Supporting Text

Materials and Methods

***Deinococcus radiodurans* R1 (DEIRA) mutant generation and characterization.** Genes shown in Tables 3 and 4 are good candidates for disruption based on their response to acute irradiation. Disruption vectors were formed by cloning PCR-generated internal segments (400-900 bp) of candidate ORFs into position 295 of the *Escherichia coli* plasmid pCR2.1 (Invitrogen, CA) according to the manufacturer's protocol. Purified disruption vectors were then transformed into DEIRA with kanamycin (Km) selection (8 μg/ml) yielding kanamycin resistant (Km^R) transformants (1). The possibility of heterozygosity (ESP DEIRA contains 4 haploid genomic copies per cell (2)), where some of DEIRA's haploid chromosomes contain a disruption while others do not, can be overcome by several rounds of selection on nutrient agar (TGY) containing Km (25 μg/ml) if the gene is non-essential; permanent heterozygosity indicates a gene is essential. For construction of the DR0070 DEIRA mutant, a 575 bp PCR-generated internal segment of ORF DR0070 (600 bp) was first cloned into pCR2.1, yielding pMD890. Purified pMD890 was then transformed into DEIRA with Km selection, giving rise to Km^R transformants (yielding DEIRA mutant MD891). Homozygosity of a disruption was confirmed by detailed mapping of a transformant's integration site. Total DNA from representative transformants was subjected to restriction endonuclease analysis, electrophoresis, and Southern blotting with diagnostic ^{32}P-radiolabeled probes as shown in Fig. 7. Stationary phase cultures (OD_{600} ~1.2) of confirmed mutants were irradiated (^{60}Co Gammacell irradiation unit [J. L. Shepard and Associates, Model 109]) to increasing doses extending to 20 kGy and compared to the survival of DEIRA strain MD68 (Daly et al. 1994b) (MD68 is the product of wild-type DEIRA transformed with the autonomously replicating Km^R-encoding plasmid pMD66). Following irradiation, cell viability was determined by appropriate dilution and selective plating for CFU on agar plates containing Km (25 μg/ml), as described previously (1, 3, 4). To investigate the effect of chronic irradiation, cells grown on rich medium (TGY with or without antibiotic selection) were exposed to continuous γ-radiation in a ^{137}Cs irradiator (50 Gy/hour) at 30°C [Atomic Energy of Canada Limited]. Control cultures were incubated in the absence of γ-radiation at the same temperature.

Comparison of expression patterns produced in microarray and real-time (RT)-PCR experiments for a set of 7 DEIRA genes. Real-time quantitative PCR protocol for Table 1: Relative transcript abundances displayed under non-irradiated and irradiated conditions by 7 selected DEIRA were measured by real-time quantitative PCR. These experiments were performed on the same RNA samples used for microarray analysis. First-strand cDNA synthesis was carried out in 10-μl reactions containing 1 μg of total RNA, 3 μg of random hexamers (Invitrogen), 10 mM dithiothreitol (DTT), 500 μM dNTP mix, and 200 U of Supescript™ II RNase H-reverse transcriptase (Invitrogen) incubated at 42°C for 60 min. The real-time quantitative PCR amplification was performed in 50-μl reaction volumes containing 0.5-μl aliquots of synthesized first-strand cDNA, gene-specific primer pairs and 20,000× diluted SYBR Green I dye (Molecular Probes, Eugene, OR) using the BioRad iCycler (Bio-Rad, Hercules, CA) according to the manufacturer's protocol. The PCR cycle parameters were set at 96°C for 15 sec, 55°C for 30 sec, 72°C for 30 sec for a total of 45 cycles. The fluorescent intensity of SYBR Green I was monitored at the end of each extension step; the copy number of the target cDNA was estimated by the threshold cycle number according to the standard curve.

Total cellular RNA was prepared from DEIRA cells at the indicated time post irradiation (hours). The first-strand cDNA was synthesized with random hexamers using Supescript™ II RNase H reverse transcriptase (Gibco-BRL) and quantified by microarray hybridization (see Materials and Methods) or by PCR amplification with gene-specific primers (Table 2) the iCycler (Bio-Rad) according to the manufacturer's instruction. Amounts of target cDNAs in the irradiated samples are expressed as folds of the non-irradiated control cells. The values of the microarray data are averages of three independent experiments of four replicates, whereas those of real-time quantitative PCR data are averages of two independent experiments of three replicates.

Results

Expression pattern correlation between genes in predicted operons and quality of microarray analysis. Operons are the principal form of gene co-regulation in prokaryotes (5), and the expression patterns of genes within an operon are expected to be strongly correlated. To test this prediction, we compared the expression profiles of genes in predicted DEIRA operons with random gene-groups.

Conserved operons in DEIRA were identified using the approach described previously (6). We considered all conserved operons common for DEIRA and at least one other completely sequenced prokaryotic genome. Only those operons that contained unidirectional genes separated by less than 100 bp were further analyzed. In total, 141 predicted operons containing 435 genes were predicted. Pearson's linear correlation coefficient (CC) was used to measure the correlation between expression patterns of any two given genes. The significance of a correlation (Pcc) was computed using the STATISTICA program. The number of genes that had a significant correlation (SC) with at least one gene from the same predicted operon was calculated for each of the predicted operons. To test the hypothesis that genes within one operon show a significant correlation between their expression profiles with a higher frequency compared to genes located at random positions in the genome, a Monte Carlo simulation was used. To create a random set of gene-groups "pseudo-operons", 435 genes were randomly chosen from the 2,976 analyzed genes and each gene was randomly assigned to one of 141 gene-groups. The number of genes within each gene-group was the same as in the analysis of the actual data, but all genes included in one random gene-group were separated by at least 10 genes in the genome. Correlation analysis was performed for 10,000 sets of random gene-groups and the number of genes that had a significant correlation with at least one gene from the same "pseudo-operon" (SC^*, SC values observed in random gene-groups) was calculated for each set.

