Figure S1

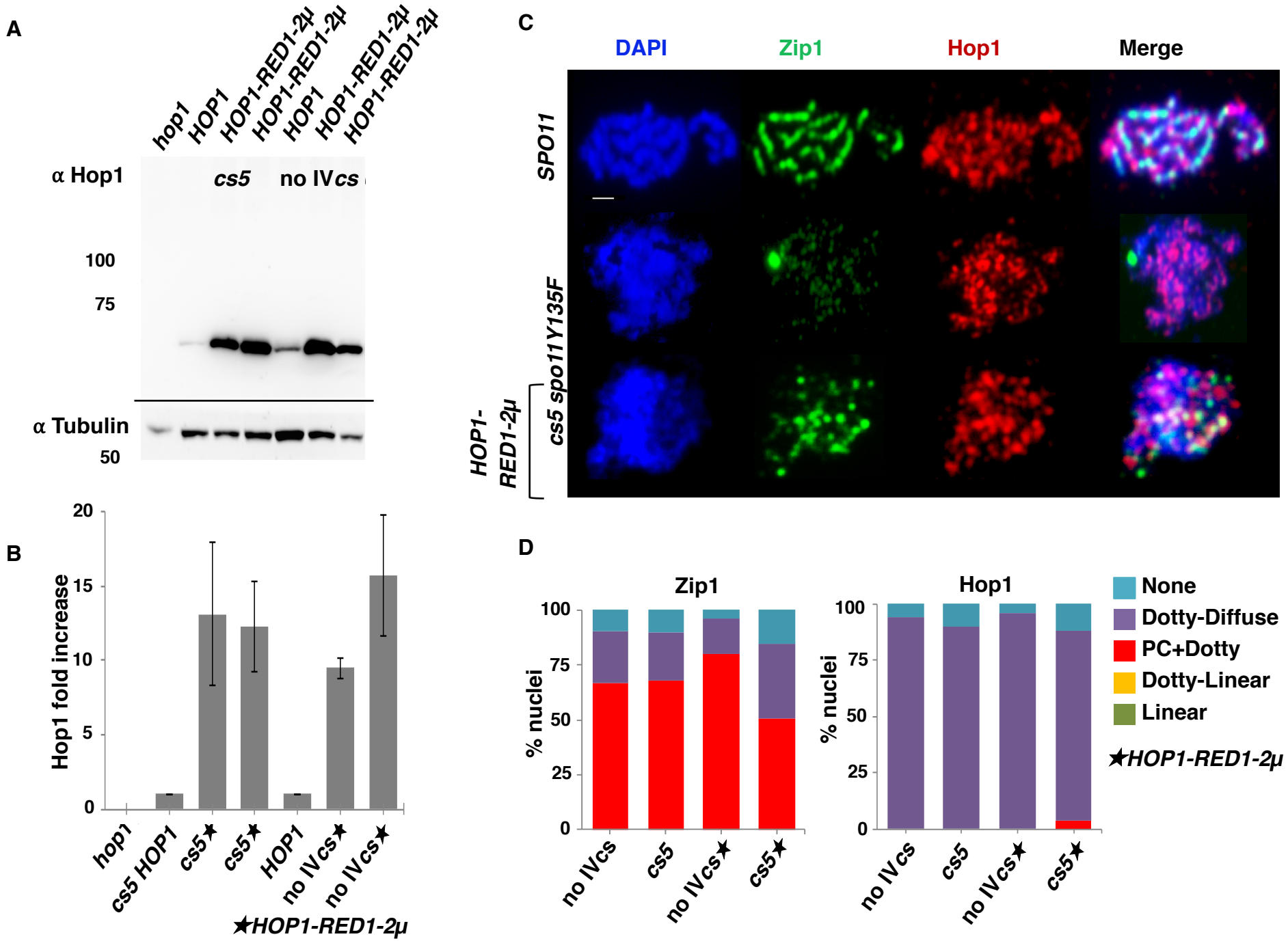

A
hop1
HOP1
HOP1-RED1-2μ
HOP1-RED1-2μ
HOP1
HOP1-RED1-2μ
HOP1-RED1-2μ
α Hop1
cs5
no IVcs
100
75
α Tubulin
50
B
Hop1 fold increase
20
15
10
5
0
hop1
cs5 HOP1
cs5★
cs5★
HOP1
no IVcs★
no IVcs★
★HOP1-RED1-2μ
C
DAPI
Zip1
Hop1
Merge
SPO11
cs5 spo11Y135F
HOP1-RED1-2μ
D
Zip1
Hop1
% nuclei
100
75
50
25
0
no IVcs
cs5
no IVcs★
cs5★
None
Dotty-Diffuse
PC+Dotty
Dotty-Linear
Linear
★HOP1-RED1-2μ

Figure S1. *Overexpression of chromosome axis proteins does not facilitate SC assembly in response to an HO-mediated meiotic DSB.*

