Genome Sequence and Transcriptome Analysis of the Radioresistant Bacterium *Deinococcus gobiensis*: Insights into the Extreme Environmental Adaptations

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Abstract

The desert is an excellent model for studying evolution under extreme environments. We present here the complete genome and ultraviolet (UV) radiation-induced transcriptome of *Deinococcus gobiensis* I-0, which was isolated from the cold Gobi desert and shows higher tolerance to gamma radiation and UV light than all other known microorganisms. Nearly half of the genes in the genome encode proteins of unknown function, suggesting that the extreme resistance phenotype may be attributed to unknown genes and pathways. *D. gobiensis* also contains a surprisingly large number of horizontally acquired genes and predicted mobile elements of different classes, which is indicative of adaptation to extreme environments through genomic plasticity. High-resolution RNA-Seq transcriptome analyses indicated that 30 regulatory proteins, including several well-known regulators and uncharacterized protein kinases, and 13 noncoding RNAs were induced immediately after UV irradiation. Particularly interesting is the UV irradiation induction of the *phrB* and *recB* genes involved in photoreactivation and recombinational repair, respectively. These proteins likely include key players in the immediate global transcriptional response to UV irradiation. Our results help to explain the exceptional ability of *D. gobiensis* to withstand environmental extremes of the Gobi desert, and highlight the metabolic features of this organism that have biotechnological potential.

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Introduction

The order Deinococcales contains 50 species of extremely ionizing radiation (IR) and UV tolerant bacteria (http://www.bacterio.cict.fr/) [1]. *D. radiodurans* R1, isolated from canned meat that had spoiled following exposure to X-rays, was sequenced first [2]. *D. radiodurans* has 200-fold greater resistance to ionizing radiation and 20-fold greater resistance to UV radiation than *Escherichia coli* [3], but it encodes approximately the same number and types of DNA repair proteins as *E. coli*, and no unique DNA repair system was found [3,4]. Recently, the genome sequences of the slightly thermophilic *D. geothermalis* DSM11300, isolated from a hot spring, *D. deserti* VCD115, isolated from the Sahara desert, *Truepera radiovictrix* RQ-24, isolated from hot spring runoff on the Island of Sao Miguel, and *D. maricopensis* LB-34, isolated from the Sonoran Desert soil, were published [5–8]. Besides, the sequence of the complete genome of *D. proteolyticus* MRP is available under GenBank accession number CP002536. Investigation of the biology and biochemistry of *Deinococcus spp.* has benefited from the availability of genomic information and the development of genetic tools, but the extreme resistance phenotype of *Deinococcus spp.* is still not fully understood [9]. Comparative genomics combined with microarray and proteomic analysis suggest that the extreme resistance phenotype results from a combination of different molecular mechanisms [5,6,10–12].

About 10% of the Earth's terrestrial surface is covered by desert. The Gobi desert of northwestern China is a cold, arid biotope with cycles of extreme temperatures, prolonged dryness, and intense solar radiation [13]. Despite the extreme challenges of the desert, diverse microorganisms have adapted and colonized this harsh environment. Thus, the desert biosphere is an excellent venue for studying evolution under extreme conditions, and it provides a useful gene pool for genetic engineering. One of the major stresses for bacteria inhabiting the surface sands of the desert is intense solar UV radiation-induced damage. In general, the capacity of prokaryotes to withstand significant UV radiation requires a wide array of physiological responses, including transcriptional regulation and cellular repair of irradiation-induced damage [11,14,15].

Several studies have focused on cellular recovery following exposure to UV irradiation and have shown that induction and repression of UV radiation-responsive genes occurs in a time-dependent manner [16–18]. Currently, very little is known about the immediate transcriptome response to UV irradiation.

