Supplementary Table S1. Strains generated for this study.

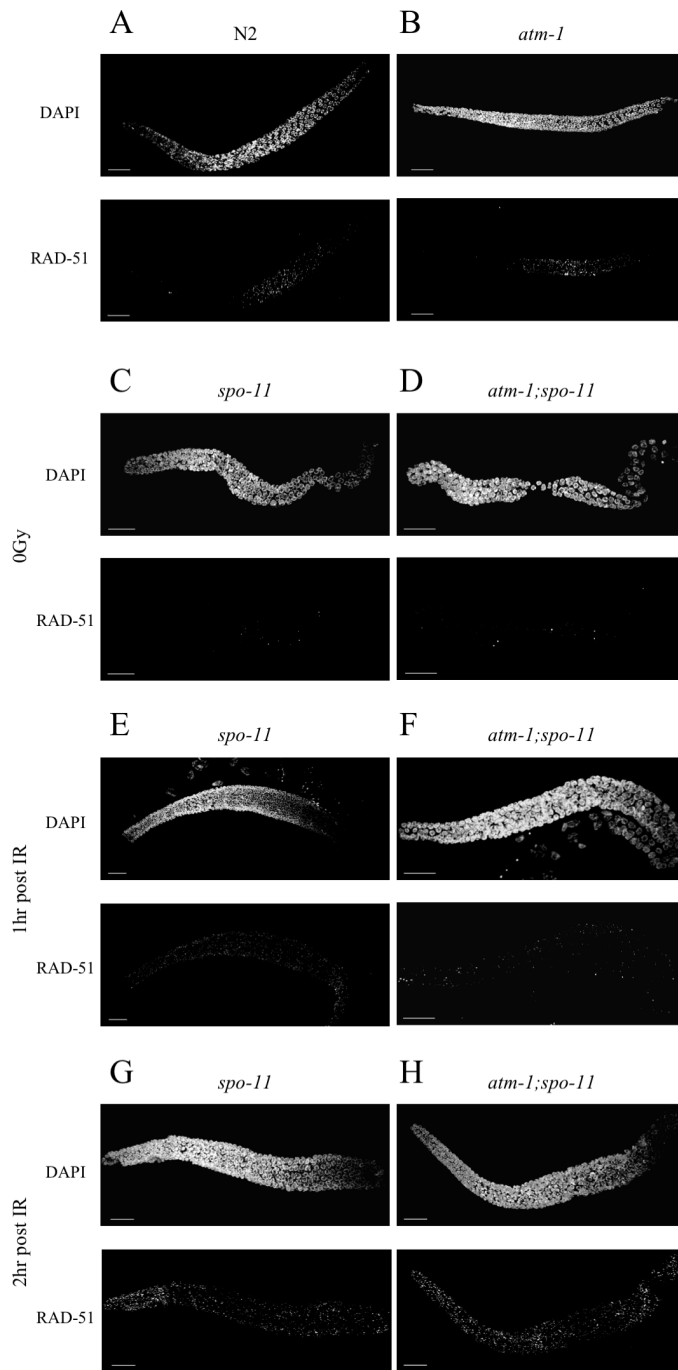| STRAIN	GENOTYPE	REFERENCE IN TEXT
QP0031	*dpy-1(e1),lon-1(e186) III*	*dpy-1,lon-1*
QP0187	*dpy-18(e364),unc-64(e246) III*	*dpy-18,unc-64*
QP1253	*atm-1(gk186) I;atl-1(tm853) V/nT1[qIs51]*	*atm-1;atl-1*
QP1302	*meIs8 II;him-5(ok1896) V/nT1[qIs51]*	*him-5;meIs8*
QP1427	*spo-11(me44) IV;atl-1(tm853) V/ nT1[qIs51]*	*spo-11;atl-1*
QP1428	*atm-1(gk186) I;syp-1(me17) V/nT1[qIs51]*	*atm-1;spy-1*
QP1429	*dsb-2(me96) II;atl-1(tm853) V/nT1[qIs51]*	*dsb-2;atl-1*
QP1430	*atm-1(gk186) I;dsb-2(me96) II;atl-1(tm853) V/ nT1[qIs51]*	*atm-1;dsb-2;atl-1*
QP1431	*atl-1(tm853),him-5(ok1896) V/nT1[qIs51]*	*atl-1,him-5*
QP1432	*atm-1(gk186) I;atl-1(tm853),him-5(ok1896) V/nT1[qIs51]*	*atm-1;atl-1,him-5*
QP1437	*atm-1(gk186) I;meIs8 II*	*atm-1;meIs8*
QP1441	*atm-1(gk186) I;brc-1(tm1145) III*	*atm-1;brc-1*
QP1635	*atm-1(gk186) I;smc-5(ok2421) II/mIn1[dpy-10(e128)]*	*atm-1;smc-5*
QP1659	*atm-1(gk186) I;dpy-18(e364),unc-64(e246) III*	*atm-1;dpy-18,unc-64*
QP1660	*atm-1(gk186) I;dpy-18(e364),unc-64(e246) III; him-5(ok1896) V*	*atm-1;him-5;dpy-18,unc-64*
QP1661	*atm-1(gk186),rad-54(ok615) I/hT2[qIs48];him-5(ok1896) V*	*atm-1;rad-54;him-5*
QP1662	*atm-1(gk186) I;spo-11(me44) IV/nT1[qIs51]*	*atm-1;spo-11*
