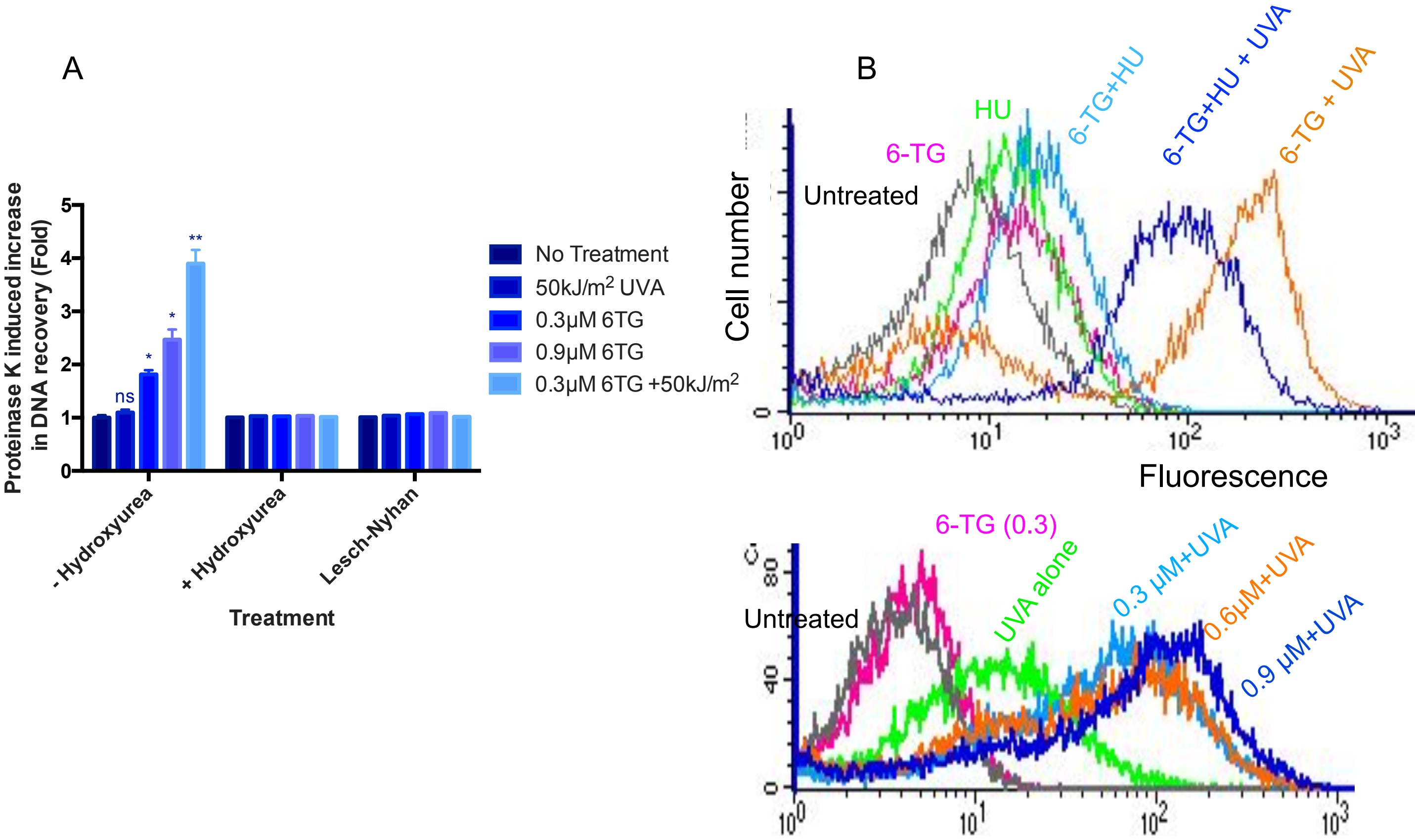
Supplementary Figure S1

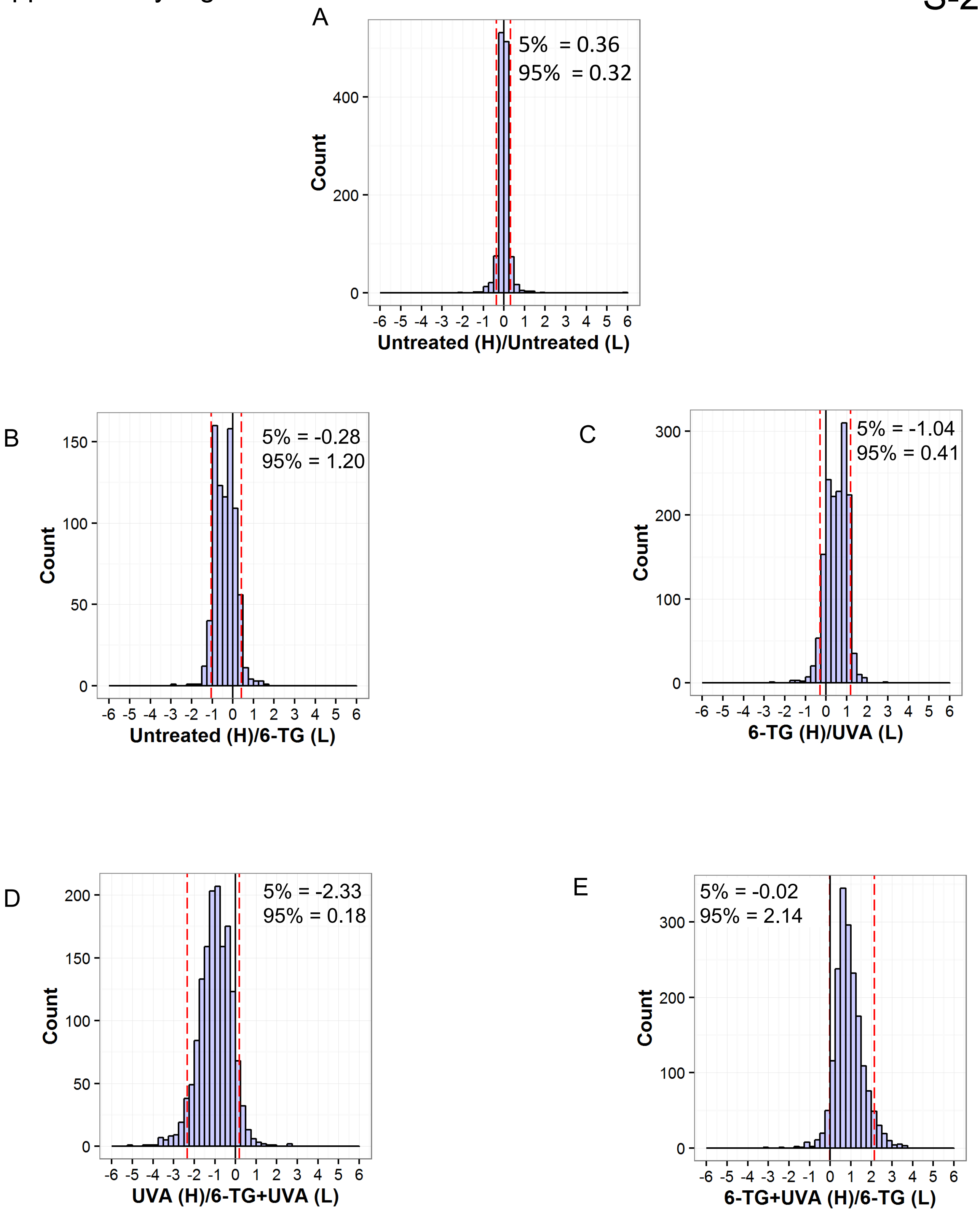


A Protease-dependent DNA recovery. CCRF-CEM or GM03467 Lesch-Nyhan cells treated with 6-TG and UVA as indicated were divided into two aliquots. DNA was extracted by the Wizard genomic purification kit (Promega). In one set of extractions, a proteinase K digestion step was included prior to DNA precipitation.
Effect of hydroxyurea. CCRF-CEM cells that had been treated with 3 mM HU for 6 h were grown for a further 24 h in 6-TG in the continued presence of HU and UVA irradiated as indicated. DNA was extracted by the Wizard genomic purification kit with or without proteinase K digestion prior to DNA precipitation. HPLC measurements confirmed that DNA 6-TG incorporation in HU treated cells was < 0.001% DNA G.

Data are expressed as the fold increase in DNA recovery resulting from proteinase K digestion. Means from three separate experiments.
Paired t-test analysis, p-values,: UVA ns 0.1359;
0.3 μM 6-TG * 0.0196;
0.9 μM 6-TG * 0.0248;
0.3μM 6-TG+UVA ** 0.0076.

