Figure S1. Characterization of GBM cell lines and PARP-1 inhibition by NU1025. (A) Representative protein expression of PTEN, AKT, $pAKT^{(476)}$ and MGMT in GBM cell lines (T98G, LN18 and U87MG). HeLa cells were used as a positive control for PTEN expression; β-actin was used as an endogenous control. The samples were analyzed by western blot analysis. (B) Effects of NU1025 agent in the reduction of poly-ADP-ribosylation promoted by PARP-1. Cells were treated with NU1025 (NU-100 and NU-200 μM) at 20 min prior to H_2O_2 treatment (20 mM for 10 min), and then analyzed by flow cytometry using PAR-antibody. $^*P<0.05$. Bars correspond to comparisons between treatments. GBM, glioblastoma; PARP-1, poly[ADP-ribose] polymerase 1; PTEN, phosphatase and tensin homologue deleted on chromosome ten; MGMT, O^6-methylguanine DNA methyltransferase.

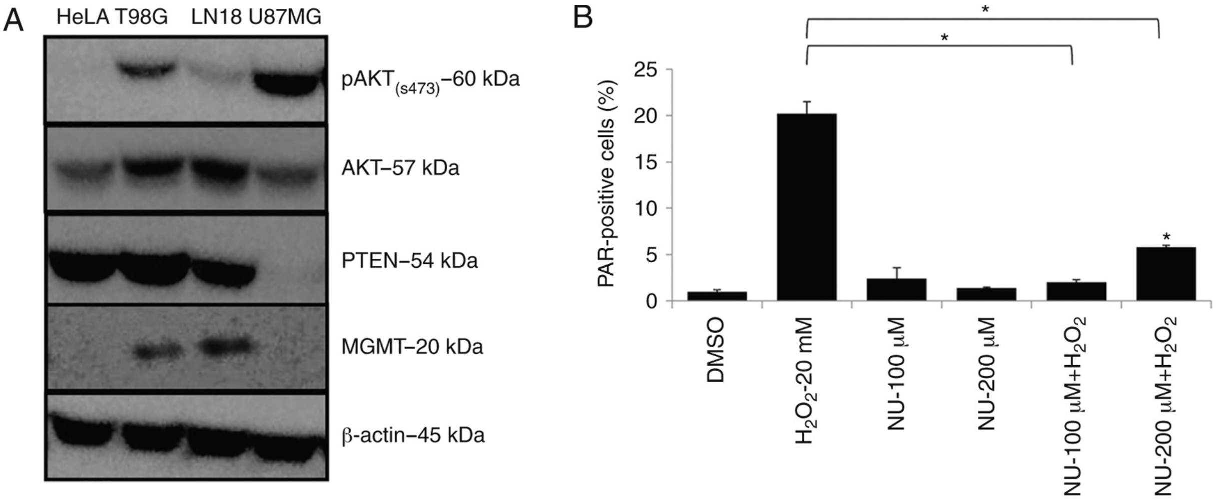

Table SI. List of genes used in expression analysis[a].

Custom genes TaqMan Array 96 - Well FAST	
Genes	Identification
TBP	Hs00427620_m1
HPRT1	Hs99999909_m1
MGMT	Hs01037698_m1
BRCA1	Hs01556193_m1
BRCA2	Hs01037414_m1
LIG4	Hs00172455_m1
RAD51B	Hs00172522_m1
RAD51C	Hs00427442_m1
RAD51D	Hs00979544_m1
RAD51	Hs00153418_m1
FEN1	Hs00748727_s1
APEX1	Hs00172396_m1
LIG1	Hs01553527_m1
PARP1	Hs00242302_m1
XRCC1	Hs00959834_m1
MSH2	Hs00953523_m1
MSH3	Hs00989003_m1
XPA	Hs00166045_m1
XPC	Hs01104206_m1
XRCC4	Hs00243327_m1
PRKDC	Hs00179161_m1
XRCC6	Hs01922652_g1
XRCC5	Hs00221707_m1

[a] as evaluated by means of custom TaqMan Array 96 - Well FAST plates (Thermo Fischer Scientific, Inc.).

Table SII. Fold change values (log2) evaluated by PCR array (Thermo Fisher Scientific, Inc.) for a set of DNA repair pathway genes in T98G cells submitted to continuous treatments of TMZ (200 μM) and NU1025 (200 μM), tested alone or in combination.