QP1663	*atm-1(gk186) I;dsb-1(we11) IV/nT1[qIs51]*	*atm-1;dsb-1*
QP1672	*atm-1(gk186) I;him-5(ok1896) V*	*atm-1;him-5*
QP1673	*atm-1(gk186) I;dsb-2(me96) II*	*atm-1;dsb-2*
QP1674	*dpy-18(e364) unc-64(e246) III;him-5(ok1896) V*	*him-5;dpy-18,unc-64*
QP1675	*atm-1(gk186) I;dpy-1(e1),lon-1(e186) III*	*atm-1;dpy-1,lon-1*
QP1676	*dpy-1(e1) lon-1(e186) III;him-5(ok1896) V*	*him-5;dpy-1,lon-1*
QP1677	*atm-1(gk186) I;dpy-1(e1) lon-1(e186) III;him-5(ok1896) V*	*atm-1;him-5;dpy-1,lon-1*
QP1678	*rad-54(ok615) I/hT2[qIs48];him-5(ok1896) V*	*rad-54;him-5*
QP1679	*smc-5(ok2421) II/min1(?);brc-1(tm1145) III*	*smc-5;brc-1*
QP1680	*atm-1(gk186) I;smc-5(ok2421) II/mIn1[dpy-10(e128)];brc-1(tm1145) III*	*atm-1;smc-5;brc-1*
QP1681	*atm-1(gk186) I;him-5(ok1896) V;meIs8[gfp::cosa-1]*	*atm-1;him-5;meIs8*
QP1682	*atm-1(gk186) I;smc-5(ok2421) II;spo-11(me44) IV/nT1[qIs51]*	*atm-1;smc-5;spo-11*
QP1683	*smc-5(ok2421) II;spo-11(me44) IV/nT1[qIs51]*	*smc-5;spo-11*

Supplemental Figure S1

Figure S1. ATM-1 limits the number of RAD-51 foci. (A, B) DAPI (top) and anti-RAD-51 (bottom) stained gonad arms of N2 (left) and *atm-1* mutant (right) day 1 adult worms. (C-H) DAPI (top) and anti-RAD-51 (bottom) stained gonad arms for time-course IR experiments of *spo-11* (left) and *atm-1;spo-11* mutant (right). Scale bar=20μm.