The Western blot in (A) indicates Hop1 protein levels in a P_{GAL}-*HOP1 ndt80* strain (LY769; lane 1), a *HOP1 spo11-Y135F* strain homozygous for *HO cs5* (LY841; lane2), the LY841 strain carrying a 2*μ-HOP1-RED1* plasmid (LY864; lane 3 and 4), a strain without a chromosome IV *HO cs* (LY846; lane 5), and this LY846 strain carrying a 2*μ-HOP1-RED1* plasmid (LY865; lanes 6, 7). Numbers at the left indicate molecular weight (kDa). The average of 3 Western experiments to detect Hop1 levels are plotted on the graph in (B), with strains listed in the same order as in (A). Tubulin levels were used to normalize Hop1 levels across samples; bars indicate standard error of the mean. (C) Representative surface spread meiotic nuclei from a *SPO11 ndt80* strain (YAM424; top row; image also shown in Figure 6), and *spo11-Y135F ndt80* strains carrying *cs5* with and without a 2*μ-HOP1-RED1* plasmid (LY841 and LY864) at 24 hours of sporulation. The *ndt80* null allele ensures the strains will not progress beyond the pachytene stage of meiosis. Percentage of nuclei exhibiting various indicated Zip1 and Hop1 phenotypes for control and 2*μ-HOP1-RED1*-carrying strains (left to right: LY846, LY841, LY865, LY864) are plotted in (D); Each bar represents a total of 50 nuclei.

Figure S2

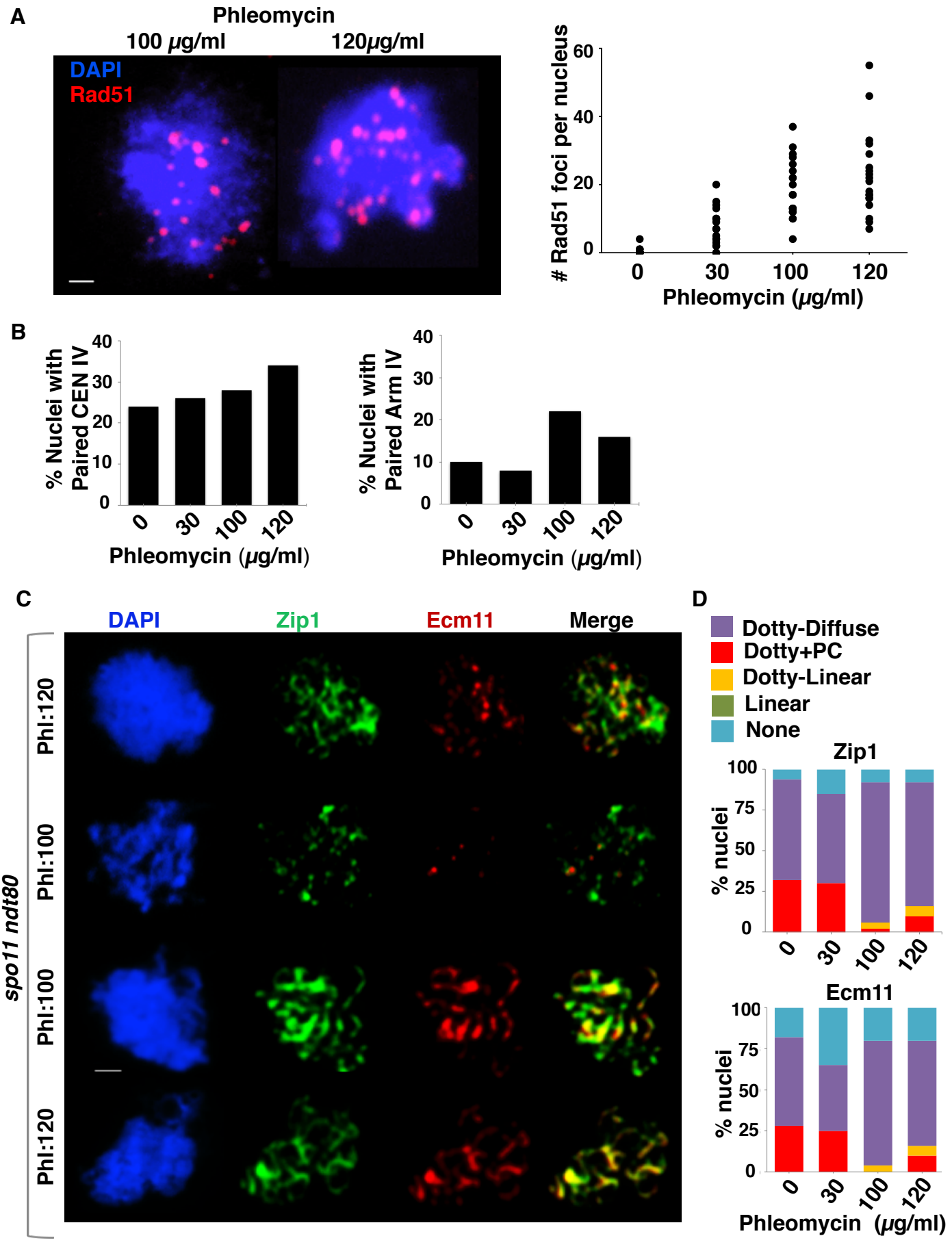
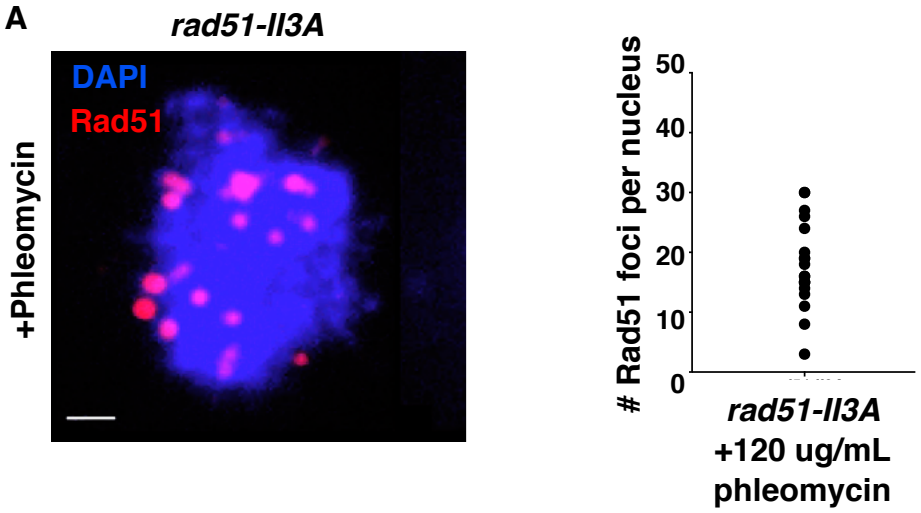
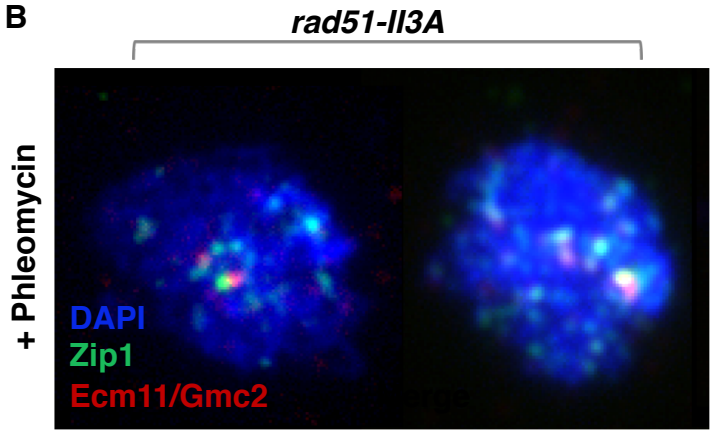