T98G cells-Transcript expression values (fold change log2)							
		Time of treatments (6 h)			Time of treatments (24 h)		
Genes	DNA repair pathway	NU1025 (200 μM)	TMZ (200 μM)	NU1025 +TMZ	NU1025 (200 μM)	TMZ (200 μM)	NU1025 +TMZ
PARP1	BER	0.17	0.10	0.38	0.31	**1.30**	-0.06
APEX1		0.05	0.20	0.50	-0.36	0.34	-0.18
FEN1		-0.61	-0.83	-0.92	0.05	**1.43**	-0.53
LIG1		0.39	0.20	1.28	-0.11	**1.90**	**1.47**
XRCC1		0.37	0.16	0.17	-0.52	0.86	-0.46
BRCA1	HR	-0.06	1.52	0.31	1.18	**1.32**	0.31
RAD51		0.97	0.20	0.65	0.60	1.16	0.02
RAD51B		0.49	-0.20	-0.21	-0.28	**1.63**	0.88
RAD51C		0.21	-0.02	-0.76	0.73	**1.68**	0.89
RAD51D		0.52	0.27	0.57	-0.51	0.49	-0.06
LIG4		**-1.98**	**-2.13**	**-1.42**	0.07	0.93	-0.69
PRKDC	NHEJ	0.61	0.03	0.30	-0.32	**1.37**	0.37
XRCC5		0.35	-0.44	0.46	0.56	0.43	-0.14
XRCC6		0.31	-0.11	0.53	-0.27	0.02	-0.45
XPA	NER	0.45	0.20	0.0	0.10	0.51	-0.40
XPC		**-1.94**	**-1.60**	-1.28	-0.58	-0.01	-1.01
XRCC4		0.27	0.20	0.40	0.13	**1.31**	0.47
MGMT	MGMT	-0.61	**-1.38**	-1.01	-0.13	1.03	0.81
MSH2	MMR	0.34	0.36	0.38	0.03	1.05	0.26
MSH3		-0.04	-0.24	-0.09	0.13	0.51	-0.28

The expression was evaluated 6 and 24 h after the start of the treatments using QuantStudio 3 Real-Time PCR Systems and software (Thermo Fisher Scientific, Inc.). *TBP* and *HPRT1* were used as reference genes. The experiments were performed with a pool of cDNA corresponding to the proportional junction of three independent experiments applied in simplicates. Fold change values >|1.3| are represented in bold. BER, base excision repair; HR, homologous recombination; NHEJ, non-homologous end joining; NER, nucleotide excision repair; MGMT, O^6-methylguanine DNA methyltransferase; MMR, mismatch repair.

Table SIII. Fold change values (log2) evaluated by PCR array (Thermo Fisher Scientific, Inc.) for a set of DNA repair pathway genes in LN18 cells submitted to continuous treatments of TMZ (200 μM) and NU1025 (200 μM), tested alone or in combination.

LN18 cells-Transcript expression values (fold change log2)							
		Time of treatments (6 h)			Time of treatments (24 h)		
Genes	DNA repair pathway	NU1025 (200 μM)	TMZ (200 μM)	NU1025 +TMZ	NU1025 (200 μM)	TMZ (200 μM)	NU1025 +TMZ
PARP1	BER	-0.16	-0.05	-0.06	-0.16	0.21	0.07
APEX1		0.11	0.33	0.05	0.13	0.79	0.64
FEN1		0.16	0.39	0.17	0.09	0.23	0.14
LIG1		-0.16	0.07	-0.08	-1.24	-0.49	-1.03
XRCC1		0.14	0.33	-0.10	-0.33	-0.11	0.22
BRCA1	HR	-0.31	-0.12	-0.33	**2.18**	0.78	0.52
RAD51		-0.51	0.01	-0.16	0.35	0.97	0.44
RAD51B		-0.18	-0.42	-0.40	0.11	0.10	-0.02
RAD51C		-0.41	0.12	-0.01	0.56	0.67	0.27
RAD51D		0.05	0.09	0.10	0.45	0.50	0.49
LIG4		-0.35	-0.42	-0.10	-0.94	0.06	-0.56
PRKDC	NHEJ	-0.32	-0.27	-0.03	0.25	-0.11	0.25
XRCC5		-0.11	0.05	-0.01	0.01	0.36	0.32
XRCC6		-0.02	0.09	0.18	**-1.81**	**-2.18**	**-2.18**
XPA	NER	-0.09	0.00	0.18	-0.39	0.15	-0.24
XPC		0.23	0.47	0.18	0.11	0.14	0.32
XRCC4		0.01	0.10	-0.04	-0.49	0.63	0.17
MGMT	MGMT	0.40	0.41	0.00	0.98	1.10	0.83
MSH2	MMR	-0.18	0.09	0.09	-0.05	0.61	0.31
MSH3		-0.30	-0.25	-0.20	0.97	0.54	0.71

The expression was evaluated six and 24 h after the start of the treatments using QuantStudio 3 Real-Time PCR Systems and software (Thermo Fisher Scientific). *TBP* and *HPRT1* were used as reference genes. The experiments were performed with a pool of cDNA corresponding to the proportional junction of three independent experiments applied in simplicates. Fold change values >|1.3| are represented in bold. BER, base excision repair; HR, homologous recombination; NHEJ, non-homologous end joining; NER, nucleotide excision repair; MGMT, O^6-methylguanine DNA methyltransferase; MMR, mismatch repair.