

Table S10. DNA repair genes in <i>D. deserti</i>, <i>D. radiodurans</i> and <i>D. geothermalis</i>				
A. Main DNA repair genes for Base Excision Repair (BER)^a				
Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Putative function of the predicted gene product
Monofunctional DNA glycosylases				
<i>alkA</i> (282 aa)	<i>Deide_08050</i> (204 aa)	<i>DR_2074</i> (190 aa)	<i>Dgeo_1660</i> (209 aa)	3-methyladenine-DNA glycosylase II
	<i>Deide_02320</i> (216 aa)	<i>DR_2584</i> (225 aa)	<i>Dgeo_0107</i> (216 aa)	
<i>tag</i> (187 aa)	-	-	-	3-methyladenine-DNA glycosylase I
<i>mutY</i> (350 aa)	<i>Deide_01970</i> (353aa)	<i>DR_2285</i> (363 aa)	<i>Dgeo_0019</i> (343 aa)	A/8oxoG adenine glycosylase
<i>mug</i> (168 aa)	<i>Deide_17530</i> (185 aa)	<i>DR_0715</i> (199 aa)	<i>Dgeo_1718</i> (195 aa)	Removes uracil, thymine or ethenocytosine opposite guanine
	-	-	<i>Dgeo_2568</i> (177 aa) (plasmid)	
<i>ung</i> or <i>udg</i> (229 aa)	<i>Deide_00830</i> (248 aa)	<i>DR_0689</i> (247 aa)	<i>Dgeo_2059</i> (245 aa)	Uracil-DNA glycosylase
	-	<i>DR_1751</i> (237 aa)	<i>Dgeo_1556</i> (230 aa)	
	-	<i>DR_0022</i> (199 aa) ^b	-	
Bifunctional DNA glycosylases (displaying also a AP lyase activity)				
<i>fpg</i> (<i>mutM</i>) (269 aa)	<i>Deide_16240</i> (276 aa)	<i>DR_0493</i> (280 aa)	<i>Dgeo_0442</i> (289 aa)	Formamidopyrimidine-DNA glycosylase
<i>nth</i> (211 aa)	<i>Deide_01790</i> (222 aa)	<i>DR_0289</i> (<i>nth1</i>)(225 aa)	<i>Dgeo_0248</i> (233 aa)	Endonuclease III; removes ring-saturated or fragmented pyrimidines
	<i>Deide_23070</i> (247 aa)	<i>DR_2438</i> (<i>nth2</i>)(259 aa)	<i>Dgeo_2290</i> (242 aa)	
	<i>Deide_12880</i> (237 aa)	<i>DR_0928</i> (338 aa)	<i>Dgeo_0785</i> (269 aa)	
<i>nei</i> (263 aa)	-	-	-	Endonuclease VIII, DNA N-glycosylase/AP lyase
AP endonucleases				
<i>nfi</i> (223 aa)	-	<i>DR_2162</i> (181 aa)	-	Endonuclease V
<i>nfo</i> (285 aa)	-	-	-	Endonuclease IV
<i>xthA</i> (268 aa)	<i>Deide_03250</i> (260 aa)	<i>DR_0354</i> (283 aa)	<i>Dgeo_0461</i> (267 aa)	Exodeoxyribonuclease III
	<i>Deide_2p01470</i> (270 aa)	-	<i>Dgeo_2484</i> (254aa) (plasmid)	
B. Main DNA repair genes for Nucleotide Excision Repair (NER)^a				
Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
<i>mfd</i> (1148 aa)	<i>Deide_06920</i> (1041 aa)	<i>DR_1532</i> (1054 aa)	<i>Dgeo_0545</i> (1041 aa)	transcription-repair coupling factor; helicase
<i>uvrA</i> (940 aa)	<i>Deide_12760</i> (1004 aa)	<i>DR_1771</i> (1016 aa)	<i>Dgeo_0694</i> (1004 aa)	DNA damage recognition protein UvrA; DNA independent ATPase and DNA binding protein
	<i>Deide_2p02060</i> (831 aa)	<i>DR_A0188</i> (922 aa)	-	
<i>uvrB</i> (673 aa)	<i>Deide_03120</i> (671 aa)	<i>DR_2275</i> (730 aa)	<i>Dgeo_1890</i> (676 aa)	DNA damage binding protein UvrB ; helicase
<i>uvrC</i> (610 aa)	<i>Deide_11450</i> (617 aa)	<i>DR_1354</i> (617 aa)	<i>Dgeo_1124</i> (616 aa)	Excision nuclease
<i>uvrD</i> (720 aa)	<i>Deide_12100</i> (744 aa)	<i>DR_1775</i> (745 aa)	<i>Dgeo_0868</i> (741 aa)	DNA helicase II

