

## SUPPLEMENTAL TABLE 1

### Primer Sets used for Quantitative RT-PCR

<b>Designation</b>	<b>Primer Sequence</b>
DR2340up	5'GTCAGCACCGGCAGCCTCAGCCTTGACCTC 3'
DR2340down	5'GATGGCGAGGGCCAGGGTGGTCTTGC 3'
DR1343up	5'CTTACCAGCCGCGAAGGGGCCTCCAAGC 3'
DR1343down	5'GCCAGCACGATGGAGAAGTCCTCGCC 3'
DR0003up	5'GTGCGGAGAGGGATGAATGAAGCGATGG 3'
DR0003down	5'GAACAGGTAGCCCGCAGCGAGCGCCAGAGC 3'
DR0070up	5'GAACGTGGAGCATGAAAGCCGGTTGCTGG 3'
DR0070down	5'CCAGTCGAAGTCGGCCTCGTTCTCGATGG 3'
DR0326up	5'GCTGCTGCAACTCGCGGCGTACATGAAGG 3'
DR0326down	5'CGTTTCGCCCTTGCTGGTGACGACTTCCG 3'
DR0423up	5'GGTGCAGGACCGACTCGACGCCGTTTGCC 3'
DR0423down	5'CCTCGCGGGTCACGCCGAGCACGGTCAGG 3'
DRA0346up	5'GAGCACGGCGGGCGTGGACAGCCAGATCG 3'
DRA0346down	5' CAGCCGCGCCTCATGGCGCAGGTGGTGCAG 3'

**SUPPLEMENTAL TABLE 2**

**Primer Sets used for Construction of the Strains and Plasmids used in the Study**

<b>Designation</b>	<b>Sequence</b>	<b>Use</b>
tnkkatA1	5'GCGAGGGCCTGAGGGCCATGGAGACCGAGGGCCCTGGACATTG AGAATGATTCTCAATATGGTGCAGGGAGCTTCGGGCC3'	Construction for pTNK101, pTNK102, pTNK103 and pTNK104
tnkcat1	5'GGTGCAGGGAGCTTCGGGCCTCTTGCCGCGCAGCAGAGCCAGC GAGGCGAAGGAGAGTGTATGGAGAAAAAATCACTGG3'	Construction for pTNK101
tnkcat2	5'TCGAAAGTTTAAACTCAGGCGTAGCAACCAGGCGTTTA3'	Construction for pTNK101
tnkkn1	5'GGTGCAGGGAGCTTCGGGCCTCTTGCCGCGCAGCAGAGCCAGC GAGGCGAAGGAGAGTGTATGAGCCATATTCAACGGGA3'	Construction for pTNK102
tnkkn2	5'TCGAAAGTTTAAACTTAGAAAACTCATCGAGCATCAA3'	Construction for pTNK102
tnkspc1	5'GGTGCAGGGAGCTTCGGGCCTCTTGCCGCGCAGCAGAGCCAGC GAGGCGAAGGAGAGTGTATGCGCTCACGCAACTGGTC3'	Construction for pTNK103
tnkspc2	5'TCGAAAGTTTAAACTTATTTGCCGACTACCTTGGTGAT3'	Construction for pTNK103
tnkhyg1	5'GGTGCAGGGAGCTTCGGGCCTCTTGCCGCGCAGCAGAGCCAGC GAGGCGAAGGAGAGTGTATGACACAAGAATCCCTGTT3'	Construction for pTNK104
tnkhyg2	5'TCGAAAGTTTAAACTCAGGCGCCGGGGGCGGTGTCCGG3'	Construction for pTNK104
tnk0003FW1	5'GCGCAAAGCGAAGTCGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK201

