Figure S1

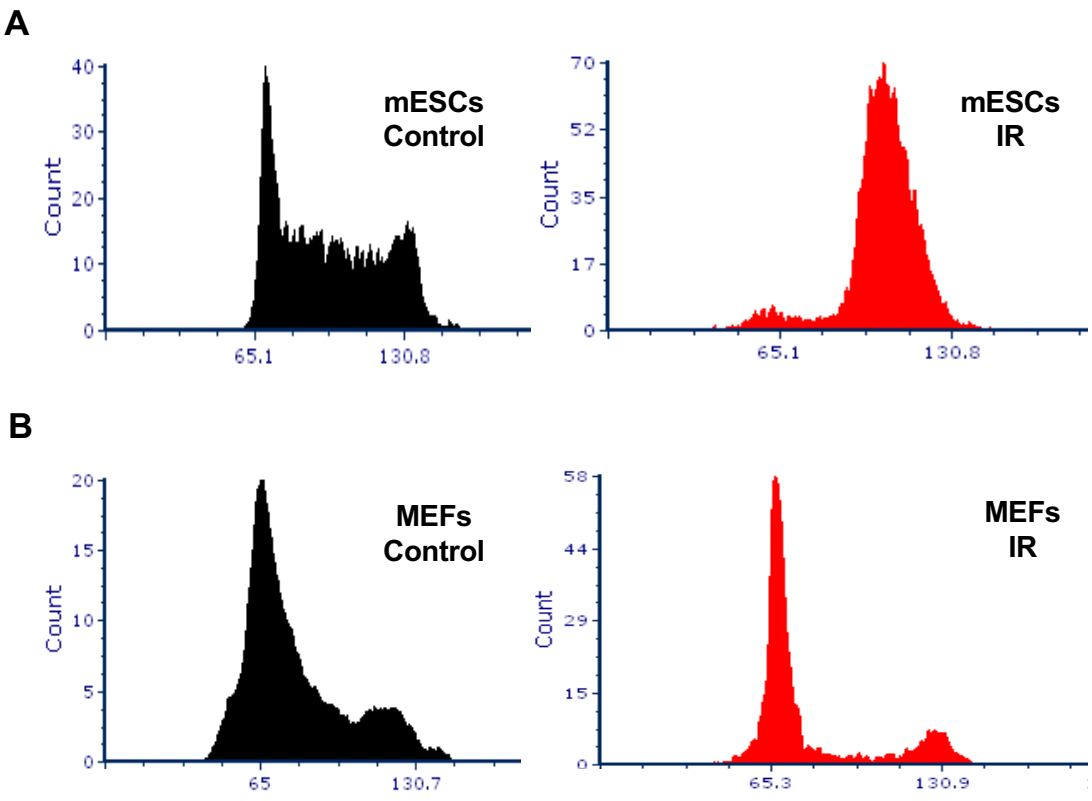

Figure S1. mESCs lack a G1 cell cycle checkpoint in response to IR-induced DNA damage.

A. Mouse embryonic stem cells (mESCs) were treated with 10 Gy of irradiation (right panel) or untreated (left panel). Eight hours after irradiation, cells were trypsinized, stained, and subjected to flow cytometry to assess cell-cycle distribution.

