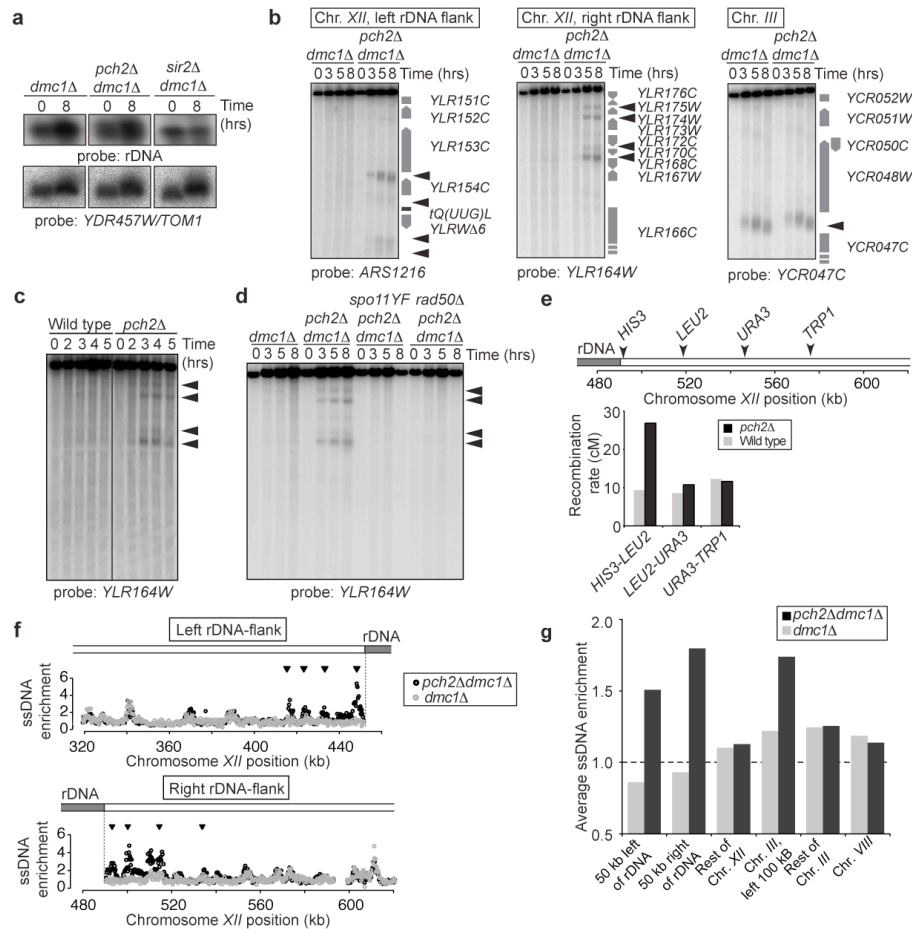
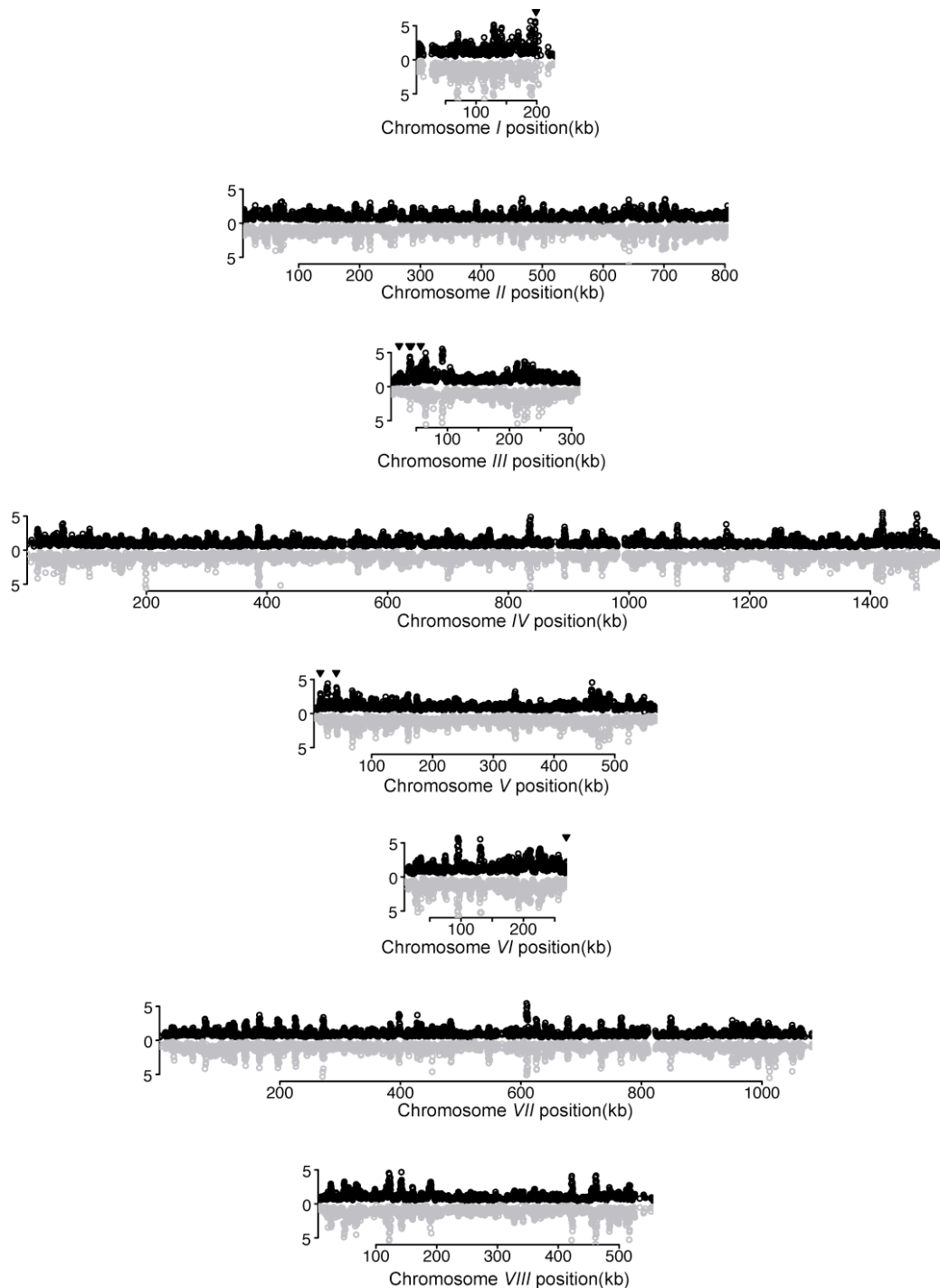


