Supporting information for Liu *et al.* (2003) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.0630387100

Table 4. Irradiation-response patterns of genes involved in replication, repair, and recombination functions in DEIRA

Gene name*	Gene ID	Protein description and comments	Pathway[†]	Relative basal level[‡]	Response to radiation, folds[§]	Time of response, h	STD	CV, %
Ogt/Ybaz	DR0248	O-6-methylguanine DNA methyltransferase	DR	0.71	0.50	3	0.32	63.99
MutT	DR0261	8-oxo-dGTPase	DR	0.33	3.85	12	1.68	43.58
AlkA	DR2074 DR2584	3-methyladenine DNA glycosylase II	DR, BER	0.48 0.51	0.70 0.93	0.5-9 0.5-9		
MutY	DR2285	8-oxoguanine DNA glycosylase and AP-lyase, A-G mismatch DNA glycosylase	BER, MMY	0.19	2.36	3	0.40	16.83
Nth-2 Nth-1	DR2438 DR0289 DR0928	Endonuclease III and thymine glycol DNA glycosylase	BER	1.11 0.49 0.47	0.36 1.09 0.89	3 0.5-9 0.5-9	0.12	32.19
YhhF	DR0643	N6-adenine-specific methylase	BER	0.70	0.39	3	0.05	11.70
MutM/Fpg	DR0493	Formamidopyrimidine and 8-oxoguanine DNA glycosylase	BER	0.68	0.46	1.5	0.09	18.71
Nfi (Yjaf)	DR2162	Endonuclease V	BER	0.31	1.36	0.5-9		
PolA	DR1707	DNA polymerase I	BER	5.81	0.86	0.5-9		
Ung	DR0689 DR1663	Uracil DNA glycosylase	BER	0.68 2.71	2.03 2.52	12 24	1.41 0.76	69.35 30.20

Gene name*	Gene ID	Protein description and comments	Pathway†	Relative basal level‡	Response to radiation, folds§	Time of response, h	STD	CV, %
Mug	DR0715	G/T mismatch-specific thymine DNA glycosylase	BER	0.85	0.17	3	0.01	7.80
	DR1751	Uracil DNA glycosylase	BER	0.86	0.64	0.5-9		
	DR0022			0.47	3.33	1.5	0.87	26.18
XthA	DR0354	Exodeoxyribonuclease III	BER	0.64	0.95	0.5-9		
RadA	DR1105	Predicted ATP-dependent protease	NER, BER	0.40	1.08	0.5-9		
Mfd	DR1532	Transcription-repair coupling factor; helicase	NER	1.25	0.69	0.5-9		
UvrA-1	DR1771	ATPase, excinuclease subunit	NER	1.44	3.52	1.5	1.15	32.56
UvrA-2	DRA0188			0.13	2.03	5	0.90	44.42
UvrB	DR2275	Helicase, excinuclease subunit	NER	0.80	4.93	3	1.81	36.76
UvrC	DR1354	Nuclease, excinuclease subunit	NER	1.02	3.78	3	0.42	11.04
UvrD	DR1775	Helicase II, excinuclease subunit; initiates unwinding from a nick	NER, mMM, SOS	1.19	3.30	1.5	1.69	51.25
MutL	DR1669	ATPase	mMM, VSP	0.42	0.99	0.5-9		
MutS	DR1976	ATPase	mMM, VSP	0.35	1.31	0.5-9		
XseA/ Nec7	DR0186	Exonuclease VII, large subunit	MM	1.07	2.19	1.5	0.83	37.89
SbcC	DR1922	ATPase, SbcCD exonuclease subunit	RER	1.36	1.39	0.5-9		
SbcD	DR1921	Exonuclease, SbcCD subunit	RER	0.55	1.82	3	0.27	15.06

Gene name*	Gene ID	Protein description and comments	Pathway†	Relative basal level‡	Response to radiation, folds§	Time of response, h	STD	CV, %
RecA	DR2340	Recombinase; ssDNA-dependent ATPase; activator of LexA autoproteolysis	RER, SOS	1.46	7.98	1.5	3.86	48.40
RecD	DR1902	DNA-dependent ATPase or helicase; in other bacteria, regulatory subunit of the RecBCD recombinase (helicase-nuclease); RecB and RecC are missing in DEIRA.	RER	1.16	0.80	0.5-9		
RecF	DR1089	ATPase; required for daughter-strand gap repair	RER	0.10	0.59	1.5	0.32	54.76
RecG	DR1916	Holliday junction-specific DNA helicase; branch migration inducer	RER	1.03	2.66	0.5	0.87	32.62
RecJ	DR1126	Nuclease	RER	1.94	0.33	12	0.12	37.43
RecN	DR1477	ATPase	RER	1.28	0.93	0.5-9		
RecO	DR0819	Biochemical activity unknown; required for daughter-strand gap repair	RER	1.34	1.10	0.5-9		
RecQ	DR2444 DR1289	Helicase; suppressor of illegitimate recombination	RER	1.85 0.34	2.43 1.19	0.5 0.5-9	0.27	11.18
RecR	DR0198	Inactivated Toprim-domain protein; required for daughter-strand gap	RER	1.71	0.90	0.5-9		