BS_ywjD (320 aa)	<i>Deide_17800</i> (301 aa)	<i>DR_1819</i> (305 aa)	<i>Dgeo_1819</i> (311 aa)	UV DNA damage endonuclease UvsE
yejH (586 aa)	<i>Deide_17320</i> (467 aa)	<i>DR_A0131</i> (895 aa)	-	DNA or RNA helicase of superfamily II (COG1061); also predicted nuclease
cho (295 aa)	-	-	-	UvrC homolog

C. Main DNA repair genes for Mismatch Repair ^a

Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
<i>mutL</i> (615 aa)	<i>Deide_15600</i> (550 aa)	<i>DR_1696</i> (547 aa)	<i>Dgeo_1538</i> (549 aa)	DNA mismatch repair protein; ATPase
<i>mutS</i> (853 aa)	<i>Deide_15540 (mutS1)</i> (849 aa)	<i>DR_1039 (mutS1)</i> (850 aa)	<i>Dgeo_1537 (mutS1)</i> (880 aa)	DNA mismatch repair protein; ATPase
	<i>Deide_05000 (mutS2)</i> (767 aa)	<i>DR_1976 (mutS2)</i> (766 aa)	<i>Dgeo_0899 (mutS2)</i> (789 aa)	MutS2 family protein; ATPase
<i>xseA</i> (456aa)	<i>Deide_22980</i> (402aa)	<i>DR_0186</i> (416aa)	<i>Dgeo_0148</i> (413aa)	Exonuclease VII, large subunit
<i>xseB</i> (80 aa)	<i>Deide_02120</i> (87 aa) ^c	<i>DR_2586</i> (85 aa) ^c	<i>Dgeo_0027</i> (83 aa) ^c	Exonuclease VII, small subunit
<i>dam</i> (278 aa)	-	-	-	Methylase GATC
<i>mutH</i> (229 aa)	-	-	-	Endonuclease GATC
<i>dcm</i> (472 aa)	-	-	-	C-5 cytosine methyltransferase
<i>vsr</i> (156 aa)	-	-	-	Very short patch repair protein; endonuclease

D. Main DNA repair genes for Direct Reversal of DNA damage (DR) ^a

Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
<i>ada</i> (354 aa)	-	-	-	O-6-methylguanine-DNA alkyltransferase; Transcription activator
<i>ogt/ybaZ</i> (171 aa/129 aa)	<i>Deide_22770</i> (118 aa)	<i>DR_0428</i> (139 aa)	<i>Dgeo_2101</i> (124 aa)	O-6-alkylguanine transferase
<i>alkB</i> (216 aa)	-	-	-	N1-methyladenine and N3-methylcytosine repair protein
<i>phrB</i> (472 aa)	-	-	-	DNA photolyase
<i>BS_splB</i> (342 aa)	Deide_3p02150 (354 aa)	-	-	DNA repair photolyase
<i>dut</i> (151 aa)	-	-	-	dUTPase
<i>dcd</i> (193 aa)	<i>Deide_16640</i> (186 aa)	-	<i>Dgeo_1880</i> (186 aa)	Deoxycytidine triphosphate deaminase
<i>yggV</i> (197 aa)	<i>Deide_19360</i> (202 aa)	<i>DR_0179</i> (200 aa)	<i>Dgeo_2209</i> (199 aa)	Xanthosine triphosphate pyrophosphatase

