

Supplemental data:

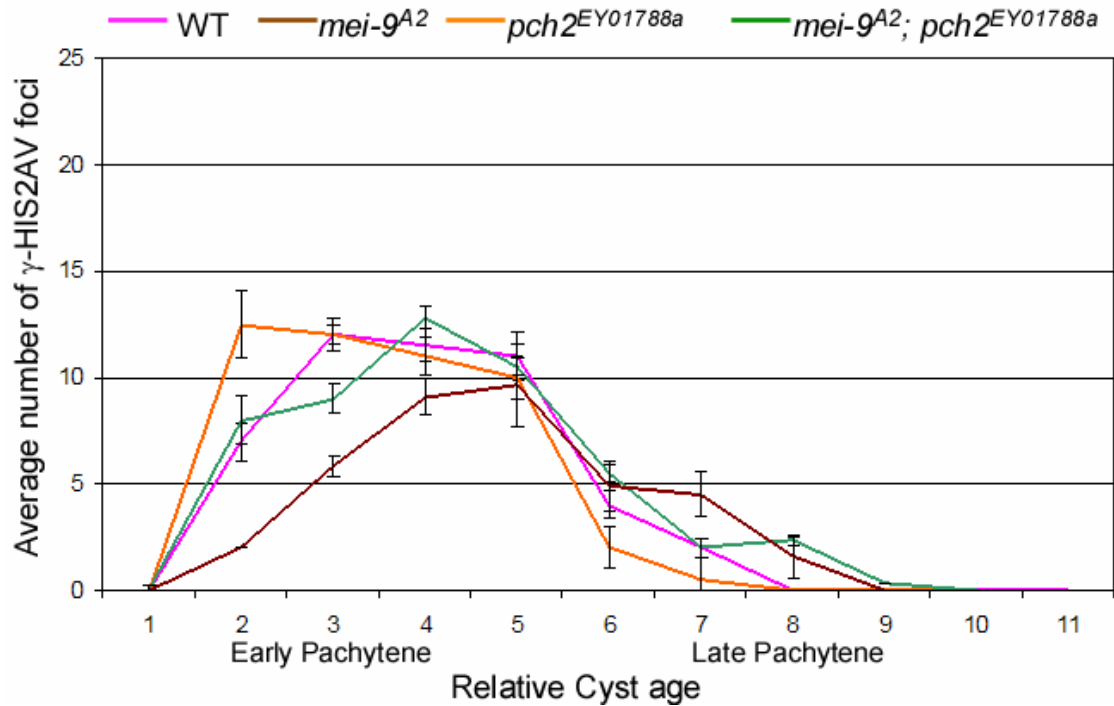


Figure S 1: Pattern of  $\gamma$ -HIS2AV staining in wild-type, *pch2* and *mei-9* mutants.

The average number of  $\gamma$ -HIS2AV foci relative to oocyte age (see Figure 3B for details). *pch2<sup>EY01788a</sup>* mutations do not alter the wild-type  $\gamma$ -HIS2AV staining pattern and suppress the delayed onset of  $\gamma$ -HIS2AV in *mei-9<sup>A2</sup>* mutants. Error bars denote the standard error of the mean.

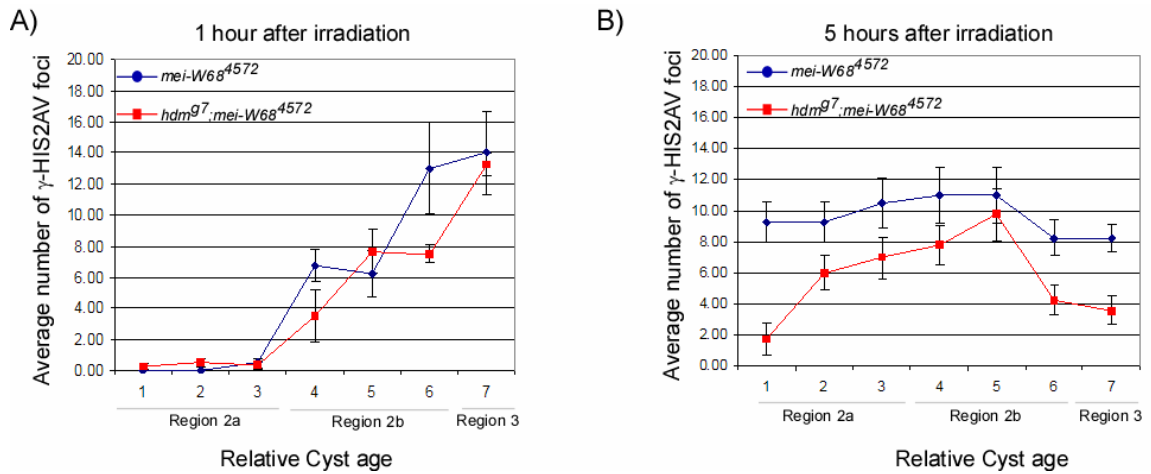


Figure S 2. *hdm* delays the response to X-ray induced DSBs.