tnk0003FW2	5'GTTGCTGGTCACCTGCCGGGCGATGAG3'	Construction for pTNK201
tnk0003FW3	5'CAAGGTAGTCGGCAAATAACAAATCAGCACGGAAG3'	Construction for pTNK201
tnk0003RV1	5'TTCCGTGCTGATTTGTTATTTGCCGACTACCTTGG3'	Construction for pTNK201
tnk0003RV2	5'CCCTCAGGCCCTCGCGACTTCGCTTTGCGCTCCCA3'	Construction for pTNK201
tnk0003RV3	5'GCACGCGCCCTCATTTGGACTGGGTTC3'	Construction for pTNK201
tnk0003FW4	5'CTAGGCGTTGGGAGCGCAAAGCGAAGT3'	Verification of <i>ddrC</i> (DR0003) deletions
tnk0003RV4	5'AAATAGCCCTGCTTCCGTGCTGATTTG3'	Verification of <i>ddrC</i> (DR0003) deletions
tnk0070FW1	5'CCCCGATGTGTTATGAATTCGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK202
tnk0070FW2	5'CTGCGGCCTTACCTCAACACCTTCTGG3'	Construction for pTNK202
tnk0070FW3	5'GGTTGCTACGCCTGAAGCTTCTGAGCGGCGAAACGTGAC3'	Construction for pTNK202
DR0070up	5'ATGTGTTATGTTATTTACGTAAGGAGGAGG3'	Verification of <i>ddrB</i> (DR0070) deletion in TNK102 and derivatives
DR0070dn	5'ACGTTTCGCCGCTCAGAACGGCGTTTCTTC3'	Verification of <i>ddrB</i> (DR0070) deletion in TNK102 and derivatives
tnk0070RV1	5'GTTTCGCCGCTCAGAAGCTTCAGGCGTAGCAACCAGGCG3'	Construction for pTNK202
tnk0070RV2	5'CCCTCAGGCCCTCGCGAATTCATAACACATCGGGGAAGCC3'	Construction for pTNK202
tnk0070RV3	5'GCGAGAACGTCAAGCAGTACGAGGTGC3'	Construction for pTNK202

tnk0070FW4	5'GACACTGGCACCGGCTTCCCCGATGTG3'	Verification of <i>ddrB</i> (DR0070) deletion in TNK122 and derivatives
tnk0070RV4	5'CCTGCTTTTTGCGTCACGTTTCGCCGC3'	Verification of <i>ddrB</i> (DR0070) deletion in TNK122 and derivatives
tnk0326FW1	5'TGCTAGAAAAAGCTCGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK204
tnk0326FW2	5'TTTCTCAGTGCTGTCTTACTTGACGAG3'	Construction for pTNK204 and verification of <i>ddrD</i> (DR0326) deletions
tnk0326RV3	5'ACGACCAGAACGACCTCGCCGTCATCC3'	Construction for pTNK204 and verification of <i>ddrD</i> (DR0326) deletions
tnk0326FW3	5'GATGAGTTTTTCTAATTTTTCAGGGTATCCATAGC3'	Construction for pTNK204
tnk0326RV1	5'GGATACCCTGAAAAATTAGAAAACTCATCGAGCA3'	Construction for pTNK204
tnk0326RV2	5'CCCTCAGGCCCTCGCGAGCTTTTTCTAGCATCCTG3'	Construction for pTNK204
tnk0423FW1	5'CAGGCTGCGGGTCATGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK205
tnk0423FW2	5'GTAGACCTTGCTCAGCGCGGTGATGTC3'	Construction for pTNK205
tnk0423FW3	5'GCCCCGGCGCCTGAGCATTTAGTTTAGAACAGAA	Construction for pTNK205
tnk0423FW4	GCTCGGCAGAGGTCAGGCTGCGGGTCA3'	Verification of <i>ddrA</i> (DR0070) deletion
tnk0423RV4	5'GGACGAAGGTAGAGGCGGCGGTGGAGG3'	Verification of <i>ddrA</i> (DR0070)