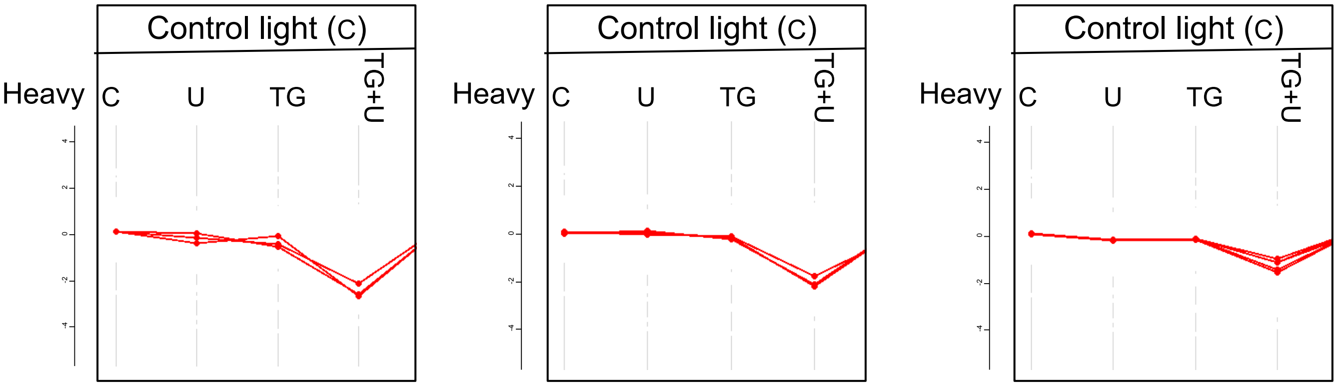
B FACS analysis of ROS. CCRF-CEM cells treated HU (6 mM, 3 h) followed by 6-TG (0, 0.9 μM for 24 h) (Upper panel) in the continued presence of HU as indicated or 0, 0.3, 0.6 or 0.9 μM 6-TG as indicated (Lower panel) were irradiated with UVA (50 kJ/m^2). ROS were determined by CM-H_2DCFDA staining and FACS.

Supplementary Figure S2



Analysis of HyBond N+ bound chromatin proteins from CCRF-CEM cells.
Perseus derived log2 SILAC H:L ratio *versus* frequency count histograms for mixes of heavy (H) and light (L) labelled cells that had received the treatments shown.

Supplementary Figure S3

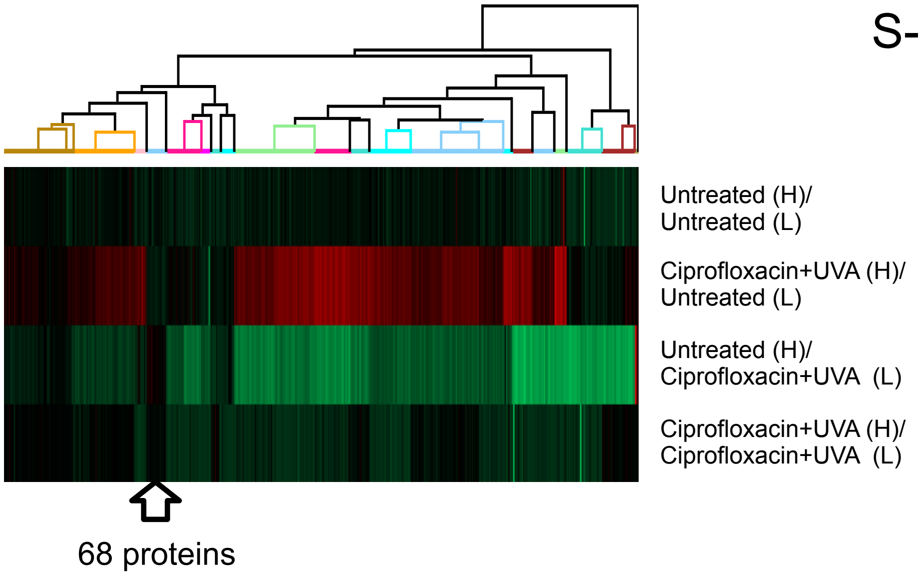


POLD MCM TOP

Loss of DNA polymerase delta subunits from extracts prepared from 6-TG+UVA treated cells.

Crosslinking plot displaying the log2 SILAC H:L ratios for POLD1-3, MCM2-7 and the topoisomerases for the comparisons indicated. The shape of the profile (red) indicates treatment-induced protein losses.