B. Same as in A except with primary mouse embryonic fibroblasts (MEFs) rather than mESCs.

Figure S2

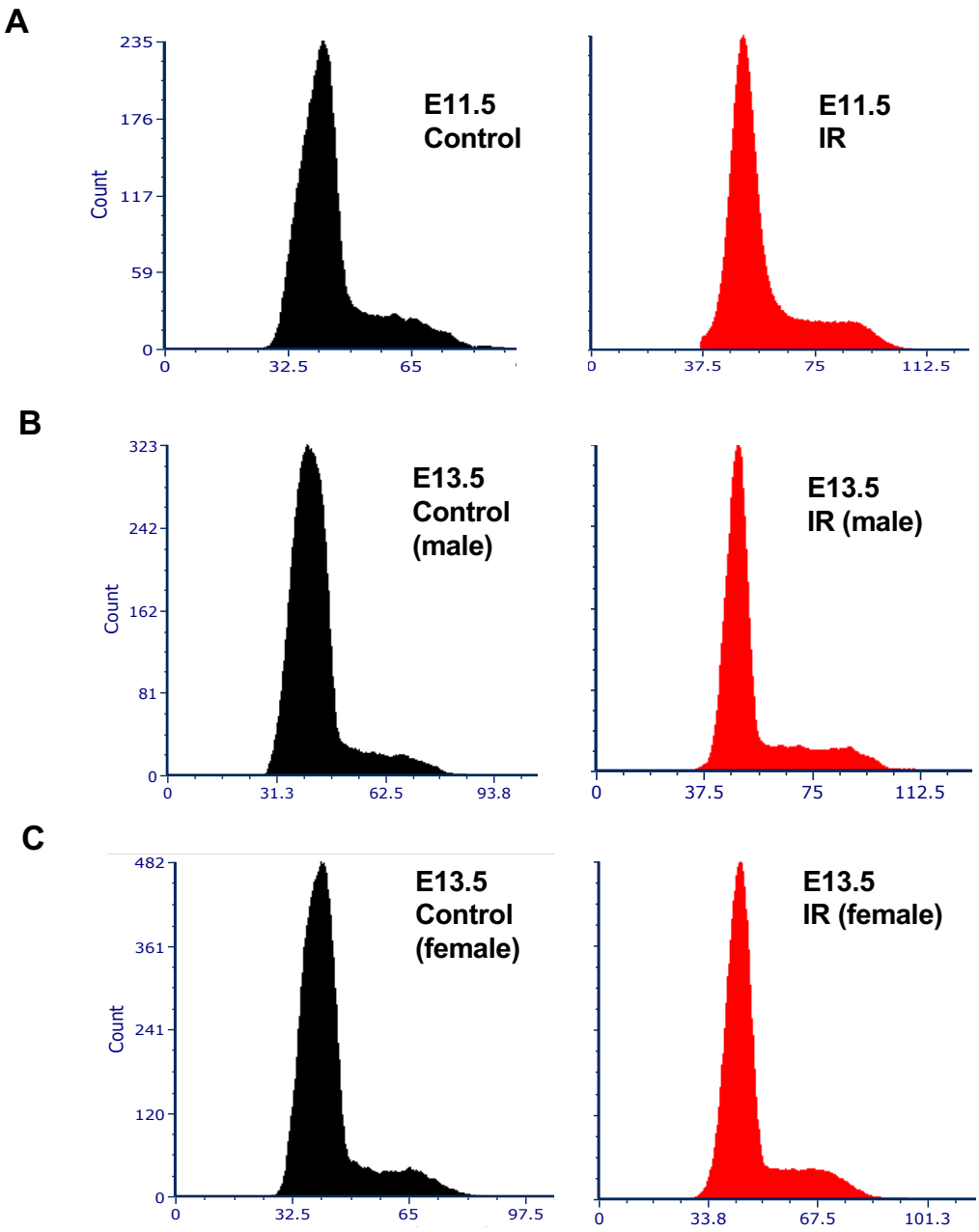

Figure S2. Cell cycle profiles of embryonic somatic cells show an intact G1 cell cycle checkpoint in response to IR-induced DNA damage.
A. Embryonic somatic cells at E11.5 were treated with 5 Gy of irradiation (right panel) or untreated (left panel). Eight hours after irradiation, cells were trypsinized, stained, and subjected to flow cytometry to assess cell-cycle distribution.
B-C. Same as in A except with male (B) and female (C) embryonic somatic cells from E13.5.

Figure S3

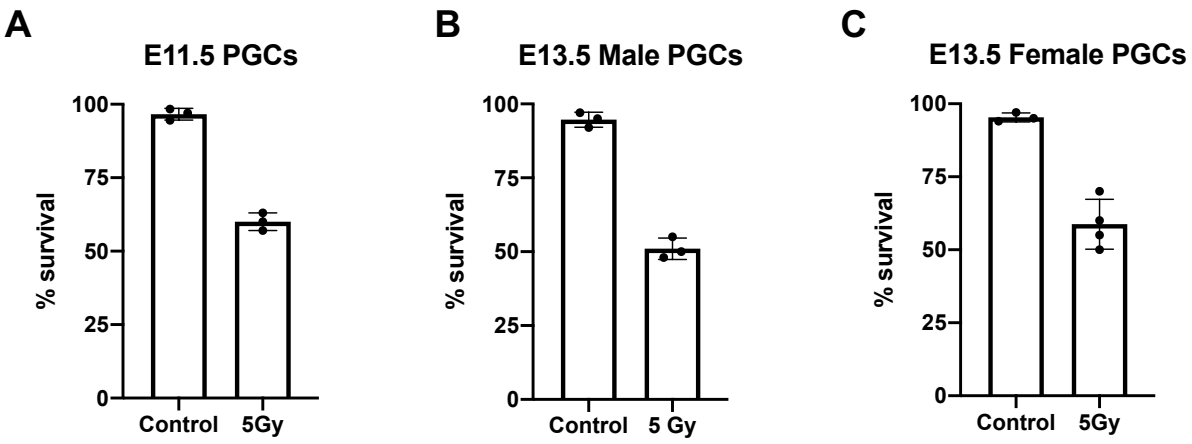

Figure S3. Irradiation leads to a reduction in embryonic germ cells 8 hours post damage.
A. Survival of E11.5 PGCs 8 hours after treatment where the percent of live PGCs (GFP+, PI- cells) was compared to the total number of PGCs (GFP+, PI- and PI+ cells). B-C. Same as in A except with male (B) and female (C) germ cells from E13.5.