## Supplemental Figures and Legends



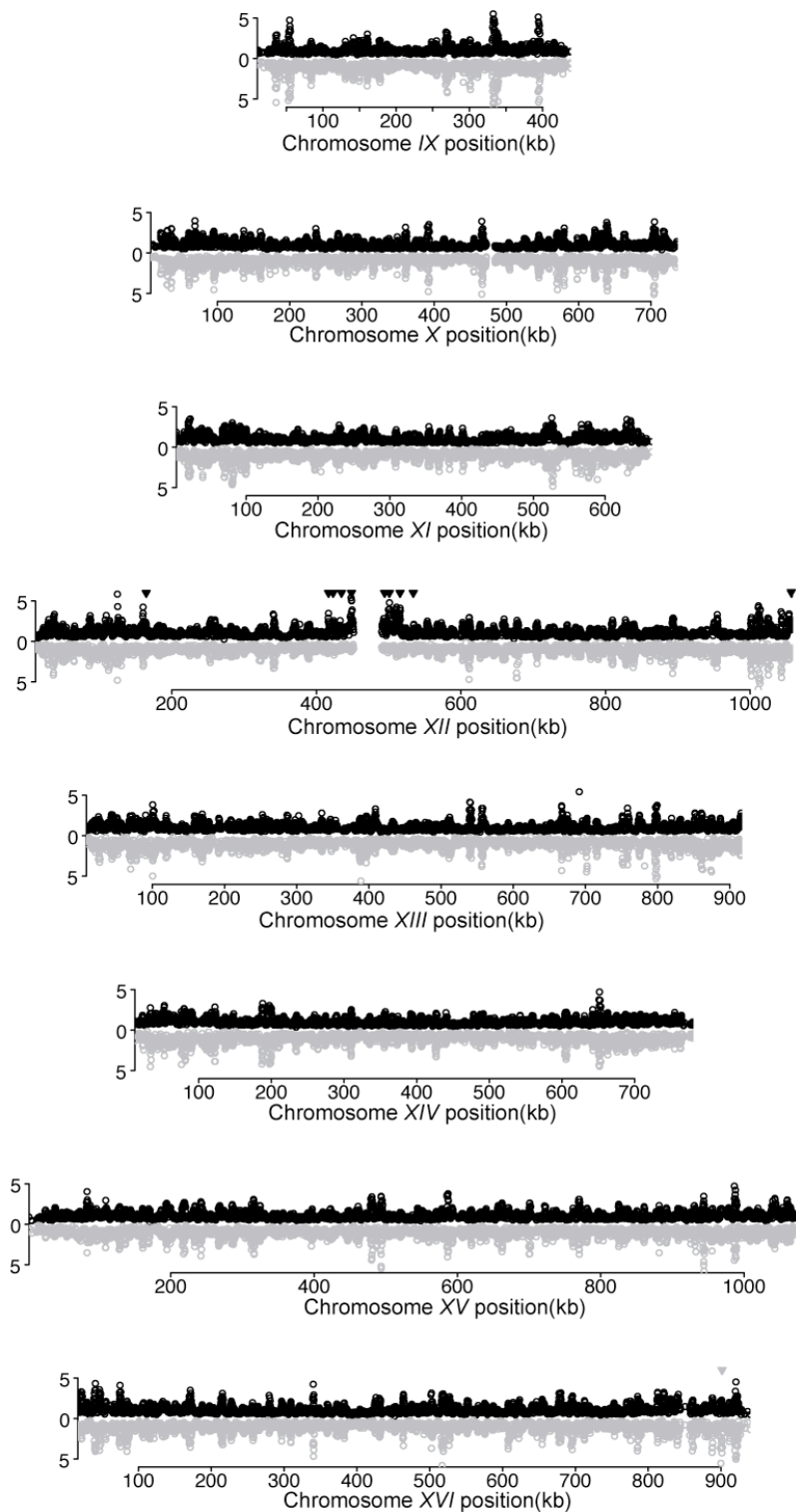
**Supplementary Figure 1. Pch2-dependent suppression of DSBs at the rDNA borders.**

