

Supplementary Materials for  
**ATM deficiency confers specific therapeutic vulnerabilities in bladder cancer**

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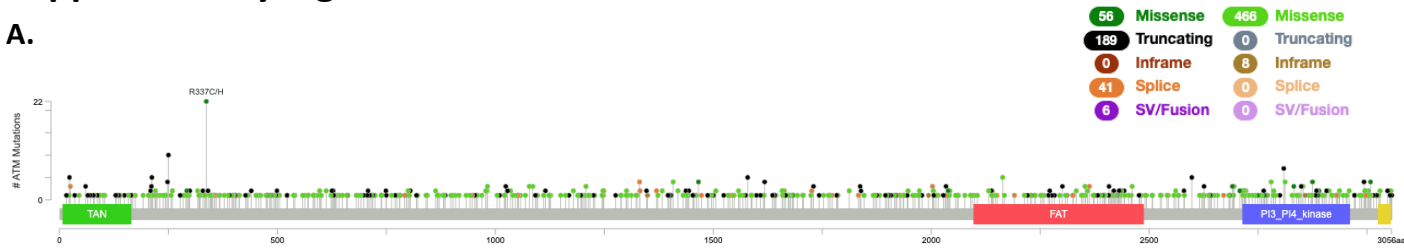
Figs S1 to S9  
Legends for tables S1 to S5  
References

**Other Supplementary Material for this manuscript includes the following:**

Tables S1 to S5

# Supplementary Figure 1

A.



B.

R337
R1466
R2832
N2875
I2888L
L2890
R3008

**Supplementary Figure 1: ATM alterations in bladder cancer and other tumor types.** A. Location of ATM mutations in The Cancer Genome Atlas (TCGA) pan-cancer cohort (n = 10,967 tumors). Alterations are color-coded by type. Data was accessed and visualized using the cBioPortal interface ([www.cbioportal.org](http://www.cbioportal.org)). B. Seven amino acid positions have been identified as ATM missense mutational hotspots ([www.cancerhotspots.org](http://www.cancerhotspots.org)).

## Supplementary Figure 2

<u>TCGA Case ID</u>	<u>Alteration</u>	<u>Mutation type</u>	<u>Germline/ Somatic</u>	<u>LOH</u>	
TCGA-FD-A3N6	M1	Startloss	Germline	No	Truncating mutations
TCGA-DK-A6AW	R250X	Stopgain	Somatic	No	
TCGA-FD-A43Y	S403X	Stopgain	Somatic	Yes	
TCGA-UY-A8OD	Q781X	Stopgain	Somatic	Yes	
TCGA-GV-A40E	W1026Lfs	Frameshift ins.	Somatic	Yes	
TCGA-XF-AAMG	Q1276X	Stopgain	Somatic	No	
TCGA-4Z-AA84	R1466X	Stopgain	Somatic	No	
TCGA-BT-A42E	Q1636X	Stopgain	Somatic	Yes	
TCGA-E7-A5KF	Q1839X	Stopgain	Somatic	Yes	
TCGA-UY-A9PF	Q1839X	Stopgain	Somatic	No	
TCGA-DK-A6B5	E1978X	Stopgain	Germline	No	
TCGA-K4-A3WU	E1996fs	Frameshift ins.	Germline	No	
TCGA-FD-A43P	E2221X	Stopgain	Somatic	No	
TCGA-KQ-A41N	X792_splice	Splice site	Somatic	No	Splice site mutations
TCGA-E7-A8O8	E1249_splice	Splice site	Somatic	No	
TCGA-FD-A3B5	X2191_splice	Splice site	Somatic	Yes	
TCGA-GV-A6ZA	X2326_splice	Splice site	Somatic	Yes	
TCGA-GD-A6C6	X2643_splice	Splice site	Somatic	No	
TCGA-XF-AAME	I323V	Nonsyn. SNV	Somatic	Yes	Missense mutations
TCGA-UY-A9FP	E2039K	Nonsyn. SNV	Somatic	No	
TCGA-ZF-AA53	V2424G*	Nonsyn. SNV	Germline	Yes	
TCGA-FD-A5BY	R2832C*	Nonsyn. SNV	Germline	Yes	