		deletion
tnk0423RV1	5'TTCTAAACTAAATGCTCAGGCGCCGGGGGCGGTGT3'	Construction for pTNK205
tnk0423RV2	5'CCCTCAGGCCCTCGCATGACCCGCAGCCTGACCTC3'	Construction for pTNK205
tnk0423RV3	5'ATCTCCGAACTCAGGCGACCTTCATAG3'	Construction for pTNK205
tnkA0346FW1	5'TAATAAAGGCAGTATGAATTCGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK207
tnkA0346FW2	5'CGGCGAGTTGTGCGGGAGCAGGTGGTC3'	Construction for pTNK207 and verification of <i>pprA</i> (DRA0346) deletion in TNK105 and derivatives
tnkA0346RV3	5'CTCCCAGAAATCCGGCTGCTCGGCCAG3'	Construction for pTNK207 and verification of <i>pprA</i> (DRA0346) deletion in TNK105 and derivatives
tnkA0346FW3	5'GAATTCTTGACTGCAGCTCGAGTGAGTCAAGAAAAGCAAAGG3'	Construction for pTNK207
tnkA0346FW5	5'CCTTCGACACCTTGATGAGCACGGCGGGCG3'	Verification of <i>pprA</i> (DRA0346) deletion in TNK123 and derivatives
tnkA0346RV7	GCACTTCGGACAGTTGGCGGGTGGTCACGC	Verification of <i>pprA</i> (DRA0346) deletion in TNK123 and derivatives
tnkA0346RV1	5'GCTTTTCTTGACTCACTCGAGTCAGGTCGAGGTGGCCCGGC3'	Construction for pTNK207
tnkA0346RV2	5'CTCGAGCTGCAGTCAAGAATTCATACTGCCTTTATTATGCCC3'	Construction for pTNK207
tnk2340FW1	5'ACCCATGAGCAAGGAATTCGCGAGGGCCTGAGGGCCATG3'	Construction for pTNK210
tnk2340FW2	5'GGCGTGGCTGATTCCGAGTGCCGAGGCGCT3'	Construction for pTNK210

tnk2340FW3	5'ATTCTGACTGCAGAAGCTTGTAACCTCCTCTTGCTGCG3'	Construction for pTNK210
tnk2340FW5	5'CGCACATCACCTCGCCCGCAAGAAGG3'	Verification of <i>recA</i> (DR2340) deletions
tnk2340RV5	5'GACGTAAAACTCCCCTGTCTTCACCC3'	Verification of <i>recA</i> (DR2340) deletions
tnk2340RV1	5'CAAGAGGAGGTTTACAAGCTTCAGGCGTAGCAACCAGGCG3'	Construction for pTNK210
tnk2340RV2	5'AAGCTTCTGCAGTCAGAATTCCTTGCTCATGGGTGCTCC3'	Construction for pTNK210
tnk2340RV3	5'CCCGCTGCTTGGTTTGCCGCACCATCGTCA3'	Construction for pTNK210

**SUPPLEMENTAL TABLE 3**

**Mean Cy5/Cy3 ratios obtained for those genes in an exponential phase population of *D. radiodurans* R1 exposed to 3,000Gy  $\gamma$  radiation.**

AMT	Identifier	Gene Name/Annotation	0 Hour		0.5 Hour		1 Hour	
			Mean	Range	Mean	Range	Mean	Range
<b><u>DNA Metabolism</u></b>								
-	<b>DR0596</b>	<i>ruvB</i> / Holliday junction DNA helicase	<b>11</b>	6-15	-	-	<b>6</b>	4-9
+*	<b>DR2340</b>	<i>recA</i> / recombinase	<b>7</b>	4-14	<b>10</b>	4-25	<b>6</b>	4-10
+	<b>DR1771</b>	<i>uvrA</i> / exonuclease ABC, subunit A	<b>6</b>	5-8	<b>7</b>	5-11	<b>5</b>	5-6

+	<b>DR2275</b>	<i>uvrB</i> / exonuclease ABC, subunit B	<b>7</b>	4-8	<b>7</b>	4-9	<b>4</b>	4-5
+	<b>DR1913</b>	<i>gyrA</i> / DNA gyrase, subunit A	<b>13</b>	4-17	<b>10</b>	7-17	-	-
+	<b>DR0906</b>	<i>gyrB</i> / DNA gyrase, subunit B	<b>8</b>	6-13	<b>8</b>	6-10	-	-

#### Adaptation to Oxidative Stress

+	<b>DR1998</b>	<i>katA</i> / catalase	<b>4</b>	3-6	-	-	-	-
+	<b>DR2220</b>	<i>terB</i> / tellurium resistance protein	<b>4</b>	4	-	-	-	-
-	<b>DR2224</b>	<i>terZ</i> / tellurium resistance protein	<b>7</b>	5-13	<b>9</b>	4-20	<b>4</b>	<b>4</b>
+	<b>DR1849</b>	<i>mrsA</i> / peptidomethionine sulfoxide reductase	<b>4</b>	3-4	<b>3</b>	3	-	-



-	<b>DRB0092</b>	Dps family	<b>5</b>	4-5	<b>8</b>	8-10	-	-
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**Metabolism / Energy Acquisition**

