Figure S1. (A) Identity and similarity of *C. elegans* ATL-1 and ATM-1 compared with *H. sapiens* ATM and ATR. The table shows the percentages for the PI3K domain. **(B) *atl-1* mutants exhibit mitotic catastrophe in the germline.** Representative images of mitotic germline nuclei stained with DAPI for the indicated genotypes (scale bar = 5μM**).**

Figure S2. +/*atl-1(tm853)* and *atl-1(RNAi)* characterization. **(A)** Representative images of fixed germlines of the indicated genotype immunostained with RPA-1 and RAD-51 antibodies and counterstained with DAPI. Quantification of the number of RPA-1 and RAD-51 foci per nucleus for the indicated genotypes is shown in the graph on the right. Error bars indicate standard error of mean from at least 20 nuclei from 10-15 worms of each genotype. **(B)** Quantification of HU-induced cell cycle arrest of mitotic germline nuclei that was determined in animals of the indicated genotype by scoring the number of nuclei in a volume of 54,000μm^3 16 hours after exposure of L4 stage animals to 40mM hyrdroxyurea, as previously described (Ahmed et al., 2001). **(C)** Quantification of IR-induced cell cycle arrest of mitotic germline nuclei in animals of the indicated genotype that was determined by scoring the number of nuclei in a volume of 54,000μm^3 12 hours after exposure of L4 stage animals to 75 Gy IR, as previously described (Gartner et al., 2000). **(D)** Germ cell apoptosis was measured by differential interference contrast (DIC) microscopy in animals of the indicated genotype at the indicated time points post IR-treatment. In B,C and D graphs the error bars indicate standard error of mean from at least ten germlines for each time point.

Figure S3. ATL-1 immunostaining and *rpa-1(RNAi)* controls. (**A**) Representative images of ATL-1 immunostaining of mitotic nuclei from untreated animals of the indicated genotype. (**B**) RPA-1 immunostaining of mitotic nuclei from animals subjected to control RNAi (L4440) and *rpa-1(RNAi)*. (**C**) Quantification of ATL-1 focus formation of the data shown in Figure 3B. Error bars indicate standard error of mean from at least ten germlines for each time point. (**D**) Representative images of ATL-1 foci in *brd-1* mutants following HU-treatment.

Figure S4. Increased ATL-1 foci in checkpoint and DNA repair mutants. (A) Representative images of ATL-1 immunostaining of mitotic nuclei from animals of the indicated genotype, 4hrs after IR-treatment (75Gy). (**B**) Quantification of the data in (A). Error bars indicate standard error of mean from at least ten germlines for each time point. **(C)** Quantification of ATL-1 foci per nucleus measured at the indicated time points after IR-treatment (75Gy) in animals of the indicated genotype. Error bars indicate standard error of mean from at least 20 nuclei from 10-15 worms of each genotype.

Figure S5. Dose response **(A) Q**uantification of IR-induced cell cycle arrest of mitotic germline nuclei in animals of the indicated genotype that was determined by scoring the number of nuclei in a volume of 54,000μm^3 12 hours after exposure of L4 stage animals to increasing doses of Gy IR, as previously described (Gartner et al., 2000). **(B)** Germ cell apoptosis was measured by differential interference contrast (DIC) microscopy in animals of the indicated genotype at the indicated doses of IR. Left graph shows 12 hs post IR-treatment, middle graph shows 24 hs post IR-treatment and right graph shows 36 hs post IR-treatment. Error bars indicate standard error of mean from at least ten germlines for each time point.