Among 435 genes within 141 predicted operons, 297 genes showed significant correlation ($CC \geq 0.67$, $Pcc \leq 0.05$), with at least one other gene from the same operon (SC = 68%). Analysis of the 10,000 SC^* values for random gene-groups showed that they formed a normal distribution, with a mean value of 45% (196 genes), and maximal and minimal SC values of 52% and 39%, respectively (standard deviation 1.7%). It should be noted that the results for random gene-groups do not necessarily represent a background of non-correlated expression because genes involved in unrelated processes might have similar expression profiles since they could be independently responding to γ-radiation. Nevertheless, the probability that the observed SC value for genes in predicted DEIRA operons (68%) belongs to the SC^* distribution was 6.9×10^{-20} (Zelterman's statistics).

Poorly characterized genes that play a role in cell recovery after irradiation. DEIRA has many expanded families of paralogous genes that have been explored in detail previously and are suggested to play some role in radiation resistance (7, 8). Indeed, many genes from expanded families are up-regulated, *e.g.*, those of the TerEDXZ/CABP/SCP2 family (DR2220-DR2225, DRA0057) and the PR1 family gene (DR1548). The most notable example of induction of genes from the same family are the members of the YfiT/DinB family, which includes homologs of DinB-like proteins that belong to the SOS regulon of *B. subtilis* (9). DEIRA has 12 members of this family (8) and four of them are strongly induced in a *recA*-like manner (DR0053, DR0841, DR1642, DR1899), supporting an important role in the irradiation-response (Table 3).

1. Daly, M. J., Ouyang, L., Fuchs, P. & Minton, K.W. (1994) *J. Bacteriol.* **176**, 3508-3517
2. Hansen, M.T. (1978) *J. Bacteriol.* **134**, 71-75.
3. Daly, M.J. & Minton, K.W. (1995) *J. Bacteriol.* **177**, 5495-5505.
4. Daly, M.J. & Minton, K.W. (1996) *J. Bacteriol.* **178**, 4461-4471.
5. Miller, J. H. & Reznikoff, W. S. E. (1978) *The Operon* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY).
6. Wolf, Y. I., Rogozin, I. B., Kondrashov, A. S. & Koonin, E. V. (2001) *Genome Res.* **11**, 356-72.
7. Makarova, K. S., Aravind, L., Daly, M. J. & Koonin, E. V. (2000) *Genetica* **108**, 25-34.
8. Makarova, K. S., Aravind, L., Wolf, Y. I., Tatusov, R. L., Minton, K. W., Koonin, E. V. & Daly, M. J. (2001) *Microbiol. Mol. Biol. Rev.* **65**, 44-79.
9. Yasbin, R. E., Cheo, D. & Bayles, K. W. (1991) *Res. Microbiol.* **142**, 885-92.

Fig. 5. Effect of high-dose acute irradiation on DEIRA growth. Diamonds, early stationary phase (ESP) cells (~1 x 10^8 cells /ml) were irradiated with 15 kGy on ice and then diluted 1/20 in fresh TGY medium. Cell growth was monitored by periodic OD_{600} measurements. At 0, 0.5, 1.5, 3, 5, 9, 12, 16, and 24 hours into recovery, about 1 x 10^9 cells were harvested for microarray analysis. Squares, non-irradiated ESP control DEIRA cells inoculated and monitored as for irradiated cells. Values are the means ± standard deviations of the triplicate experiments (n = 9).

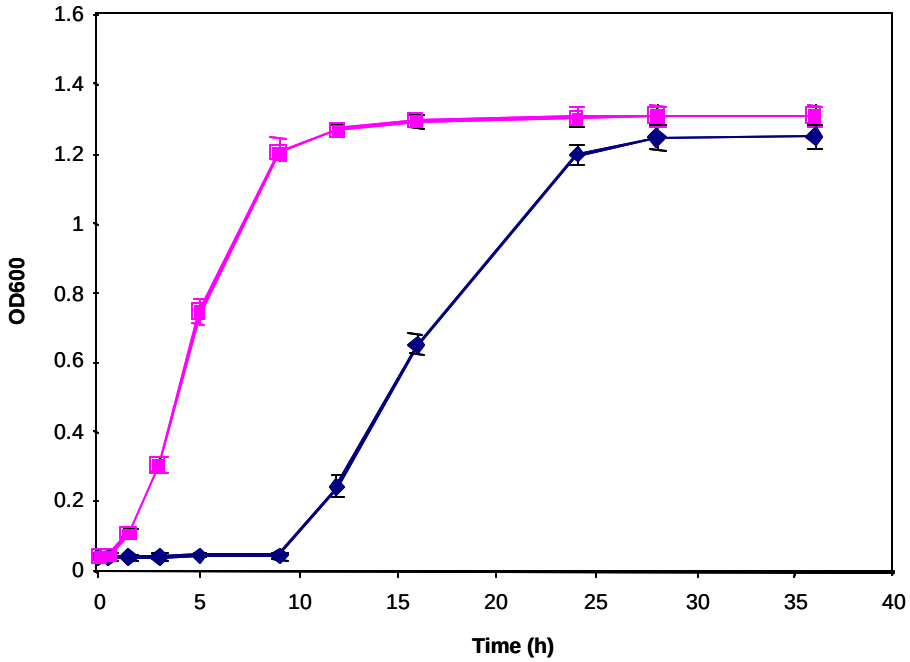
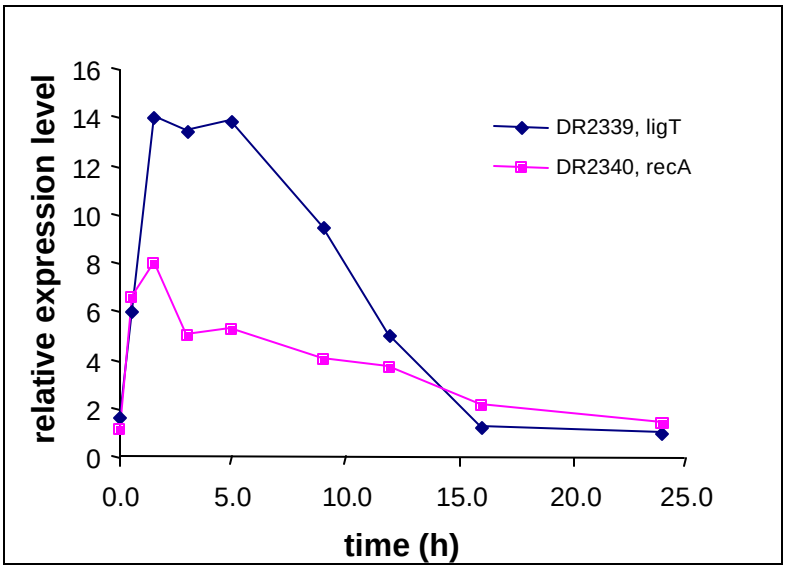