**a**, Example of a CHEF gel/Southern blot of *dmc1Δ* (H5217), *dmc1Δ pch2Δ* (H5216), and *dmc1Δ sir2Δ* (H2933) cells harvested at the indicated time points as analysed in Figure 1a. rDNA was released from chromosome XII by in-gel digest with XhoI. Blot was probed for rDNA (NTS1) sequence and YDR457W/TOM1, a DSB coldspot that served to correct for copy number changes associated with DNA replication and as loading control. The ratio of full-length fragments after DSB formation (8h after meiotic induction) over unbroken (0h) was calculated. See supplementary methods for electrophoresis conditions and probe information. **b**, Meiotic time course analysis of *dmc1Δ* (H118) and *dmc1Δ pch2Δ* cells (H2629). Southern blots of the left rDNA flank (HindIII; probe: ARS1216), the right rDNA flank (ApaI; probe: YLR164W), and chromosome III (HindIII; probe: YCR047C). Grey boxes indicate the positions of open reading frames; black arrows highlight major DSB sites. **c**, Southern blot analysis of the right rDNA flank in wild-type (H119) and *pch2Δ* (H2817) cells. **d**, Southern blot of right rDNA flank in *dmc1Δ* (H118), *dmc1Δ pch2Δ* (H2629), *dmc1Δ pch2Δ spo11-Y135F* (H3102), and *dmc1Δ pch2Δ rad50Δ* cells (H3239). **e**, Crossover recombination in single-copy regions flanking the right border of the rDNA in wild-type (H3037, n=207) and *pch2Δ* (H3065; n=164) cells. Recombination rates are provided in centiMorgans (cM). Schematic indicates the chromosomal locations of analysed genetic markers. **f**, ssDNA profiles of *dmc1Δ* (H118, grey), and *dmc1Δ pch2Δ* (H2629, black) cells in the regions directly abutting the rDNA array on Chromosome XII. Significantly different peaks are indicated with black triangles (*dmc1Δ pch2Δ* over *dmc1Δ*). Definition of significance and coordinates of significantly different peaks are indicated in Table S1. **g**, Average enrichment for *dmc1Δ* (H118, grey), and *dmc1Δ pch2Δ* (H2629, black) is plotted for the indicated chromosomal regions. The genome-wide average is indicated by the dotted line. See Supplementary Methods for chromosomal coordinates of the analysed regions.



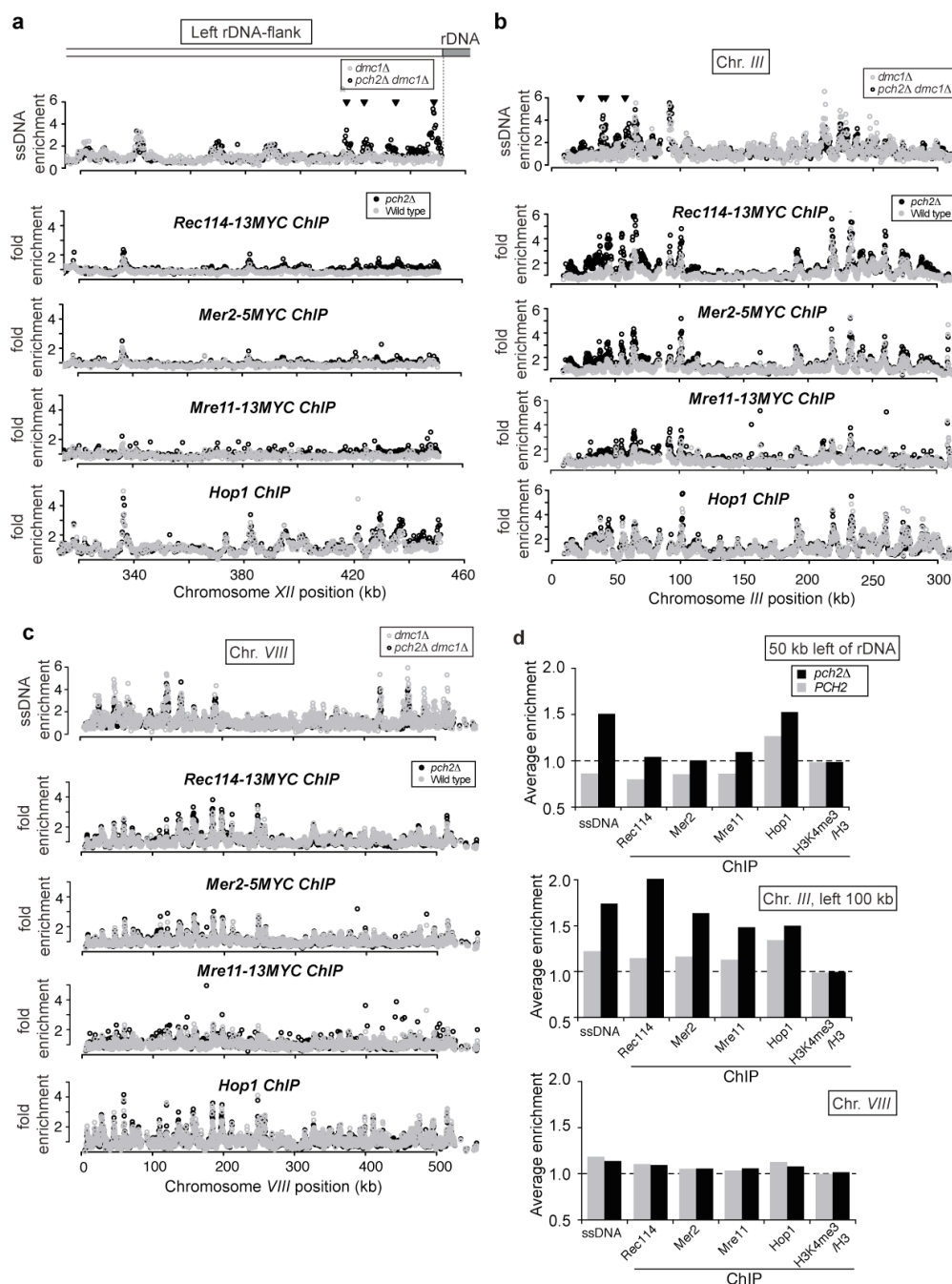
**Supplementary Figure 2. Effects of Pch2 on DSB formation across the genome.**

