Supplementary data

Requirement of MTA1 in ATR-mediated DNA Damage Checkpoint Function

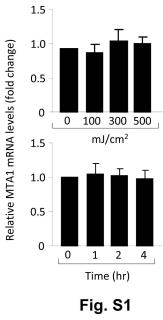
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Figure Legends

- Figure S1. HaCaT cells were untreated or treated with different doses of UV and harvested at the indicated time points. Total RNA was isolated and subjected to qPCR analysis of MTA1 mRNA levels. The expression levels of MTA1 were normalized to those of actin, and average values from three independent experiments are shown with indicated standard deviations.
- Figure S2. (A) HaCaT cells were transfected with control siRNAs or specific siRNAs targeting MTA1 (Qiagen) and then subjected to Western blot analysis with the indicated antibodies. (B) Control siRNA- or MTA1 siRNA-transfected HaCaT cells were exposed to 200 mJ/cm² of UV and harvested at the indicated time points for Western blot as described in Figure 4C.
- *Figure S3*. MTA1^{+/+} or MTA1^{-/-} MEFs were treated with or without 200 mJ/cm² of UV and harvested at the indicated time points for FCAS analysis. The graph data represent the average values of cell-cycle distribution from two independent experiments.
- Figure S4. MTA1^{+/+} or MTA1^{-/-} MEFs were treated with 200 mJ/cm² of UV and fixed after 1 hour for immunofluorescent staining with an anti-phospho-H2AX (Ser139) antibody. The nuclei were visualized by DAPI staining. Representative confocal images of γ-H2AX foci were shown.
- Figure S5. HaCaT cells were transfected with control siRNA or specific siRNA targeting MTA1. After 48 hours of transfection, cells were irradiated with UV and then subjected to γ -H2AX staining as described in Fig. S3. Representative confocal images of γ -H2AX foci were shown.



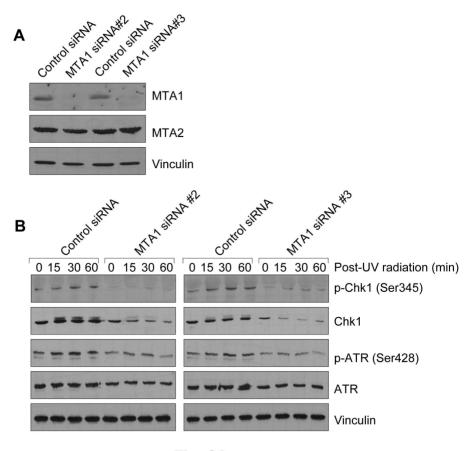


Fig. S2

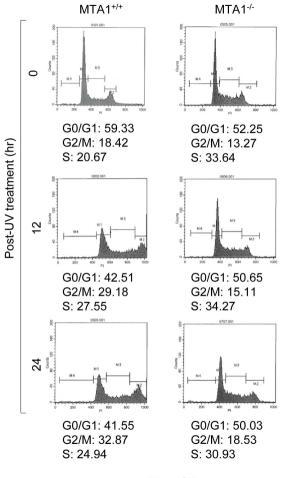


Fig. S3

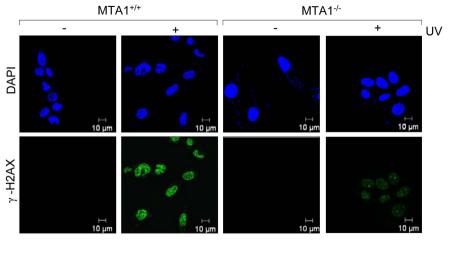


Fig. S4

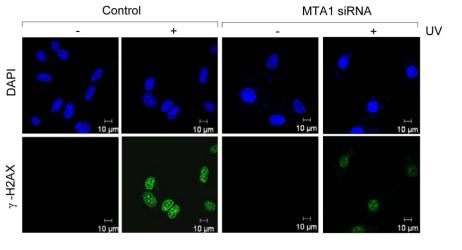


Fig. S5