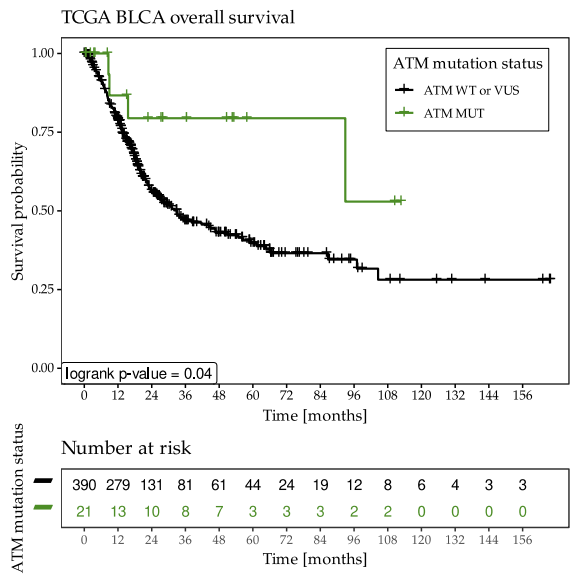
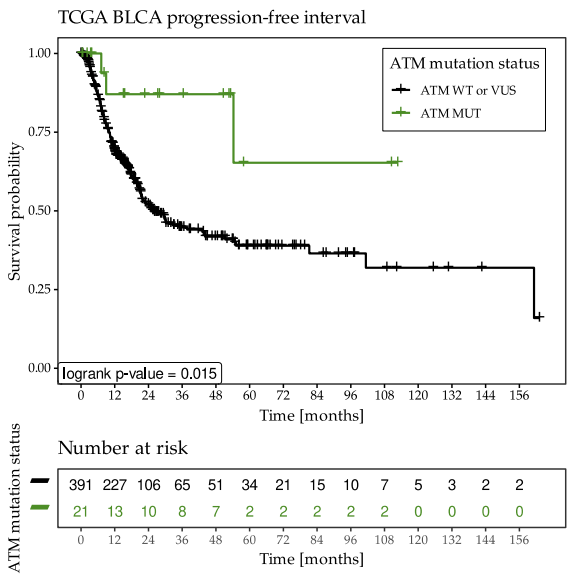
**Supplementary Figure 2: Complete list of predicted deleterious ATM alterations in the bladder cancer (BLCA) The Cancer Genome Atlas (TCGA) cohort.** See Methods for additional details regarding mutation calling. Cases are color-coded by alteration type (orange, truncating; pink, splice site; red, missense).

### Supplementary Figure 3

	ATM-mutant (n=22)	ATM wild-type (n=384)
<b>Age</b> (mean $\pm$ s.d)	66 $\pm$ 12	68 $\pm$ 11
<b>Sex</b>		
Female	4 (4%)	104 (96%)
Male	17 (6%)	287 (94%)
<b>Stage at diagnosis</b>		
1	0 (0%)	1 (<1%)
2	10 (48%)	121 (31%)
3	7 (33%)	134 (35%)
4	4 (19%)	132 (34%)

**Supplementary Figure 3: Clinical characteristics of ATM-altered and unaltered cases in TCGA bladder cancer (BLCA) cohort.**