ssDNA profiles of the 16 budding yeast chromosomes in *dmc1Δ* (H118, grey) and *dmc1Δ pch2Δ* cells (H2629, black) cells. Chromosomes 1-8 are shown; see Figure S2-continued (next page) for chromosomes 9-16. Significantly different peaks are marked with black (*dmc1Δ pch2Δ* over *dmc1Δ*) and grey arrowheads (*dmc1Δ* over *dmc1Δ pch2Δ*). Definition of significance and coordinates of significantly different peaks are indicated in Table S1.



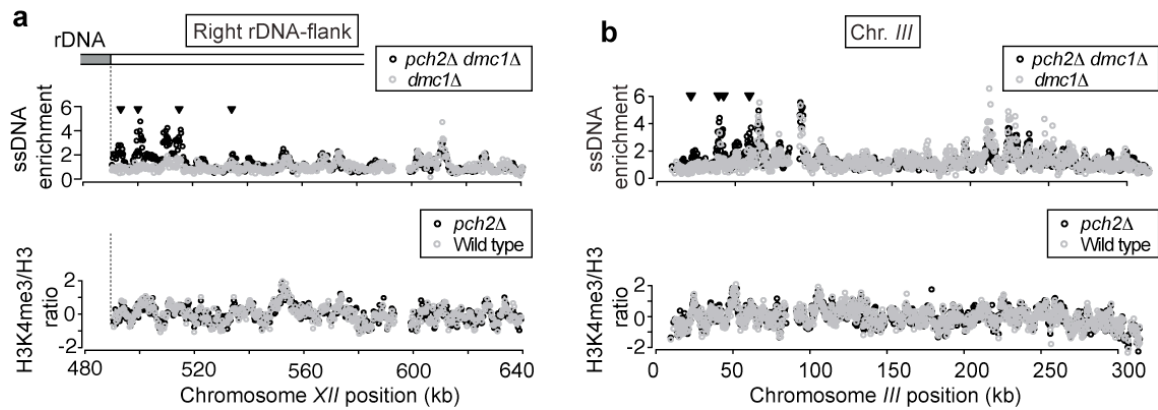
**Supplementary Figure 2-continued. Effects of Pch2 on DSB formation across the genome.**

ssDNA profiles of the Chromosomes 9-16 in *dmc1Δ* (H118, grey) and *dmc1Δ pch2Δ* cells (H2629, black) cells.



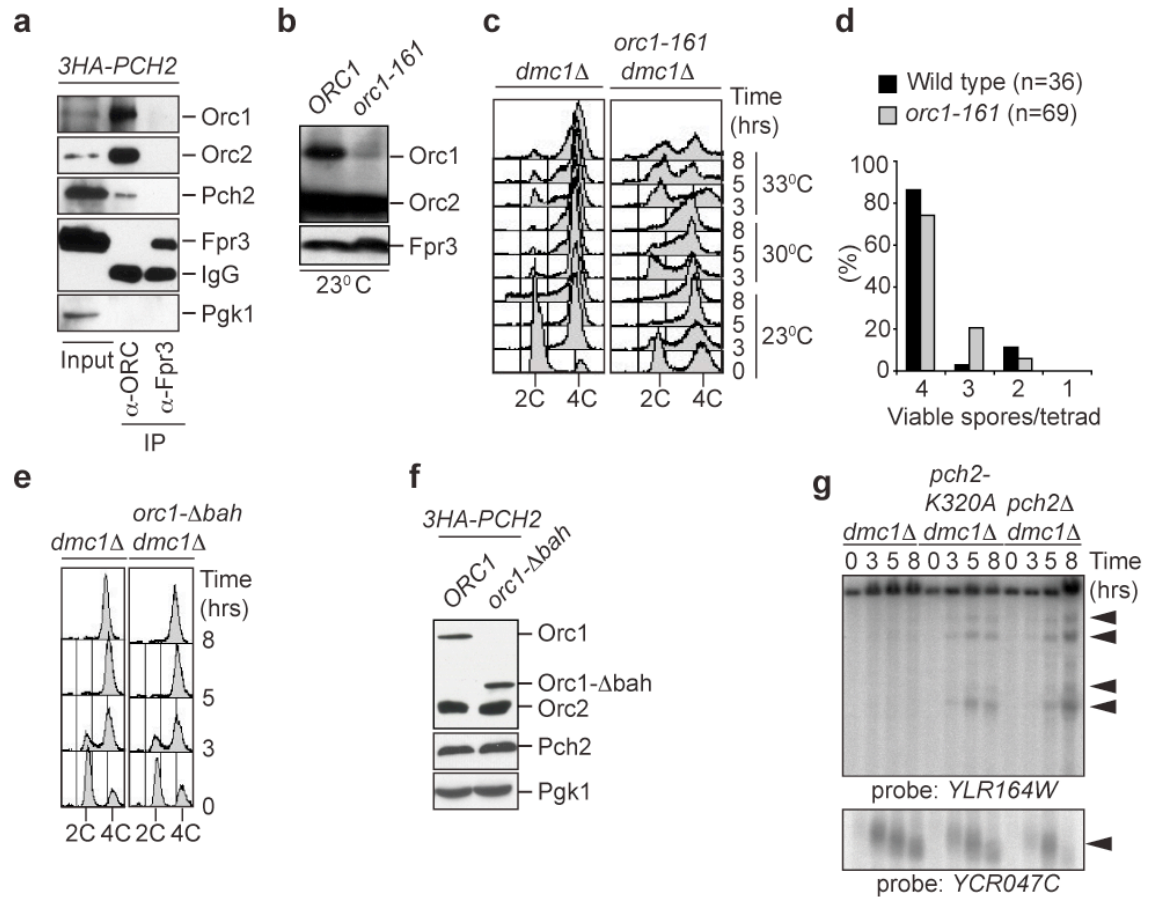
### Supplementary Figure 3. Effects of Pch2 on DSB factor distribution at the left rDNA flank and on chromosomes III and VIII.