Fig. 6. Coordinated expression of genes belonging to the same operon or multi-subunit complex. (*A*) Predicted operon consisting of 2'-5' RNA ligase, LigT, and recombinational ATPase, RecA. (*B*) Subunits of the UvrABCD excinuclease

A



B

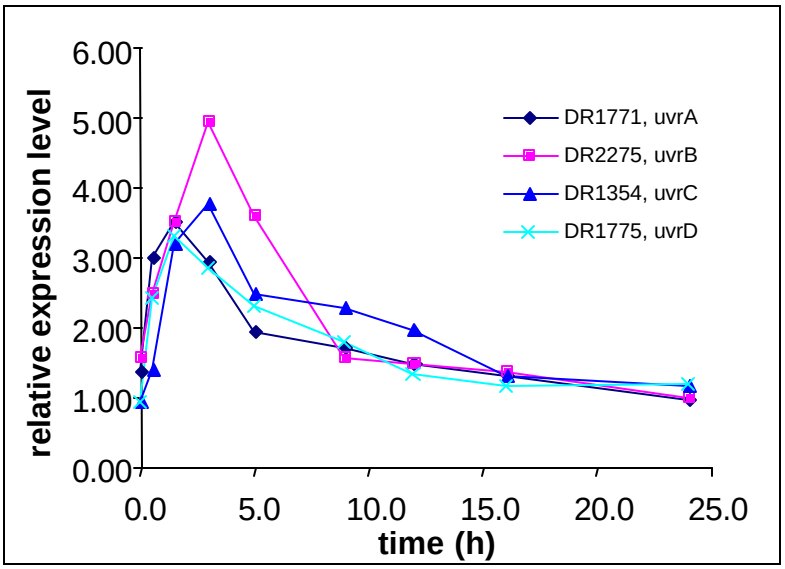


Fig. 7. Resistance phenotype, construction, and genomic structure for the DR0070 knockout mutant**.** **(***A***)** Survival of DEIRA strains MD891 (DR0070 disruption) and MD68 (DEIRA wild type strain R1/pMD68) following gamma irradiation. Cells were grown to the early plateau phase and irradiated on ice to the indicated doses. Aliquots were withdrawn at intervals, diluted, and plated on TGY agar that was supplemented with kanamycin. Symbols: squares, MD68; circles, MD891. Values are the means ± standard deviations of three independent experiments. (*B***)** Predicted DNA band-sizes of wild-type DR0070 arising from cleavage with the indicated restriction endonucleases. ATG and TGA, DR0070 initiation and termination codons, respectively. (*C***)** Predicted DNA band-sizes of disrupted DR0070 following integration of pCR2.1, arising from cleavage with the indicated restriction endonucleases. ATG and TGA, as in Panel B. (*D***)** MD891 was subjected to a detailed mapping of the DR0070 integration site using restriction enzymes indicated in panels B and C, Southern blotting, and probing with a 575 bp radiolabeled DR0070 fragment shown in Panel B. Abbreviations: wt, wild-type (DEIRA R1); m, mutant (MD891). Molecular size standards (kbp): 1, DNA Ladder, Mix (Fermentas); 2, 200bp DNA step ladder (Promega); 3, 2-Log DNA Ladder (New England Biolabs).