Figure S4

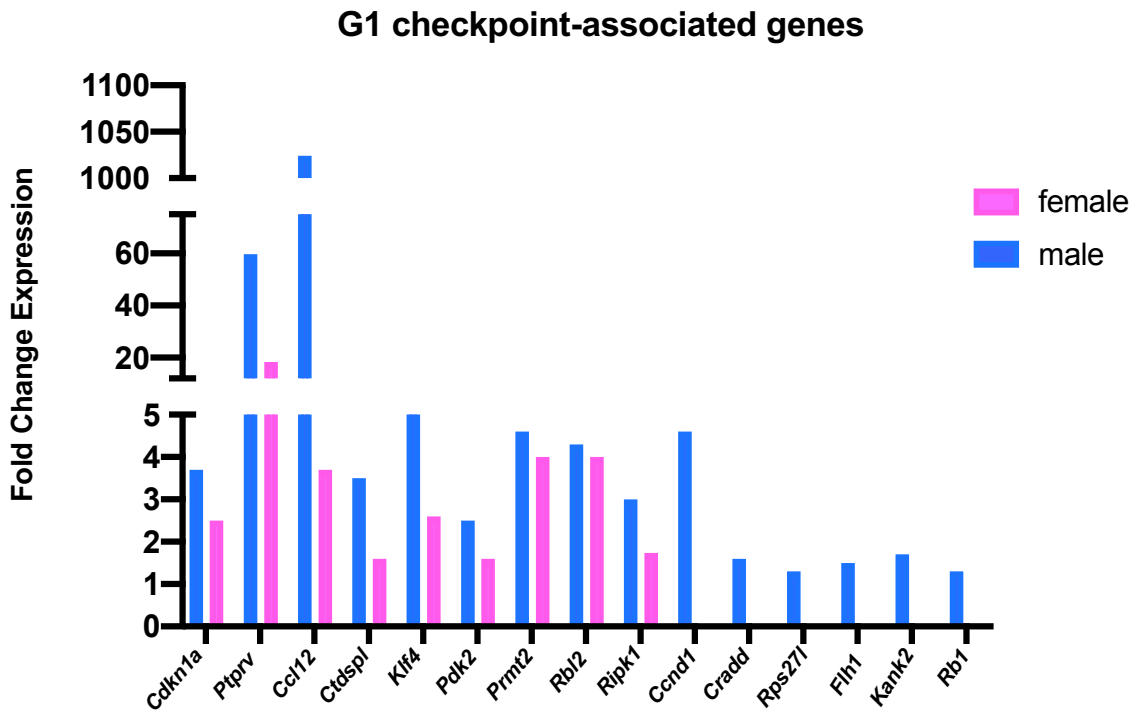

Figure S4. Expression of G1 checkpoint-associated genes are up-regulated in response to IR in E13.5 male germ cells.
Expression of genes in the GO term category “negative regulation of G1/S transition” (#2000143). All the genes are more highly expressed in response to IR in male germ cells and 6/15 genes are only differentially expressed in male cells. .

