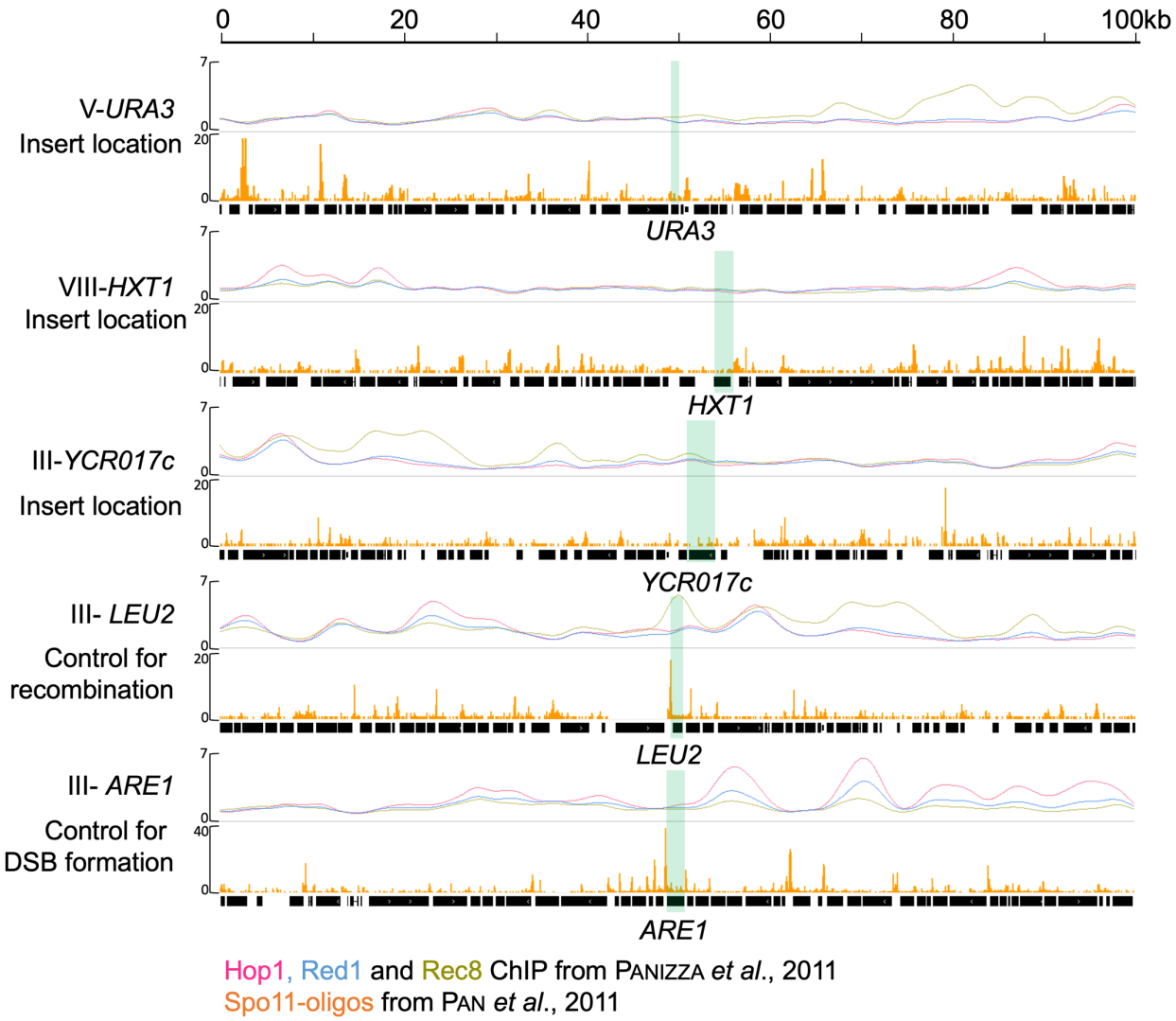

Figure S1. Genome-wide axis protein localization
Line plots—levels of Hop1 (pink), Red1 (blue) and Rec8 (olive green), at the locations of the three inserts and at the two control loci, expressed as decile-normalized ChIP/WCE, data from PANIZZA *et al.* (2011). Orange bars-–levels of Spo11 DSBs, counts of Spo11-linked oligonucleotides (hPM/bp), data from PAN *et al.* (2011). Green boxes—gene positions.

