Supplementary Material

Supplementary table 1 Primer sets for ChIP-qPCR analysis

	Gene	Location (TSS)		Sequence (5’-3’)
ChIP	MGMT	+221247, +221336	Forward	AGTGGCACAGGTGTCAGGGG
			Reverse	GTGCACCTTCGCTCCAGTGT
	MLH1	+42365, +43454	Forward	TCACTGCAACCACCACCTCC
			Reverse	CAGGCGTGGTGGCACATGCT
mRNA				
	BRCA1		Forward	CCTTCTACTGTCCTGGCTACTA
			Reverse	CAGATTTCCAAGGGAGACTTCA
	MGMT		Forward	CTGGCCGAAACTGAGTATGT
			Reverse	GGACACTGCCACTTCCTTTA
	MLH1		Forward	GATGAGGAAGGGAACCTGATTG
			Reverse	CTCAGTGGCTAGTCGAAGAATG
	PARP1		Forward	GCCGAGATCATCAGGAAGTATG
			Reverse	ATTCGCCTTCACGCTCTATC
	XPC		Forward	CTGCCATCCTTGGGTATTGT
			Reverse	CCTCACCACTCTTGCTTTCT
	XRCC1		Forward	CTTCTCAAGGCAGACACTTACC
			Reverse	TGTGTATCTGCTCCTCCTTCT
	GAPDH		Forward	GGTGTGAACCATGAGAAGTATGA
			Reverse	GAGTCCTTCCACGATACCAAAG

TSS: transcriptional starting site.

Supplementary table 2 Association between DDR genes expression and urinary 1-OHP or DNA damage

	1-OHP	OTM	Tail DNA%	H3K4me3	H3K9me3	H3K27me3	H3K36me3
BRCA1	-0.105 (0.117)	-0.073 (0.321)	0.023 (0.751)	-0.025 (0.708)	-0.134 (0.043)	-0.071 (0.283)	-0.034 (0.635)
MGMT	-0.237 (0.001)	-0.186 (0.016)	-0.274 (<0.001)	0.033 (0.641)	-0.013 (0.850)	-0.170 (0.013)	-0.242 (0.001)
MLH1	-0.160 (0.019)	-0.238 (0.001)	-0.256 (0.001)	0.038 (0.585)	-0.167 (0.014)	-0.200 (0.003)	-0.290 (<0.001)
PARP1	0.021 (0.752)	0.002 (0.982)	0.138 (0.058)	0.007 (0.919)	-0.124 (0.059)	0.016 (0.803)	0.039 (0.577)
XPC	-0.069 (0.297)	-0.030 (0.679)	0.039 (0.595)	-0.076 (0.255)	-0.049 (0.456)	-0.058 (0.375)	-0.012 (0.861)
XRCC1	-0.078 (0.250)	-0.075 (0.317)	0.006 (0.938)	0.101 (0.142)	-0.040 (0.552)	-0.013 (0.852)	-0.047 (0.509)

Spearman correlation coefficients (*P* value) analysis was applied. Variables were ln-transformed to improve model fit.