Figure S2. Additional data and analyses. (A) Fraction of cells completing meiosis I, scored in DAPI-stained samples as cells with 2 or more nuclei. (B) VDE-initiated DSBs, scored as percent total lane signal in Southern blots containing *Hin*dIII digests (MEDHI *et al*, 2016). Data for inserts at *HIS4* and *URA3* are from Medhi et al (2016); data for all other insert loci are from a single experiment. (C) Combined data for COs and NCOs for all four genotypes, using values presented in Figures 2C, E and 3A, C. (D) NCO/CO ratios for *PCH2* strains, calculated from mean values presented in Figure 2C, E. (E) NCO/CO ratios for *pch2Δ* strains, calculated from mean values presented in Figure 3A, C. For panels (D) and (E), error bars represent the sum of fractional standard deviations for each mean value. In panel (D), NCO/CO ratios in *MLH3* differ significantly from *mlh3Δ* only for inserts at *FIR1*, *HSP30*, and *HIS4* (adjusted *p* values of 0.02, 0.008 and 0.00001, respectively). In panel (E), NCO/CO ratios in *MLH3 pch2Δ* differ significantly from *mlh3Δ pch2Δ* for all inserts (adjusted *p* values ≤ 0.03).