# Supplementary Figure 4



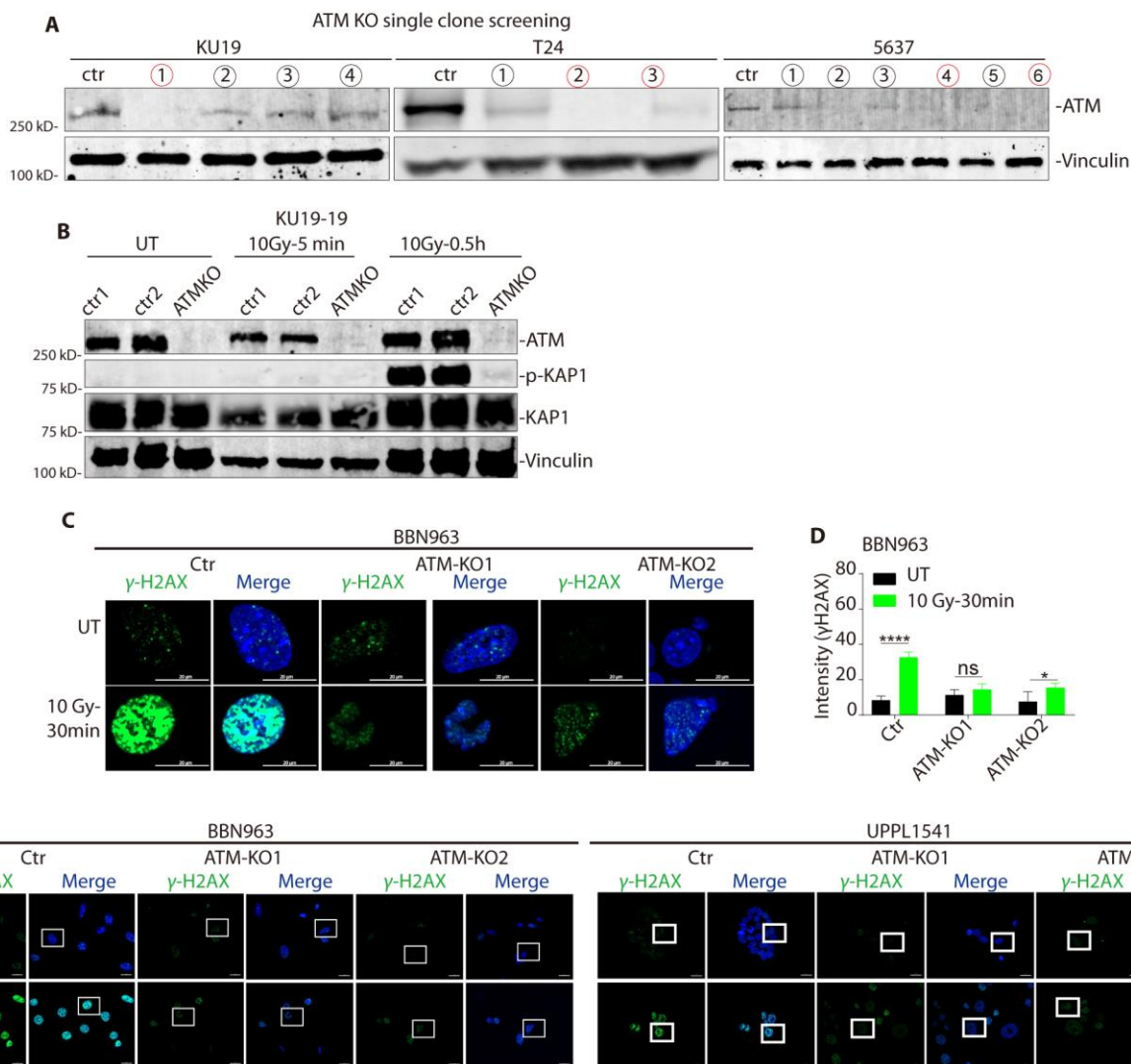
**Supplementary Figure 4: Overall survival (OS) and progression-free survival (PFS) in ATM altered vs unaltered cases in the TCGA bladder cancer (BLCA) cohort. PFS and OS were significantly longer in ATM-altered compared to ATM-unaltered cases.**

## Supplementary Figure 5

<u>Case No.</u>	<u>Alteration</u>	<u>Mutation type</u>
1	R250X	stopgain
2	E343X	stopgain
3	E343lfs*2	frameshift deletion
4	E390X	stopgain
5	Q513X	stopgain
6	K828Sfs*8	frameshift deletion
7	Q1017Rfs*5	frameshift deletion
8	Q1116X	stopgain
9	V1268*	stopgain
10	S1589X	stopgain
11	Q1636X	stopgain
12	R1730X	stopgain
13	I1792Nfs*9	frameshift insertion
14	E1991X	stopgain
15	E2157X	stopgain
16	Q2433X	stopgain
17	R2598X	stopgain
18	Q2615X	stopgain
19	W2960X	stopgain
20	R2547_S2549del	nonframeshift deletion
21	splice	splicing
22	splice	splicing
23	splice	splicing
24	splice	splicing
25	splice	splicing
26	P292L	nonsynonymous SNV
27	E2039K	nonsynonymous SNV
28	E2039K	nonsynonymous SNV
29	S2394L	nonsynonymous SNV
30	V2424G	nonsynonymous SNV
31	R2832C	nonsynonymous SNV
32	R3008C	nonsynonymous SNV

**Supplementary Figure 5: Complete list of predicted deleterious ATM alterations in the Dana-Farber/Brigham & Women's Cancer Center (DFBWCC) urothelial tumor cohort.** See Methods for additional details regarding mutation calling. Cases are color-coded by alteration type (orange, truncating; green, non-frameshift deletion; pink, splice site; red, missense).

