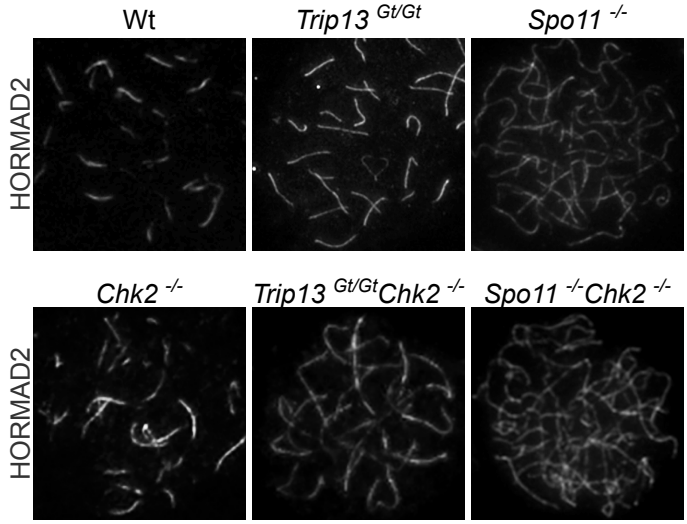


Figure S1. Related to Figure 4 - CHK2 is not required for HORMAD localization to meiotic chromosome axes of *Spo11*$^{-/-}$ or *Trip13*$^{Gt/Gt}$ oocytes. Shown are zygotene and zygotene-like nuclei from indicated genotypes.

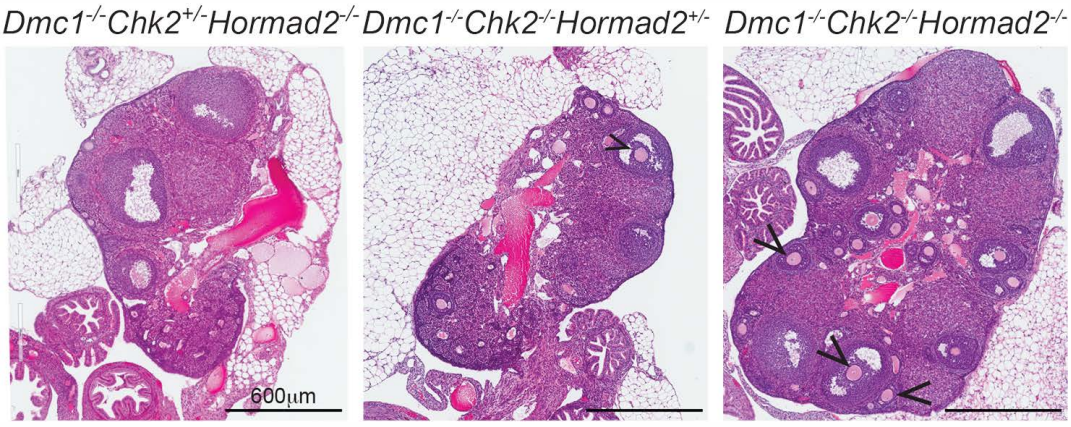


Figure S2. Related to Figure 3 - H&E stained histological sections of 8 week old ovaries of speci-fied genotypes. Black arrowheads indicate antral follicles.