The average number of  $\gamma$ -HIS2AV foci observed in pro-oocytes and oocytes of *mei-W68<sup>4572</sup>* (blue) and *hdm<sup>97</sup>; mei-W68<sup>4572</sup>* (red) females at (A) 1 hour and (B) 5 hours after irradiation. This graph shows how the response time to DSBs decreases as the pro-oocytes progress from early (region 2a) to late (region 3) pachytene. At one hour after irradiation, the number of  $\gamma$ -HIS2AV foci gradually increases between region 2a and 3, indicating the response time to X-ray induced DSBs gradually decreased from early to late pachytene oocytes. In region 3, the maximum number of  $\gamma$ -HIS2AV foci was observed within one hour after irradiation, which is similar to the response in somatic cells (MADIGAN *et al.* 2002). At five hours after irradiation, all pro-oocytes showed a uniform level of  $\gamma$ -HIS2AV foci throughout the germarium. The data in Figure 4 corresponds to cyst 1 in this Figure. Error bars denote the standard error of the mean.

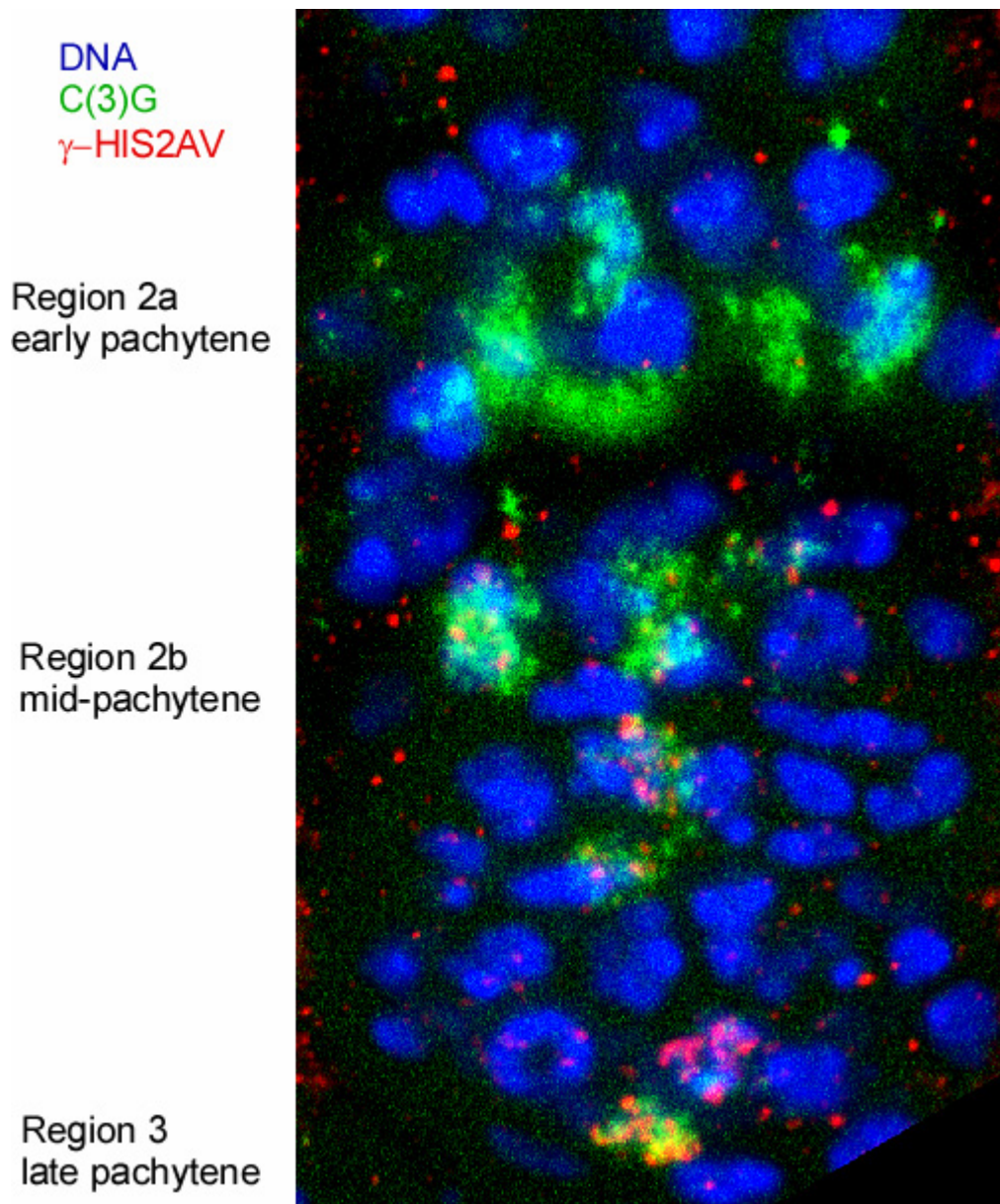


Figure S 3: Effect of *mei-41* on DSB repair

A *mei-41*<sup>D3</sup> mutant gerarium stained for  $\gamma$ -HIS2AV shows a delay in the onset and a persistence of  $\gamma$ -HIS2AV phenotype similar to DSB repair mutants. Unlike DSB repair mutants, however, mutation in *mei-41* did not cause a persistence of  $\gamma$ -HIS2AV foci in nurse cells, suggesting these cells repair their DSBs with wild-type kinetics.