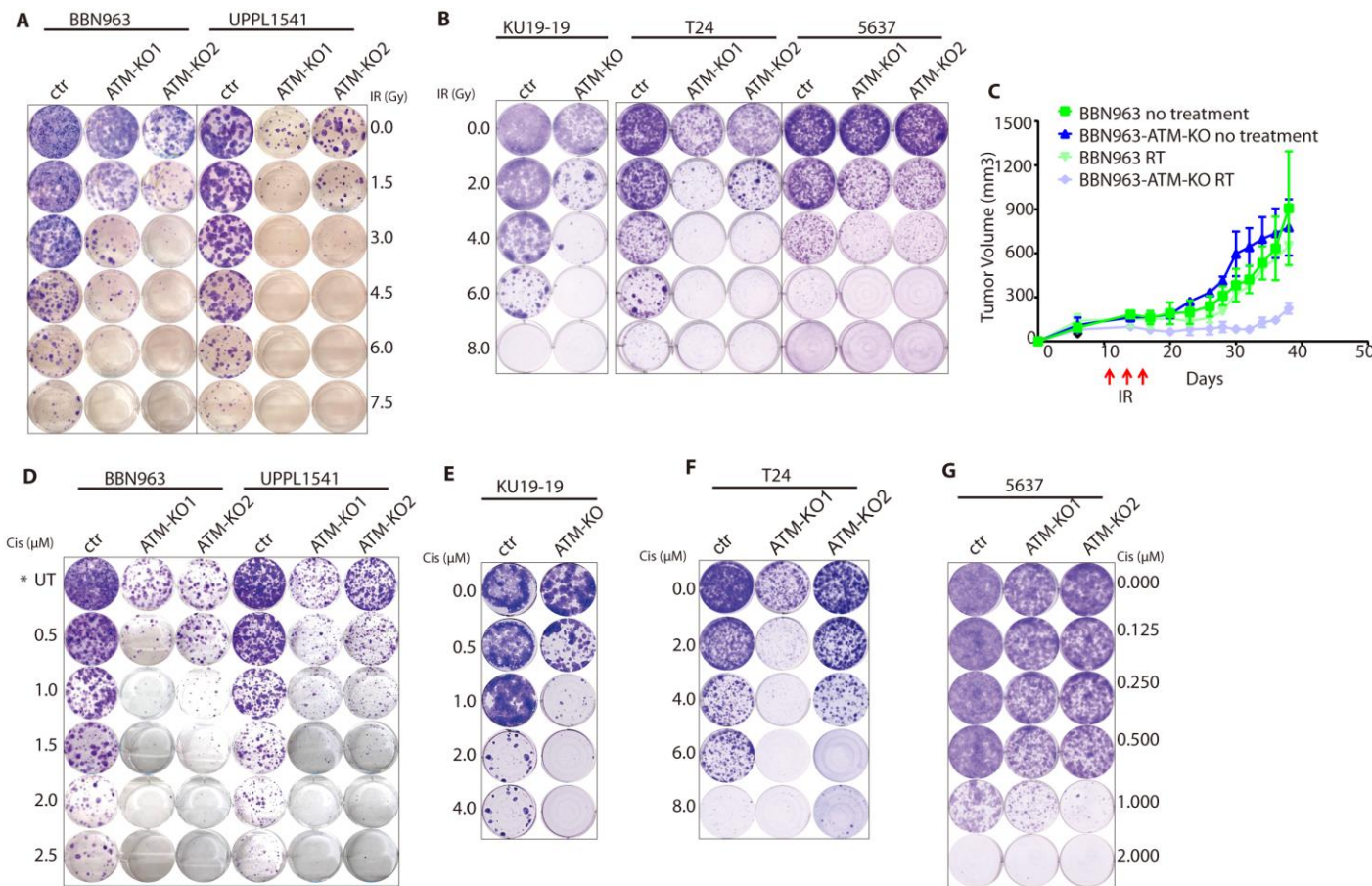
# Supplementary Figure 6



## Supplementary Figure 6: ATM deletion in bladder cancer cell lines and DNA repair properties of ATM-deleted models.

**A.** Following nucleofection of Cas9/sgRNA ribonucleoparticles, single cells were sorted and clones were expanded and then screened by ATM immunoblot to identify clones with loss of ATM protein expression. Clones with red circles were selected as ATM-deleted clones. **B.** KAP1 is a primary target of ATM phosphorylation following DNA damage and radiation-induced phosphorylation of KAP1 was markedly reduced in ATM-deleted vs WT ATM (control, 'ctr') KU19-19 bladder cancer cells. **C.** ATM phosphorylates histone H2A following DNA damage and radiation-induced  $\gamma$ H2AX (Ser139) foci were significantly decreased in ATM-deleted compared to WT ATM BBN bladder cancer cells. **D.** Quantification of  $\gamma$ H2AX (Ser139) foci from experiment represented in panel C. \*\*\*\*,  $p < 0.0001$ . **E.** Full scale images (20X) of  $\gamma$ H2AX (Ser139) foci in ATM-deleted and ATM WT BBN and UPPL cells. Cells in white boxes were amplified and displayed representatively in Figure 2C and and Supplementary Figure 6C.