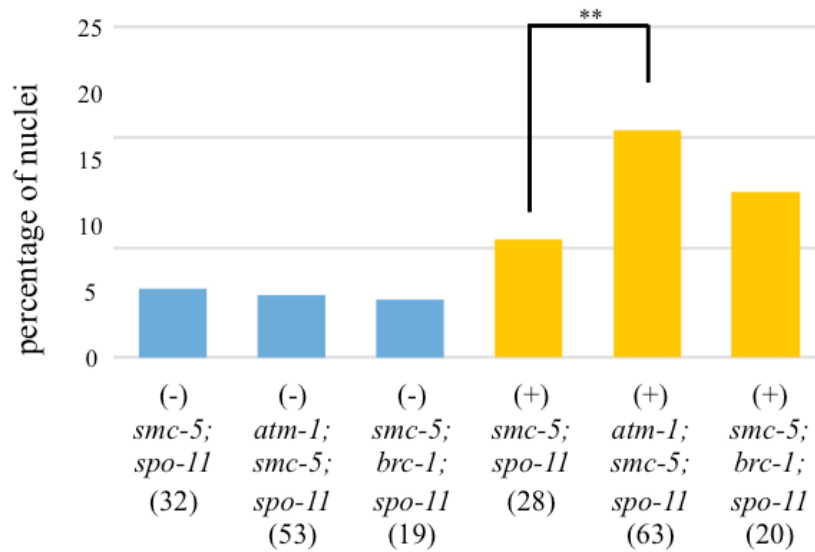
Supplemental Figure S2

Figure S2. The impact of *atm-1* on inter-sister repair is independent of SPO-11 induced breaks. Mutant nuclei contain more IR-induced fragments in *atm-1; spo-11* compared to *spo-11* when inter-sister repair is impaired by loss of *smc-5* or *brc-1*. Percentage of -1 nuclei containing fragments are shown. Numbers below each genotype indicate the numbers of nuclei analyzed/genotype. (-): non-irradiated; (+): irradiated with 10Gy. **P<0.01, χ^2 test.
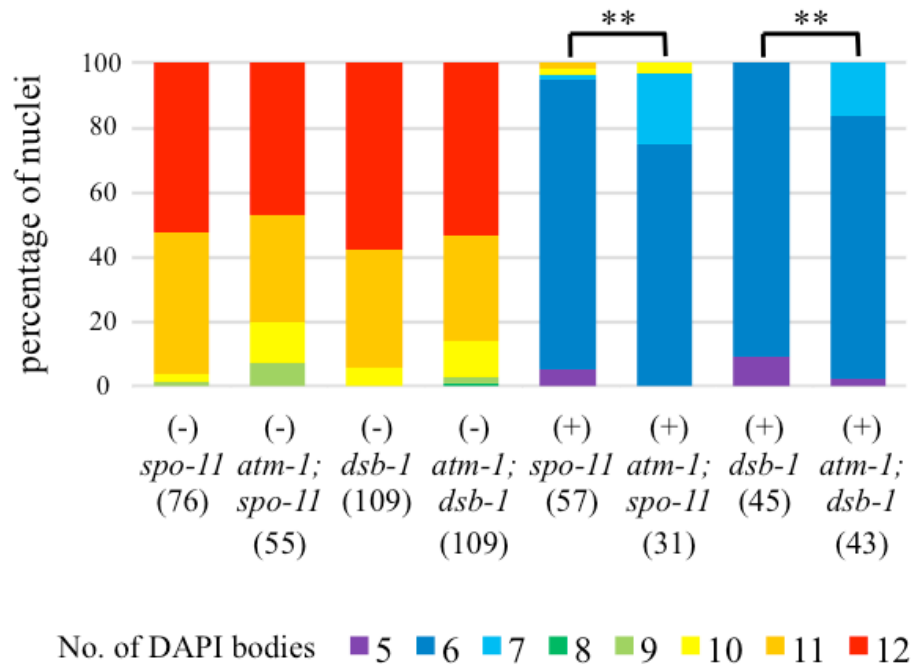
Supplemental Figure S3

Figure S3. CO formation is impaired in *atm-1* mutants independently of SPO-11. Quantification of -1 nuclei containing the indicated number of DAPI bodies. (-): non-irradiated; (+): irradiated with 10Gy. Numbers below each genotype indicate the numbers of nuclei analyzed for that column. **P<0.01, wo-tailed Mann Whitney test.