Analysis of ssDNA enrichment in *dmc1Δ* (H118, grey) and *pch2Δ dmc1Δ* (H2629, black) cells (first panel) and ChIP-chip analysis for Rec114-13Myc (second panel, wild type:H4890; *pch2Δ*:H4893), Mer2-5Myc (third panel, wild type:H5916; *pch2Δ*:H5917), Mre11-13Myc (fourth panel, wild type:H5547; *pch2Δ*:H5947) and Hop1 (fifth panel, wild type:H1556; *pch2Δ*:H2817), in wild-type (grey) and *pch2Δ* cells (black) on the left rDNA flank on Chromosome XII (**a**), and along Chromosome III (**b**), and Chromosome VIII (**c**). **d**, Average enrichment for the different *PCH2* and *pch2Δ* ssDNA and ChIP-strains (see **a-c**) in the indicated chromosomal regions is plotted. The genome-wide average is indicated by the dotted line. See Supplementary Methods for chromosomal coordinates of the analysed regions.



**Supplementary Figure 4. Pch2 does not affect histone H3K4 trimethylation near the rDNA.**

Analysis of ssDNA profiles (upper panel; *dmc1Δ* (H118, grey) and *dmc1Δ pch2Δ* cells (H2629, black)) and H3K4me3/H3 ratios for wild-type (H119, grey) and *pch2Δ* cells (H2817, black) in the region directly abutting the rDNA array on Chromosome XII (a), and along Chromosome III (b).



### Supplementary Figure 5. Pch2 interacts with Orc1 and its ATPase activity is required to suppress DSBs.

**a**, Co-immunoprecipitation of 3HA-Pch2 with ORC. Co-IPs performed with  $\alpha$ -ORC (using a pan-ORC antibody that recognises all 6 ORC subunits) or  $\alpha$ -Fpr3 (as negative control) in 3HA-PCH2 cells (H3463). Samples were probed for: Orc1 ( $\alpha$ -ORC), Orc2 ( $\alpha$ -ORC), Fpr3, and Pgk1 as a cytoplasmic control. **b**, Western blot showing Orc1 and Orc2 protein levels in meiotic wild-type (H4962) and *orc1-161* (H5033) cells grown at the permissive temperature (23°C). Samples were taken 3h after meiotic induction. Fpr3 was used as loading control. **c**, FACS analysis of *dmc1* $\Delta$  (H118) and *orc1-161 dmc1* $\Delta$  (H5137) cells at various times in meiosis, while incubated at 23°C, 30°C, and 33°C. **d**, Spore viability of wild-type (H13) and *orc1-161* cells (H5033) sporulated at 23°C. **e**, FACS analysis of *dmc1* $\Delta$  (H5838) and *orc1- $\Delta$ bah *dmc1* $\Delta$*  (H5865) cells at various times in meiosis while incubated at 30°C. **f**, Western blot showing protein levels of Orc1, Orc1- $\Delta$ bah, Orc2, and 3HA-Pch2 in meiotic 3HA-PCH2 (H5772) and 3HA-PCH2 *orc1- $\Delta$ bah* (H5894) cells. Samples were taken 3h after meiotic induction. Pgk1 was used as loading control. **g**, Meiotic time course in *dmc1* $\Delta$  (H118), *pch2-K320A dmc1* $\Delta$  (H4509), and *pch2* $\Delta$  *dmc1* $\Delta$  cells (H2629) analysed by Southern blotting of the right rDNA flank (ApaLI; probe: YLR164W) and of chromosome III (HindIII; probe: YCR047C). *pch2-K320A* was a kind gift of Akira Shinohara.



# Supplementary Tables

## Supplementary Table 1. Regions of ssDNA enrichment in *pch2Δ dmc1Δ* versus *dmc1Δ*

Sites of differential ssDNA enrichment between *dmc1Δ* (H118) and *pch2Δ dmc1Δ* (H2629) strains are listed. Sites were selected at which the ssDNA signal was increased >2 fold at more than 3 data points within 500 bp of each other. To exclude false positives due to background fluctuations, regions were only considered significant when the region overlapped with an ssDNA peak within the enriched dataset. Using these criteria, we identified 173 enriched features in 18 regions that were significantly increased in *pch2Δ dmc1Δ* over *dmc1Δ* cells, of which 110 features (in 8 regions) were directly flanking the rDNA array (shown in bold).