E. Main DNA repair genes for recombinational repair (RER) ^a

Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
<i>recA</i> (353 aa)	Deide_19450 (355 aa)	<i>DR_2340</i> (363 aa)	<i>Dgeo_2138</i> (358 aa)	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
	Deide_1p01260 (344 aa)			
	Deide_3p00210 (344 aa)			
<i>recB</i> (1180 aa)	- ^d	-	-	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ss DNA endonuclease
<i>recC</i> (1122 aa)	-	-	-	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ss DNA endonuclease

<i>recD</i> (608 aa)	<i>Deide_16210</i> (710 aa)	<i>DR_1902</i> (715 aa)	<i>Dgeo_0826</i> (726 aa)	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease
<i>recE</i> (866 aa)	-	-	-	Exonuclease VIII, dsDNA exonuclease, 5'=>3' specific
<i>recF</i> (357 aa)	<i>Deide_14250</i> (363 aa)	<i>DR_1089</i> (359 aa)	<i>Dgeo_1620</i> (358 aa)	Recombinational repair protein
<i>recG</i> (693 aa)	<i>Deide_09960</i> (780 aa)	<i>DR_1916</i> (784 aa)	<i>Dgeo_1139</i> (776 aa)	Holliday junction-specific DNA helicase; branch migration inducer
<i>recJ</i> (577 aa)	<i>Deide_07130</i> (714 aa)	<i>DR_1126</i> (684 aa)	<i>Dgeo_1599</i> (702 aa)	ssDNA exonuclease, 5'=>3' specific
<i>recN</i> (553 aa)	<i>Deide_12310</i> (534 aa)	<i>DR_1477</i> (564 aa)	<i>Dgeo_1194</i> (555 aa)	Recombination and repair protein
<i>recO</i> (242 aa)	<i>Deide_13810</i> (247 aa)	<i>DR_0819</i> (244 aa)	<i>Dgeo_0855</i> (243 aa)	Bacterial recombinational repair protein
<i>recQ</i> (609 aa) (one HRDC domain)	<i>Deide_11320</i> (731 aa) (two HRDC domains)	<i>DR_1289</i> (824 aa) ^c (three HRDC domains)	<i>Dgeo_1226</i> (195 aa !) frameshift? (one HRDC domain) (no RQC domain)	ATP-dependent DNA helicase RecQ
	<i>Deide_02180</i> (591 aa) (one HRDC domain)	<i>DR_2444</i> (603 aa) ^c (one HRDC domain)	<i>Dgeo_0021</i> (653 aa) (one HRDC domain)	Nucleic acid-binding protein, HRDC family