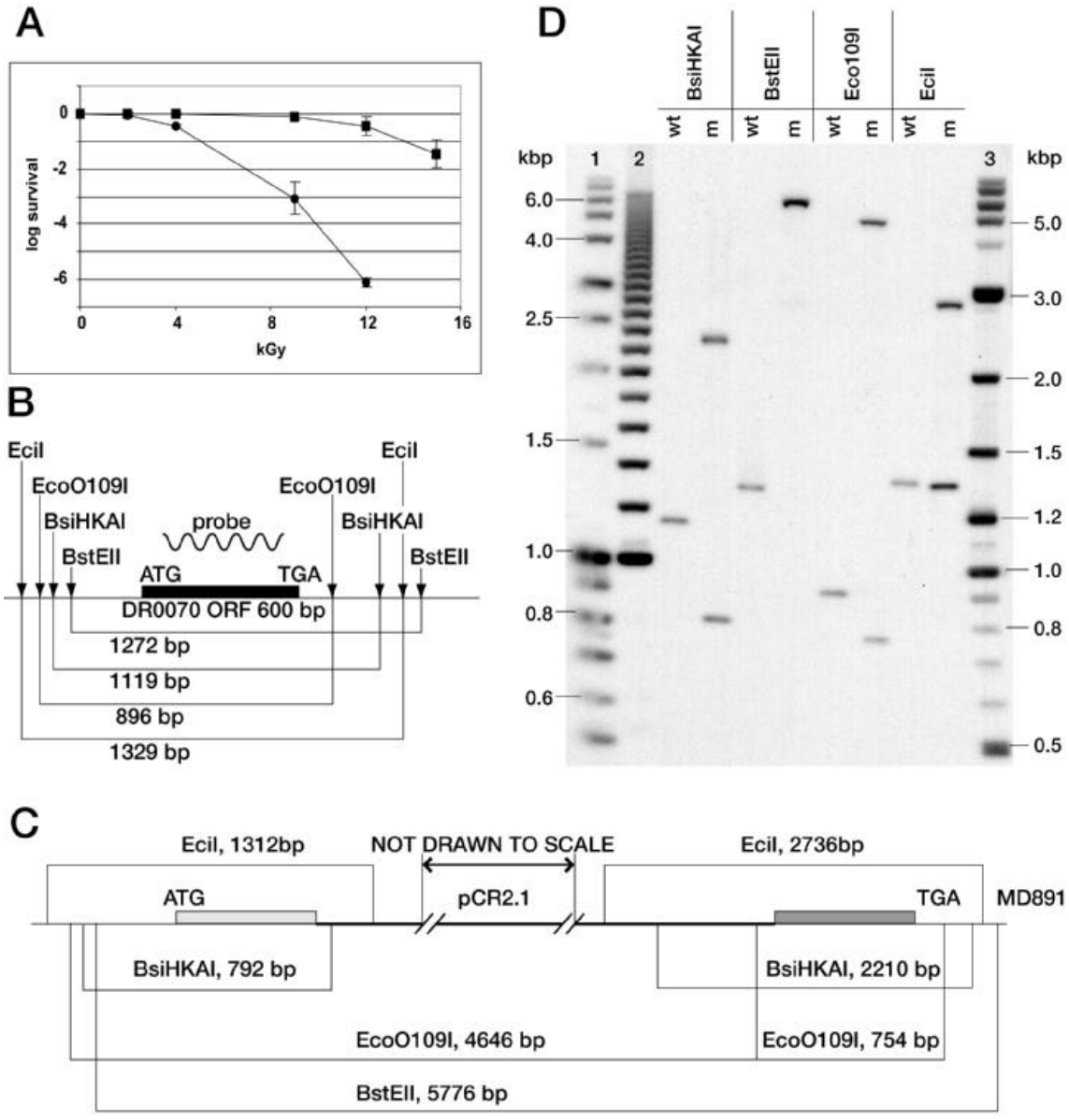
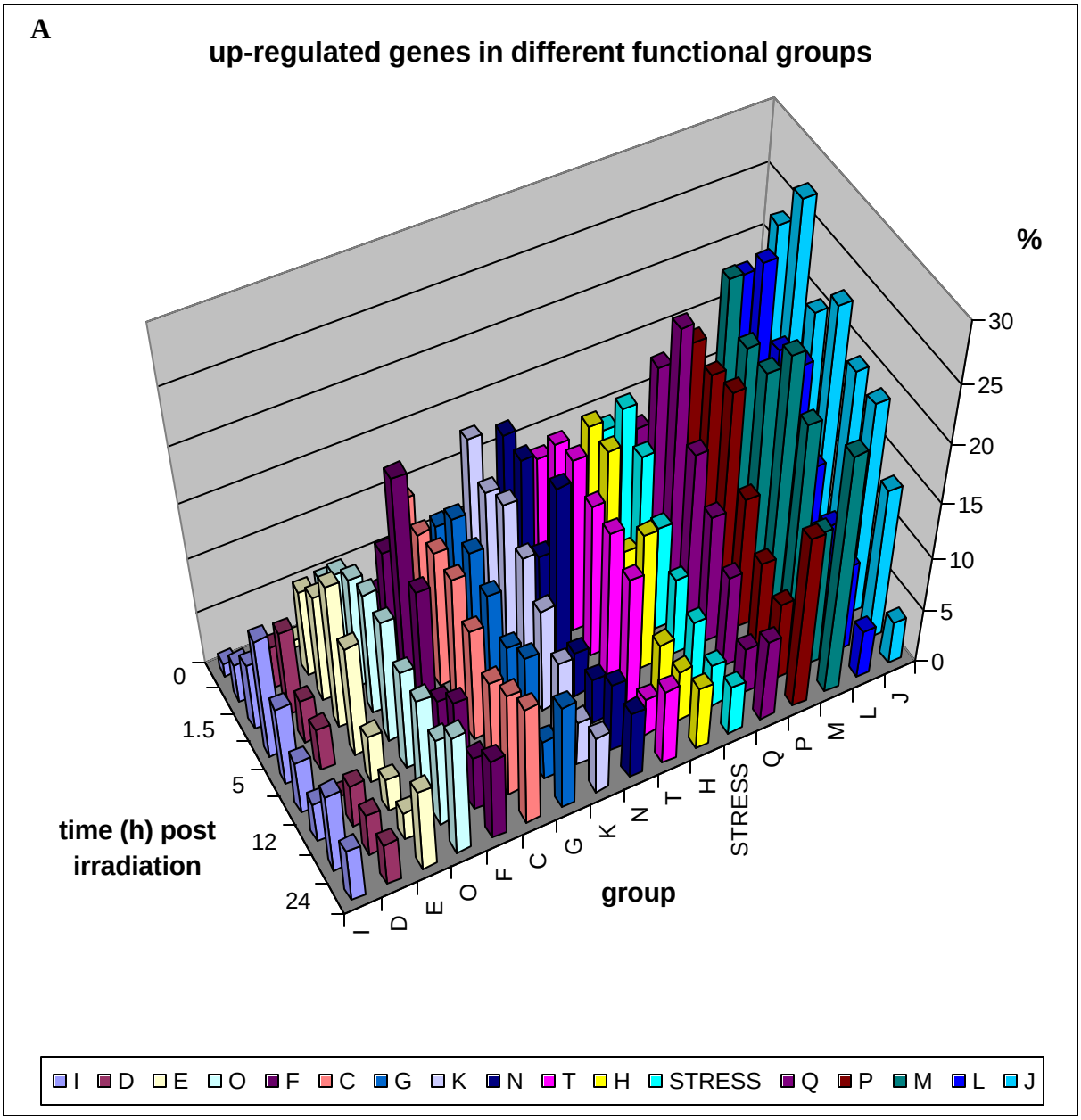
