scale bar indicates 10  $\mu$ m. **B.** Quantification of fraction  
1082 of rows of transition zone nuclei in 3 germlines in *syp-1<sup>T452A</sup>* (maroon) and *pch-2;syp-1<sup>T452A</sup>* (light blue)  
1083 mutants.

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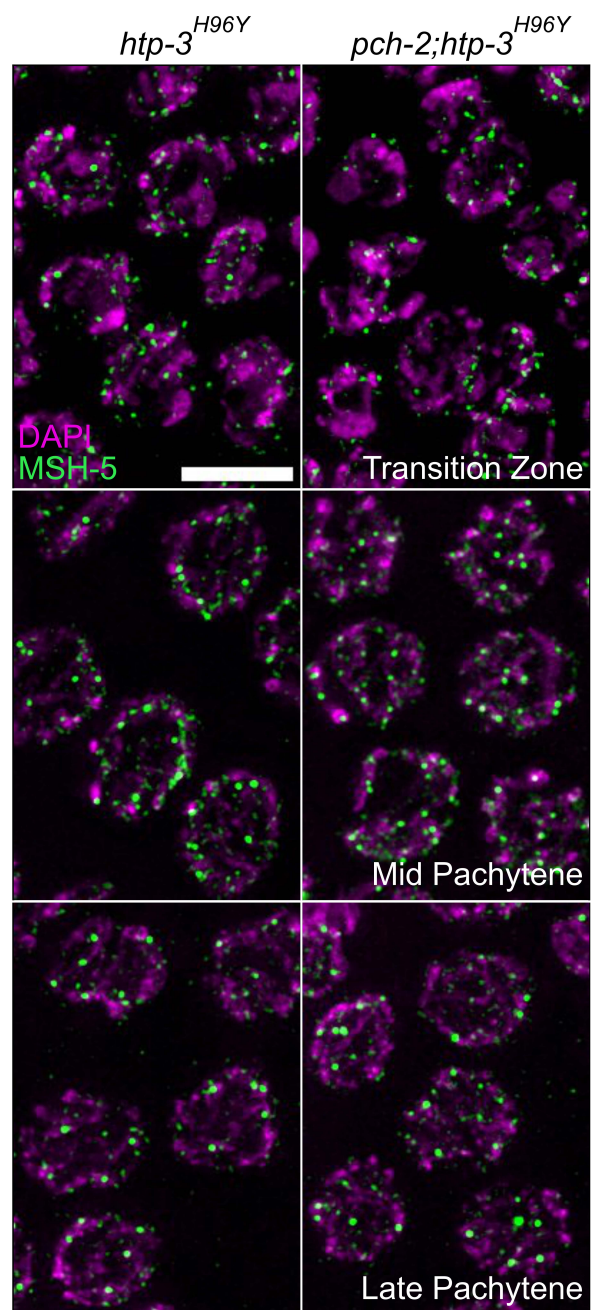
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**Supplementary Table 1: Single nucleotide polymorphisms used for recombination assay**

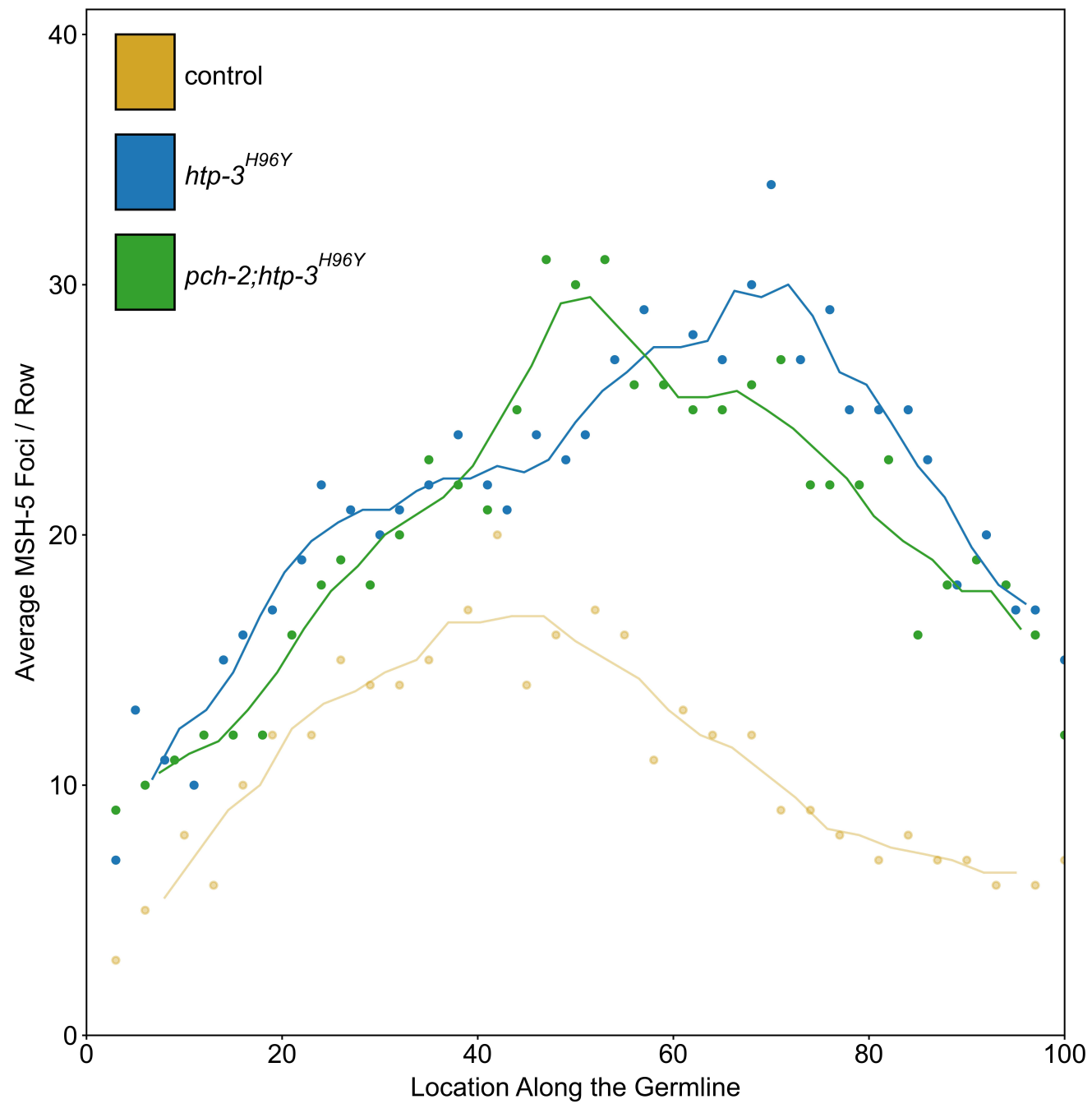
Chromosome and SNP	Primer Name	Primer Genetic Location	Primer Sequence FOR	Primer Sequence REV	Restriction enzyme	N2	HI