Chromosome	Start enriched region (bp)	End enriched region (bp)	Peak (bp)	Fold enrichment at peak	No. of features within region	Distance from <sup>a</sup> rDNA, <sup>b</sup> telomere or <sup>c</sup> HML	Enriched Dataset
1	196719	198671	198671	4.61	6	30632 <sup>b</sup>	<i>pch2Δdmc1Δ</i>
3	22131	24379	22524	3.42	7	7182 <sup>c</sup>	<i>pch2Δdmc1Δ</i>
3	37036	39665	38859	7.37	8	22087 <sup>c</sup>	<i>pch2Δdmc1Δ</i>
3	40789	42066	41829	4.28	7	25840 <sup>c</sup>	<i>pch2Δdmc1Δ</i>
3	56386	60034	57095	3.40	11	41437 <sup>c</sup>	<i>pch2Δdmc1Δ</i>
5	13642	15812	15348	7.02	7	13642 <sup>b</sup>	<i>pch2Δdmc1Δ</i>
5	41108	42923	41665	4.25	4	41108 <sup>b</sup>	<i>pch2Δdmc1Δ</i>
6	267700	269851	268697	3.07	4	0 <sup>b</sup>	<i>pch2Δdmc1Δ</i>
12	164572	165524	164572	3.49	5	164572 <sup>b</sup>	<i>pch2Δ dmc1Δ</i>
<b>12</b>	<b>416092</b>	<b>417652</b>	<b>416758</b>	<b>7.52</b>	<b>6</b>	<b>35278<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>423165</b>	<b>423965</b>	<b>423165</b>	<b>2.90</b>	<b>4</b>	<b>28205<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>431663</b>	<b>434643</b>	<b>434643</b>	<b>3.92</b>	<b>8</b>	<b>19707<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>444578</b>	<b>451090</b>	<b>448541</b>	<b>6.51</b>	<b>21</b>	<b>6792<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>491066</b>	<b>494638</b>	<b>494316</b>	<b>4.77</b>	<b>15</b>	<b>535<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>498803</b>	<b>511779</b>	<b>500878</b>	<b>6.72</b>	<b>37</b>	<b>8272<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>512872</b>	<b>517689</b>	<b>515671</b>	<b>3.78</b>	<b>15</b>	<b>22341<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
<b>12</b>	<b>533975</b>	<b>535512</b>	<b>533975</b>	<b>2.14</b>	<b>4</b>	<b>43444<sup>a</sup></b>	<b><i>pch2Δdmc1Δ</i></b>
12	1057155	1057952	1057155	2.86	4	19942 <sup>b</sup>	<i>pch2Δdmc1Δ</i>
16	899524	901317	901317	2.28	4	46379 <sup>b</sup>	<i>dmc1Δ</i>

**Supplementary Table 2. rDNA recombination in *pch2Δ* and wild-type cells**

Recombination frequencies as measured by tetrad dissection using strains that carry different *URA3* integrations within the rDNA array (see Figure 1c,d). Strain numbers are indicated. CO-associated repeat number changes were determined by CHEF gel analysis of XhoI-digested chromosomes (probe: *NTS1/2*).

Number of rDNA repeats between left flank and <i>URA3</i> insertion	Genotype	Total array length (repeats)	Tetrads analysed	Cross-over events <i>HIS3-URA3</i>	Cross-over events <i>URA3-TRP1</i>	Fraction of total crossovers in <i>HIS3-URA3</i> interval	Fraction of total rDNA repeats in <i>HIS3-URA3</i> interval	CO-associated repeat number changes for <i>HIS3-URA3</i> interval
1	<i>pch2Δ</i> (H4611)	103	465	8	46	15%	1%	2 of 5 (+1, 0, +6, 0, 0)
3	<i>pch2Δ</i> (H4613)	99	533	12	36	25%	3%	9 of 12 (-1, 0, +4, 0, +2, +1, +15, +8, +1, +3, 0, +3)
10	<i>pch2Δ</i> (H3823)	110	494	20	33	38%	9%	6 of 11 (+3, 0, +2, 0, -2, +13, 0, -7, 0, +6, 0)
12	<i>pch2Δ</i> (H4612)	110	367	19	30	39%	11%	16 of 19 (0, -5, +2, 0, +6, +7, +2, -4, -3, +5, +9, 0, +3, -4, +13, +12, -2, -7, +19)
29	<i>pch2Δ</i> (H3820)	108	503	20	26	44%	27%	
49	<i>pch2Δ</i> (H3821)	99	308	27	24	53%	50%	
12	wild type (H4881)	110	2350	4	10	30%	11%	3 of 4 (+1, +2, 0, -3)