We recently characterized a new bacterial species, *Deinococcus gobiensis* I-0, that was isolated from the upper sand layers of the cold Gobi desert of the Xinjiang region in China [19]. This strain shows higher tolerance for gamma radiation and UV light than all other known *Deinococcus* strains [19]. To obtain a comprehensive understanding of the molecular mechanisms underlying the resistance phenotype of *Deinococcus*, the genome of *D. gobiensis* was sequenced and compared to those of the three most closely related sequenced bacterial strains, *D. radiodurans* R1, *D. geothermalis* DSM11300, and *D. deserti* VCD115, which were isolated from canned meat, a hot spring, and the hot Sahara desert, respectively [3–6]. This study also provides the first transcriptome analysis investigating the UV resistance of *Deinococcus*. In particular, we identified a subset of poorly characterized UV irradiation-induced genes that may provide clues to the adaptation of *Deinococcus* to extreme environments.

Results

Genome features

The genome of *D. gobiensis* I-0 is composed of seven replicons: a 3.1 Mb main chromosome and six plasmids from 433 to 53 kb (Figure 1 and Table 1, GenBank accession numbers CP002191–CP002197 for the main Chromosome and Plasmids P1–P6, respectively). The chromosome and the 433 kb plasmid P1 have an average GC content of 71%, higher than that of the six other sequenced Deinococcales species (Table S1), and similar to that of the extreme thermophile *Thermus thermophilus* [20]. The genome of *D. gobiensis* contains 4,340 predicted coding sequences (CDSs), 46 tRNA genes, and 15 rRNA genes, and is larger than those of the six other published Deinococcales species (Table S1).

Phylogenetic analyses using only the orthologous proteins that occur in 14 sequenced strains from the phylum Deinococcus-Thermus showed that *Deinococcus* strains belong to the same branch (Figure S1). Further phylogenetic analyses showed that *D. gobiensis*, *D. radiodurans*, *D. geothermalis* and *D. deserti* belong to the same deeper branch and *D. gobiensis* was more closely related to *D. radiodurans* than to *D. deserti* and *D. geothermalis* (Figure 2). Pairwise comparisons of the *Deinococcus* genomes revealed limited synteny (Figure S2). The most striking feature was the cross patterns that indicate frequent symmetrical exchanges of genes, possibly by recombination between the bidirectional replication forks [21,22]. There were no long stretches of synteny, indicating that the *Deinococcus* genomes exhibit remarkable plasticity involving gene rearrangements, acquisition, and loss (Figure S2). A 354-kb stretch of the main chromosome that is populated by 316 genes lacks a single functional COG prediction (Figure 1, circles 2 and 3; grey DGo_CA0296–DGo_CA0612, 306 kb–660 kb). BLAST searches revealed that 262 (83%) of the 316 genes have counterparts in other *Deinococcus* species, although they were dispersed throughout the genomes. We suggest the name "Grey Heaven of *D. gobiensis*" for this intriguing gene cluster which appears to underpin the unprecedented resistance of deinococci.

Of the 4,340 CDSs, 55% (2,376/4,340) were classified by Clusters of Orthologous Groups (COGs), a lower percentage than for the other deinococci (75% in *D. radiodurans*, 85% in *D. deserti* and 79% in *D. geothermalis*). 1,534 (35%) of the *D. gobiensis* CDSs were hypothetical proteins, and 834 (19%) were orphans without precedent. To identify the functional gene categories that characterize the cold desert adaptation in deinococci, we compared the genomes of *D. gobiensis* and other three related *Deinococcus* species (Figure 3). *D. gobiensis* and *D. deserti* are similar in each COG category. Notably, the two desert species have more genes than the other two published species in most categories, especially in energy production and conversion, carbohydrate transport and metabolism, transcription, cell wall/membrane/envelope biogenesis, inorganic ion transport and metabolism, signal transduction mechanisms. *D. gobiensis* also has more genes for replication, recombination and repair, cell motility, intracellular trafficking, secretion, and vesicular transport, and defense mechanisms, but fewer genes for translation and nucleotide metabolism genes. This COG characteristic is similar to functional gene categories that are associated with cold adaptation of the psychrophilic *Methanococcoides burtonii* [23].

