Supplementary information

Materials and methods

Chemicals

Methyl methanesulfonate (MMS) and oxaliplatin were purchased from Sigma-Aldrich. The Non-radioactive aqueous cell proliferation assay kit was purchased from Promega.

Primers

Following primer sequences were ordered from IDT.

UNG Forward (5'- AGAAGGGCAGTGCCATTGATAGG- 3')

UNG Reverse (5'- TCAATGGGCTTCTTGCCAGACTTCT- 3')

MBD4 Forward (5'-GGACAACAACTGCTCACCAACCAG- 3')

MBD4 Reverse (5'-CCTTCTTTCTATCTGTGTTCGTGGGATGG- 3')

SMUG1 Forward (5'-TGAACCCTGGACCTTTTGGCATG- 3')

SMUG1 Reverse (5'-CACTGGTCGTTTAGGATGCTCTTGGG- 3')

XRCC1 Forward (5'-GCAGGCGAGAAGACCATCTCTGT-3')

XRCC1 Reverse (5'-CTGTGTATCTGCTCCTCCTTCTCCAA- 3')

MTS assay

~8000 cells were plated in 96 well plates. The cells were allowed to attach overnight and treated the following day with varying concentrations of MMS for 24 hr in complete media or

oxaliplatin for 2 hr in serum free media. 20 µL of MTS reagent was added to each well and incubated at 37 ºC. The absorbance was read at 490 nm. The readings from untreated wells were normalized to 100 % survival.

Figure legends

Supplementary Figure 1. RT PCR analysis for percentage of (A) UNG Knockdown (B) SMUG1 knockdown and (C) MBD4 knockdown. The cells were harvested at 96 hr time points after infection. RNA was isolated and reverse transcribed and the cDNA was used for RT-PCR. (D) *In vitro* glycosylase assay, DNA (5nM) was incubated with 4 µg of MEF extract. Lane 1, undamaged DNA alone. Lane 2, undamaged DNA treated with UDG and APE1 to generate a 19 mer product. Lane 3, reaction of the undamaged DNA substrate treated with UDG, APE1 and 1 unit of UGI. Lanes 4, undamaged DNA incubated with MEF extract; Lanes 5 reactions in which MEF extract was preincubated with the indicated concentrations of UGI before adding the undamaged DNA substrate. Lanes 6-10 follow the same set up as lanes 1-5, but with ICL substrate. The substrate contains a 3' Cy3 label. Extract was preincubated with the indicated concentrations of UGI before adding the undamaged DNA substrate. (E) *In vitro* glycosylase assay, DNA (5nM) was incubated with 4 µg of MEF $Ung^{-/-}$ extract. Lane 1, undamaged DNA alone. Lane 2, undamaged DNA treated with UDG and APE1 to generate a 19 mer product. Lane 3, reaction of the undamaged DNA substrate treated with UDG, APE1 and 1 unit of UGI. Lanes 4, undamaged DNA incubated with MEF $Ung^{-/-}$ extract; Lanes 5 reactions in which MEF $Ung^{-/-}$ extract was supplemented with UDG. Lanes 6-10 follow the same set up as lanes 1-5, but with ICL substrate. The substrate contains a 3' Cy3 label.

Supplementary Figure 2. (A) MTS assay with HeLa shControl and shApe1 cells treated with varying concentrations of cisplatin for 2 hr as described in Materials and Methods. (B) Western blot analysis in HeLa shControl (open circles) and shApe1 (closed triangles) cells at 96 hr and 120 hr time points post infection. (C) MTS assay with WT MDA-MB-231 shcontrol (open circles) and shApe1 (closed triangles) cells treated with varying concentrations of oxaliplatin. Results are represented as mean ± SE from 3 independent experiments.

Supplementary Figure 3. MTS assay with pretreatment of myricetin (closed triangles) and methoxyamine (closed circles) followed by treatment with MMS for 24 hr compared with treatment with MMS alone (open circles). Results are represented as mean ± SE from 3 independent experiments.

Supplementary Figure 4. (A) MTS assay with WT MDA-MB-231 (open circles) and K72A MDA-MB-231 (closed circles) treated with varying concentrations of MMS for 24 hr. (B) MTS assay with WT MDA-MB-231 cells treated with cisplatin alone (open circles), WT MDA-MB-231 cells pretreated with myricetin followed by cisplatin (closed triangles), K72A MDA-MB-231 cells treated with cisplatin alone (closed circles), K72A MDA-MB-231 cells pretreated with myricetin followed by cisplatin (open squares).

Supplementary Figure 5. Transcript analysis for XRCC1 in WT MDA-MB-231 cells infected with either shControl or shXRCC1. The cells were harvested at 96 hr time points post infection. The knockdown efficiency was analyzed using RT-PCR.