**Supplementary Table 3. Genotypes of yeast strains used in this study.**

<b>Strain No.</b>	<b>Relevant genotype</b>	<b>Reference</b>
H13 (=A4962)	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>his3::hisG</i> , <i>trp1::hisG</i> <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>his3::hisG</i> , <i>trp1::hisG</i>	<sup>1</sup>
H118 (=NKY1455)	H119, but <i>dmc1Δ::ARG4/dmc1 Δ::ARG4</i>	<sup>2</sup>
H119 (=NKY1551)	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>his4X::LEU2-URA3</i> , <i>ura3</i> , <i>arg4-Bgl2</i> , <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>his4B::LEU2</i> , <i>ura3</i> , <i>arg4-Nsp</i>	<sup>3</sup>
H2629	H118, but <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study
H2817	H119, but <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study
H2953	H118, but <i>sir2::TRP1/sir2::TRP1</i>	This study
H3026	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>his3::hisG</i> , <i>trp1::hisG</i> <i>MATalpha</i> , <i>ho::LYS2</i> , <i>trp1::hisG</i> , <i>his3::hisG</i> , <i>leu2::hisG</i> , <i>ura3</i> , <i>pch2Δ::KanMX/+</i> , <i>YLR162W-A::TRP1</i> , <i>ARS1216::HIS3</i>	This study
H3027	H3026, but <i>pch2Δ::KanMX/pch2Δ::KanMX</i>	This study
H3037	H13, but <i>pch2Δ::KanMX/+</i> , <i>MAS1::HIS3</i> , <i>HMX1::URA3</i> , <i>IFH1::TRP1</i> , <i>ylr184w::LEU2</i>	This study
H3038	H2953, but <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study
H3065	H13, but <i>pch2Δ::KanMX/pch2Δ::KanMX</i> , <i>MAS1::HIS3</i> , <i>HMX1::URA3</i> , <i>IFH1::TRP1</i> , <i>ylr184w::LEU2</i>	This study
H3102	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3::hisG</i> , <i>leu2::hisG</i> , <i>arg4-Bgl</i> <i>II</i> , <i>his4B::LEU2</i> , <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3::hisG</i> , <i>leu2::hisG</i> , <i>arg4-Bgl II</i> , <i>his4B::LEU2</i> , <i>spo11-Y135F-HA-URA3/spo11-Y135F-HA-URA3</i> , <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i> , <i>dmc1Δ::ARG4/</i> <i>dmc1Δ::ARG4</i>	This study
H3239	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>his4B::LEU2</i> , <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>his4B::LEU2</i> , <i>dmc1Δ::ARG4/dmc1Δ::ARG4</i> , <i>rad50::URA3/</i> <i>rad50::URA3</i> , <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study
H3261	H3262, but <i>leu2::SIR2::LEU2</i>	This study
H3262	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>ura3</i> , <i>trp1::hisG</i> , <i>his3::hisG</i> , <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>ura3</i> ,	This study

	<i>trp1::hisG, his3::hisG, pch2Δ::KanMX4/ pch2Δ::KanMX4, dmc1Δ::HIS3/ dmc1Δ::HIS3, sir2::TRP1/sir2::TRP1</i>	
H3282	H3262, but <i>leu2::sir2-345::LEU2</i>	This study
H3463	<i>MATa, ho::LYS2, lys2, ura3, leu2::hisG, his4B::LEU2, arg4-Bgl II, MATalpha, ho::LYS2, lys2, ura3, leu2::hisG, his4B::LEU2, arg4-Bgl II, pch2::URA3:pPCH2(300bp):3HA-PCH2/pch2::URA3:pPCH2(300bp):3HA-PCH2</i>	This study
H3820	<i>MATalpha, lys2, ho::LYS2, trp1::hisG, his3::hisG, leu2::hisG, ura3 ARS1216::HIS3, YLR162W-A::TRP1, MATa, lys2, ho::LYS2, trp1::hisG, his3::hisG, leu2::hisG, ura3, pch2Δ::KanMX/ pch2Δ::KanMX rDNA::URA3 (@29<sup>th</sup> repeat)</i>	This study
H3821	H3820, but <i>rDNA::URA3 (@49<sup>th</sup> repeat)</i>	This study
H3823	H3820, but <i>rDNA::URA3 (@10<sup>th</sup> repeat)</i>	This study
H4509	H118, but <i>pch2-K320A/ pch2-K320A</i>	This study
H4611	H3820, but <i>rDNA::URA3 (@1<sup>st</sup> repeat)</i>	This study
H4612	H3820, but <i>rDNA::URA3 (@12<sup>th</sup> repeat)</i>	This study
H4613	H3820, but <i>rDNA::URA3 (@3<sup>rd</sup> repeat)</i>	This study
H4737	H2629, but <i>rdnΔΔ::HIS3/ rdnΔΔ::HIS3, [pRDN-hyg::URA3::leu2-8]/[pRDN-hyg::URA3::leu2-8], flo8 (unmarked)/+</i>	This study
H4798	H2629, but <i>t(Chr.2;Chr12) lys2::hphMX4::pGPD-loxP-ADE2/t(Chr.2;Chr12) lys2::hphMX4::pGPD-loxP-ADE2 t(Chr.12;Chr2) YLR162W-A::natMX4::loxP /t(Chr.12;Chr2) YLR162W-A::natMX4::loxP</i>	This study
H4890	<i>MATa, ho::LYS2, TRP1, his3::hisG, ura3, lys2, leu2::hisG, MATalpha, ho::LYS2, trp1::hisG, his3::hisG, URA3, lys2, LEU2, REC114-13MYC::HIS3/REC114-13MYC::HIS3</i>	This study
H4893	H4890, but <i>pch2Δ::KanMX/ pch2Δ::KanMX</i>	This study
H4952	H118, but <i>pch2Δ::KanMX/+, orc1::orc1-161 /orc1::orc1-161</i>	This study
H5028	H13, but <i>orc1::orc1-161/ orc1::orc1-161</i>	This study
H5033	H5033, but <i>orc1::orc1-161/orc1::orc1-161</i>	This study
H5137	<i>MATa, ho::LYS2, lys2, trp1::hisG, leu2::hisG, his4X::LEU2-URA3, his3::hisG, ura3, arg4-nsp(?), dmc1Δ::ARG4, orc1::orc1-161 MATalpha, ho::LYS2, lys2, ura3, leu2::hisG, his4B::LEU2, arg4-Bgl II (?),</i>	This study