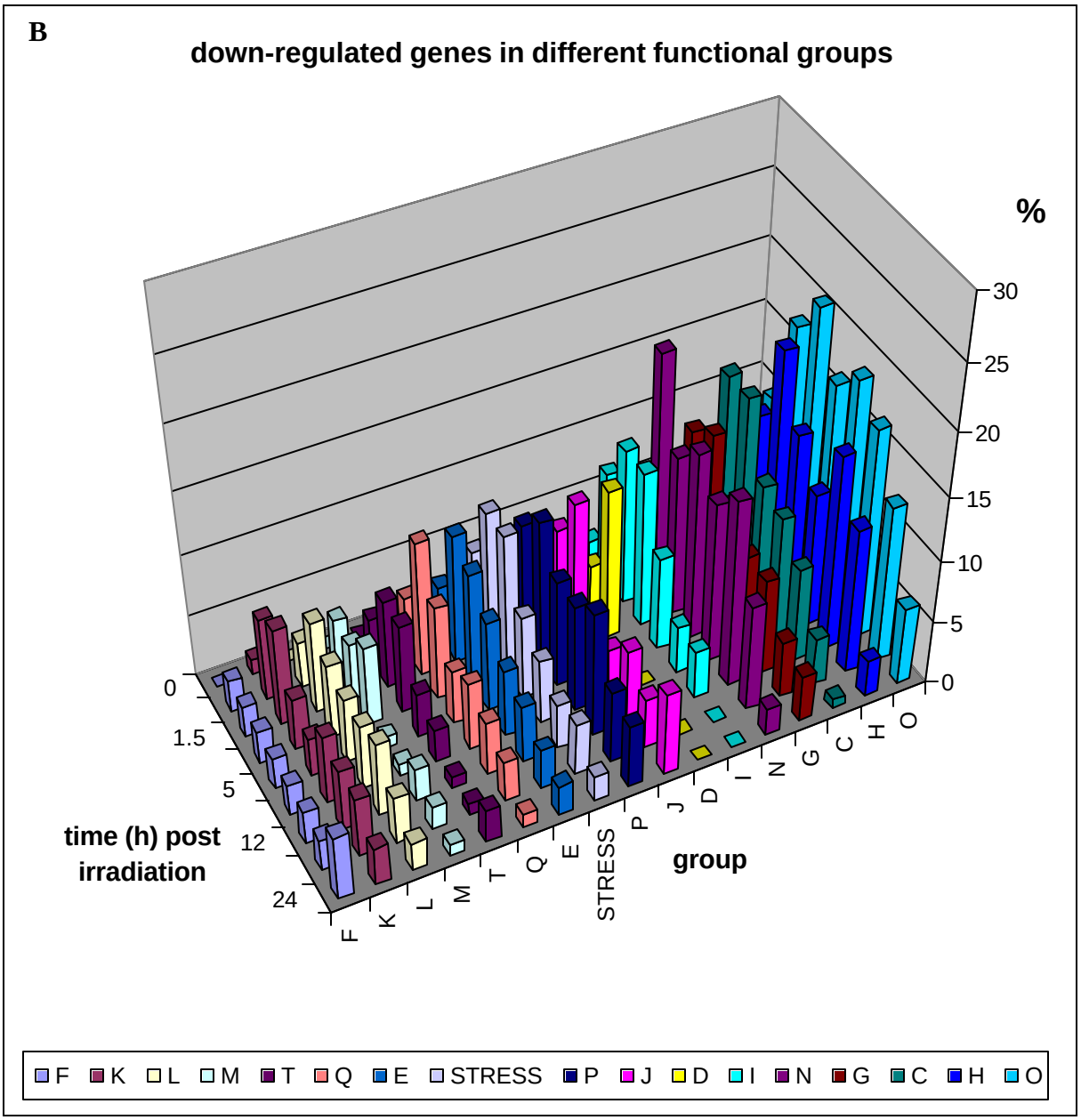