	<i>Deide_1p01280</i> (548 aa) (no RQC and HRDC domains)	-	-	ATP-dependent DNA helicase, RecQ family; partial COG0514
	<i>Deide_06510_3</i> (1683 aa) (no RQC and HRDC domains)	-	-	Multidomain protein: 1 is DnaQ, 2 is DinG, 3 is RecQ ^f
<i>recR</i> (201 aa)	<i>Deide_06340</i> (198 aa)	<i>DR_0198</i> (220 aa)	<i>Dgeo_1513</i> (222 aa)	Recombination and repair protein
<i>recT</i> (269 aa)	-	-	-	Recombinase, DNA renaturation
<i>recX</i> (166 aa)	<i>Deide_12350</i> (195 aa)	<i>DR_1310</i> (204 aa)	<i>Dgeo_1433</i> (191 aa)	Regulatory protein
<i>radA</i> (sms) (460 aa)	<i>Deide_12660</i> (449 aa)	<i>DR_1105</i> (503 aa)	<i>Dgeo_1212</i> (449 aa)	DNA repair protein RadA
<i>rusA</i> (<i>ybcP</i>) (120 aa)	-	-	-	Endonuclease/Holliday junction resolvase
<i>ruvA</i> (203 aa)	<i>Deide_09360</i> (202 aa)	<i>DR_1274</i> (201 aa)	<i>Dgeo_0726</i> (198 aa)	Holliday junction helicase subunit A; branch migration
<i>ruvB</i> (336 aa)	<i>Deide_18350</i> (334 aa)	<i>DR_0596</i> (333 aa)	<i>Dgeo_0404</i> (331 aa)	Holliday junction helicase subunit B; branch migration
<i>ruvC</i> (173 aa)	<i>Deide_20630</i> (169 aa)	<i>DR_0440</i> (179 aa)	<i>Dgeo_0327</i> (168 aa)	Holliday junction endonuclease
<i>ygqF</i> (138 aa)	<i>Deide_04280</i> (139 aa)	<i>DR_2509</i> (136 aa)	<i>Dgeo_0425</i> (232 aa)	Putative Holliday junction resolvase
<i>sbcB</i> (475 aa)	-	-	-	exodeoxyribonuclease I
<i>sbcC</i> (1048 aa)	<i>Deide_16170</i> (911 aa)	<i>DR_1922</i> (909 aa)	<i>Dgeo_0823</i> (910 aa)	ATP dependent dsDNA exonuclease
<i>sbcD</i> (400 aa)	<i>Deide_16180</i> (393 aa)	<i>DR_1921</i> (416 aa)	<i>Dgeo_0824</i> (395 aa)	ATP dependent dsDNA exonuclease
<i>ssb</i> (178 aa)	<i>Deide_00120</i> (297 aa)	<i>DR_0099</i> (301 aa)	<i>Dgeo_0165</i> (301 aa) (+ <i>Dgeo_2964</i> (283 aa), <i>Dgeo_2969</i> (352 aa), <i>Dgeo_3087</i> (200 aa) on plasmid)	Single-stranded DNA-binding protein