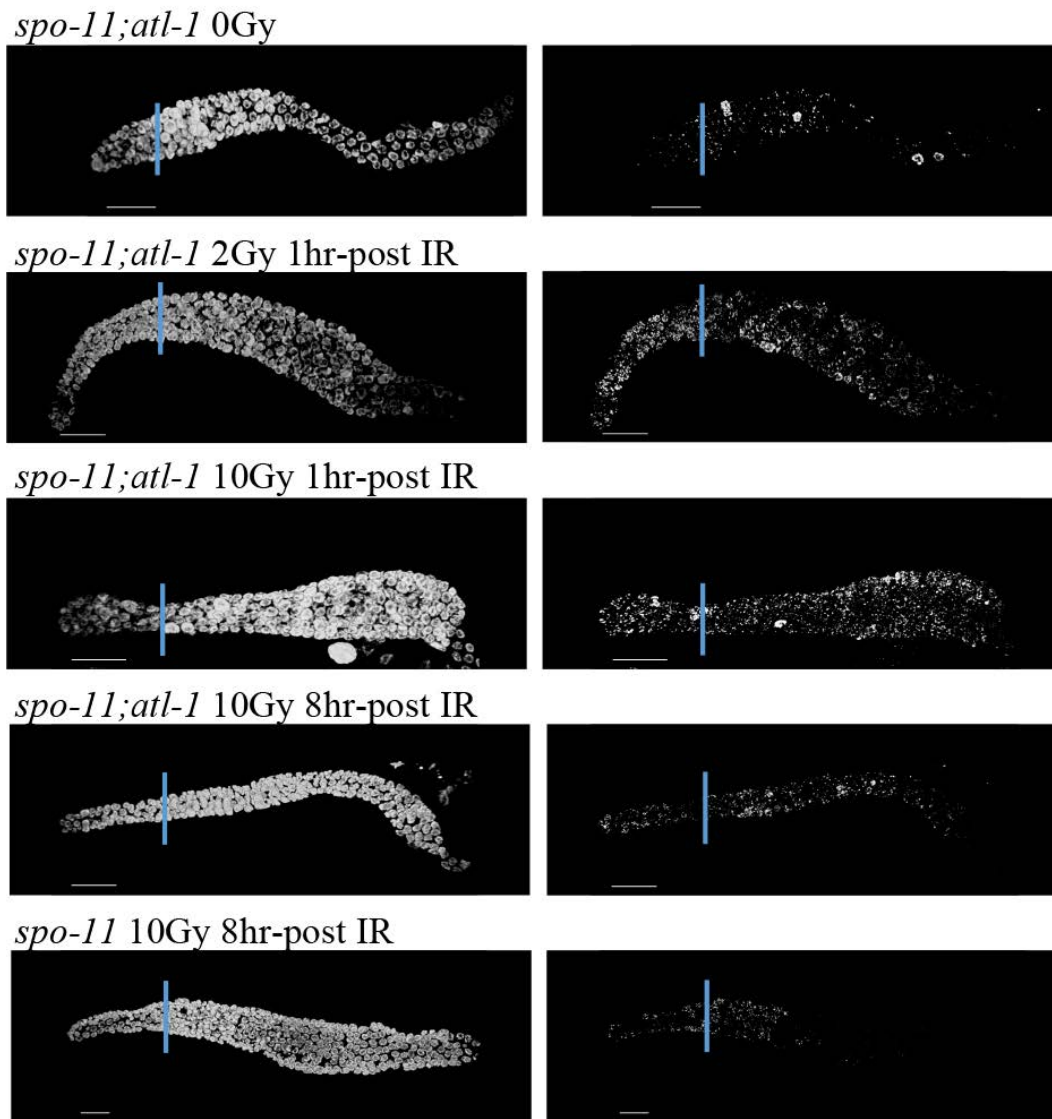
Figure S4. RAD-51 analysis in *atl-1* mutants. DAPI (left) and anti-RAD-51 (right) stained gonad arms of indicated genotypes in unirradiated control and irradiated animals. The blue line marks the start of the transition zone. Scale bar = 20 μm.