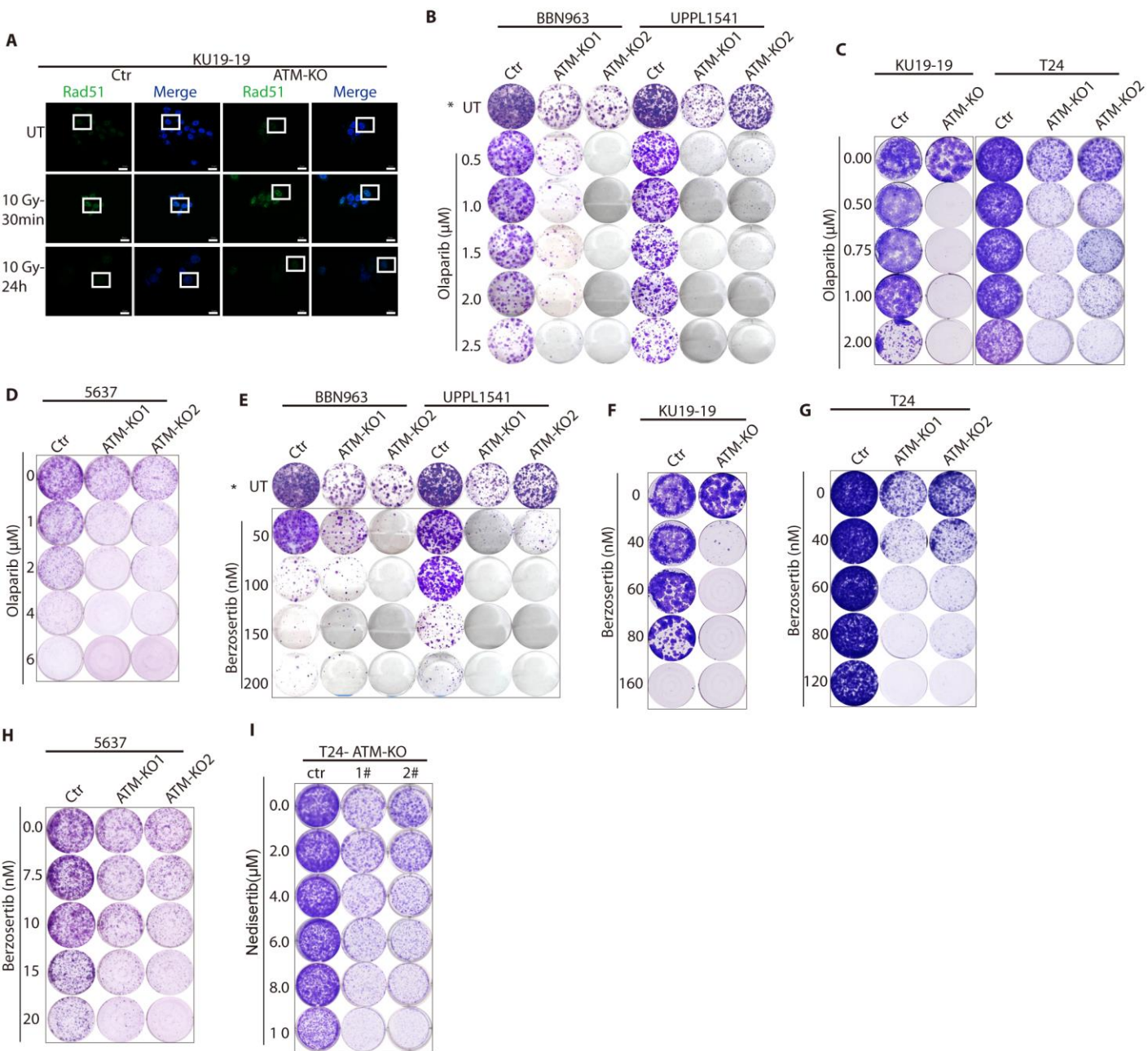
# Supplementary Figure 7



**Supplementary Figure 7: ATM deletion increases sensitivity to DNA damaging agents. A-B.** Representative images of crystal violet stained wells from cell survival assays following ionizing radiation. **C.** Xenograft growth curves for ATM-deleted and WT ATM BBN xenografts. The ATM-deleted and WT ATM models grow at a similar rate in untreated conditions (dark blue and dark green lines, respectively), but only the ATM-deleted xenograft model has growth delay following treatment with 3 Gy x 3 of tumor-directed radiation. Radiation treatments are denoted by red arrows. **D-G.** Representative images of crystal violet stained wells from cell survival assays following cisplatin treatment. For the BBN and UPPL cell lines, the same untreated (“UT”) data was used for cisplatin, olaparib and berzosertib sensitivity assays because these three experiments were run in parallel.