F. Other DNA repair related genes ^a

Gene name	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
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<i>mutT</i> and other Nudix hydrolases	18 proteins containing Nudix box	23 proteins containing Nudix box ^g	14 proteins containing Nudix box	Nudix hydrolases
<i>dnlJ</i> (671 aa)	Deide_12290 (686 aa) ^h Deide_1p00290 (686 aa) ^h	<i>DR_2069</i> (700 aa)	<i>Dgeo_0696</i> (684 aa)	DNA ligase, NAD-dependent
<i>gyrA</i> (875 aa)	<i>Deide_12520</i> (811 aa)	<i>DR_1913</i> (812 aa)	<i>Dgeo_1016</i> (809 aa)	DNA gyrase subunit A
<i>gyrB</i> (804 aa)	<i>Deide_15490</i> (674 aa)	<i>DR_0906</i> (663 aa)	<i>Dgeo_0546</i> (711 aa)	DNA gyrase subunit B
<i>topA</i> (865 aa)	<i>Deide_07410</i> (966 aa)	<i>DR_1374</i> (1021 aa)	<i>Dgeo_2001</i> (964 aa)	DNA topoisomerase I (Topo IA)
-	<i>Deide_00840</i> (344 aa)	<i>DR_0690</i> (346 aa)	<i>Dgeo_2058</i> (349 aa)	DNA topoisomerase IB
<i>radC</i> (222 aa)	-	-	-	DNA repair protein
<i>xni</i> (281 aa)	Deide_1p00132 (244 aa)	-	-	5'-3' exonuclease; exonuclease IX
-	-	<i>DR_1757</i> (328 aa)	-	nuclease-related domain (NERD) protein
<i>lexA</i> (202 aa)	<i>Deide_1p01870</i> (211 aa) <i>Deide_01180</i> (240 aa)	<i>DR_A0344 (lexA1)</i> (210 aa) <i>DR_A0074 (lexA2)</i> (248 aa)	<i>Dgeo_1366</i> (236 aa)	Transcriptional regulator, repressor of the SOS regulon, autoprotease
<i>polA</i> (928 aa)	<i>Deide_15130</i> (926 aa)	<i>DR_1707</i> (956 aa)	<i>Dgeo_1666</i> (907 aa)	DNA polymerase I
<i>polB</i> (783 aa)	Deide_1p00180 (765 aa)	-	-	DNA polymerase II
<i>dnaE</i> (1160 aa)	<i>Deide_21950</i> (1341 aa) Deide_1p01900 (1058 aa)	<i>DR_0507</i> (1335 aa)	<i>Dgeo_0255</i> (1322 aa)	DNA polymerase III alpha subunit Putative error-prone DNA polymerase DnaE2
<i>dnaQ</i> (243 aa)	<i>Deide_17790</i> (202 aa) Deide_05970 (204 aa) Deide_06510_1 (1683 aa) multidomain protein ^f : 1 is DnaQ, 2 is DinG, 3 is RecQ	<i>DR_0856</i> (197 aa)	<i>Dgeo_1818</i> (180 aa)	DNA polymerase III epsilon subunit (3'-5' exonuclease subunit)
<i>holE</i> (76 aa)	-	-	-	DNA polymerase III theta subunit
<i>dnaN</i> (366 aa)	<i>Deide_00020</i> (360 aa)	<i>DR_0001</i> (393 aa)	<i>Dgeo_0003</i> (360 aa) <i>Dgeo_3063</i> (367 aa) (plasmid)	DNA polymerase III beta subunit
<i>dnaX</i> (643 aa)	<i>Deide_01610</i> (762 aa)	<i>DR_2410</i> (615 aa)	<i>Dgeo_2135</i> (737 aa)	DNA polymerase III tau/gamma subunit
<i>holA</i> (343 aa)	<i>Deide_10170</i> (300 aa)	<i>DR_1244</i> (300 aa)	<i>Dgeo_0745</i> (312 aa)	DNA polymerase III delta subunit
<i>holB</i> (334 aa)	<i>Deide_21710</i> (318 aa)	<i>DR_2332</i> (321 aa)	<i>Dgeo_2262</i> (316 aa)	DNA polymerase III delta prime subunit
<i>holC</i> (147 aa)	-	-	-	DNA polymerase III chi subunit
<i>holD</i> (137 aa)	-	-	-	DNA polymerase III psi subunit
BS <i>yshC</i> (570 aa)	<i>Deide_07030</i> (568 aa)	<i>DR_0467</i> (572 aa)	<i>Dgeo_1609</i> (572 aa)	DNA polymerase, family X
<i>umuC</i> (422 aa)	-	-	-	DNA polymerase type-Y family; error-prone DNA polymerase; in conjunction with UmuD and RecA catalyses translesion DNA synthesis
<i>umuD</i> (139 aa)	-	-	-	In conjunction with UmuC and RecA facilitates translesion DNA synthesis; autoprotease
<i>dinB</i> (<i>dinP</i>) (351 aa)	-	-	-	Pol IV, DNA polymerase type-Y family, contains 1 UmuC domain