A
Phleomycin
100 μg/ml
120μg/ml
DAPI
Rad51
Rad51 foci per nucleus
60
40
20
0
0
30
100
120
Phleomycin (μg/ml)
B
% Nuclei with Paired CEN IV
40
30
20
10
0
0
30
100
120
Phleomycin (μg/ml)
% Nuclei with Paired Arm IV
40
30
20
10
0
0
30
100
120
Phleomycin (μg/ml)
C
DAPI
Zip1
Ecm11
Merge
spo11 ndt80
Phl:120
Phl:100
Phl:100
Phl:120
D
Dotty-Diffuse
Dotty+PC
Dotty-Linear
Linear
None
Zip1
% nuclei
100
75
50
25
0
0
30
100
120
Ecm11
% nuclei
100
75
50
25
0
0
30
100
120
Phleomycin (μg/ml)

Figure S2. *DSBs generated via phleomycin exposure alter SC protein distribution but do not promote robust SC assembly in* spo11 *meiotic nuclei*.

(A) Image displays representative surface-spread meiotic nuclei from a *spo11 ndt80* strain (LY471) exposed to 100 μg/mL (left) or 120 μg/mL phleomycin; DNA is labeled by DAPI (blue) and Rad51 targeted by an antibody (red). Graph plots the number of Rad51 foci measured per nucleus in LY471 meiotic cells sporulated for 24 hours with different doses of Phleomycin (n= 20). Graphs in (B) plot the frequency of *CEN IV* pairing or chromosome IV arm pairing in a *spo11* strain (LY176) with increasing concentration of Phleomycin (n= 50). Cells were assessed at 15 hours of sporulation. ($P > 0.1$ for all strains relative to the control) (C) Representative surface spread meiotic nuclei from a *spo11 ECM11-MYC ndt80* strain (LY471), exposed to 0, 30, 100 or 120μg/ml phleomycin at t = 0 of meiosis. Top two rows give representative images of the Zip1 and Ecm11-MYC 'dotty-diffuse' phenotype, while the bottom two rows give representative images of the less frequent 'dotty-linear' phenotype where Zip1 and Ecm11 co-assemble short linear structures. The proportion of nuclei with different Zip1 and Ecm11 distribution phenotypes are plotted in (D); n= 20-50 for each concentration of phleomycin (indicated on *x* axis).