Gene name*	Gene ID	Protein description and comments	Pathway[†]	Relative basal level[‡]	Response to radiation, folds[§]	Time of response, h	STD	CV, %
		repair						
RuvA	DR1274	Holliday-junction-binding subunit of the RuvABC resolvasome	RER	0.89	0.95	0.5-9		
RuvB	DR0596	Helicase subunit of the RuvABC resolvasome	RER	2.58	3.22	0.5	1.31	40.82
RuvB	DR0440	Endonuclease subunit of the RuvABC resolvasome	RER	3.99	0.20	24	0.09	45.47
DnaC	DR0507	Polymerase subunit of the DNA polymerase III holoenzyme	MP	0.81	0.43	12	0.15	35.32
DnaQ	DR0856	3'-5' exonuclease subunit of the DNA polymerase III holoenzyme	MP	0.31	1.97	0.5	1.04	52.62
DnlJ	DR2069	NAD-dependnet DNA ligase	MP	1.58	0.17	3	0.05	28.26
Ssb	DR0099	Single-strand binding protein; D. radiodurans R1 has three incomplete ORFs corresponding to different fragments of Ssb; it remains unclear whether D. radiodurans has a functional Ssb.	MP	3.92	3.01	0.5	1.20	39.80
LexA	DRA0344 DRA0074	Transcriptional regulator, repressor of the SOS regulon, autoprotease	SOS	0.51 4.74	1.80 0.80	1.5 0.5-9	1.08	59.92
YcjD	DR0221	Predicted very short patch	VSP?	0.37	1.94	3	0.81	41.73

Gene name*	Gene ID	Protein description and comments	Pathway†	Relative basal level‡	Response to radiation, folds§	Time of response, h	STD	CV, %
	DR2566	repair nuclease		0.42	4.10	3	1.09	26.48
HAM1/YggV	DR0179	Xantosine triphosphate pyrophosphatase, prevents 6-N-hydroxylaminopurin mutagenesis	DR	0.35	1.00	0.5-9		
Uve1/BS_Ywjd	DR1819	UV-endonuclease	NER	0.29	1.06	0.5-9		
Yejh/Rad25	DRA0131	Helicase of superfamily II, predicted nuclease; DRA0131 has an additional McrA nuclease domain	NER	0.07	0.51	3	0.32	62.57
	DR0690	Topoisomerase IB, probably of eukaryotic origin	?	0.41	1.10	0.5-9		
	DR1721	3'->5' nuclease	?	0.54	1.36	0.5-9		
Rsr	DR1262	RNA-binding protein Ro; ribonucleoproteins complexed with several small RNA molecules. Involved in UV-resistance in Deinococcus	?	0.68	1.04	0.5-9		
Mrr Mrr-1 Mrr-2	DR1877 DR0508 DR0587	Nuclease	?	0.44 0.59 0.78	0.79 0.78 0.95	0.5-9 0.5-9 0.5-9		
XerC	DRA0155		RER	0.26	0.95	0.5-9		

Gene name*	Gene ID	Protein description and comments	Pathway†	Relative basal level‡	Response to radiation, folds§	Time of response, h	STD	CV, %
XerD	DRB0104	Integrase/recombinase		0.94	0.53	3	0.11	20.56
XerC/D	DRC0018			0.10	2.72	12	0.77	28.19
GyrA	DR1913	DNA gyrase, subunitA	general	4.12	3.29	0.5	1.56	47.51
GyrB	DR0906	DNA gyrase, subunitB	general	2.75	4.41	0.5	2.98	67.46
DnaE	DR0601	DNA primase	general	1.36	0.59	3	0.04	7.40
TopA	DR1374	DNA topoisomerase	general	2.58	0.45	9	0.10	23.03
DnaN	DR0001	DNA polymerase III, beta subunit	general	2.28	2.71	0.5	0.45	16.69
	DR2332	DNA polymerase III gamma and tau subunit, inactivated AAA superfamily ATPase	general	0.05	2.73	12	1.74	63.70
	DR2410	DNA polymerase III, gamma and tau subunit, AAA superfamily ATPase	general	4.15	0.29	9	0.14	47.65

Red, up-regulated; blue, down-regulated; pink, no changes.

*The gene names are from *E. coli*, whenever an *E. coli* ortholog exists, or from *B. subtilis* (with the prefix BS_).

†Abbreviations of DNA repair pathways: DR, direct damage reversal; BER, base excision repair; NER, nucleotide excision repair; mMM, methylation-dependent mismatch repair; MMY, MutY, dependent mismatch repair; VSP, very short patch mismatch repair; RER, recombinational repair; SOS, SOS repair; MP, multiple pathways. Potential new repair pathways are indicated by a question mark; general, genes that are also involved in replication; ?, unknown.

‡The ratio of the fluorescent intensity of a particular gene to the average intensity of all arrayed genes when nonirradiated sample is used as a labeled probe.

§The maximum, minimum, or average ratio of the irradiated sample(s) harvested at the "Time of response" to the nonirradiated control. There is no SD and coefficient of variation (CV) for an average ratio of several time points.