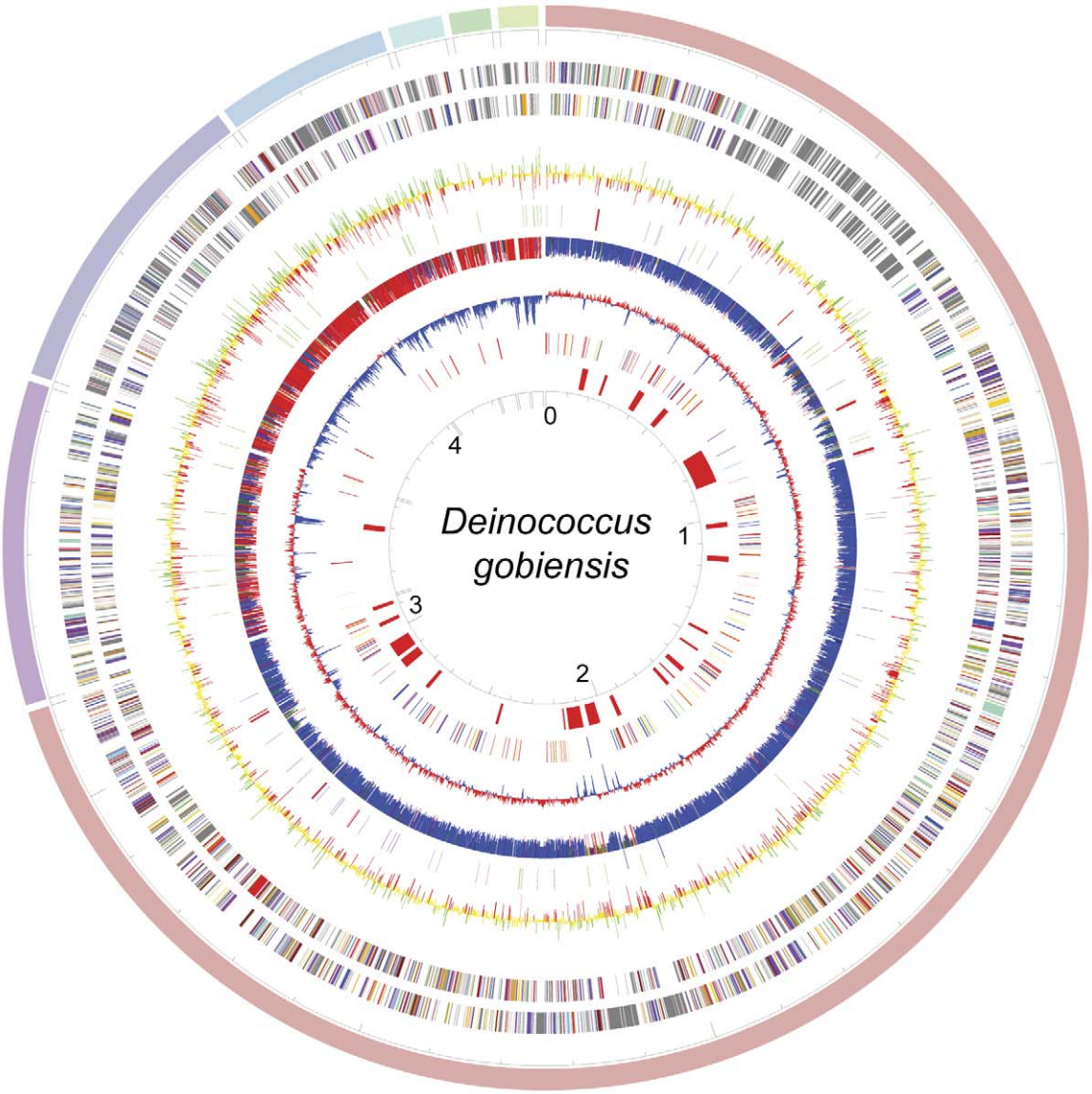
Transcriptome profiling

The transcriptome was analyzed using high throughput cDNA sequencing (RNA-Seq), that uses deep sequencing to assess the transcriptional activity of annotated genes, reveal previously unannotated genes and identify non-coding RNAs (ncRNAs) [24,25]. We found that 4,325 of the 4,340 CDSs and 45 non-coding RNAs were detected under normal growth conditions (The RNA-Seq raw data of are available from the NCBI Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE29088). The accuracy of the RNA-seq data was verified by quantitative real-time RT-PCR analysis (using 16 S rRNA as a control) of eight selected genes qRT-PCR (Table S2). In total, 638 plausible transcriptional start sites (TSS) were identified on the chromosome, and 362 on the six plasmids (Table S3). Furthermore, cDNAs for almost all of the CDSs of unknown function (2,029/2,041) were detected.