Figure S5

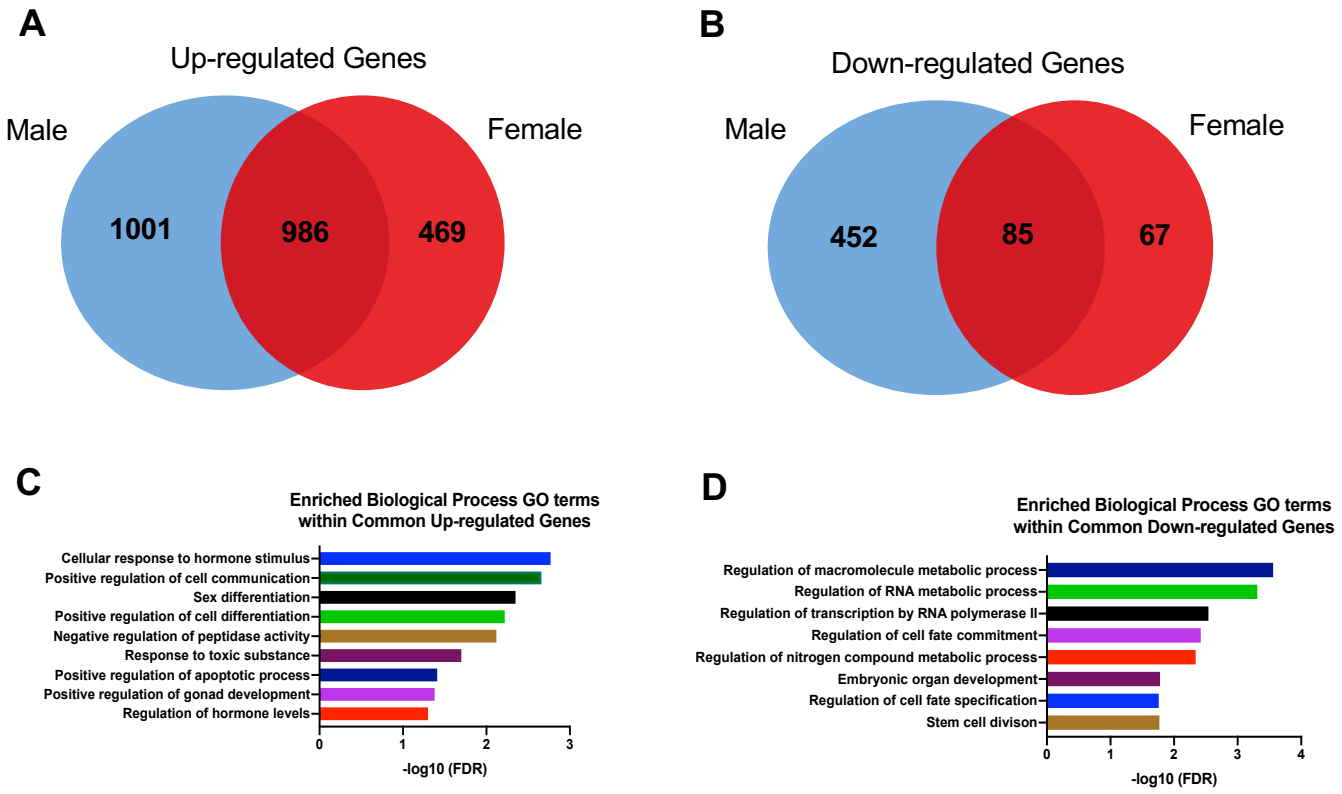

Figure S5 Comparison of the irradiation-induced DNA damage response in E13.5 female and male germ cells.

A. The number of up-regulated genes expressed at least 2-fold or higher in male germ cells only, female germ cells only or shared between the sexes in response to IR at E13.5.

B. Same as in A, but with down-regulated genes.

C. Significantly enriched GO terms among commonly-upregulated genes in male and female E13.5 germ cells in response to IR.

D. Same as in C, but with down-regulated genes.

Figure S6

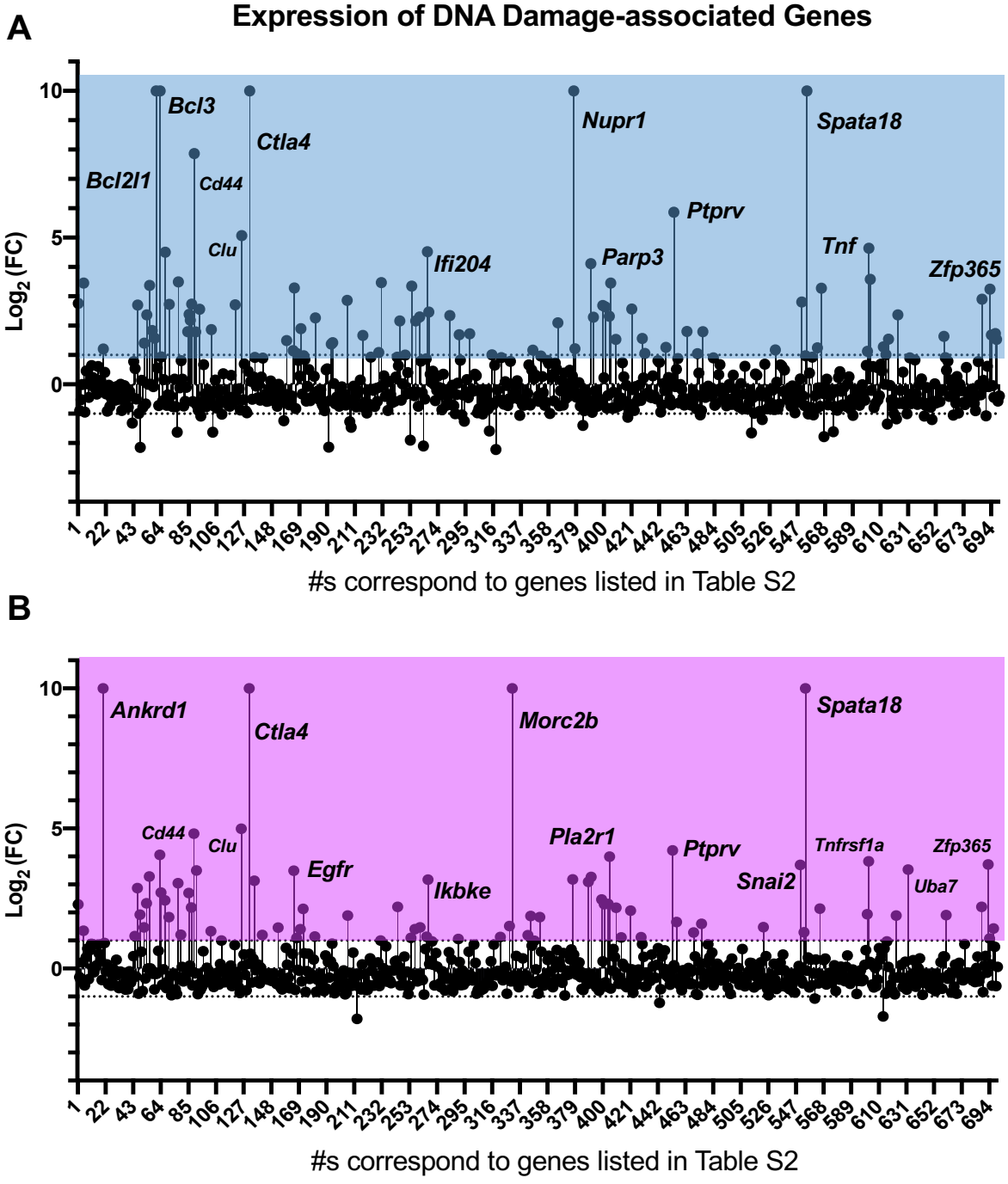

Figure S6. Expression of DNA damage-associated genes in irradiated E13.5 male and female germ cells.