Fig. 8. Activation (*A*) and repression (*B*) of different functional groups of DEIRA genes. Designations of functional groups (from the COG database): J - Translation, ribosomal structure and biogenesis; K – Transcription; L - DNA replication, recombination and repair; D - Cell division and chromosome partitioning; O - Posttranslational modification, protein turnover, chaperones; M - Cell envelope biogenesis, outer membrane; N - Cell motility and secretion; P - Inorganic ion transport and metabolism; T - Signal transduction mechanisms; C - Energy production and conversion; G - Carbohydrate transport and metabolism; E - Amino acid transport and metabolism; F - Nucleotide transport and metabolism; H - Coenzyme metabolism; I - Lipid metabolism; Q - Secondary metabolites biosynthesis, transport and catabolism; R - General function prediction only; S - Function unknown. STRESS – genes involved in stress response, based on previous analyses of the DEIRA genome (Makarova et al. 2001).



B


down-regulated genes in different functional groups
%
30
25
20
15
10
5
0
time (h) post irradiation
0
1.5
5
12
24
group
F
K
L
M
T
Q
E
STRESS
P
J
D
I
N
G
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H
O

Fig. 9. Expression patterns of predicted transcriptional regulators potentially involved in the regulation of DEIRA's irradiation-response.

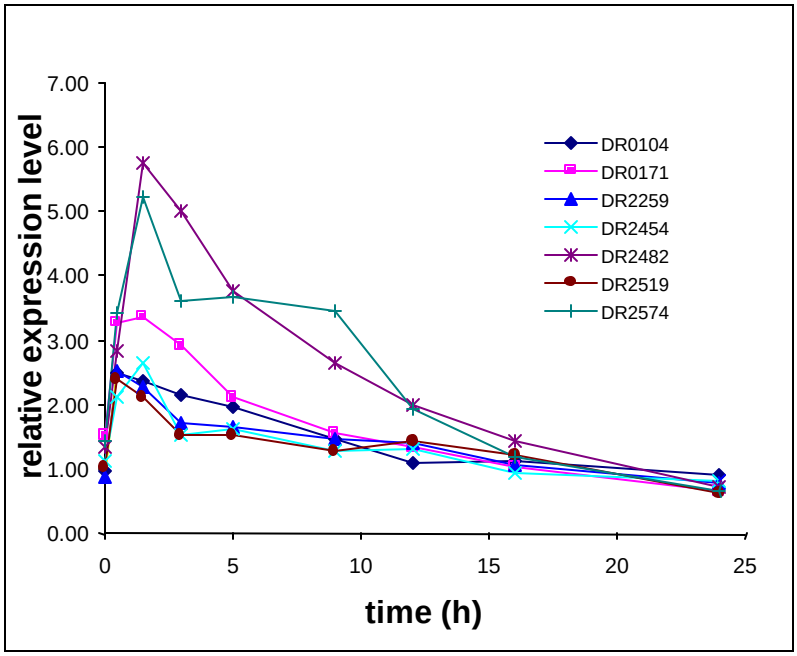

Table 1. Comparison of expression levels produced in microarray and real-time (RT) – PCR experiments for a set of 7 DEIRA genes.

Gene ID	Annotation	Method	Time (h) post irradiation Responds to radiation (folds)								
			0	0.5	1.5	3	5	9	12	16	24
DR0007	Unknown	Microarray	1.02	3.93	2.99	1.39	1.73	1.53	1.88	1.17	1.78
		RT PCR	0.21	0.37	1.77	0.69	0.95	1.31	1.38	1.89	1.49
DR2340	RecA	Microarray	1.13	6.62	7.98	5.02	5.27	4.06	3.70	2.15	1.44
		RT PCR	0.65	1.67	9.96	11.23	2.06	0.63	0.91	0.30	0.10
DRB0100	DNA ligase	Microarray	1.63	1.47	9.24	14.43	9.42	6.24	4.42	4.16	2.28
		RT PCR	2.38	7.98	17.82	12.18	8.64	4.14	3.97	3.93	1.68
DR2339	LigT-RNA ligase	Microarray	1.68	6.00	14.06	13.44	13.85	9.50	5.01	1.22	1.03
		RT PCR	3.51	6.52	14.24	2.88	1.51	2.48	2.94	0.52	1.42
DR0422	SAM-dependent melyltransferase	Microarray	1.28	13.99	18.85	10.95	8.18	4.39	2.69	1.79	1.14
		RT PCR	3.00	16.86	18.32	5.27	4.92	4.48	1.77	3.28	3.36
DR0053	DinB family	Microarray	1.67	4.49	10.16	10.25	6.10	3.67	2.30	1.35	1.30
		RT PCR	0.68	3.61	10.70	11.31	9.83	2.42	3.63	3.13	0.15
DR0207	ComA	Microarray	2.14	2.83	10.89	15.47	12.40	3.86	3.87	1.87	1.35
		RT PCR	1.37	5.41	18.68	19.96	33.22	21.12	16.95	3.30	4.34

Table 2. Sequences of the primers used in the real-time quantitative PCR

DR #	Gene product	Primer sequence	PCR product size (bp)
DR0007	Unknown	CAGTGGTGCTGATCGTGAGT ATAGACGAGTTCGCGCAGTT	116
DR2340	RecA protein	CCCCTTCAAGGAAGTCGAAC CGCCGTAGGAGTAGAAGCTG	125
DRB0100	DNA ligase	GCGAGTCAAATACCCTTCCA GGTAGAGGCTGGTGTTTTCG	146
DR2339	2'-5' RNA ligase	AACACCAACCGTCCACCTAC AGGTACGAGAGGGTGACGTG	145
DR0422	SAM-dependent melyltransferase	GCTTCGACCTGCTGTACTCC GTCGTGATTTGCTGGAACCT	128
DR0053	DinB/YfiT family	CCGCAGGTAAGCACTGAGAT TGGACCTCGTTGTCAATCAA	101
DR0207	ComA protein	CCCGGTAAACGTCAACACTG GCCTTTGACCTTTTTGACCA	133

Table 3. Selected genes and operons of DEIRA with a *recA*-like expression pattern