+	<b>DR0702</b>	v-type ATP synthase, D subunit	-	-	<b>3</b>	3-4	-	-
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+	<b>DR0970</b>	<i>etfA</i> / electron transfer flavoprotein, $\alpha$ subunit	<b>4</b>	3-4	<b>4</b>	4	<b>3</b>	<b>3</b>
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+	<b>DR0971</b>	<i>etfB</i> / electron transfer flavoprotein, $\beta$ subunit	<b>5</b>	4-6	<b>4</b>	3-4	-	-
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+	<b>DR1019</b>	<i>glpD</i> / glycerol-3-phosphate dehydrogenase	-	-	<b>3</b>	3	-	-
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+	<b>DR2195</b>	glucan phosphorylase,	<b>4</b>	3-6	<b>7</b>	5-9	<b>3</b>	<b>3</b>
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+	<b>DR2206</b>	<i>citE</i> /citrate lyase, beta subunit	-	-	<b>9</b>	3-20	<b>5</b>	4-7
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+	<b>DR2594</b>	<i>chII</i> / Mg-chelatase	-	-	<b>4</b>	4-5	-	-
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### Putative Regulatory Proteins

+	<b>DR0692</b>	<i>glnB</i> /nitrogen regulatory protein P-II	-	-	<b>9</b>	8-9	-	-
+	<b>DR1082</b>	light-repressed protein A, putative	<b>3</b>	3	-	-	-	-
+	<b>DR2338</b>	<i>cinA</i> /competence inducible protein	<b>5</b>	3-9	<b>4</b>	4-6	<b>5</b>	4-8

### RNA Metabolism

-	<b>DR2010</b>	16S rRNA processing protein RimM, putative	<b>3</b>	3	-	-	-	-
-	<b>DR2339</b>	2'-5' RNA ligase, putative	<b>6</b>	4-7	<b>5</b>	5-6	<b>5</b>	4-6
-	<b>DR1262</b>	<i>rsr</i> /ribonucleotide Ro/SS-A- related protein	-	-	<b>4</b>	4-5	-	-

+	<b>DR2374</b>	<i>nrdA</i> / ribonucleoside reductase, alpha subunit	-	-	-	-	<b>4</b>	3-4
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**Protein Synthesis**

+	<b>DR0101</b>	<i>rspR</i> /ribosomal protein S18	<b>4</b>	4	<b>4</b>	4	-	-
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**Protein Fate**

+	<b>DR0349</b>	<i>lon2</i> /ATP-dependent protease LA	-	-	<b>6</b>	4 - 8	-	-
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-	<b>DR1114</b>	heat shock protein, HSP20 family	<b>11</b>	9-12	<b>4</b>	4	-	-
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+	<b>DR1459</b>	putative serine protease, subtilase family	<b>3</b>	3	<b>3</b>	3	-	-
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+	<b>DR2325</b>	putative serine protease, subtilase family	-	-	-	-	<b>6</b>	4-7
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interrupted by transposon

**Transport**

+	<b>DR0561</b>	<i>malE</i> / maltose transporter	-	-	<b>4</b>	3-5	-	-
-	<b>DR0693</b>	<i>amtB</i> / ammonium transporter	-	-	<b>4</b>	4-5	-	-
+	<b>DR1709</b>	NRAMP protein	<b>6</b>	4-7	-	-	-	-
+	<b>DRA0135</b>	putative ABC transporter	-	-	<b>4</b>	4	-	-

**Unknown Function**

-	<b>DR0003</b>	hypothetical	<b>12</b>	6-36	<b>12</b>	4-32	<b>8</b>	6-13
+	<b>DR0025</b>	hypothetical	<b>3</b>	3	-	-	-	-
+	<b>DR0052</b>	hypothetical	<b>5</b>	4-5	-	-	<b>4</b>	4
-	<b>DR0053</b>	hypothetical	<b>5</b>	4-6	-	-	-	-
+	<b>DR0070</b>	hypothetical	<b>13</b>	4-27	<b>7</b>	3-20	<b>8</b>	3-13