Figure S3


A
rad51-II3A
DAPI
Rad51
+Phleomycin
Rad51 foci per nucleus
50
40
30
20
10
0
rad51-II3A
+120 ug/mL
phleomycin


B
rad51-II3A
+ Phleomycin
DAPI
Zip1
Ecm11/Gmc2

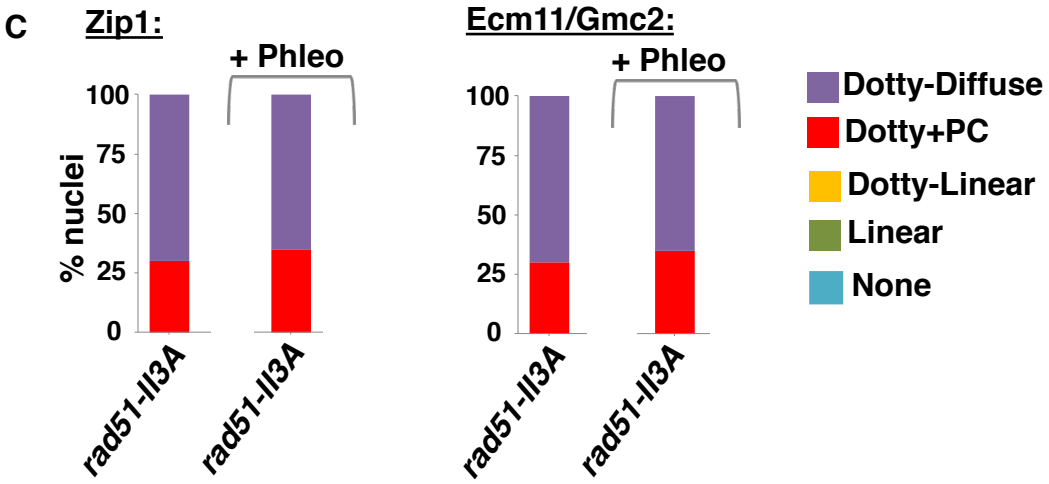

C
Zip1:
+ Phleo
% nuclei
100
75
50
25
0
rad51-II3A
rad51-II3A
Ecm11/Gmc2:
+ Phleo
100
75
50
25
0
rad51-II3A
rad51-II3A
Dotty-Diffuse
Dotty+PC
Dotty-Linear
Linear
None

Figure S3. *Forced use of the Dmc1 recombinase does not lead to SC assembly triggered by HO-mediated or phleomycin DSBs during meiosis.*

(A) Image displays a representative surface-spread meiotic nucleus from a *spo11 spo13 rad51-II3A* strain (LY935) sporulated for 20 hours with 120μg/ml phleomycin (n=20); DNA is labeled by DAPI (blue) and Rad51 targeted by an antibody (red). Graph plots the number of Rad51 foci measured per nucleus in the *spo11 spo13 rad51-II3A* strain. (B) Representative surface spread nuclei from each strain (indicated) immune-stained to show Zip1 (green) and Ecm11/Gmc2 (red); DNA is labeled by DAPI (blue). (C) The percentage of nuclei displaying indicated distributions of Zip1 and Ecm11/Gmc2 is plotted for *rad51-II3A* (LY935) strains, with and without the 120μg/ml phleomycin treatment (n=20 per strain and condition).

Table S1. HO-mediated meiotic recombination at the *MAT* locus in two-spore- and one-spore-viable dyad progeny of select mutants

A.

	% Mating phenotype and genotype of *spo11 spo13* two-spore-viable dyads												
Genotype	nm *MAT**a*** / *MAT* α	nm *MAT**a*** / *MAT* α	a *MAT**a*** / *MAT**a***	a *MAT**a*** / *MAT**a***	α *MATα* / *MATα*	α *MATα* / *MATα*	nm *MAT**a*** / *MATα*	a *MAT**a*** / *MAT**a***	nm *MAT**a*** / *MATα*	α *MATα* / *MATα*	a *MAT**a*** / *MAT**a***	α *MATα* / *MATα*	Total dyads
ho	99.8		0.0		0.0		0.0		0.0		0.2		589
P_{SPO13}-*HO*	60.2		12.2		12.5		8.5		5.9		0.7		543
P_{SPO13}-*HO cs5 rad51*	99.0		0.0		0.0		0.0		1.0		0.0		105
P_{SPO13}-*HO cs5 rad51 dmc1*	96.4		0.0		0.0		1.4		2.2		0.0		139
P_{SPO13}-*HO cs5 rad51-II3A*	53.4		11.8		14.6		11.8		8.4		0.0		178
P_{SPO13}-*HO cs5 mre11*	53.8		7.7		0.0		23.1		7.7		7.7		13
P_{SPO13}-*HO cs5 xrs2*	68.5		5.5		9.4		6.6		9.4		0.6		181

B.