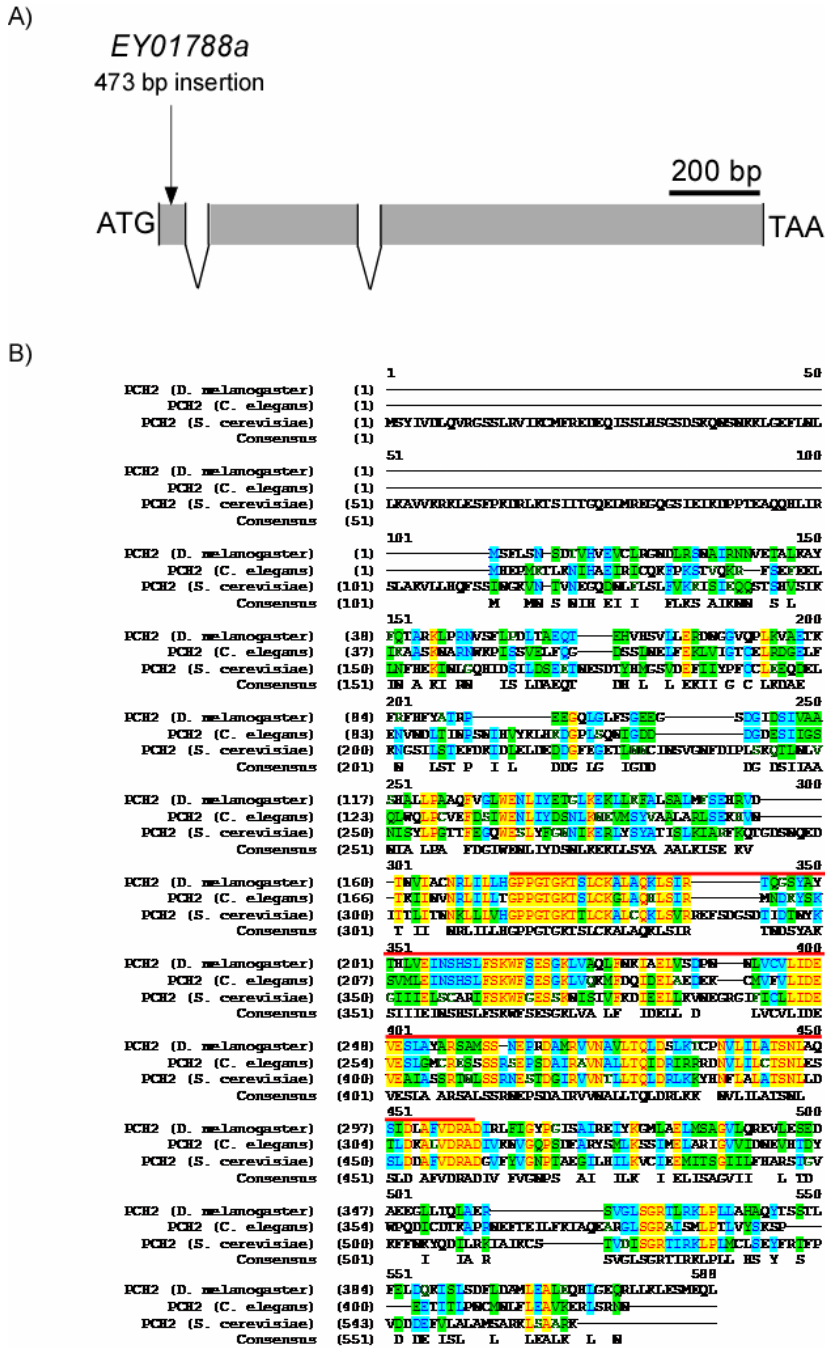


Figure S 4. Alignment of PCH2 orthologs.

A) Schematic of the *Drosophila pch2* transcript (CG31453) showing the splice pattern and the location of the P-element insertion *EY01788a*. The coding region is shown in grey and the untranslated regions in black. B) Full-length protein sequence alignment of PCH2 homologs from *Drosophila*, *C. elegans* and *S. cerevisiae*. The location of the conserved AAA-ATPase domain is shown with an orange line.