

Table S2: Complete gene list from the DNA damage signaling PCR array. The 16 significantly affected genes are listed in the top of the table. The associated DNA repair pathway is indicated for each gene and the fold change and p values in doxorubicin- and mixture-treated cells are detailed.

Cell cycle	Apoptosis	DNA repair	Symbol	Description	Doxorubicin		Mixture	
					Fold Change	p-value	Fold Change	p-value
		Mgmt	Mgmt	O-6-methylguanine-DNA methyltransferase	5,04	0,009	4,32	0,012
		Other	Polh	Polymerase (DNA directed), eta	2,67	0,005	2,32	0,050
		Multiple	Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	2,14	0,003	1,70	0,011
		Other	Rev1	REV1 homolog (S. cerevisiae)	2,05	0,000	1,91	0,001
		BER	Ung	Uracil-DNA glycosylase	0,54	0,000	0,47	0,000
		Other	Gadd45g	Growth arrest and DNA-damage-inducible, gamma	1,48	0,003	1,64	0,002
		Other	Gadd45a	Growth arrest and DNA-damage-inducible, alpha	1,76	0,017	1,61	0,049
		Multiple	Bard1	BRCA1 associated RING domain 1	1,57	0,005	1,40	0,233
			Bbc3	Bcl-2 binding component 3	7,00	0,000	9,13	0,006
			Bax	Bcl2-associated X protein	2,64	0,000	2,52	0,001
			Cdkn1a	Cyclin-dependent kinase inhibitor 1A	11,17	0,000	11,85	0,000
			Ppp1r15a	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	1,63	0,015	2,29	0,011
			Terf1	Telomeric repeat binding factor (NIMA-interacting) 1	1,50	0,001	1,23	0,008
			Ppm1d	Protein phosphatase 1D magnesium-dependent, delta isoform	2,24	0,000	2,18	0,003
			Ddit3	DNA-damage inducible transcript 3	1,90	0,006	1,93	0,030
			Cdc25c	Cell division cycle 25 homolog C (S. pombe)	1,53	0,001	1,50	0,056
		BER	Mbd4	Methyl-CpG binding domain protein 4	1,47	0,124	1,44	0,174
		BER	Wrn	Werner syndrome	1,25	0,097	1,28	0,017
		BER	Fen1	Flap structure-specific endonuclease 1	1,25	0,176	1,25	0,292
		BER	Mpg	N-methylpurine-DNA glycosylase	1,02	0,737	0,84	0,130
		BER	Apex1	APEX nuclease (multifunctional DNA repair enzyme) 1	0,99	0,940	0,67	0,295
		NER	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	1,24	0,124	1,20	0,229
		NER	Pold3	Polymerase (DNA-directed), delta 3, accessory subunit	1,20	0,131	1,05	0,619
		NER	Ercc1	Excision repair cross-complementing rodent repair deficiency, complementation group 1	1,14	0,433	1,36	0,216
		NER	Xpc	Xeroderma pigmentosum, complementation group C	1,13	0,286	1,07	0,531
		NER	Fancc	Fanconi anemia, complementation group C	1,12	0,251	1,26	0,061
		NER	Ddb2	Damage specific DNA binding protein 2	1,04	0,689	0,88	0,380
		NER	Ercc2	Excision repair cross-complementing rodent repair deficiency, complementation group 2	1,01	0,843	0,98	0,933
		DSB	Rad52	RAD52 homolog (S. cerevisiae)	1,42	0,001	1,49	0,002
		DSB	Rad51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	1,27	0,000	1,40	0,007
		DSB	Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	1,25	0,024	1,25	0,034
		DSB	Blm	Bloom syndrome, RecQ helicase-like	1,23	0,002	1,19	0,007
		DSB	Nbn	Nibrin	1,15	0,212	1,00	0,988
		DSB	Mre11a	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	1,14	0,114	1,10	0,130
		DSB	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	1,09	0,433	0,81	0,413
		MMR	Mlh1	MutL homolog 1 (E. coli)	1,17	0,271	0,93	0,973