	% Mating phenotype and genotype of *spo11 spo13* one-spore-viable dyads						
Genotype	dead	nm *MAT**a*** / *MATα*	dead	a *MAT**a**** / *MAT**a***	dead	α *MATα** / *MATα*	Total dyads
P_{SPO13}-*HO cs5 rad51*	98.9		0.0		1.1		181
P_{SPO13}-*HO cs5 rad51 dmc1*	98.6		0.3		1.1		363
P_{SPO13}-*HO cs5 rad51-II3A*	70.9		16.9		12.2		189
P_{SPO13}-*HO cs5 mre11*	55.0		28.3		16.7		60
P_{SPO13}-*HO cs5 xrs2*	84.0		9.2		6.8		206

Table S1. *HO-mediated meiotic recombination at the MAT locus in two-spore- and one-spore-viable dyad progeny of select mutants*. HO-mediated interhomolog recombination at the *MAT* locus during *spo11 spo13* meiosis can result in spores homozygous for *MAT**a*** or *MAT*α (Figure 1). The table in (A) gives the percentage of two-spore-viable dyads carrying spores of a specific phenotype (bold) and inferred genotype (unbold) from select *spo11 spo13* strains carrying mutations that confer low spore viability (genotypes listed in column 1); companion spores in a dyad are separated by a vertical line. The total number of two-spore-viable dyads in the analysis is given in the final column. The table in (B) lists the percentage of one-spore-viable dyads whose viable spore exhibits a specific phenotype (bold) and inferred genotype (unbold) from the *spo11 spo13* strains with low spore viability; the viable spore is indicated to the right of its dead companion (separated by a vertical line). The total number of one-spore-viable dyads in the analysis is given in the final column. *One-spore-viable dyads carrying a spore with the capacity to mate could reflect either a meiotic gene conversion or chromosome loss; in the case of chromosome loss the strains carry only a single chromosome III.

Table S2. Sporulation efficiency of strains used to assess recombination

Genotype	Strain	% Sporulation efficiency (n)
spo11 spo13	LY407	33 (1068)
spo11 spo13 lys2::P_{SPO13}-HO	LY208	25 (1030)
LY208 cs2	LY555	18 (1025)
LY208 cs7	LY324	19 (1035)
LY208 cs6	LY322	20 (1092)
LY208 cs5	LY207	26 (1063)
LY207 rad51	LY459	25 (1087)
LY207 rad51 dmc1	LY393	17 (1133)
LY207 dmc1	LY290	26 (1040)
LY207 mek1	LY904	24 (1052)
LY407 mek1	LY907	19 (1164)
LY207 red1	LY939	28 (1116)
LY207 rad51-II3A	LY935	27 (1026)
LY207 xrs2	LY910	14 (1227)
LY407 xrs2	LY913	17 (1220)
LY207 mre11	LY916	13 (1238)
LY407 mre11	LY919	21 (1137)
LY207 zip1	LY288	20 (1059)
LY207 zip2	LY289	21 (1033)
LY207 zip3	LY341	38 (1156)
LY207 msh4	LY299	30 (1122)
LY207 mlh3	LY363	38 (1337)
LY207 mlh3 zip3	LY413	25 (1103)
LY207 mlh3 msh4	LY410	24 (1130)
LY207 mer3	LY376	30 (1016)
LY207 P_{CLB2}-MMS4	LY291	27 (1089)
LY207 yen1 P_{CLB2}-MMS4	LY388	25 (1060)
LY207 slx1 mlh3 yen1 P_{CLB2}-MMS4	LY868	28 (1114)
LY207 sgs1-ΔC795	LY850	45 (1080)
LY324 zip3	LY382	37 (1103)
LY324 slx1 mlh3 yen1 P_{CLB2}-MMS4	LY871	26 (1106)

Table S2. *Sporulation efficiency of strains used to assess recombination*. Strains were sporulated on plates for 5 days at 30°C and the frequency of dyad spores was evaluated by light microscopy (n >1000).