Gene_ID[a]	Function group[b]	Protein description and comments	Relative basal level	Maximum induction level (fold)	STD	CV	Maximum induction time (hr)
DR0003	-	Uncharacterized protein	1.32	14.03	5.53	39.39	1.5
DR0046	-	Leucine-rich repeat protein	0.18	2.14	0.35	16.21	3
DR0047	-	Uncharacterized protein	0.11	2.48	1.40	56.42	3
DR0048	S	Uncharacterized membrane protein, YcaP ortholog	0.33	3.90	0.55	14.01	3
DR0050	L	DinB/YfiT family protein	0.53	3.84	0.93	24.23	3
DR0051	S	Small cysteine-rich protein of the HesB family	0.70	5.93	3.32	55.97	3
DR0052	-	Uncharacterized conserved protein	0.34	6.50	2.15	33.14	1.5
DR0053	L	DinB/YfiT family protein	0.44	10.25	2.36	23.00	3
DR0070	ST?	Uncharacterized protein	0.08	3.89	1.72	44.18	9
DR0103	R	Predicted metal-binding protein	0.57	6.46	4.02	62.22	1.5
DR0140	-	Uncharacterized protein	0.97	6.44	2.87	44.60	1.5
DR0160	-	Conserved membrane protein	0.42	3.90	0.86	22.09	1.5
DR0161	S	AmsJ/WcaK related protein, possibly involved in exopolysaccharide biosynthesis	0.97	8.12	4.07	50.14	1.5
DR0203	R	Uncharacterized membrane protein	0.28	3.82	0.86	22.43	1.5
DR0204	-	Uncharacterized membrane protein	0.51	6.01	1.35	22.52	3
DR0205	Q	ABC transporter ATPase	0.49	4.10	2.45	59.75	3
DR0206	-	Uncharacterized protein	0.19	5.45	2.65	48.56	3
DR0207	L	ComEA related protein, secreted	0.26	15.47	10.31	66.66	3
DR0324	E	Predicted glutamate formiminotransferase	0.31	3.30	1.47	44.50	0.5
DR0363	E	ABC-type dipeptide transporter periplasmic binding protein, DppA	2.79	4.09	1.75	42.74	24
DR0365	E	ABC-type dipeptide transporter, permease ,DppC	2.11	1.48	0.84	56.88	5
DR0394	ST	Predicted kinase antibiotic/homoserine kinase homolog	0.29	7.51	2.76	36.69	1.5
DR0395	G	MDR-type permease	1.09	4.40	2.12	48.16	1.5
DR0396	-	Uncharacterized protein	1.15	5.57	2.39	42.78	1.5
DR0421	-	Uncharacterized protein	0.68	4.94	2.30	46.60	1.5
DR0422	Q	Trans-aconitate methylase	0.68	18.85	7.46	39.59	1.5
DR0477	E	Membrane permease, DhlC	0.56	4.63	1.71	36.85	1.5

		homolog					
DR0478	E	Aminopeptidase P	0.77	2.86	0.55	19.36	0.5
DR0479	M	Penicillin-binding protein 1	0.77	7.07	2.42	34.21	1.5
DR0599	ST	Aminoglycoside N3'-acetyltransferase family	1.31	4.24	1.41	33.31	1.5
DR0609	R	Predicted kinase, adenylate kinase homolog	0.47	2.43	1.14	46.95	3
DR0610	-	Uncharacterized protein	0.25	6.10	4.51	73.93	3
DR0665	-	Uncharacterized protein	0.54	11.66	5.74	49.24	3
DR0694	C	Phage protein homolog	0.60	5.57	2.02	36.28	1.5
DR0812	O	Extracellular alkaline serine protease	0.59	3.32	1.24	37.52	3
DR0841	L	DinB/YfiT family protein	0.48	5.93	1.47	24.84	1.5
DR0842	ST	NimC-like (5-nitroimidazole antibiotics resistance) protein	2.62	1.89	0.69	36.67	24
DR0911	K	DNA-directed RNA polymerase beta' subunit	1.62	1.99	1.37	68.70	0.5
DR0912	K	DNA-directed RNA polymerase beta subunit	0.54	3.19	0.80	24.90	0.5
DR1143	-	Uncharacterized protein	0.49	8.85	4.26	48.13	1.5
DR1144	-	Uncharacterized conserved protein	1.10	2.69	1.31	48.82	1.5
DR1356	R	ABC transporter, ATPase subunit	0.40	9.85	5.98	60.68	3
DR1357	R	ABC transporter, permease subunit	0.31	6.79	2.56	37.67	1.5
DR1358	M	ABC transporter, periplasmic subunit	0.38	22.73	13.73	60.39	1.5
DR1359	M	ABC transporter, periplasmic subunit	0.50	24.83	11.13	44.82	1.5
DR1398	-	Uncharacterized protein	0.24	4.17	1.04	24.83	1.5
DR1548	T	Bacillus ykwD ortholog, Divergent member of the secreted PRP1, plant pathogenesis related protein superfamily	0.48	5.62	2.34	41.32	3
DR1556	-	Membrane-associated sensor histidine kinase	2.27	3.61	1.71	47.23	1.5
DR1557	T	Uncharacterized protein	1.37	5.06	1.57	31.04	1.5
DR1558	-	Receiver domain (flavodoxin, CheY family) of a two component system, contains a C- terminal helix-turn-helix (HTH) DNA-binding domain	1.12	5.64	1.49	26.43	1.5
DR1559	E	Uncharacterized protein	0.87	4.39	1.60	36.47	1.5
DR1639	L	Uncharacterized protein	1.15	4.41	1.84	41.73	1.5
DR1641	L	DinB/YfiT family protein	2.52	1.88	0.78	41.24	5
DR1642	-	DinB/YfiT family protein	0.27	3.71	1.30	35.02	1.5