A. Expression of genes within the "cellular response to DNA damage stimulus" GO category (#0006974) in response to IR in male germ cells at E13.5. 83/701 genes are up-regulated 2-fold or higher (see Table S7 for a list of genes and their associated Log_2(Fold) expression change).

B. Same as in A, but in female cells. 73/701 genes are up-regulated 2-fold or higher (see Table S7 for a list of genes and their associated Log_2(Fold) expression change).

Figure S7

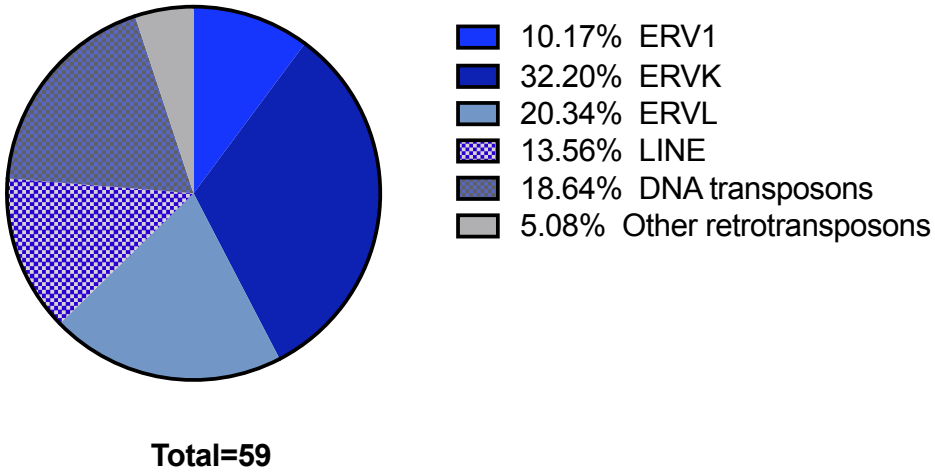

Figure S7. Expressed TE families in E13.5 male germ cells (related to Figure 2). Distribution of transposon family classes represented among the differentially expressed transposons with adjusted p-values<0.05.