Table S3. Spore viability of various strains used to assess recombination

Genotype	Strain	n	% Distribution of dyad types			% Spore viability
			2-sv	1-sv	0-sv	
spo11 spo13	LY407	728	81	16	3	89
spo11 spo13 lys2::P_{SPO13}-HO	LY208	624	87	10	3	92
LY208 cs2	LY555	936	60	23	18	71
LY208 cs7	LY324	728	70	23	7	81
LY208 cs6	LY322	832	73	22	6	84
LY208 cs5	LY207	2581	60	27	13	74
LY207 zip1	LY288	572	65	24	11	77
LY207 zip2	LY289	624	66	19	15	76
LY207 zip3	LY341	1508	67	21	12	78
LY207 msh4	LY299	754	58	25	18	70
LY207 mlh3	LY363	1508	73	18	9	82
LY207 mlh3 zip3	LY413	604	51	32	18	66
LY207 mlh3 msh4	LY410	780	60	26	15	72
LY207 mer3	LY376	390	78	14	8	85
LY207 P_{CLB2}-MMS4	LY291	520	68	22	10	79
LY207 yen1 P_{CLB2}-MMS4	LY388	458	68	22	10	79
LY207 slx1 mlh3 yen1 P_{CLB2}-MMS4	LY868	1144	49	31	19	65
LY207 sgs1-ΔC795	LY850	1144	63	24	13	75
LY324 zip3	LY382	676	62	23	15	73
LY324 slx1 mlh3 yen1 P_{CLB2}-MMS4	LY871	1300	44	32	24	60

Table S3. *Spore viability of various strains used to assess recombination*. The percentage of total dyads (n) from *spo11 spo13* diploids homozygous for various mutant alleles carrying two viable spores (2-sv), one viable spore (1-sv) and 0 viable spores (0-sv) is shown. The percentage of the total number of spores (nx2) that are viable is given for each strain in the final column (% Spore viability).

Table S4. Strains used in this study

STRAIN	GENOTYPE
BR1919	*his4-260,519 leu2-3,112 MATa ho trp1-289 ura3-1 thr1-4 ade2-1* *his4-260,519 leu2-3,112 MAT ho trp1-289 ura3-1 thr1-4 ade2-1*
LY208	BR1919 *lys2::P_{SPO13}-HO lacO::LEU2@450kb iTHR1@1,416kb spo11::ADE2 spo13::URA3* *lys2::P_{SPO13}-HO CENIV 1,416kb spo11::ADE2 spo13::URA3*
LY207	LY208 homozygous *cs5::natMX4@836kb ChrIV*
LY322	LY208 homozygous *cs6::natMX4@1,162kbChrIV*
LY324	LY208 homozygous *cs7::natMX4@1,056 kb ChrIV*
LY555	LY208 *447kb cs2::natMX4@449kb CENIV* *LEU2@ChrIV cs2::natMX4@449kb CENIV*
LY407	BR1919 *spo11::ADE2 spo13::URA3* *spo11::ADE2 spo13::URA3*
LY299	LY207 homozygous *msh4::kanMX4*
LY291	LY207 homozygous *kanMX4-P_{CLB2}-MMS4*
LY363	LY207 homozygous *mlh3::kanMX4*
LY288	LY207 homozygous *zip1::kanMX4*
LY289	LY207 homozygous *zip2::kanMX4*
LY341	LY207 homozygous *zip3::kanMX4*
LY376	LY207 homozygous *mer3::kanMX4*
LY290	LY207 homozygous *dmc1::kanMX4*
LY459	LY207 homozygous *rad51::kanMX4*
LY393	LY207 homozygous *dmc1::kanMX4 rad51::hphMX4*
LY904	LY207 homozygous *mek1::kanMX4*
LY907	LY407 homozygous *mek1::kanMX4*
LY939	LY207 homozygous *red1::kanMX4*
LY954	LY925 homozygous *dmc1::hphMX4*
LY935	LY207 homozygous *rad51-II3A::kanMX4*
LY957	LY935 homozygous *dmc1::hphMX4*
LY910	LY207 homozygous *xrs2::kanMX4*
LY913	LY407 homozygous *xrs2::kanMX4*
LY916	LY207 homozygous *mre11::kanMX4*
LY919	LY407 homozygous *mre11::kanMX4*
LY410	LY207 homozygous *mlh3::kanMX4 msh4::hphMX4*
LY413	LY207 homozygous *mlh3::kanMX4 zip3::hphMX4*
LY388	LY207 homozygous *yen1::hphMX4 kanMX4-P_{CLB2}-MMS4*
LY850	LY207 homozygous *sgs1-ΔC795*
LY868	LY207 homozygous *yen1::hphMX4 kanMX4-P_{CLB2}-MMS4 slx1::hphMX4 mlh3::kanMX4*
LY871	LY324 homozygous *yen1::hphMX4 kanMX4-P_{CLB2}-MMS4 slx1::hphMX4 mlh3::kanMX4*
LY382	LY324 homozygous *zip3::kanMX4*
LY458	LY324 homozygous *rad51::kanMX4*
LY457	LY322 homozygous *rad51::kanMX4*
LY481	LY459 homozygous *LYS2* (*LYS2* replaces *P_{SPO13}-HO*)
LY492	LY208 homozygous *cs4::natMX4@1,241kbChrIV rad51::kanMX4*
LY456	LY208 homozygous *cs2::natMX4@449kbChrIV rad51::kanMX4*
LY491	LY208 homozygous *cs1::natMX4 rad51::kanMX4*
LY500	LY393 homozygous *LYS2* (*LYS2* replaces *P_{SPO13}-HO*)