	MMR	Msh2	MutS homolog 2 (E. coli)	1,12	0,382	0,88	0,797
	MMR	Exo1	Exonuclease 1	1,11	0,454	1,02	0,759
	MMR	Pms2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	1,10	0,390	0,95	0,945
	MMR	Msh3	MutS homolog 3 (E. coli)	1,07	0,545	0,85	0,645
	MMR	Pms1	Postmeiotic segregation increased 1 (S. cerevisiae)	1,04	0,547	0,95	0,808
	MMR	Abl1	C-abl oncogene 1, receptor tyrosine kinase	1,03	0,718	0,84	0,667
	MMR	Mlh3	MutL homolog 3 (E. coli)	0,89	0,098	0,87	0,212
	Other	Fancg	Fanconi anemia, complementation group G	1,33	0,003	1,21	0,036
	Other	Poli	Polymerase (DNA directed), iota	1,19	0,076	1,03	0,720
	Other	Rad18	RAD18 homolog (S. cerevisiae)	1,18	0,002	1,26	0,000
	Other	Fanca	Fanconi anemia, complementation group A	1,12	0,063	0,99	0,954
	Other	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	1,12	0,026	1,08	0,011
	Other	Rad51b	RAD51 paralog B	1,10	0,088	1,08	0,015
	Other	Wrnip1	Werner helicase interacting protein 1	1,07	0,274	1,01	0,851
	Other	Rad51c	Rad51 homolog c (S. cerevisiae)	1,05	0,249	0,92	0,114
	Other	Smc3	Structural maintenance of chromosomes 3	1,03	0,410	1,00	0,960
	Other	Rad1	RAD1 homolog (S. pombe)	0,99	0,792	0,99	0,949
	Other	Pttg1	Pituitary tumor-transforming 1	0,97	0,780	0,85	0,051
	Other	Atrx	Alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0,85	0,261	0,91	0,553
	Multiple	Rad50	RAD50 homolog (S. cerevisiae)	1,45	0,000	1,38	0,003
	Multiple	Nth1	Nth (endonuclease III)-like 1 (E.coli)	1,43	0,006	1,27	0,054
	Multiple	Brca2	Breast cancer 2	1,31	0,123	1,29	0,249
	Multiple	Rpa1	Replication protein A1	1,25	0,001	1,08	0,149
	Multiple	Topbp1	Topoisomerase (DNA) II binding protein 1	1,22	0,028	1,18	0,103
	Multiple	Fancd2	Fanconi anemia, complementation group D2	1,18	0,001	1,14	0,060
	Multiple	Rnf8	Ring finger protein 8	1,17	0,255	1,05	0,643
	Multiple	Smc1a	Structural maintenance of chromosomes 1A	1,17	0,119	1,17	0,130
	Multiple	Rad17	RAD17 homolog (S. pombe)	1,16	0,265	1,13	0,454
	Multiple	Pole	Polymerase (DNA directed), epsilon	1,13	0,107	1,13	0,075
	Multiple	Lig1	Ligase I, DNA, ATP-dependent	1,11	0,269	1,06	0,570
	Multiple	Ogg1	8-oxoguanine DNA glycosylase	1,11	0,128	0,96	0,826
	Multiple	Pcna	Proliferating cell nuclear antigen	1,02	0,788	1,02	0,824
	Multiple	Hus1	HUS1 checkpoint homolog (S. pombe)	1,00	0,980	1,00	0,960
	Multiple	Parp1	Poly (ADP-ribose) polymerase 1	0,99	0,868	0,85	0,035
	Multiple	Parp2	Poly (ADP-ribose) polymerase 2	0,94	0,247	0,87	0,024
	ATM	Csk2a2	Casein kinase 2, alpha prime polypeptide	1,03	0,653	0,92	0,716
	DSB	Tp53bp1	Tumor protein p53 binding protein 1	1,05	0,581	0,91	0,550
	DSB	Prkdc	Protein kinase, DNA activated, catalytic polypeptide	0,97	0,722	1,02	0,799
	NER	Sirt1	Sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	1,24	0,127	1,12	0,417
	Other	Rad21	RAD21 homolog (S. pombe)	0,97	0,689	0,88	0,185
	Multiple	Brca1	Breast cancer 1	1,21	0,132	1,24	0,303
	Multiple	Rad9	RAD9 homolog (S. pombe)	1,07	0,566	1,08	0,560
	Multiple	Tp53	Tumor protein p53	1,26	0,007	1,46	0,000
	Multiple	Chek2	CHK2 checkpoint homolog (S. pombe)	1,07	0,437	0,93	0,614
	Multiple	Atm	Ataxia telangiectasia mutated homolog (human)	1,02	0,770	0,76	0,714

	Multiple	Chk1	CHK1 checkpoint homolog (S. pombe)	1,02	0,760	0,93	0,482
	ATM	Cdc25a	Cell division cycle 25 homolog A (S. pombe)	1,24	0,007	1,23	0,116
		Mif	Macrophage migration inhibitory factor	0,92	0,178	1,00	0,982