+	<b>DR0194</b>	conserved hypothetical	<b>4</b>	4	-	-	-	-
+	<b>DR0219</b>	hypothetical	<b>6</b>	6	<b>4</b>	3-4	-	-
+	<b>DR0227</b>	hypothetical	<b>4</b>	4-5	-	-	-	-
+	<b>DR0326</b>	hypothetical	<b>12</b>	6-26	<b>13</b>	5-20	<b>8</b>	5-13
-	<b>DR0361</b>	predicted hydrolase	-	-	-	--	<b>4</b>	3-4
+	<b>DR0423</b>	hypothetical	<b>18</b>	7-50	<b>18</b>	5-26	<b>16</b>	4-25
-	<b>DR0438</b>	hypothetical	<b>3</b>	3-4	-	-	-	-
+	<b>DR0491</b>	conserved hypothetical	<b>4</b>	4-5	<b>6</b>	3-8	-	-
+	<b>DR0533</b>	hypothetical	<b>4</b>	4	<b>3</b>	3	<b>5</b>	5
-	<b>DR0659</b>	<i>frnE</i> / predicted dithiol- disulfide isomerase	<b>4</b>	4	-	-	-	-
-	<b>DR0997</b>	predicted cyclic nucleotide- binding domain /CRP family	<b>4</b>	3-6	-	-	-	-
+	<b>DR1142</b>	hypothetical	<b>5</b>	4-8	-	-	-	-
+	<b>DR1143</b>	hypothetical	<b>5</b>	4-8	-	-	-	-

+	<b>DR1263</b>	conserved hypothetical	-	-	<b>4</b>	4-6	-	-
-	<b>DR1264</b>	hypothetical	-	-	<b>6</b>	4-8	-	-
+	<b>DR1315</b>	hypothetical	-	-	<b>5</b>	3-8	-	-
+	<b>DR1370</b>	hypothetical	-	-	<b>4</b>	3-6	-	-
+	<b>DR1422</b>	hypothetical	-	-	<b>4</b>	3-4	-	-
+	<b>DR1439</b>	hypothetical	-	-	<b>6</b>	3-11	-	-
-	<b>DR1440</b>	authentic frameshift	<b>5</b>	3-9	<b>10</b>	9-13	-	-
+	<b>DR1465</b>	hypothetical	-	-	<b>4</b>	3-4	-	-
+	<b>DR1803</b>	hypothetical	<b>4</b>	3-4	-	-	<b>5</b>	4-5
+	<b>DR2073</b>	hypothetical	<b>5</b>	3-7	<b>4</b>	4-5	<b>4</b>	4-6
-	<b>DR2309</b>	hypothetical	-	-	-	-	<b>4</b>	4
-	<b>DR2414</b>	hypothetical	-	-	<b>4</b>	3-4	-	-
-	<b>DR2441</b>	hypothetical	<b>9</b>	4-15	<b>7</b>	4-11	<b>6</b>	5-6
+	<b>DR2563</b>	hypothetical			<b>3</b>	3	-	-
-	<b>DR2574</b>	predicted helix-turn-helix	<b>8</b>	3-14	<b>7</b>	3-11	<b>6</b>	4-11

XRE - family

+	<b>DRA0346</b>	pprA / DNA damage repair protein	<b>15</b>	6-20	<b>12</b>	8-13	<b>9</b>	4-14
+	<b>DRB0100</b>	hypothetical	<b>4</b>	4-5	-	-	-	-
-	<b>DRB0110</b>	hypothetical	-	-	-	-	<b>4</b>	3-5
-	<b>DRB0141</b>	<i>hicB</i> / uncharacterized protein	-	-	<b>4</b>	4-5	-	-
+	<b>DRB0142</b>	hypothetical	-	-	<b>4</b>	4	-	-

\* A (+) sign indicates that an accurate mass tag has been reported for the protein encoded by this locus (LIPTON *et al.* 2002).

## SUPPLEMENTAL TABLE 4

Relative expression of seven genes induced following the exposure of *D. radiodurans* R1 to 3,000 Gy  $\gamma$  radiation

Identifier	Gene Name	Mean Ratio (Range)		
		0 Hour	0.5 Hour	1 Hour
DR2340	<i>recA</i>	8 (4-12)	12 (10-14)	6 (3-7)
DR1343	<i>gap</i>	1 (0.1-1.2)	1 (0.4-1.5)	1 (0.4-3)
DR0003	hypothetical	7 (5-10)	8 (4-12)	15 (10-21)
DR0070	hypothetical	42 (41-43)	39 (37-41)	12 (12-13)
DR0326	hypothetical	11 (7-16)	11 (10-13)	4 (4)
DR0423	hypothetical	11 (8-19)	27 (26-28)	12 (10-16)
DRA0346	hypothetical	5 (4-6)	7 (7)	4 (3-5)

Values are the means of three independent experiments. The ranges of values obtained are found within adjacent parentheses.