LY42	BR1919 *tetR-mCherry::hphMX4@92kb ChrIII* *tetR-mCherry::hphMX4@92kb ChrIII* *lacO::LEU2@450kb CENIV tetO::THR1@1,242kb ChrIV lacI-GFP::URA3* *lacO::LEU2@450kb CENIV tetO::THR1@1,242kb ChrIV lacI-GFP::URA3*
LY176	LY42 *lys2::P_{SPO13}-HO spo11::ADE2* *lys2::P_{SPO13}-HO spo11::ADE2*
LY173	LY176 homozygous *cs2::natMX4@449kb ChrIV*
LY174	LY176 homozygous *cs5::natMX4@836kb ChrIV*
LY175	LY176 homozygous *cs4::natMX4@1,241kb ChrIV*
LY331	LY176 *ChrIV*: *cs9::natMX4 cs10::natMX4 449kb cs5::natMX4 1,056kb cs6::natMX4 1,241kb 1,417kb* *302kb 386kb cs2::natMX 836kb cs7::natMX4 1,162kb cs4::natMX4 cs8::natMX4*
LY887	LY42 *lys2::P_{SPO13}-HO cs5::natMX4@836kbChrIV spo11-Y135F::kanMX4* *lys2::P_{SPO13}-HO cs5::natMX4@836kbChrIV spo11-Y135F::kanMX4*
LY552	LY176 homozygous *ndt80::TRP1*
LY371	LY331 homozygous *ndt80::TRP1*
YAM424	BR1919 homozygous *ndt80::URA3*
LY430	YAM424 *ZIP1-GFP spo11::ADE2* *ZIP1-GFP spo11::ADE2*
LY846	BR1919 *lys2:: P_{SPO13}-HO spo11-Y135F::kanMX4 ndt80::LEU2* *lys2:: P_{SPO13}-HO spo11-Y135F::kanMX4 ndt80::LEU2*
LY841	LY846 *cs5::natMX4@836kbChrIV* *cs5::natMX4@836kbChrIV*
LY865	LY846 *2μ-HOP1-RED1:URA3* (pNH219)
LY864	LY841 *2μ-HOP1-RED1:URA3* (pNH219)
LY886	LY846 *2μ-URA3* (pRS426)
LY885	LY841 *2μ-URA3* (pRS426)
LY890	LY841 *2μ-REC8-13xMYC:ADE2* (BAM356)
LY891	LY846 *2μ-REC8-13xMYC:ADE2* (BAM356)
LY892	LY372 *2μ-REC8-MYC:ADE2* (BAM356)
LY893	BR1919 *cs5::natMX4 spo11-Y135F::kanMX4 ndt80::LEU2 REC8-13xMYC::kanMX4* *836kb ChrIV spo11-Y135F::kanMX4 ndt80::LEU2 REC8-13xMYC::kanMX4*
LY769	BR1919 *ndt80::LEU2 TRP1-P_{GAL}-HOP1* *ndt80::LEU2 TRP1-P_{GAL}-HOP1*
LY471	BR1919 *ECM11-MYC::kanMX4 spo11::ADE2 ndt80::LEU2* *ECM11 spo11::ADE2 ndt80::LEU2*
LY303	BR1919 *lacO::LEU2@CENIII 836kb ChrIV lacI-GFP::URA3 spo11::ADE2* *lacO::LEU2@CENIII cs5::natMX4 lacI-GFP::URA3 spo11::ADE2*
LY356	BR1919 *92kb ChrIII tetO::THR1@1,242kb ChrIV* *tetR-mCherry::hphMX4 tetO::THR1@1,242kb ChrIV* *lacO::LEU2@CENV lacI-GFP::URA3 spo11::ADE2* *lacO::LEU2@CENV lacI-GFP::URA3 spo11::ADE2*
LY357	BR1919 *92kb ChrIII lacO::LEU2 1,242kbChrIV CENV lacI-GFP::URA3* *tetR-mCherry::hphMX4 CENIII tetO::THR1 lacO::LEU2 lacI-GFP::URA3* *spo11::ADE2 CTF19-13xMYC::kanMX4* *spo11::ADE2 CTF19*
LY358	BR1919 *CENIII lacO::LEU2 836kb lacI-GFP::URA3 spo11::ADE2* *lacO::LEU2 CENIV cs5::natMX lacI-GFP::URA3 spo11::ADE2*

Table S4. *Strains used in this study*. All strains are derived from a BR1919-8B background (ROCKMILL AND ROEDER 1998).