Figure S8

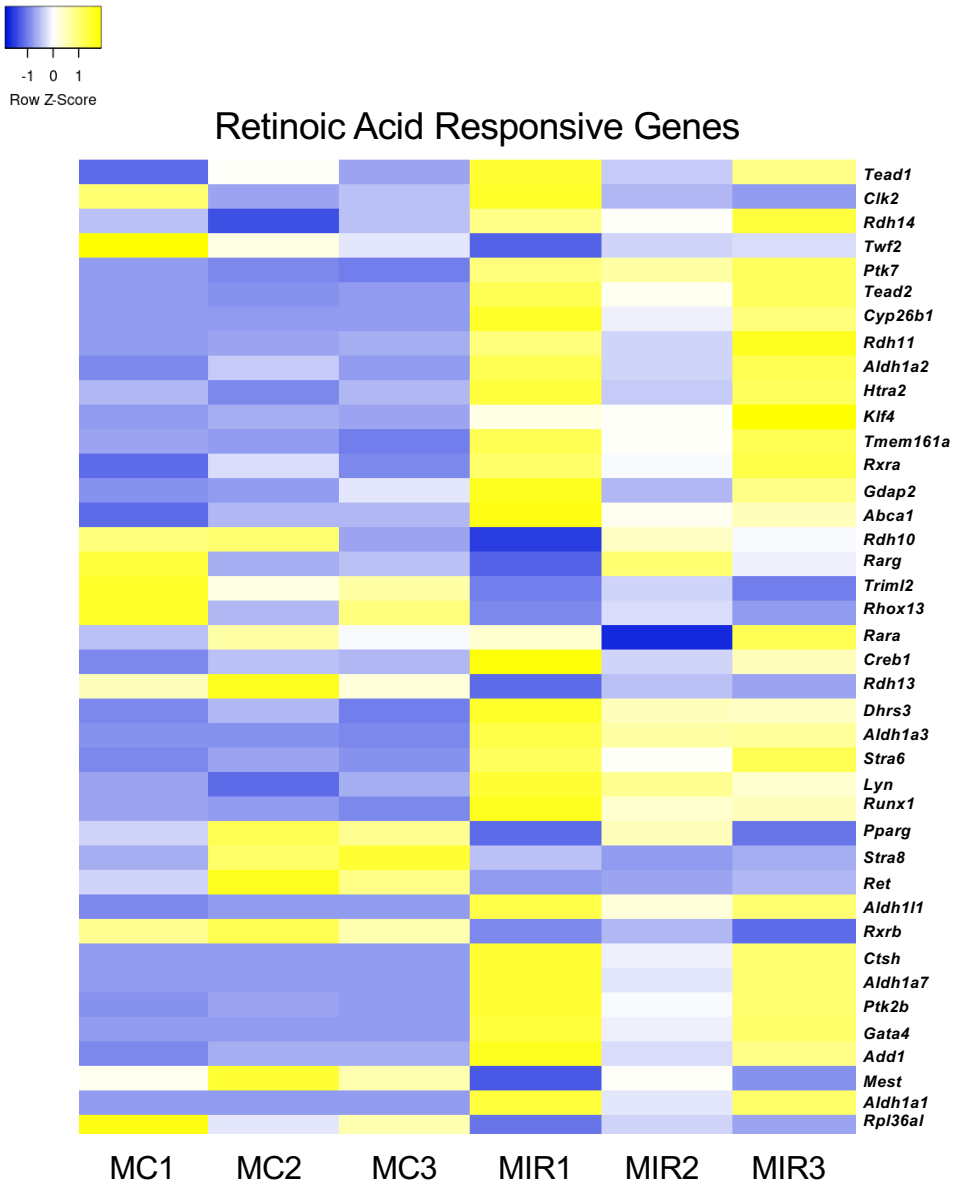

Figure S8. Irradiation exposure at E13.5 leads to an up-regulation of retinoic acid responsive genes.
Expression of retinoic acid responsive genes in control and irradiated E13.5 male germ cells.

Figure S9

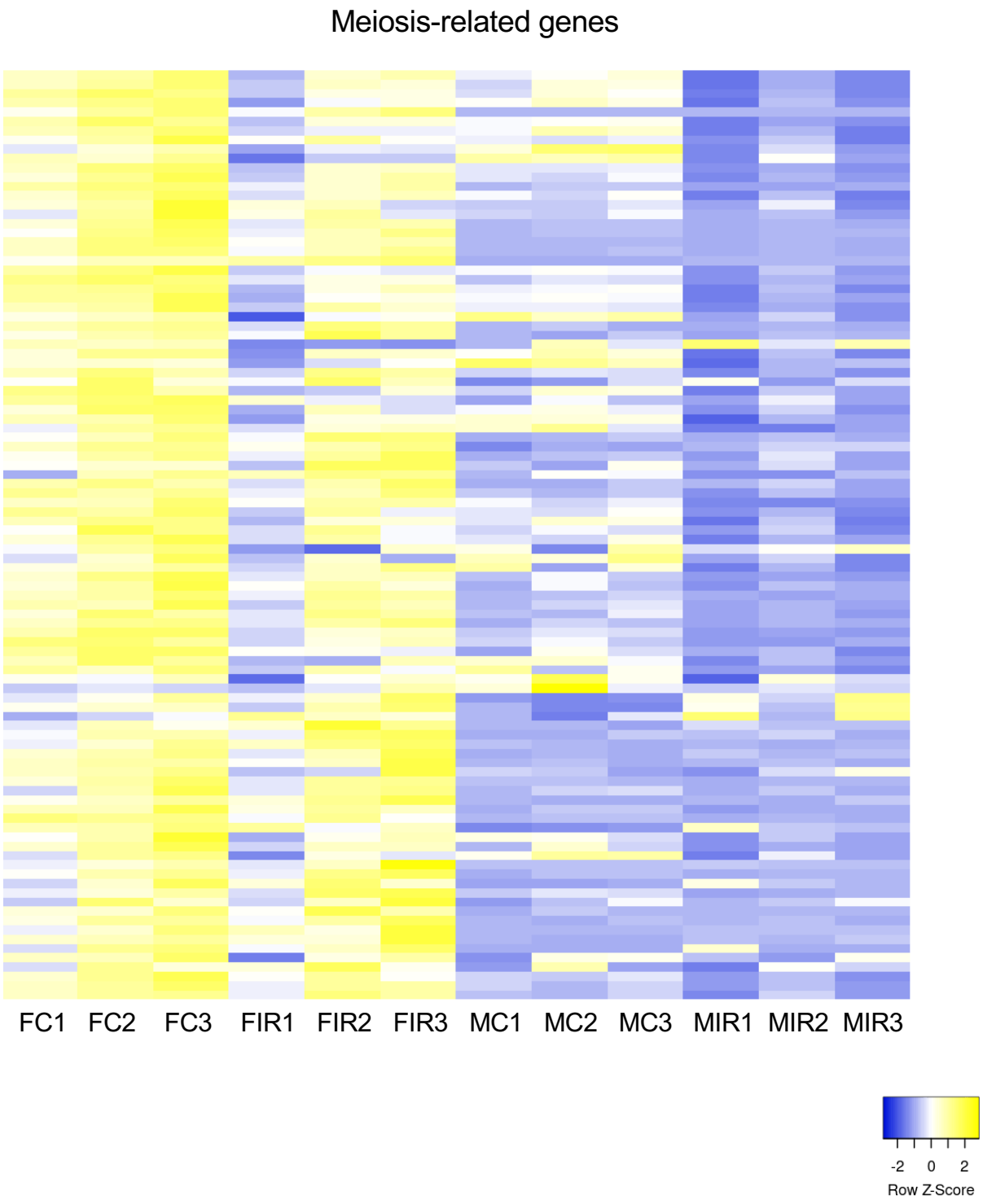

Figure S9. Meiosis-related genes are similarly expressed in female PGCs and are down-regulated in male PGCs in response to IR (related to Figure 3 and 5).

Expression of meiosis-related genes in control and irradiated E13.5 female and male germ cells. See Table S4 for the gene list.