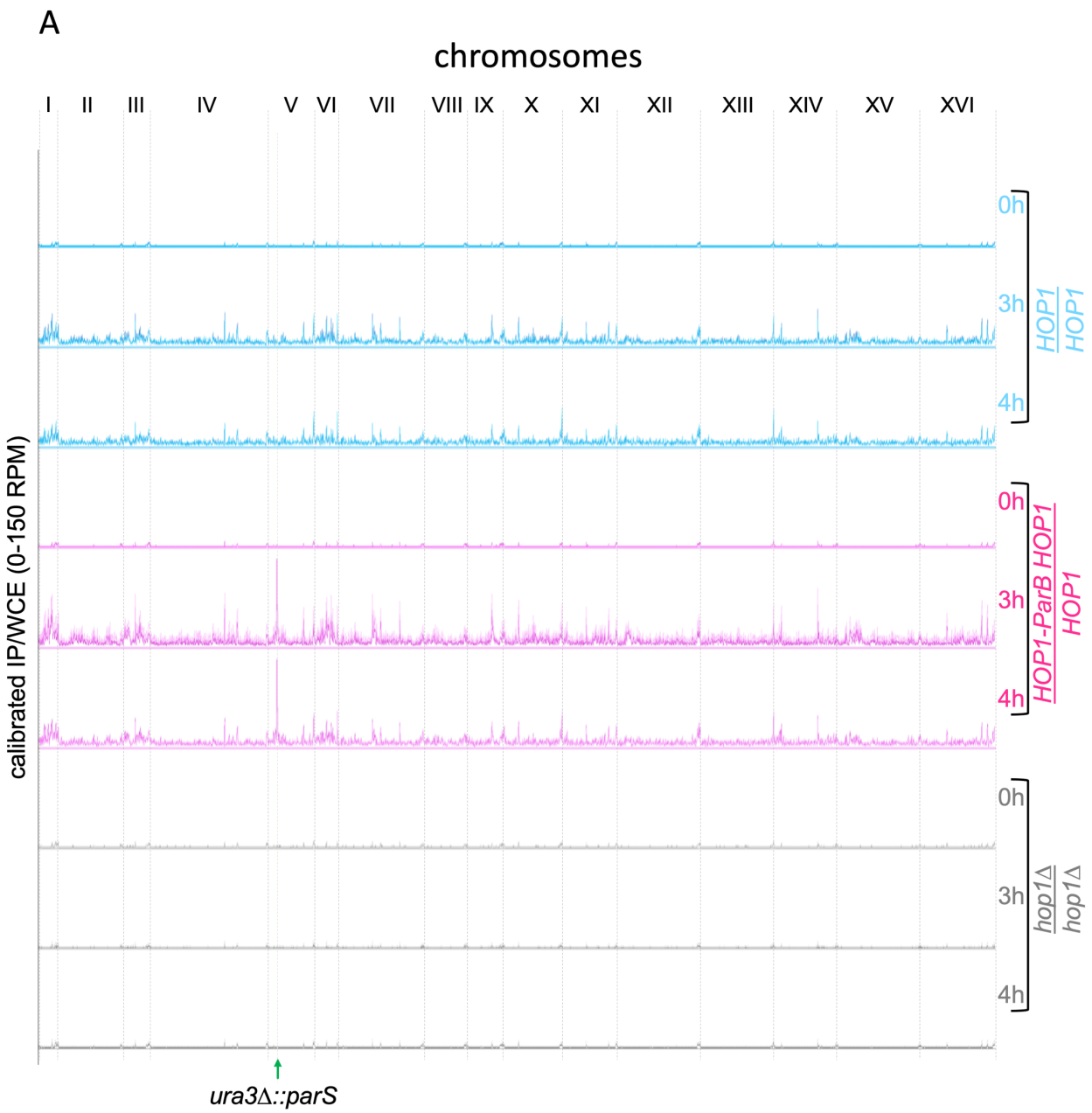

Figure S2. Genome-wide Hop1 localization

Whole-genome Hop1 occupancy (immunoprecipitate/whole cell extract) determined by calibrated ChIP-seq of samples taken at 0h, 3h and 4h in meiosis from strains with a *URA3-tel-arg4-parB* insert at *URA3* and the indicated *HOP1* genotype, plotted using a bin size of 7kb. Vertical grey lines—chromosome boundaries. Vertical green line—*parS* insert location (chr. *V*). The two replicates are indicated by dark and light lines.