Table S5. Primers used in this study

PRIMER	SEQUENCE
AJM763	CTCCCTATAGTGAGTCGTATTTTGTCCTGGAAGTCTCATGG
AJM764	CGTGTTTTCAGAAAGCATAATTATTCTCGACTCAACTTCAATCCG
AJM765	ATGCTTTCTGAAAACACG
AJM766	TCTGAG GAAAGTTGATCAAGACCC
AJM760	TCATAAATAAACGTATGAGAAGCTTGGCTGCAGGTCAACC
AJM750	TTTTATATTCAAAAACAAGAAAACAAAAGAGAAAACATTAACATGTAATTTTGTAGTTCATAAATAAACGTATGAG
AJM751	TTTTATATTCAAAAACAAGAAAACAAAAGAGAAAACATTAACATGTAATTTTGTAGTTCATAAATAAACGTATGAG
AJM752	AACTTGTATCCTAGGTTATCTATGCTGTCTCACCATAGAGAATATTACCTATGTAGTTCATAAATAAACGTATGAG
AJM753	TTGTGTATTATATGTATTTACCCGGCGAATCATGGACATACATTCTGAAAAATACGACTCACTATAGGGAG
AJM756	TAAGTATTGTGGGTAAATGATATATAAATTTTTATAAAAACTCTTGGCCAATGTAGTTCATAAATAAACGTATGAG
AJM757	TTTAATAATAATGATAACGTTACGTTTAGACATAGTCTTTTTTTTTTTTCAATACGACTCACTATAGGGAG
AJM975	TAGAAAGATAGAACGGGACGAGGGGCCGGTTCAACAACTATCATACTTTCTGTAGTTCATAAATAAACGTATGAG
AJM976	TCTTGTCTCGTAGCTTTTTTATTATTTGGGTTAATCGCGTTGTTGAACAAAATACGACTCACTATAGGGAG
AJM1137	TTAACAATTCTTCCTTTGTTCCTCTGAAAGCACGGGCCGGCGCACTCCAATGTAGTTCATAAATAAACGTATGAG
AJM1138	TGTTCACATGTTCATCCCCCTGCTACTACTTGGAAATTAATGTAGGGGTAAAATACGACTCACTATAGGGAG
AJM1141	TTCTCTATCTTTTTCACTTGCACAGCTTAATAAGCTTTTCGACCTCCTGTTGTAGTTCATAAATAAACGTATGAG
AJM1142	GCGCGACTGCCCGAAGAAGGACGCGGGGTGAGGGAATAAGACAATAGGAAAATACGACTCACTATAGGGAG
AJM1145	CGCCATCCTAGAAGGCTACAAAGTGATGCACGTATGATGATATCGGACATTGTAGTTCATAAATAAACGTATGAG
AJM1146	GCTGTGACATATCACAATTTTATGTGTACCTGTTGTATGTATACGCTCTAAATACGACTCACTATAGGGAG
AJM1255	ATCACTCAAAGTTGTCTCGGCTTCTTGTTCGAGCAGTTCAACAGAAAATTTGTAGTTCATAAATAAACGTATGAG
AJM1256	CGTGCTCCAAAGGTGTATTGTCATCGACAAATTCACCCAAATCGATTCTCAATACGACTCACTATAGGGAG
AJM1259	TTGTCATCAATTCTATCAGCAGTCGCTGAATTTGTGAGCAAGGCCGCAAATGTAGTTCATAAATAAACGTATGAG
AJM1260	AGGTATCCACATCATTCATAAGAAAACTACTAATATCATTTTGCCTCCTAAATACGACTCACTATAGGGAG
AJM1702	TGGTACATTAGCAGCCAGAGGAAACATTATGCAGTTTTTAAAGGCTCAACGGCCGAGCGGTCTAAGGCGCC
AJM1698	GCTTTATCCAGAAATTGTTCAACTTTATTGTTTTGTATATTAGATAAAAAGGTGCCCTCCTCCTTGTC
AJM2164	ACACTTATAAACGGTTTAAAAACAGCTTTATCTCAGAAAAGTCAGGAATTATGGCACCTCTTTTCGTTGAAC
AJM2165	GTTGAAGAAGTGCCTGTTTAAATGATGAGCATAATATAATTCGGTTTTCGTTATTTAGAAGTGGCGCGAATTCACTAGTGATTGATTAATTTTTG
AJM650	ATAAAGCTTTAGGCAATCAAGCGAAGC
AJM651	ATTGCATGCTTGCTCACTCCAAAAGCC

AJM666	TTAATAGACGTCAACCGTGATCCTGCGTCG
AJM667	ATATATGAGCTCAGAAAAGACGGGTAACGG
AJM838	CTTCTTGCTGACCGCTTCTA
AJM839	TTACTCTAGATGCTCAACCTTAAGC
AJM1241	GTATTCAATTTGCTAAAAAGTTGTTTTATTTAAATATTCCTTCTGAGTCACAAACCGTGATCCTGCGTCG
AJM1242	AATGGAAACACCAATGGATTTGAGAATTTTAACGCTATTCACGATGACCGGATAGAAAAGACGGGTAACGG

Table S5. *Primers used in this study*. Underlined letters indicate nucleotides on plasmids, short underlined letters indicate a restriction site and non-underlined letters indicate nucleotides on chromosomes.