-	Deide_1p01880 (423 aa)	-	-	Related to putative Y-family DNA polymerase
<i>dinG</i> (716 aa)	Deide_06510_2 (1683 aa) multidomain protein ^f : 1 is DnaQ, 2 is DinG, 3 is RecQ	-	-	Predicted helicase; SOS inducer in <i>E. coli</i>
-	Deide_06520 (849 aa)	-	-	UvrD/REP helicase; COG0210, UvrD, Superfamily I DNA and RNA helicases
BS_ywqA (922 aa)	Deide_08980 (1132 aa)	<i>DR_1259</i> (600 aa) + <i>DR_1258</i> (916 aa) (2 genes or frameshift?)	<i>Dgeo_1491</i> (1126 aa)	DNA helicase SNF2/Rad54 family
-	Deide_17480 (689 aa)	<i>DR_1572</i> (frameshift)	-	Superfamily I DNA and RNA helicases (COG3973)
<i>dnaA</i> (467 aa)	Deide_00010 (459 aa)	<i>DR_0002</i> (466 aa)	<i>Dgeo_0001</i> (470 aa)	Chromosomal replication initiator protein
<i>dnaB</i> (471 aa)	Deide_04710 (448 aa)	<i>DR_0549</i> (448 aa)	<i>Dgeo_2037</i> (849 aa; intein-mediated protein splicing)	Replicative DNA helicase
<i>dnaC</i> (245 aa)	-	-	-	DNA replication protein
<i>dnaG</i> (581 aa)	Deide_04900 (572 aa)	<i>DR_0601</i> (571 aa)	<i>Dgeo_1910</i> (587 aa)	DNA primase
<i>dnaT</i> (179 aa)	-	-	-	Primosomal protein 1
<i>priA</i> (732 aa)	Deide_00480 (857 aa)	<i>DR_2606</i> (925 aa)	<i>Dgeo_0271</i> (841 aa)	Primosomal protein N ^o
<i>priB</i> (104 aa)	-	-	-	Primosomal replication protein n
<i>priC</i> (175 aa)	-	-	-	Primosomal replication protein N ^o
<i>rarA</i> (<i>mgsA</i> , <i>ycaJ</i>) (447 aa)	Deide_04980 (451 aa)	<i>DR_1898</i> (434 aa)	<i>Dgeo_1401</i> (451 aa)	Replication-associated recombination protein
G. Other radiation tolerance-associated genes in <i>D. deserti</i>, <i>D. radiodurans</i> and <i>D. geothermalis</i>^{a,i}				
<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description	
Deide_03030 (281 aa)	<i>DR_0167</i> (328 aa)	<i>Dgeo_0395</i> (289 aa)	IrrE, regulator of <i>recA</i> expression in <i>D. radiodurans</i>	
Deide_2p01380 (294 aa)	<i>DR_A0346</i> (300 aa)	<i>Dgeo_2628</i> (302 aa) (plasmid)	DNA damage repair protein PprA	
Deide_09150 (201 aa)	<i>DR_0423</i> (208 aa)	<i>Dgeo_0977</i> (201 aa)	DNA damage response protein DdrA; Rad52/22 double-strand break repair protein	
Deide_02990 (178 aa)	<i>DR_0070</i> (199 aa)	<i>Dgeo_0295</i> (178 aa)	DdrB	
Deide_23280 (232 aa)	<i>DR_0003</i> reversed (231 aa)	<i>Dgeo_0047</i> reversed (229 aa)	DdrC (<i>DR_0003</i> and <i>Dgeo_0047</i> probably incorrectly annotated, see main text)	
Deide_01160 (158 aa)	<i>DR_0326</i> (198 aa)	<i>Dgeo_2186</i> (160 aa)	DdrD	
Deide_11220 (228 aa)	<i>DR_0194</i> (227 aa)	<i>Dgeo_1282</i> (226 aa)	DdrE; Related to zinc metallopeptidase	
-	<i>DR_0219</i> (444 aa)	-	DdrF	
-	<i>DR_0227</i> (242 aa)	-	DdrG	
Deide_20641 (82 aa)	<i>DR_0438</i> reversed (92 aa)	<i>Dgeo_0322</i> (82 aa)	DdrH (<i>DR_0438</i> probably incorrectly annotated, see main text)	
Deide_12530 (205 aa)	<i>DR_0997</i> (260 aa)	<i>Dgeo_1015</i> (204 aa)	DdrI; Transcriptional regulator, Crp/Fnr family	