IA	F56C11	-19	ATGCCAG TGATAAG GAACGG	TCACATCC CTTGTCGA TGAA	DraI	354, 146	500
IB	Y71G12	-12.3	GACAATG ACCAATA AGACG	GATCCGT GAAATTGT TCCG	BsrI	440, 125	364, 125, 76
IC	K04F10	0.9	ATCATTCT CCAGGCC ACGTTAC	CTGAACTA GTGGAAC AAACCCC	NdeI	594	300, 294
ID	T07D10	13.6	CTTGGTG TGGGGA GAGTATA GG	TTTGTCCG GATTGACT CTGC	Sau3AI	303, 63	207, 96, 63
IE	ZK909	28.8	CACAAGT GGTTTGG AAGTACC G	CAACAAAG GGATAGAT CACGGG	HindIII	450	236, 214
IIIA	pkP3081	-26.98	AGCAAGA ATGAGCC GATTG	GTCGGCC GTTTTCAA ATAACTG	TaqI	222, 149	195, 145, 27
IIIB	pkP3095	-5.12	TCTCGTC AATTGTC GCCTG	TTATTTGC AATCCAAC GGC	ApoI	308	168, 140
IIIC	pkP3101	-0.9	CCAAGTG CAAATA TGGTGC	ATAAACAA TTTCAGTG CCGC	HinfI	495	282, 213