Supplementary Figure S4



Treatment	Protein names	Gene names
6-Thioguanine+UVA	Histone H2A.x	H2AFX
	Core histone macro-H2A.1;Histone H2A	H2AFY
	Histone H2A.Z;Histone H2A.V;Histone H2A	H2AFZ;H2AFV
	Histone H2A type 1-B/E;Histone H2A;Histone H2A type 3	HIST1H2AB;HIST3H2A
	Histone H2A type 1-D;Histone H2A	HIST1H2AD
	Histone H2A; Histone H2A type 1; Histone H2A type 1-H; Histone H2A type 2-A; Histone H2A type 1-J; Histone H2A.J; Histone H2A type 2-C	HIST1H2AK; HIST1H2AG; HIST1H2AH; HIST2H2AA3; HIST1H2AJ; H2AFJ; HIST2H2AC
	Histone H2B type 1-D;Histone H2B	HIST1H2BD
	Histone H2B;Histone H2B type 1-C/E/F/G/I	HIST1H2BF;HIST1H2BC
	Histone H2B type 1-K	HIST1H2BK
	Histone H2B type 1-L	HIST1H2BL
	Histone H2B type 1-M	HIST1H2BM
	Histone H2B type 1-N	HIST1H2BN
	Histone H2B type 1-O	HIST1H2BO
	Histone H2A type 2-B	HIST2H2AB
	Histone H2B type 2-F;Histone H2B type 1-H;Histone H2B	HIST2H2BF;HIST1H2BH
Ciprofloxacin+UVA	Histone H2A.x	H2AFX
	Core histone macro-H2A.1;Histone H2A	H2AFY
	Histone H2A.Z;Histone H2A.V;Histone H2A	H2AFZ;H2AFV
	Histone deacetylase 3	HDAC3
	Histone H2A type 1-C	HIST1H2AC
	Histone H2B type 1-B	HIST1H2BB
	Histone H2B type 1-D;Histone H2B	HIST1H2BD
	Histone H2B type 1-K	HIST1H2BK
	Histone H2B type 1-L	HIST1H2BL
	Histone H2B type 1-M	HIST1H2BM
	Histone H2B type 1-N	HIST1H2BN
	Histone H3.1;Histone H3;Histone H3.1t;Histone H3.3C	HIST1H3A;HIST3H3;H3F3C;H3F3A
	Histone H4	HIST1H4L;HIST1H4A;HIST1H4H
	Histone H2A type 2-A;Histone H2A type 2-C	HIST2H2AA3;HIST2H2AC
	Histone H2A type 2-B	HIST2H2AB
	Histone H2B type 2-F;Histone H2B type 1-H;Histone H2B	HIST2H2BF;HIST1H2BH
	Histone H3.2	HIST2H3A
	Histone H3	HIST2H3PS2

Heat map of ciprofloxacin+UVA crosslinking. The arrow indicates possible false positives. These were confirmed by crosslink profile analysis (not shown). The table indicates that histones are highly represented among these false positives that show significant overlap with those generated during 6-TG+UVA analysis.

Supplementary Table S1

Protein	6-Thioguanine+UVA	Ciprofloxacin+UVA
APEX1 (APE1)	+	+
BLM	+	+
DDB1	+	+
DUT	+	+
FEN1 (DNase IV)	+	+
LIG1	+	+
LIG3	+	+
MRE11A	+	+
MSH2	+	+
MSH6	+	+
PARP1 (ADPRT)	+	+
PCNA	+	+
POLD1	+	+
POLD3	+	+
POLE3	+	+
PRPF19 (PSO4)	+	+
RAD50	+	+
RECQL (RECQ1)	+	+
RPA1	+	+
XRCC1	+	+
XRCC5 (Ku80)	+	+
XRCC6 (Ku70)	+	+
MGMT	+	-
MMS19	+	-
MPG	+	-
NBN (NBS1)	+	-
NUDT MTH1	+	-
POLE1	+	-
PRKDC	+	-
UBE2N (UBC13)	+	-
CHAF1A (CAF1)	-	+
FANCD2	-	+
FANCI	-	+
MSH3	-	+
TP53	-	+
TP53BP1 (53BP1)	-	+
WRN	-	+

DNA repair proteins most vulnerable to crosslinking by 6-TG+UVA and ciprofloxacin+UVA.