Figure S10

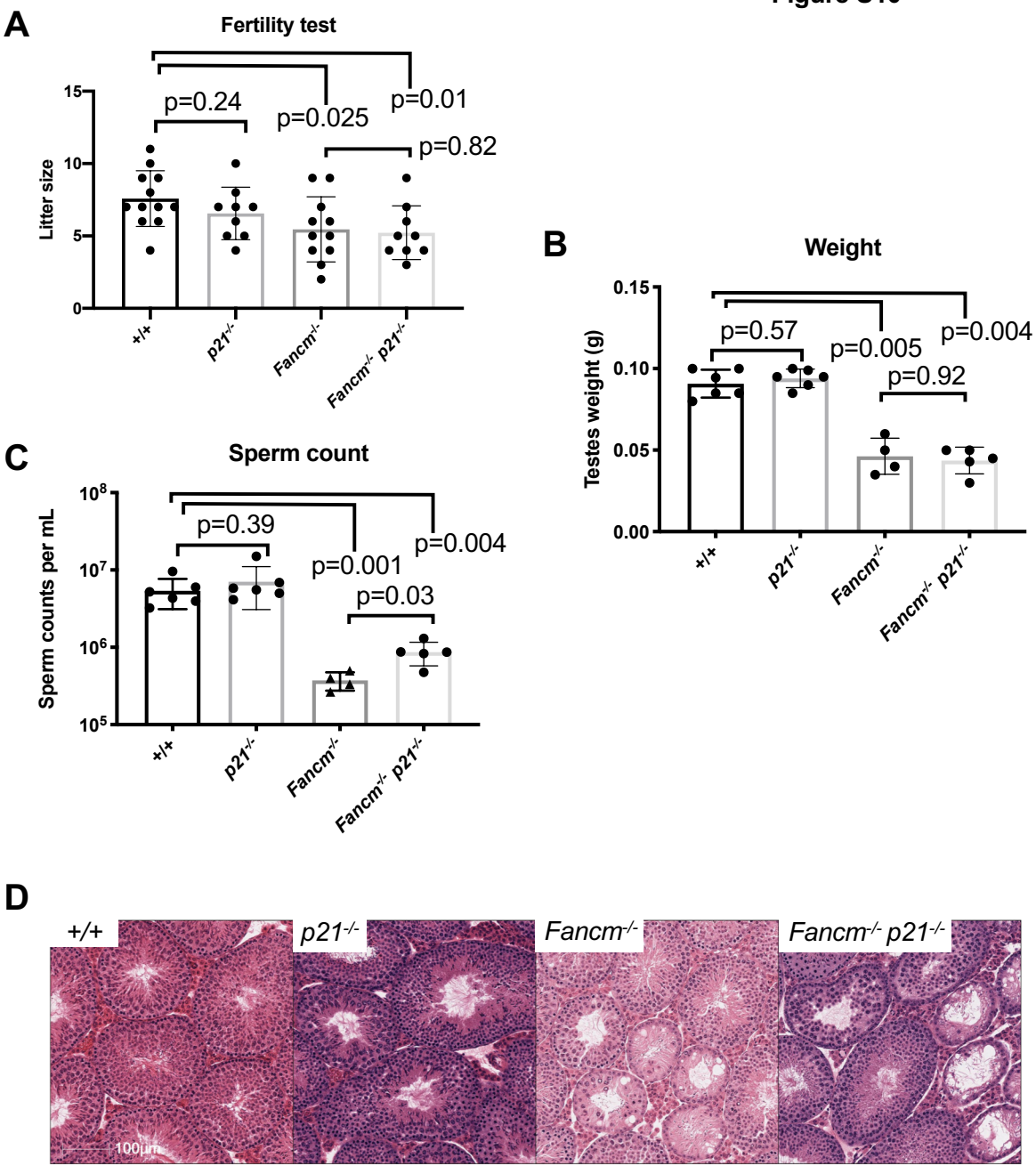

Figure S10. Loss of *p21* partially rescues germ cells in *Fancm*-deficient mutants.
A) Quantification of litter sizes produced from males of the indicated genotypes mated to wild type females.
B) Quantification of testes weights from males of the indicated genotypes.
C) Quantification of caudal epididymis sperm from males of the indicated genotypes.
D) Hematoxylin and eosin (H&E) staining of testis cross-sections from 8 week old males. Scale bar=100um