A. Y axis scale of 0-150 RPM to illustrate Hop1 occupancy across the whole genome; the signal peak at the *parS* insert location is truncated.

(figure continued below)

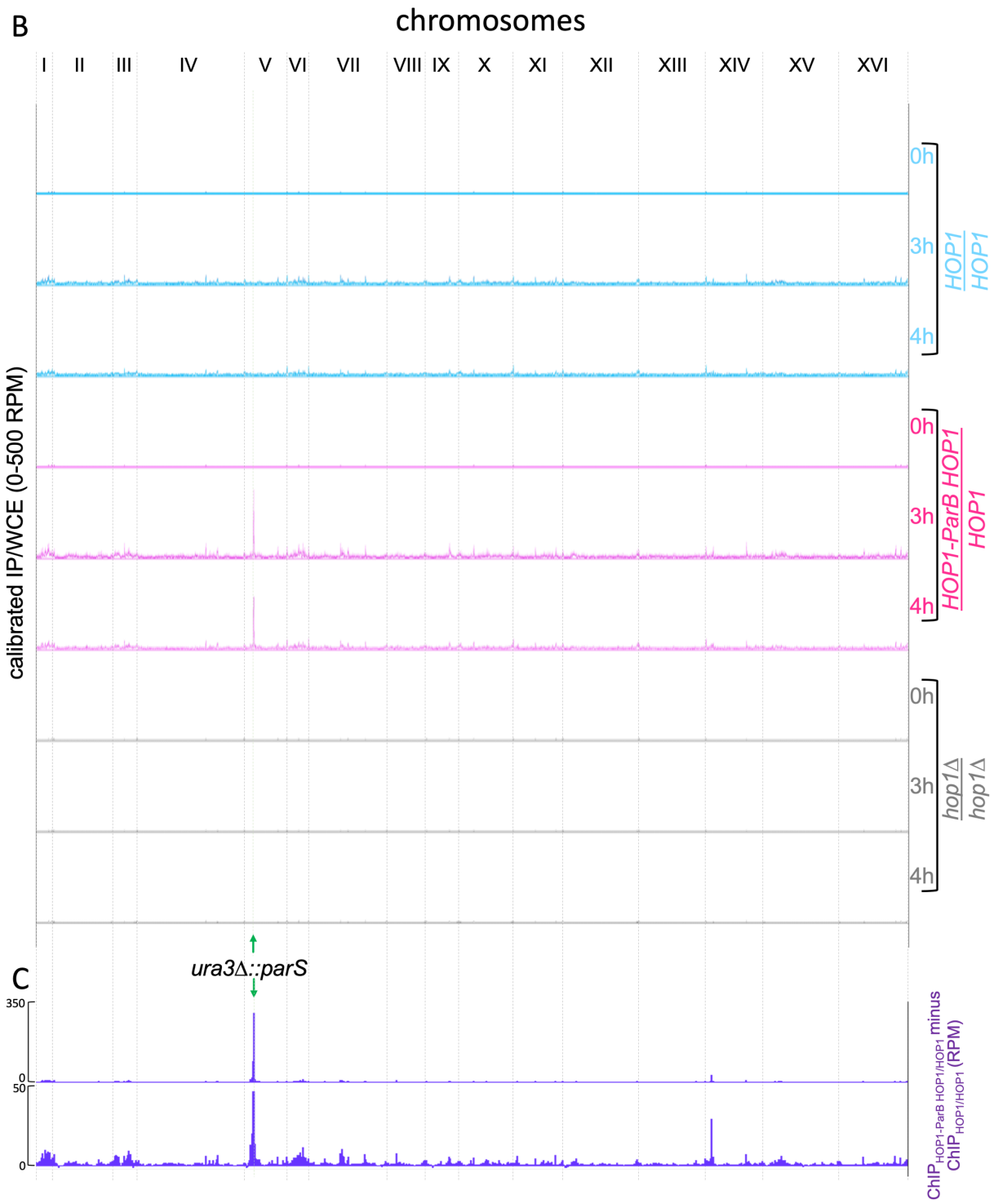

Figure S2 (continued)
B. As in panel A, but with Y axis scale of 0-500 RPM to illustrate the full range of Hop1 occupancy.
C. Difference plot calculated by subtracting the calibrated ChIP/WCE for Hop1/Hop1 (mean of both replicates) from that for Hop1-ParB Hop1/Hop1 (mean of both replicates) for the whole genome with Y scale as indicated to illustrate full range of difference and difference in signal across the genome.