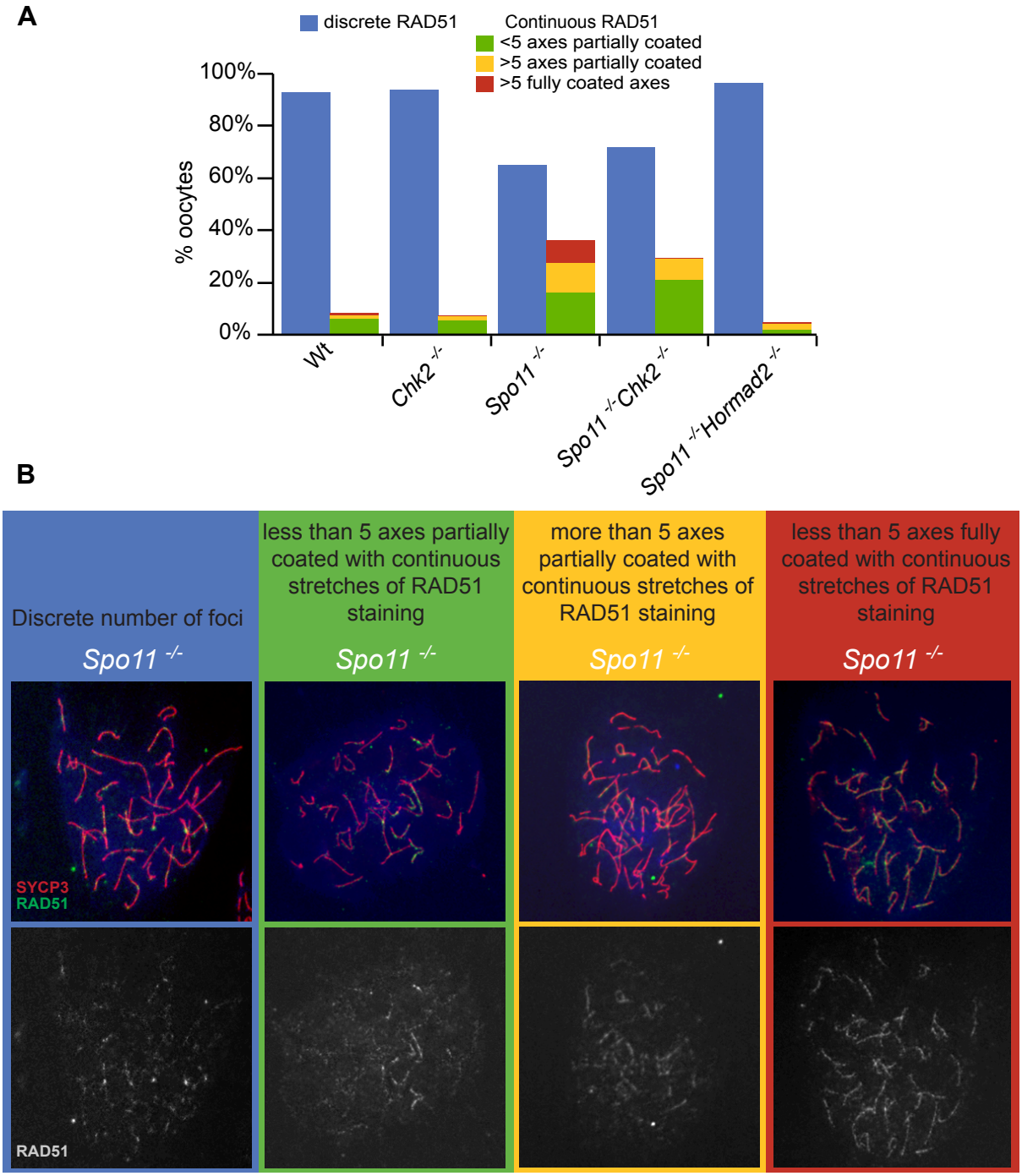


Figure S3. Related to Figure 6C - Patterns of RAD51 staining on oocyte meiotic chromosomes of various genotypes. **(A)** The plots shows the percentage of oocytes from the specified geno-types, color coded for either discrete foci or varying levels of continuous staining patterns. **(B)** Classification of the different levels of continuous RAD51 immunostaining. All chromosome spreads are derived from newborn mice. RAD51 quantification was performed in images derived from an objective with 0.45µm resolving power. At this resolution, the RAD51 signals could be classified as discrete or continuous (coating AEs and/or SCs). It is likely that these continuous staining regions consist of numerous distinct foci. Because these were not enumerated in the calculation of discrete SPO11-independent DSBs, the actual number of SPO11-independent DSBs is probably higher than reported here.