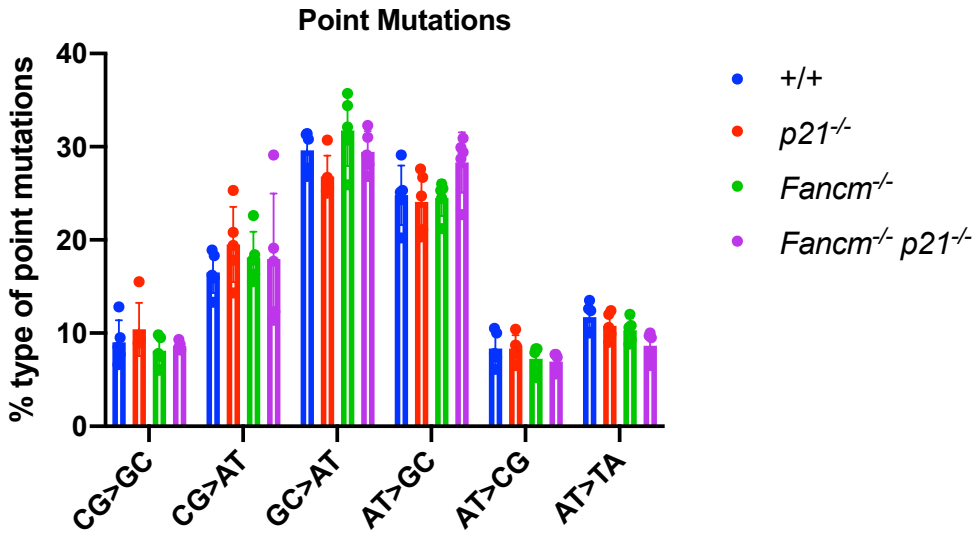

Figure S11. Point Mutation Distribution Between Genotypes Shows No Bias Towards a Specific Class of Mutations
Point mutation classes per genotype are shown as a percentage of the total point variants identified in each cell.

Figure S12

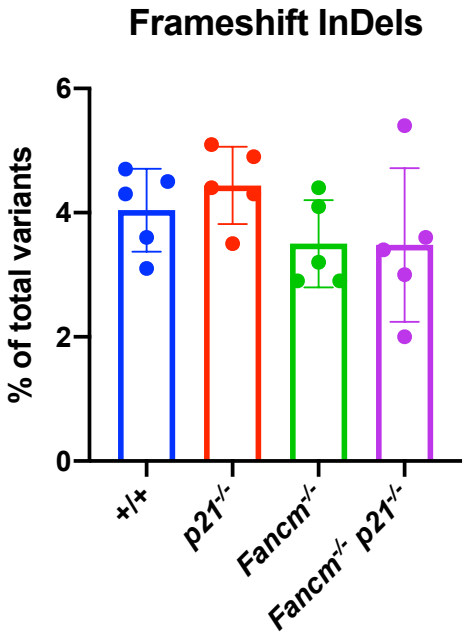

Figure S12. Insertions of deletions predicted to cause frameshift mutations are not enriched in double mutant samples.
Predicted frameshift causing mutations shown as a percentage of the total number of InDel variants identified in each cell. [Statistical significance was assessed using the Kruskal-Wallis test correcting for multiple comparisons with the Benjamini False Discovery Rate.]

Figure S13

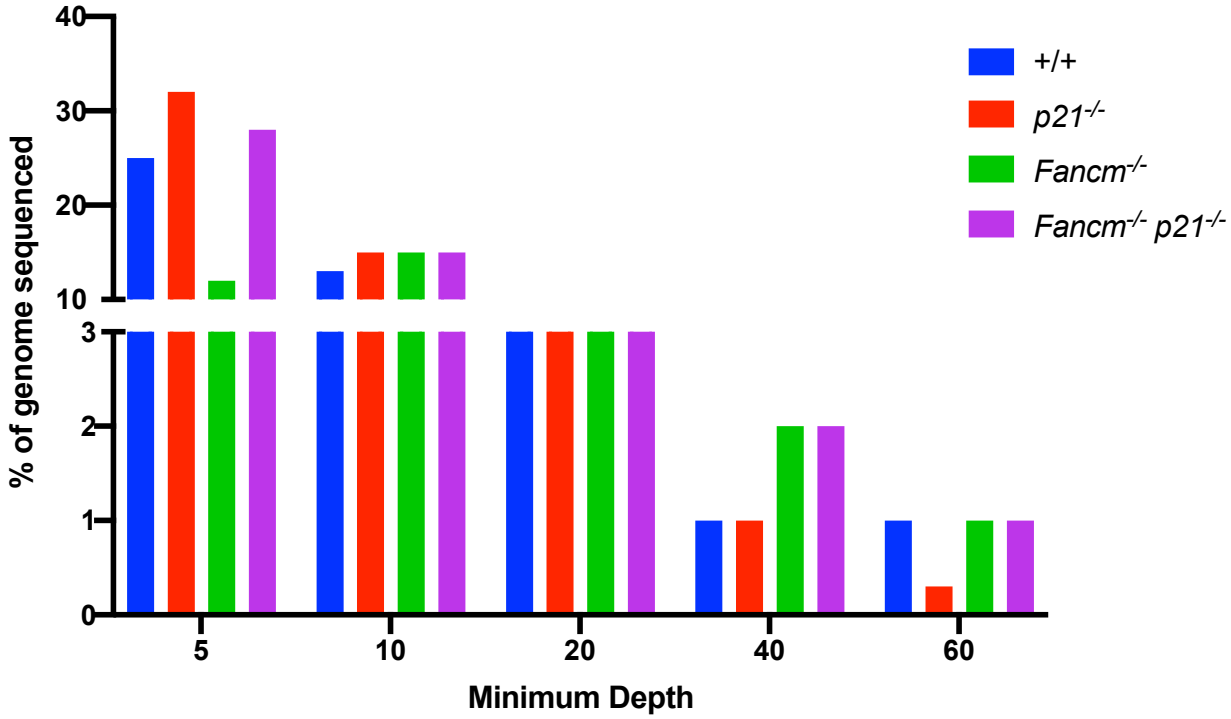

Figure S13. The percentage of the genome sequenced at specified minimum depths varies across genotypes.