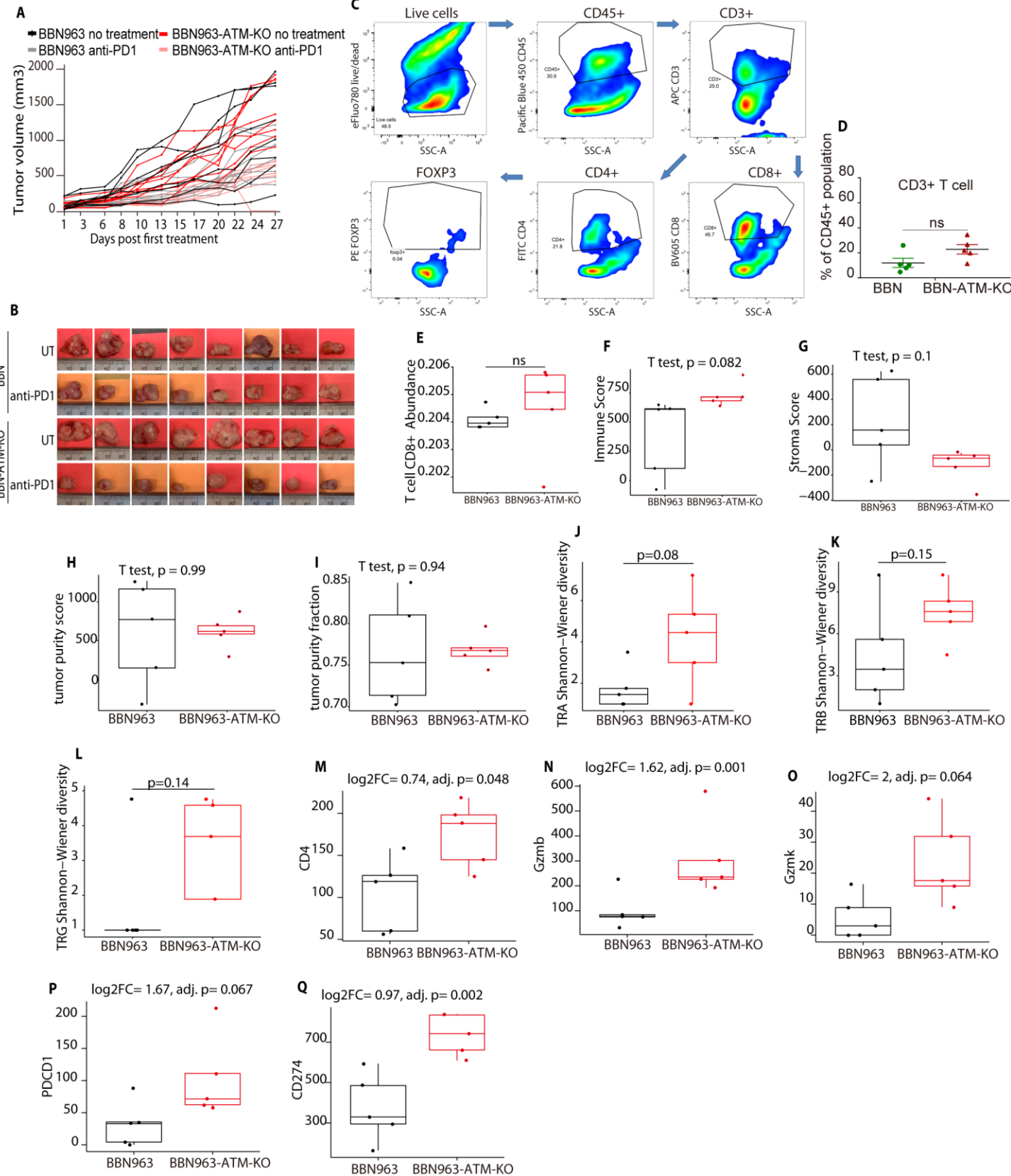
# Supplementary Figure 8



## Supplementary Figure 8: ATM deletion increases sensitivity to DNA repair directed agents.

**A.** Full scale images (20X) of Rad51 immunofluorescence in ATM-deleted and ATM WT KU19-19 cells. Cells in white boxes were amplified and displayed representatively in Figure 3A. **B-C.** Representative images of crystal violet stained wells from cell survival assays following treatment with the PARP inhibitor olaparib. **D-H.** Representative images of crystal violet stained wells from cell survival assays following treatment with the ATR inhibitor berzosertib. **I.** Representative images of crystal violet stained wells from cell survival assays following treatment with the DNA-PK inhibitor nedisertib. For the BBN and UPPL cell lines, the same untreated ("UT") data was used for cisplatin, olaparib and berzosertib sensitivity assays because these three experiments were run in parallel.

# Supplementary Figure 9



**Supplementary Figure 9: Impact of ATM loss on immune properties and anti-PD1 response.** **A.** Individual xenograft growth curves for ATM-deleted and WT ATM BBN tumor-bearing mice treated with versus without anti-PD1 (n=8 mice per group). **B.** Photographs of harvested xenografts from all mice represented in panel A. **C.** Overview of T cell flow cytometry gating strategy. **D.