	<i>dmc1Δ::ARG4,orc1::orc1-161</i>	
H5216	<i>MATa, ho::LYS2, lys2, ura3, leu2::hisG, his4B::LEU2, arg4-Bgl II</i> <i>MATalpha, ho::LYS2, lys2, ura3, leu2::hisG, his4B::LEU2, arg4-Bgl II?</i> <i>dmc1Δ::ARG4/dmc1Δ::ARG4,</i> <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study
H5217	<i>MATa, ho::LYS2, lys2, leu2::hisG, trp1::hisG, ura3, ARG4, his3::hisG?, his4B::LEU2,</i> <i>MATalpha, ho::LYS2, lys2, leu2::hisG, ura3, arg4-Bgl2, his4B::LEU2, dmc1Δ::ARG4/dmc1Δ::ARG4</i>	This study
H5547	<i>MATa, ho::LYS2, TRP, his3::hisG, ura3, LEU2</i> <i>MATalpha, ho::LYS2, trp1::hisG, his3::hisG, URA3, leu2::hisG</i> <i>MRE11-13MYC::HIS3</i> <i>MRE11-13MYC::HIS3</i>	This study
H5583	<i>MATa, ho::LYS2, lys2, leu2::hisG, TRP1, his4B::LEU2, ura3, ARG4,</i> <i>MATalpha, ho::LYS2, lys2, leu2::hisG, TRP1, his4B::LEU2, ura3, ARG4, ,dmc1Δ::ARG4/</i> <i>dmc1Δ::ARG4, rDNA::URA3 (@1<sup>st</sup> repeat)/rDNA::URA3 (@1<sup>st</sup> repeat)</i>	This study
H5622	H5583, but <i>pch2Δ::KanMX/pch2Δ::KanMX</i>	This study
H5636	H5622, but <i>rDNA::URA3 (@3<sup>rd</sup> repeat)/rDNA::URA3 (@3<sup>rd</sup> repeat)</i>	This study
H5706	H5622, but <i>rDNA::URA3 (@10<sup>th</sup> repeat)/rDNA::URA3 (@10<sup>th</sup> repeat)</i>	This study
H5772	<i>MATa, ho::LYS2, lys2, ura3, leu2::hisG, TRP1, HIS3(?)</i> <i>his4B::LEU2, pch2::URA3:pPCH2(300bp):3HA-PCH2</i> <i>orc1::TRP1, ura3::ORC1::URA3</i> <i>MATalpha, ho::LYS2, lys2, ura3, leu2::hisG, TRP1, HIS3(?)</i> <i>his4B::LEU2, pch2::URA3:pPCH2(300bp):3HA-PCH2</i> <i>orc1::TRP1, ura3::ORC1::URA3</i>	This study
H5838	<i>MATalpha, ho::LYS2, lys2, leu2::hisG, TRP1, ura3, arg4-Bgl2, dmc1Δ::ARG4, orc1::TRP1, ura3::ORC1::URA3</i> <i>MATa, ho::LYS2, lys2, leu2::hisG, trp1::hisG, his4B::LEU2, ura3, arg4-Bgl2, dmc1Δ::ARG4, orc1::TRP1, ura3::ORC1::URA3</i>	This study
H5865	<i>MATalpha, ho::LYS2, lys2, leu2::hisG, his4B::LEU2, ura3, arg4-Bgl2(?), dmc1Δ::ARG4, orc1::TRP1, ura3::orc1deltaNTD(1-235)::URA3</i> <i>MATa, ho::LYS2, lys2, leu2::hisG, his4B::LEU2, ura3,</i>	This study

	<i>arg4-Bgl2</i> , <i>dmc1Δ::ARG4</i> , <i>orc1::TRP1</i> , <i>ura3::orc1deltaNTD(1-235)::URA3</i>	
H5894	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>TRP1(?)</i> , <i>HIS3(?)</i> , <i>arg4-Bgl II (?)</i> , <i>pch2::URA3:pPCH2(300bp):3HA-PCH2</i> <i>orc1::TRP1</i> , <i>ura3::orc1deltaNTD(1-235)::URA3</i> <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>TRP1(?)</i> , <i>HIS3(?)</i> <i>his4B::LEU2</i> , <i>ARG4</i> , <i>pch2::URA3:pPCH2(300bp):3HA-PCH2</i> <i>orc1::TRP1</i> , <i>ura3::orc1deltaNTD(1-235)::URA3</i>	This study
H5916	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>TRP</i> , <i>his3::hisG</i> <i>his4X::LEU2-(Bam)-URA3</i> , <i>arg4-Nsp</i> <i>pch2Δ::KanMX</i> , <i>mer2(rec107)::MER2-5myc</i> <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>HIS3+,,</i> <i>trp1::hisG,arg</i> , <i>pch2Δ::KanMX</i> , <i>pch2::KanMX4 mer2(rec107)::MER2-5myc</i> , <i>mer2(rec107)::MER2-5myc</i> ,	This study
H5917	<i>MATa</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>TRP</i> , <i>his3::hisG</i> <i>his4X::LEU2-(Bam)-URA3</i> , <i>arg4-Nsp (?)</i> , <i>mer2(rec107)::MER2-5myc</i> <i>MATalpha</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>leu2::hisG</i> , <i>HIS3+,,</i> <i>trp1::hisG,arg(?)</i> , <i>mer2(rec107)::MER2-5myc</i> , <i>pch2::KanMX4</i>	This study
H5947	H5547, but <i>pch2Δ::KanMX4/pch2Δ::KanMX4</i>	This study

### Supplementary references

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- <sup>3</sup> Storlazzi, A., Xu, L., Cao, L., and Kleckner, N., Crossover and noncrossover recombination during meiosis: timing and pathway relationships. *Proc Natl Acad Sci U S A* **92** (18), 8512 (1995).