Bacteria generally have a global transcriptional response after UV irradiation that initiates subsequent recovery from the radiation damage. Immediately following UV irradiation, a total of 390 genes (9% of the genome) were induced, and 754 genes (17%) were repressed (Table S4). Approximately 8% of all *D. gobiensis* genes were predicted to be involved in regulation, which is the same as for *D. radiodurans* and also for *E. coli*. The regulators include six sigma factors (*rpoD*, *sigE*, *sigK*, *sig3*, *sig4* and *sig5*), 54 sensor kinases and 129 transcriptional regulators. Among those, 30 were induced, and 60 were repressed. In bacteria, noncoding RNAs often coordinate the adaptation to environmental changes, integrate environmental signals, and control target-gene expression [26]. We observed that 13 ncRNAs were upregulated, and 22 were downregulated. Moreover, a total of 61 predicted proteins were constitutively expressed at high levels ($\geq$1% of total mRNA) before and after UV irradiation, including a heat shock protein (IbpA), a phage shock protein (PspA), cold shock proteins (PprM1 and PprM2), DNA damage response proteins (DdrE and DdrO), chaperones (DnaK, DnaJ, GrpE and GroEL) and CDSs of unknown function, some of which may be responsible for cold desert adaptation.

Deinococcus-specific genes and horizontal gene transfer

The six sequenced *Deinococcus* strains share 1,474 genes. Among them, 39 genes of unknown function had no close orthologs in other species that don't belong to Deinococcales (Table S5). Furthermore, 10 previously predicted DNA damage-responsive genes (*ddr*) induced in response to IR and desiccation in *D. radiodurans* [14] were also found in *D. gobiensis*. Recently, *ddrB* was identified as a member of a new family of bacterial single-stranded DNA binding proteins which are induced by ionizing radiation [27,28]. We observed that the expression of some *ddr* genes was



Circle 2 & 3:

- [C] Energy production and conversion
- [D] Cell division and chromosome partitioning
- [E] Amino acid transport and metabolism
- [F] Nucleotide transport and metabolism
- [G] Carbohydrate transport and metabolism
- [H] Coenzyme metabolism
- [I] Lipid metabolism
- [J] Translation, ribosomal structure and biogenesis
- [K] Transcription
- [L] DNA replication, recombination, and repair
- [M] Cell envelope biogenesis, outer membrane
- [N] Cell motility and secretion
- [O] Posttranslational modification, protein turnover, chaperones
- [P] Inorganic ion transport and metabolism
- [Q] Secondary metabolites biosynthesis, transport and catabolism
- [R] General function prediction only
- [T] Signal transduction mechanisms
- [U] Intracellular trafficking, secretion, and vesicular transport
- [V] Defense mechanisms
- Cannot assign to COG or [S] Function unknown

Circle 5:

- rRNA
- tRNA
- ncRNA

Circle 6:

- Deinococcus
- Thermus
- Proteobacteria
- Actinobacteria
- Bacteroidetes
- Chlorobi
- Chloroflexi
- Cyanobacteria
- Firmicutes
- other
- unallocate
- unique

Circle 8:

- DNA-repair
- Desiccation
- General & Hot
- Osmotic
- Other
- Oxidative&detoxication
- Starvation