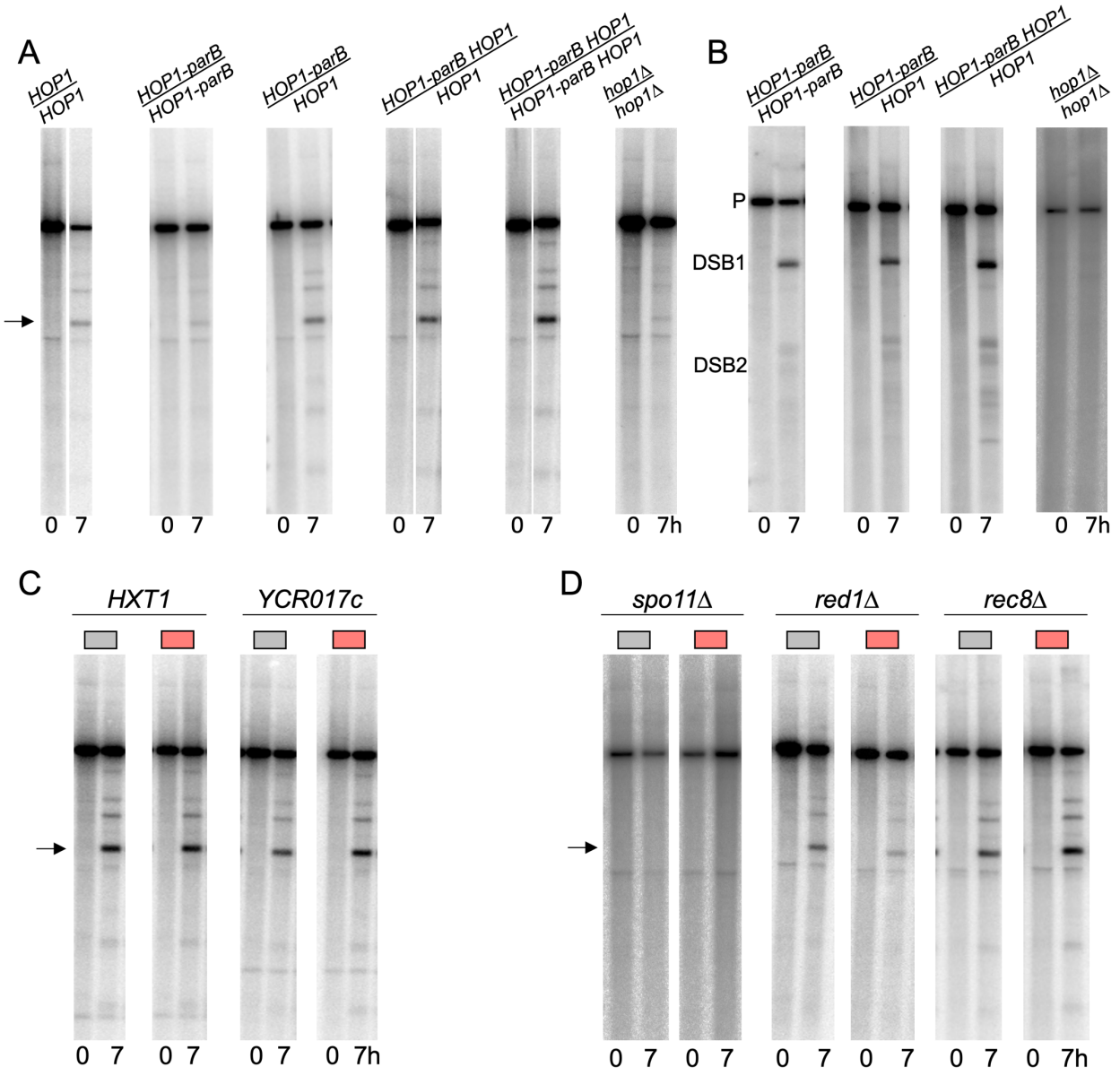

Figure S3. Representative Southern blots of meiotic DNA from *sae2*Δ cells

A. Southern blots containing DNA from *sae2*Δ cells with the *URA3-arg4-parS* insert at *URA3*, expressing Hop1 and/or Hop1-ParB as indicated, digested with *Bgl*II and probed to detect DSBs at the *ARE1* control locus. Arrow indicates DSB band that was quantified.

B. Southern blots of the same DNA, but digested with *Sbf1* and probed with *parS* sequences to detect DSBs in the *URA3-arg4-parS* insert at *URA3*.

C. DSBs at the *ARE1* control locus, in strains with inserts at *HXT1* or *Ycr017C*, expressing either *HOP1* (grey) or *HOP1-parB HOP1* (salmon). Digests and probes were as in panel A. Arrow indicates DSB band that was quantified.

D. DSBs at the *ARE1* control locus in *spo11*Δ, *red1*Δ or *rec8*Δ strains homozygous either for *HOP1* (grey) or *HOP1-parB HOP1* (salmon), digested and probed as in panel A. Arrow indicates DSB band that was quantified.

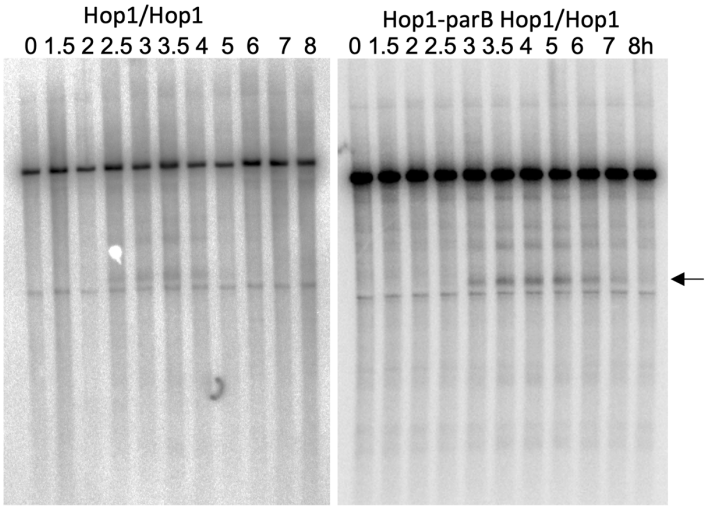

Figure S4. DSBs at *ARE1* in *SAE2* cells
Southern blots of meiotic DNA from *SAE2* cells, corresponding to those used in Figure 7A, digested with *Bgl*II and probed to detect DSBs at the *ARE1* control locus. Arrow indicates DSB band that was quantified.