-	<i>DR_1263</i> (222 aa)	-	DdrJ
-	<i>DR_1264</i> (140 aa)	-	DdrK
-	<i>DR_1439</i> (175 aa)	-	DdrL
<i>Deide_02930</i> (180 aa)	<i>DR_2441</i> (170aa)	<i>Dgeo_0078</i> (168aa)	DdrN
<i>Deide_20570</i> (129 aa) ^j <i>Deide_3p02170</i> (129 aa) ^j	<i>DR_2574</i> (131aa)	<i>Dgeo_0336</i> (140aa)	DdrO; transcriptional regulator, XRE family
-	<i>DR_B0100</i> (210 aa)	-	DdrP
-	<i>DR_B0141</i> (168 aa)	-	HicB-related protein
-	<i>DR_1262</i> (531 aa)	-	ribonucleoprotein Ro/SS-A-related protein; involved in UV resistance in <i>D. radiodurans</i>
-	<i>DR_0171</i> (230 aa)	-	IrrI

^a The gene names are from *E. coli* whenever an *E. coli* ortholog exists, or from *B. subtilis* (with the prefix BS_). The sizes of the predicted gene products (in number of amino acid residues) are indicated. *D. deserti* genes in **blue and bold face** indicate supplementary genes when compared to *D. radiodurans* and *D. geothermalis*. Grey indicates gene products identified in proteome analysis after standard cultivation of *D. deserti*.

^b DR_0022 did not demonstrate any appreciable uracil-DNA glycosylase activity in a study by Sandigursky et al (1)

^c DR_2586 contains domain COG1722; this domain is not found in the DR_2586 homologs *Deide_02120* and *Dgeo_0027*

^d *D. deserti* plasmid P2 contains a “pseudogene” (*Deide_2p00840-Deide_2p00850-Deide_2p00860*, interrupted by 2 stop codons), whose putative product has 27% identity with BS_AddA, and which is probably in operon with *Deide_2p00830* encoding a protein with 25% identity with BS_AddB

^e In *D. radiodurans*, DR_1289 is required for resistance to DNA damaging agents, whereas DR_2444, which does not contain helicase and RQC domains, is not (2). All three HRDC domains are involved in DR_1289 RecQ function (3, 4)

^f A homolog of this multidomain protein *Deide_06510* is found in *Thermus thermophilus* HB27: TT_P0128 (1649 aa)

^g Most, if not all, of the *D. radiodurans* Nudix hydrolases are probably not functional homologs of MutT (5)

^h *Deide_12290* and *Deide_1p00290* have 57% identity

ⁱ DdrA, DdrE, DdrI and DdrN homologs with more than 40% identity are present in *T. thermophilus*. Other common genes/proteins are specific to *Deinococcus*.

^j *Deide_20570* and *Deide_3p02170* have 84% identity

1. Sandigursky M, Sandigursky S, Sonati P, Daly MJ, Franklin WA (2004) Multiple uracil-DNA glycosylase activities in *Deinococcus radiodurans*. DNA Repair (Amst) 3: 163-169.
2. Huang LF, Zhang SW, Hua XT, Gao GJ, Hua YJ (2006) Construction of the recQ double mutants and analysis of adversity in *Deinococcus radiodurans*. Wei Sheng Wu Xue Bao 46: 205-209.
3. Killoran MP, Keck JL (2006) Three HRDC domains differentially modulate *Deinococcus radiodurans* RecQ DNA helicase biochemical activity. J Biol Chem 281: 12849-12857.
4. Huang L, Hua X, Lu H, Gao G, Tian B, et al. (2007) Three tandem HRDC domains have synergistic effect on the RecQ functions in *Deinococcus radiodurans*. DNA Repair (Amst) 6: 167-176.
5. Xu W, Shen J, Dunn CA, Desai S, Bessman MJ (2001) The Nudix hydrolases of *Deinococcus radiodurans*. Mol Microbiol 39: 286-290.