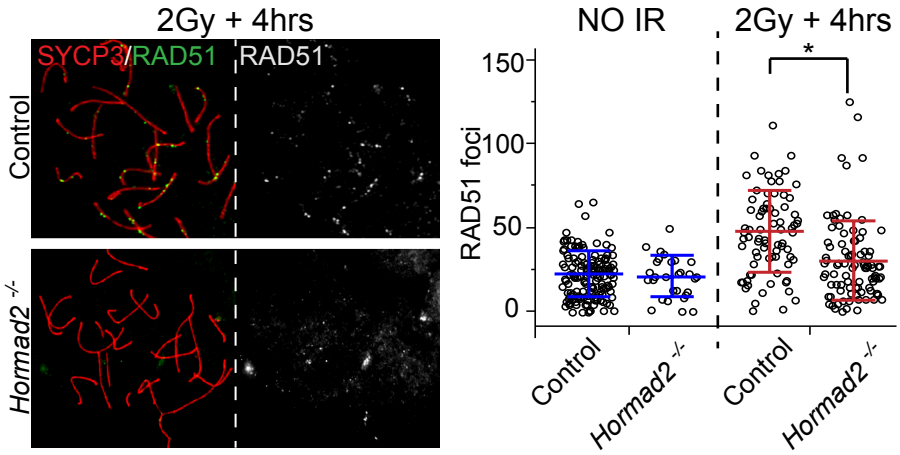
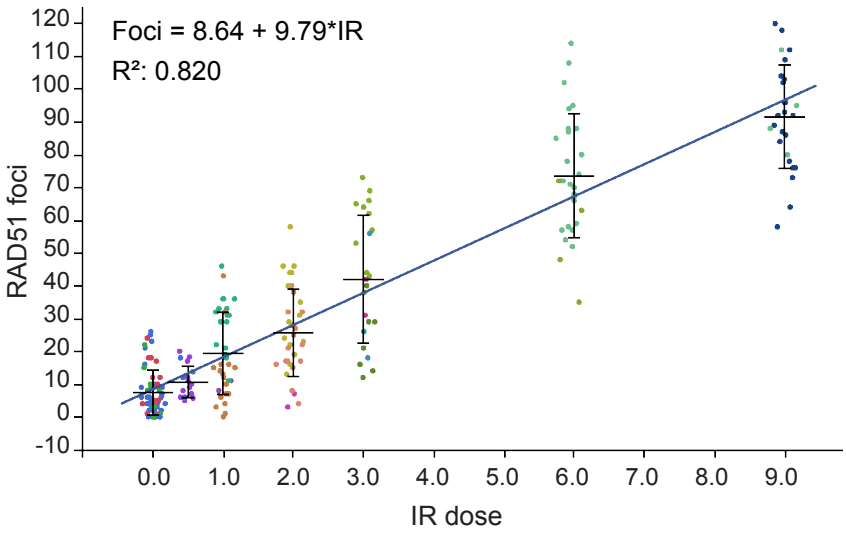


Figure S4. Related to Figure 5 - *Hormad2*$^{-/-}$ oocytes exhibit accelerated repair of radiation-induced DSBs. IR = ionizing radiation.

A



B

RAD51 foci count		
IR(Gy)	Mean	Std Dev
0	7.63	6.93
0.5	10.85	4.86
1	19.58	12.60
2	25.82	13.26
3	42.09	19.47
6	73.64	18.81
9	91.65	15.82

Figure S5. Related to Figure 6A - Raw data for statistical analysis presented in figure 6A. A) Linear fit of data without accounting for intrinsic animal variation as random effect. Dots represent RAD51 counts per pachytene cell. The colors indicate different animals. B) Mean and standard deviation of RAD51 foci count for each radiation dose.