Figure 1. *D. gobiensis* I-0 genome structure. The seven replicons were opened at sequence position 1 and concatenated. Circle 1, red, chromosome (3.1 Mb); violet, plasmid 1 (P1, 433 kb); indigo, P2 (425 kb); blue, P3 (232 kb); light blue, P4 (72 kb); dark green, P5 (55 kb); light green, P6 (53 kb). Circles 2 and 3, predicted protein coding sequences (CDSs) clockwise and anticlockwise, respectively. Coloring is according to COG. Circle 4, Fold change in the immediate global transcriptional response to UV irradiation for each gene: green, upgulated; red, down-regulated; yellow, not changed significantly. Circle 5, red, rRNA; purple, tRNA; green, ncRNAs (noncoding). Circle 6, blue, genes with homologues in other *Deinococcus* genomes; red, genes found only in *D. gobiensis* I-0; other colors, genes with closest homologues in other phyla. Circle 7, deviation from the average 69.15% total genomic GC content: red, higher; blue, lower. Circle 8, previously reported genes that are involved in DNA repair and stress-responses. Circle 9, location of the 23 genomic islands. Circle 10, Mb scale.
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induced significantly by UV, including *ddrA* (a double-strand break repair protein), *ddrB* (a radiation-induced single-stranded DNA binding protein), *ddrC*, *ddrE*, *ddrI* and *ddrP*. Although the precise functions of these genes are not clear, they may contribute to a novel mechanism for adaptation to the extreme desert environment.

Horizontal gene transfer has played a major role in the evolution of bacteria and archaea. The total genome of *D. gobiensis* is about 1 Mb larger than the other *Deinococcus* genomes, probably due to gene acquisition by horizontal gene transfer. *D. gobiensis* contains more DNA sequences that are indicative of mobile elements than the other deinococci, including 77 putative transposases, 17 integrases or recombinases, and 2 prophages. In addition, we found that the *D. gobiensis* plasmid P1 was similar to the *D. deserti* plasmid P2, the *D. geothermalis* plasmid pDSM11300 (DG574) and the *D. radiodurans* chromosome 2, suggesting that these similar sequences may have come from a common ancestor (Figure 1 and Figure S2). The *D. gobiensis* plasmids P2–P6 contain a high proportion of genes that were exclusive to *D. gobiensis* (Figure 1). Furthermore, most of the genes on *D. gobiensis* P3–P6 had no homologs in the NCBI database. This indicated that the *D. gobiensis* plasmids have different evolutionary histories. Furthermore, the *D. gobiensis* genome contained 23 sequences, which were classified as genetic islands (GI) and may have been acquired by horizontal gene transfer (Table S6). For example, genes for tRNAs flank GI 19, while the others contain integrase genes (GI 7–10 and 15). In addition, GIs 9 and 10 resemble prophages, and most of their genes have their closest homologs outside the genus *Deinococcus*.

The closest ortholog of the 2,728 CDSs in the *D. gobiensis* genome was in the phylum Deinococcus-Thermus. However, 1,612 CDSs were indicative of horizontal gene transfer, 691 of which seemed to originate from *Proteobacteria*, *Actinobacteria* and *Firmicutes*. These horizontally acquired genes are mostly involved in sugar transport, signal transduction, transcriptional regulation and transposition. Notably, the two desert species *D. gobiensis* and *D. deserti* contain more insertion sequence (IS) associated orphan genes without *Deinococcus* orthologs than *D. radiodurans*. This difference likely reflects the evolutionary development of the efficient adaptive strategy derived by IS-associated horizontal acquisition of additional genes. Further transcriptome analysis indicated that the expression of more than 35% of the horizontally acquired genes were changed by UV light, strongly suggesting the involvement of these genes in resistance to UV irradiation.

Metabolic pathways and transport

As expected, the *D. gobiensis* genome possesses most of the genes for the central metabolic pathways, including glycolysis, the pentose phosphate (PP) pathway, the tricarboxylic acid (TCA) cycle, biosynthesis of amino acids, and *de novo* purine and pyrimidine biosynthesis. This set of predicted pathways is similar to that found in the other *Deinococcus* strains. Transport systems are key components for the communication of bacteria with their environments. For example, *D. gobiensis* has approximately 300 genes coding for transporters. We found that the *rbs* genes encoding ribose ABC transporters are present in two desert species but absent from *D. radiodurans* and *D. geothermalis*. In addition to having more Mn ABC transporter proteins that are similar to those found in *D. deserti*, *D. gobiensis* is also rich in ABC transporters for oligopeptides, amino acids and sugars relative to *D. radiodurans* and *D. geothermalis*. Eighteen of the 80 amino acid or peptide transporter proteins and 16 of the 54 proteins for sugar transport are specific to *D. gobiensis*.