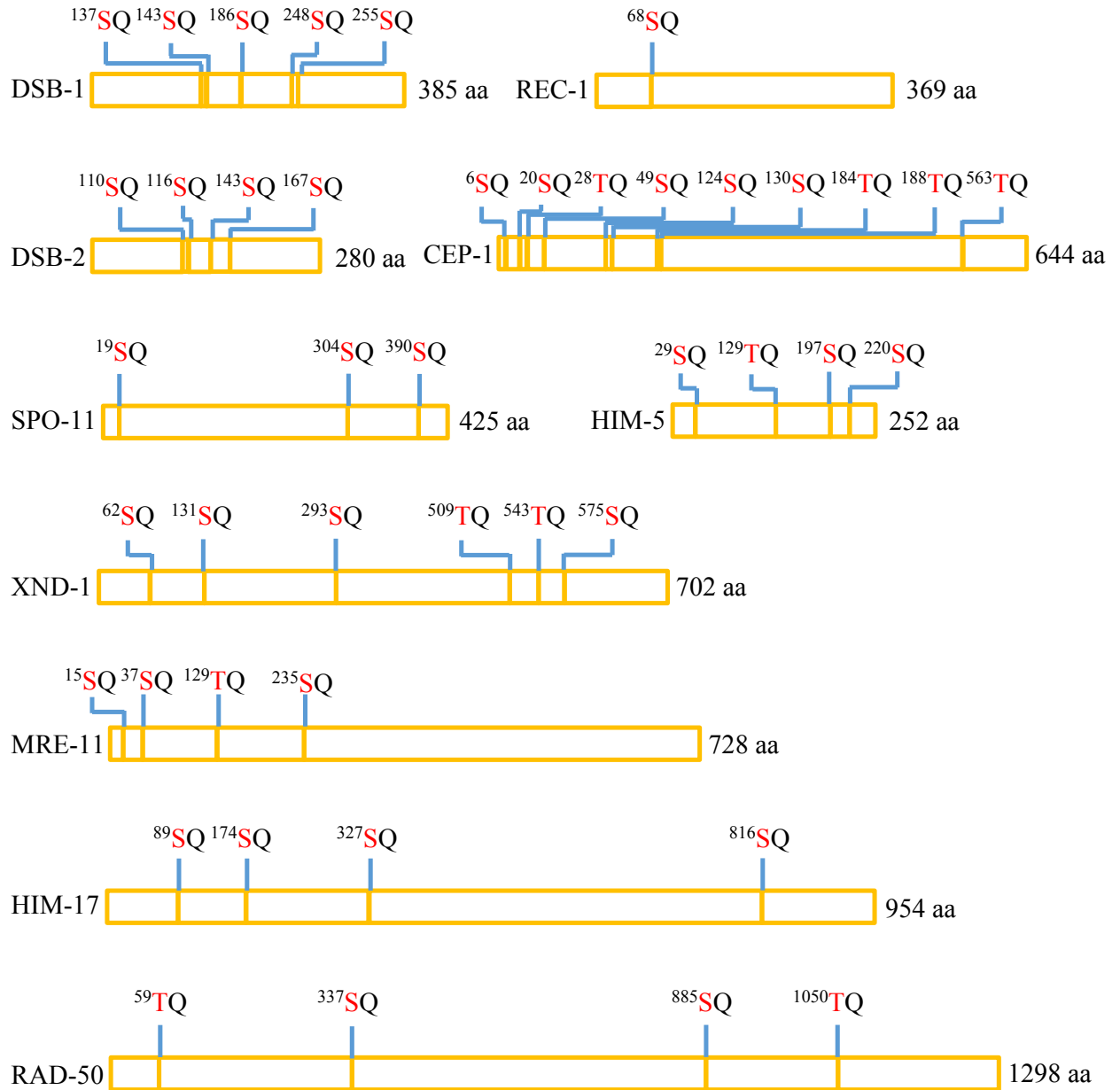
Supplemental Figure S5

Figure S5. Bioinformatic analysis of ATM/ATR potential phosphorylation targets.
(S/T)Q consensus sites for ATM/ATR signaling are shown in 10 DSB proteins.