**SUPPLEMENTAL TABLE 5**

**Mean Cy5/Cy3 ratios obtained for those genes in an exponential phase population of *D. radiodurans* R1 recovering from desiccation**

AMT	Identifier	Gene Name/Annotation	0 Hour		0.5 Hour		1 Hour	
			Mean	Range	Mean	Range	Mean	Range
<b><u>DNA Metabolism</u></b>								
-	<b>DR0596</b>	<i>ruvB</i> / Holliday junction DNA helicase	4	4	4	3-5	-	-
+*	<b>DR2340</b>	<i>recA</i> / recombinase	4	3-5	4	4-5	3	3
+	<b>DR1771</b>	<i>uvrA</i> / exinuclease ABC, subunit A	3	3	-	-	-	-

+	<b>DR2275</b>	<i>uvrB</i> / exonuclease ABC, subunit B	-	-	5	4-6	3	3
+	<b>DR1913</b>	<i>gyrA</i> / DNA gyrase, subunit A	6	5-7	4	3-5	5	3-12
+	<b>DR0906</b>	<i>gyrB</i> / DNA gyrase, subunit B	4	3-4	5	4-5	-	-

### Adaptation to Oxidative Stress

+	<b>DR2220</b>	<i>terB</i> / tellurium resistance protein	4	4	5	4-5	-	-
-	<b>DR2224</b>	<i>terZ</i> / tellurium resistance protein	4	4	4	4	-	-

### Metabolism / Energy Acquisition

+	<b>DR0567</b>	<i>ilvA</i> / threonine dehydratase	4	4-5	-	-	-	-
-	<b>DR2562</b>	<i>ubiE</i> , methylase	-	-	4	3-4	-	-

### Putative Regulatory Proteins

-	<b>DR2306</b>	<i>merR</i> / transcriptional regulator	3	3-4	-	-	-	-
+	<b>DR2338</b>	<i>cinA</i> /competence inducible protein	4	4	3	3-4	-	-

### RNA Metabolism

-	<b>DR2339</b>	2'-5' RNA ligase, putative	3	3	4	4-5	-	-
-	<b>DR1262</b>	rsr/ribonucleotide Ro/SS-A- related protein	-	-	3	3-4	-	-

### Protein Synthesis

-	<b>DR0825</b>	<i>rpmE</i> / ribosomal protein L13	-	-	-	-	3	3
+	<b>DR2043</b>	<i>rplL</i> / /ribosomal protein L7/L12	4	4-5	-	-	-	-

### Protein Fate

+	<b>DR0349</b>	<i>lon</i> / ATP dependent protease	-	-	4	4-5	-	-
+	<b>DR0606</b>	<i>groES</i> / chaperonin	-	-	4	4	-	-
+	<b>DR0607</b>	groEL / chaperonin	-	-	3	3-4	-	-
-	<b>DR1114</b>	heat shock protein, HSP20 family	12	6-15	12	5-15	10	8-14
+	<b>DR1046</b>	<i>clpB</i> / ATP-dependent Clp protease,	10	10	-	-	-	-

### Transport

+	<b>DR1709</b>	NRAMP protein	5	4-6	4	4	-	-
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-	<b>DR2589</b>	iron ABC transporter, permease protein	4	3-4	-	-	-	-
+	<b>DR2118</b>	<i>livF</i> , ABC-type branched-chain amino acid transport	5	3-10	-	-	3	3

### **Unknown Function**

-	<b>DR0003</b>	hypothetical	10	5-16	8	4-13	10	4-13
+	<b>DR0070</b>	hypothetical	8	6-10	7	5-13	9	4-13
-	<b>DR0138</b>	conserved hypothetical	4	3-4	-	-	-	-
-	<b>DR0145</b>	hypothetical	4	4-5	-	-	-	-
+	<b>DR0194</b>	conserved hypothetical	5	5	4	4-5	-	-
-	<b>DR0203</b>	conserved hypothetical	-	-	-	-	3	3
+	<b>DR0219</b>	hypothetical	6	4-8	5	4-5	3	3
+	<b>DR0227</b>	hypothetical	4	4	-	-	4	4
+	<b>DR0253</b>	hypothetical	5	4-5	-	-	-	-