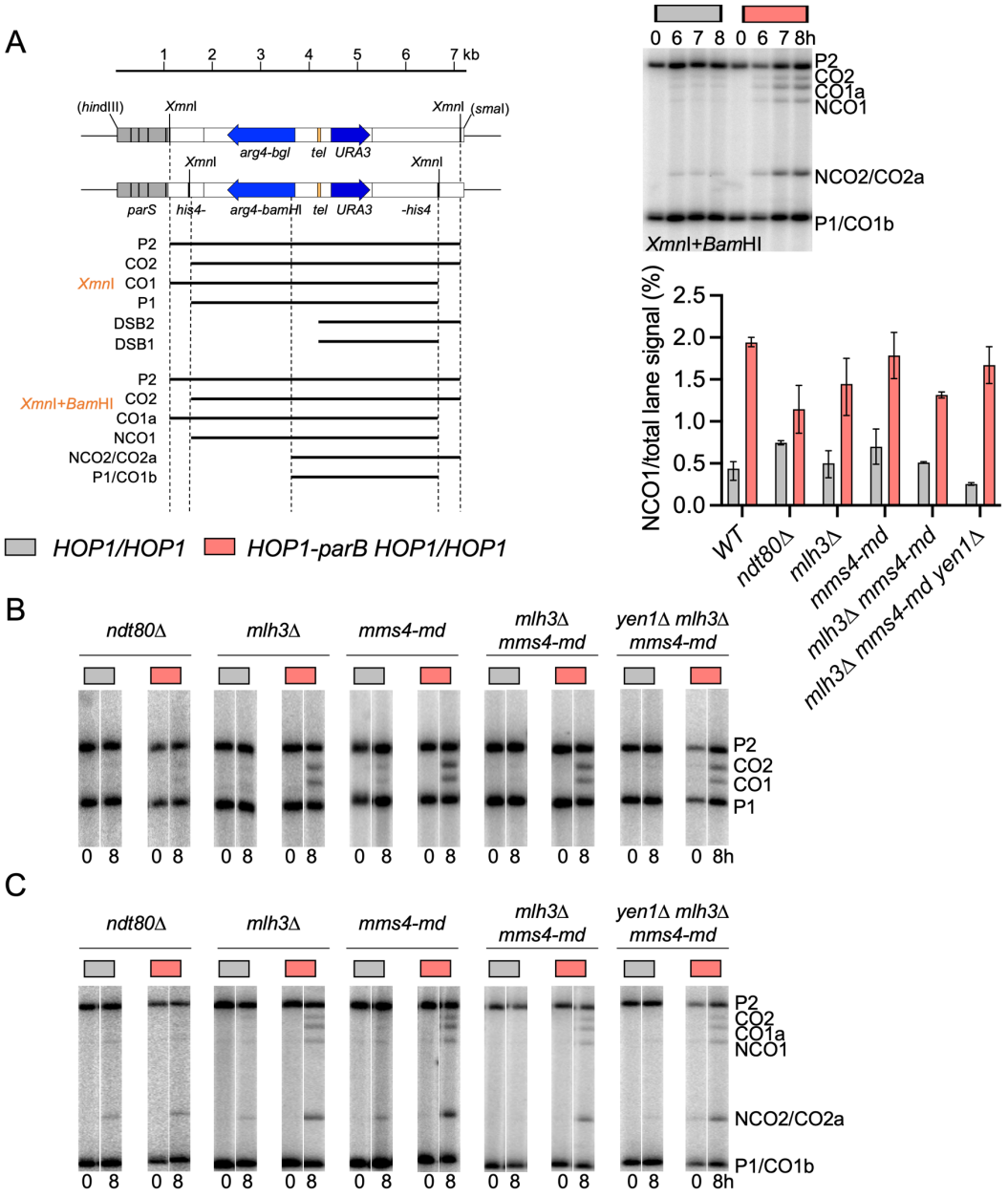

Figure S5. Crossovers and non-crossovers in U*RA3-tel-arg4-parS* insert at *URA3*

A. Schematic for the *URA3-tel-arg4-parS,* showing diagnostic fragment lengths. Top right— Southern blots to detect NCO1. DNA from *SAE2* strains was digested with *Xmn*I+*Bam*HI and probed with *URA3* sequences. Bottom— Quantification of NCO1 in *HOP1/HOP1* (grey) or *HOP1-ParB HOP1/HOP1* (salmon) in samples taken 8h after meiotic induction in the indicated mutants. Values in graphs are the average of two or more independent experiments; error bars denote range.

B. Southern blots showing COs (CO1 + CO2) in *HOP1/HOP1* (grey) or *HOP1-ParB HOP1/HOP1* (salmon) for samples taken 0 and 8h after meiotic induction in the indicated mutants.

C. Southern blots showing NCO1. Details as in B.

See also File S1, sheet 11.