IIID	pkP3035	0.9	CGTAAAC TACCAA CTCGGTG	GGTCTACT ACAACAT ACAGGC	Eco0109I	732	419, 313
IIIE	pkP3080	21.29	CGGTGGT GGTAAAA GTGTAAC	CAACATTC AGGCTGT GCTTTCC	Hpy188III	365, 76, 68, 35	241, 124, 76, 68, 35
IVA	F56B3	-24	TGATGGT GTGTCTG CGTACC	AGAGCTG GAGAGCA CGGATA	DraI	301, 128, 71	429, 71
IVB	F52C12	-14.9	ACATTTA GTCACGC GTAGGG	GCCCGAA TCTAGCAC ATAAG	HpaII	191, 137, 22	328, 22
IVC	B0273	1.8	AATACAG CAGTCGT TCCGTTT	TGAACTTC ATGAACCA GCTTG	DraI	288, 144	432

IVD	K10D11	6.7	GATTATTT CAGAGGA GCAGAGC	CATAGCAC GTGGAATA ACCAC	HindIII	420	245, 175
IVE	T02D1	16.8	TGCTTAA AGTCATC GTGTCCA C	TGTAAACC GTATCGAA TCCGAC	EcoRI	174, 235	408
XA	pkP6139	-19.97	AAGAGTG AACCTTT TCCGTGA G	TGATGCAA TTTATACA CACGCC	MseI	401, 31	279, 122, 31
XB	pkP6120	-10.46	TCGTGGC ACCATAA AAGTG	GATTCAGA TCAAACAG AGGTGG	DraI	243	128, 115
XC	pkP6157	-0.14	GGGGTAT AATGAAC CAACCTG	TGTAGGAA CCGTTTGT TTCTTC	ApoI	261, 48	150, 111, 48
XD	pkP6161	9.38	ATCGACC CCAACAA TGAC	TCCGTCAT CCAAATCT CCG	AseI	542	287, 255
XE	pkP6170	24.07	CGCTGTC ACAATCT CTAAAAT G	AAACCCTC CCCACCTT GTTGTC	ApoI	249, 118, 56	197, 118, 56, 52

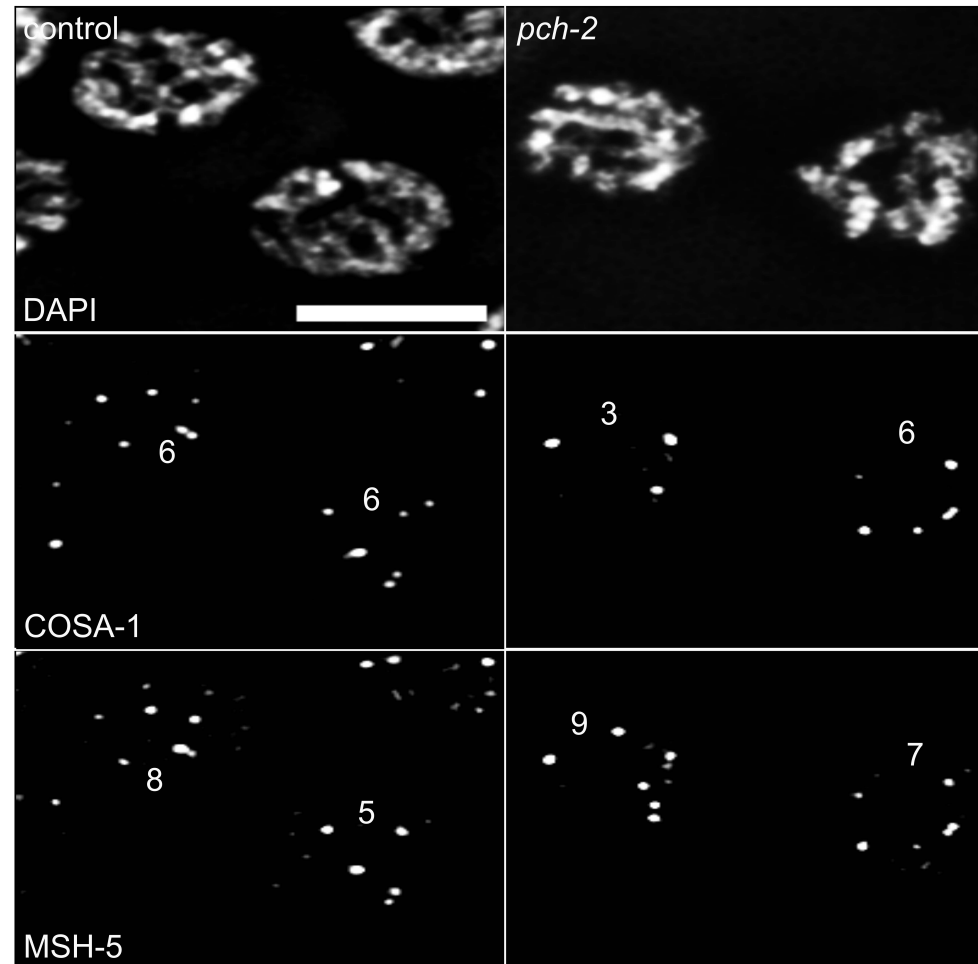
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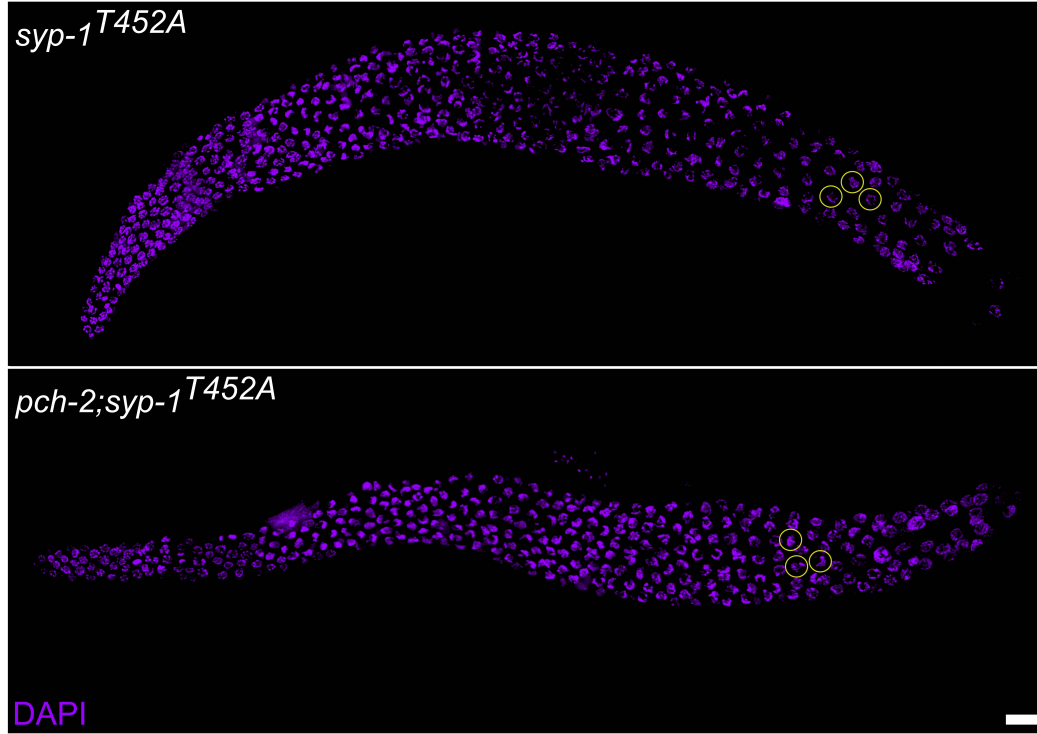
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