-	<b>DR0270</b>	<i>elaC</i> / metal-dependent hydrolases	3	3-4	-	-	-	-
+	<b>DR0326</b>	hypothetical	9	6-11	6	4-9	6	3-10
+	<b>DR0337</b>	hypothetical	4	3-4	-	-	-	-
-	<b>DR0338</b>	hypothetical	4	4	4	3-5	-	-
-	<b>DR0404</b>	hypothetical	5	5-6	9	5-12	-	-
-	<b>DR0422</b>	conserved hypothetical	-	-	5	5	-	-
+	<b>DR0423</b>	hypothetical	12	10-15	8	3-10	8	4-12
-	<b>DR0438</b>	hypothetical	5	4-6	4	3-6	5	3-10
+	<b>DR0475</b>	predicted ABC transporter with duplicated ATPase domains	4	3-4	-	-	-	-
+	<b>DR0491</b>	conserved hypothetical	4	4-5	6	3-8	-	-
-	<b>DR0492</b>	conserved hypothetical	7	4-8	-	-	-	-
+	<b>DR0621</b>	Predicted ATPase MoxR family	4	4-5	-	-	-	-
-	<b>DR0659</b>	fnE / predicted dithiol-disulfide	6	4-7	-	-	5	3-6

		isomerase							
-	<b>DR0661</b>	hypothetical	-	-	3	3-4	-	-	-
+	<b>DR0800</b>	hypothetical	4	3-5	-	-	-	-	-
+	<b>DR0955</b>	hypothetical			5	5	-	-	-
+	<b>DR0985</b>	conserved hypothetical	3	3	-	-	-	-	-
-	<b>DR0997</b>	predicted cyclic nucleotide-binding domain /CRP family	11	9-12	5	4-7	6	5-7	-
-	<b>DR1004</b>	emrE / predicted cation transporter	-	-	6	5-7	-	-	-
+	<b>DR1263</b>	conserved hypothetical	4	4	3	3-4	-	-	-
-	<b>DR1264</b>	hypothetical	4	4	5	4-7	5	5	-
+	<b>DR1439</b>	hypothetical	4	3-4	3	3-4	-	-	-
-	<b>DR1440</b>	authentic frameshift	4	3-4	-	-	-	-	-
-	<b>DR1994</b>	hypothetical	4	4-5	4	3-4	4	4-5	-
-	<b>DR2142</b>	conserved hypothetical	4	4	4	3-5	5	4-5	-

+	<b>DR2143</b>	conserved hypothetical	5	4-5	3	3-4	-	-
-	<b>DR2187</b>	<i>cfa</i> , cyclopropane fatty acid synthase, putative	3	3	-	-	-	-
+	<b>DR2218</b>	hypothetical	-	-	-	-	4	3-4
+	<b>DR2279</b>	predicted Zn-dependent dehydrogenase	3	3	-	-	-	-
-	<b>DR2436</b>	hypothetical	4	3-4	-	-	-	-
-	<b>DR2441</b>	hypothetical	4	3-5	4	3-5	5	4-6
-	<b>DR2494</b>	conserved hypothetical	-	-	3	3-4	3	3-4
-	<b>DR2573</b>	hypothetical	-	-	3	3-4	-	-
-	<b>DR2574</b>	predicted helix-turn-helix XRE - family	5	3-9	6	4-8	7	4-8
+	<b>DRA0345</b>	hypothetical	3	3-4	-	-	-	-
+	<b>DRA0346</b>	<i>pprA</i> / DNA damage repair protein	9	4-10	5	3-8	-	-



+	<b>DRB0100</b>	hypothetical	-	-	5	4-5	-	-
-	<b>DRB0141</b>	<i>hicB</i> / uncharacterized protein	3	3	-	-	-	-
-	<b>DRC0020</b>	authentic frameshift	-	-	4	4-6	-	-
-	<b>DRC0021</b>	hypothetical	-	-	5	3-8	-	-

\*A (+) sign indicates that an accurate mass tag has been reported for the protein encoded by this locus (LIPTON *et al.* 2002).