** Flow cytometric analysis showed no significant difference in CD3+ T cell population in ATM-deleted versus WT ATM BBN tumors. **E.** RNA-seq based immune cell fraction estimation using TIMER revealed a trend towards increased CD8+ T cells in ATM-deleted compared to WT ATM xenografts. **F-I.** Immune deconvolution of RNA-seq data using ESTIMATE revealed a trend towards higher immune score in the ATM-deleted xenografts, higher stroma score in the WT ATM xenografts, and no difference in the tumor purity score or fraction. **J-L.** BBN-ATM-KO samples showed increased TRA, TRB and TRG diversity. **M-Q.** RNA-seq normalized counts for selected immune-related genes showed differences in expression levels of CD4, granzyme B (Gzmb), granzyme K (Gzmk), PD-1 (PDCD1), and PD-L1 (CD274) between WT and KO tumors with higher levels in the ATM KO tumors. P-values were adjusted using the Benjamini-Hochberg procedure; log<sub>2</sub>FC, log-transformed fold-change.

**Supplementary Table 1:** Genomic and clinical data for DFBWCC urothelial cohort.

**Supplementary Table 2:** Differential RNA expression data for BBN963 ATM WT and KO cell lines.

**Supplementary Table 3:** ATM IHC data for DFBWCC bladder cancer cohort.

**Supplementary Table 4:** ATM IHC data for MGH bladder cancer cohort.

**Supplementary Table 5:** Reagent details.

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