DR1643	-	Uncharacterized protein	0.61	4.06	2.21	54.45	1.5
DR1644	Q	Uncharacterized protein	0.77	2.45	0.56	22.82	1.5
DR1672	-	SAM-dependent methyltransferase	0.41	1.24	0.73	59.15	12
DR1673	-	Predicted dehydrogenase	1.05	4.53	1.29	28.54	1.5
DR1744	L	Uncharacterized protein	1.47	5.02	1.64	32.69	1.5
DR1776	-	Nudix/MutT family pyrophosphatase	0.84	4.70	2.83	60.18	1.5
DR1850	L	Uncharacterized protein	0.62	4.36	1.13	26.00	1.5
DR1899	-	DinB/YfiT family protein	0.35	1.60	0.65	40.30	1.5
DR1900	-	Uncharacterized protein	0.51	3.14	1.04	33.14	1.5
DR1901	-	Uncharacterized protein	0.51	10.74	4.85	45.17	1.5
DR2097	E	Uncharacterized protein	0.14	6.95	2.08	29.93	1.5
DR2118	E	ABC-type branched amino acid transporter	0.26	3.04	1.38	45.32	5
DR2122	E	Branched amino acid periplasmic binding protein, LivBP	0.20	2.46	0.29	11.94	3
DR2128	ST	RNA polymerase alpha subunit	2.26	4.03	2.80	69.48	1.5
DR2220	ST	Tellurium resistance protein, TerB homolog	0.45	3.13	1.49	47.61	5
DR2221	ST	Tellurium resistance/cAMP-binding family protein	0.59	5.24	2.94	56.05	3
DR2223	ST	Tellurium resistance/cAMP-binding family protein	0.39	3.63	1.36	37.45	3
DR2225	-	Tellurium resistance/cAMP-binding family protein	0.58	2.14	0.41	19.30	3
DR2265	-	Large membrane protein	0.44	5.45	1.46	26.84	3
DR2337	T	Uncharacterized protein	0.11	7.41	5.71	77.05	1.5
DR2415	T	Receiver domain, CheY family and HTH	0.16	1.72	1.26	73.28	5
DR2416	-	Sensor histidine kinase	0.84	5.75	1.33	23.09	1.5
DR2481	K	Uncharacterized protein	0.39	4.66	1.27	27.17	1.5
DR2482	L	Predicted transcription regulator, HTH domain related to that of sigma factors	0.36	5.75	2.92	50.84	1.5
DR2483	R	McrA family nuclease	0.80	5.43	1.22	22.49	1.5
DR2484	L	WD40 repeat protein	0.71	5.12	2.53	49.39	1.5
DR2566	-	Homolog of HpaII repair protein, small, conserved bacterial protein	0.42	4.10	1.09	26.48	3
DR2573	E	Uncharacterized protein	0.22	3.93	2.57	65.55	0.5
DR2610	R	Periplasmic binding protein, FliY	1.01	4.13	1.67	40.46	0.5
DRA0008	T	Conserved membrane protein (possible transporter)	0.26	6.60	2.00	30.26	3
DRA0009	T	Membrane-associated sensor histidine kinase	0.19	3.03	1.25	41.30	5

DRA0010	P	CheY-like sensor regulator and HTH domain	0.28	4.66	2.12	45.44	5
DRA0013	P	Sulfite reductase	0.65	8.27	1.84	22.31	24
DRA0014	E	PAPS synthase (APS kinase domain), CysC	0.37	4.33	1.66	38.36	24
DRA0015	P	PAPS reductase	0.54	11.42	5.73	50.18	24
DRA0016	T	Sulfate adenylyltransferase	0.42	12.12	5.83	48.07	24
DRA0049	T	Response regulator CheY family, flavodoxin	0.12	3.16	1.70	53.75	9
DRA0050	-	Phytochrome-like histidine kinase and GAF domain	0.30	2.18	1.21	55.52	3
DRA0234	E	Uncharacterized protein	0.17	12.76	5.27	41.29	1.5
DRA0249	K	Metalloprotease, leishmanolysin-like	1.61	6.47	4.43	68.42	3
DRA0344	ST	LexA repressor, HTH domain and protease	0.51	1.80	1.08	59.92	1.5
DRA0345	ST	Predicted esterase, homologs of *E. coli* erythromycin esterase type II (EreB)	0.68	10.05	4.39	43.72	1.5
DRA0346	R	PprA protein, possibly involved in DNA damage resistance mechanisms	0.65	3.52	1.94	55.14	0.5
DRB0067	O	Extracellular nuclease containing fibronectin III domains	0.29	4.37	1.21	27.58	3
DRB0069	R	Subtilisin family serine protease	0.92	3.18	1.39	43.62	3
DRB0070	-	ABC-class ATPase	0.64	4.00	1.91	47.74	1.5
DRB0071	H	Uncharacterized protein	0.11	2.60	0.53	20.51	3
DRB0072	E	Salicylate 1-monooxygenase	0.37	4.91	2.31	47.04	1.5
DRB0133	E	D-alanine permease	0.46	3.51	1.39	39.61	1.5
DRB0145	-	Uncharacterized protein	0.67	4.77	1.80	37.63	1.5

[a.] Note: Expression profile information in two last columns is shown only for one gene in an operon. All genes selected here are significantly induced (determined by statistical analyses)

[b.] Designations of functional groups (from the COG database): see the legend for SM_Fig. IV

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

Gene Name[a]	Gene_ID	Protein description and comments	Pathway[b]	Relative basal level[c]	Response to radiation (folds)[d]	Time of response (hr)	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
Mug	DR0715	G/T mismatch-specific thymine DNA glycosylase	BER	0.85	0.17	3	0.01	7.80
	DR1751 DR0022	Uracil DNA glycosylase	BER	0.86 0.47	0.64 3.33	0.5-9 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 UvrA-2	DR1771 DRA0188	ATPase, excinuclease subunit	NER	1.44 0.13	3.52 2.03	1.5 5	1.15 0.90	32.56 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
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 repair	RER	1.71	0.90	0.5-9		
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	MP	1.58	0.17	3	0.05	28.26

		ligase						
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 DR2566	Predicted very short patch repair nuclease	VSP?	0.37 0.42	1.94 4.10	3 3	0.81 1.09	41.73 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 XerD XerC/D	DRA0155 DRB0104 DRC0018	Integrase/recombinase	RER	0.26 0.94 0.10	0.95 0.53 2.72	0.5-9 3 12	 0.11 0.77	 20.56 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

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

[b.] 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

[c] The ratio of the fluorescent intensity of a particular gene to the average intensity of all arrayed genes when non-irradiated sample is used as a labeled probe.

[d] The maximum, or minimum, or average ratio of the irradiated sample(s) harvested at the 'Time of response' to the non-irradiated control. There is no standard deviation (STD) and coefficient of variation (CV) for an average ratio of several time points.

Color coding: red – up regulated, blue – down regulated, brown – no changes.