Significant induction of most of the genes encoding metabolic pathways was not detected immediately after UV irradiation. Specifically, among the 286 transporters, 22, including two for K^+

Table 1. General features of the *D. gobiensis* genome.

Molecule	Chromosome	Plasmids						All
		P1	P2	P3	P4	P5	P6	
Size(bp)	3,137,147	432,699	424,524	231,600	72,036	54,602	53,428	4,406,036
GC content (%)	70.8	69.81	63.89	62.97	60.44	61.87	54.72	69.15
Coding density (%)	84.8	86	83.8	83.7	80.2	74.9	74.1	85.4
Protein-coding genes	2959	383	523	282	70	79	44	4340
(Average length, nt)	(899)	(971)	(679)	(687)	(825)	(511)	(900)	(863)
Pseudo genes	19	0	0	0	0	0	0	19
tRNAs	46	-	-	-	-	-	-	46
5 S rRNA	5	-	-	-	-	-	-	5
16 S rRNA	5	-	-	-	-	-	-	5
23 S rRNA	5	-	-	-	-	-	-	5
ncRNA	19	7	7	5	1	0	6	46

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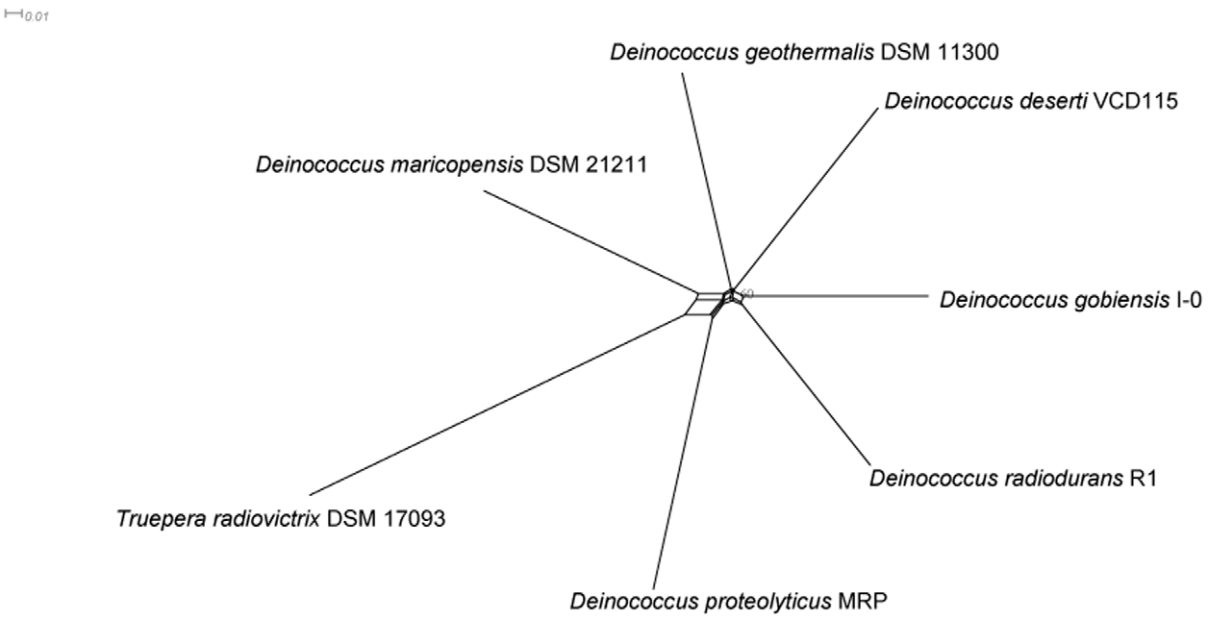

Figure 2. Unrooted Deinococcales neighbor-joining phylogenetic tree deduced from the nucleotide acid sequences of the orthologous proteins that occur in all 14 sequenced strains from the phylum Deinococcus-Thermus. *D. gobiensis* and *D. radiodurans* are most closely related. Numbers indicate bootstrap values below 100.
doi:10.1371/journal.pone.0034458.g002

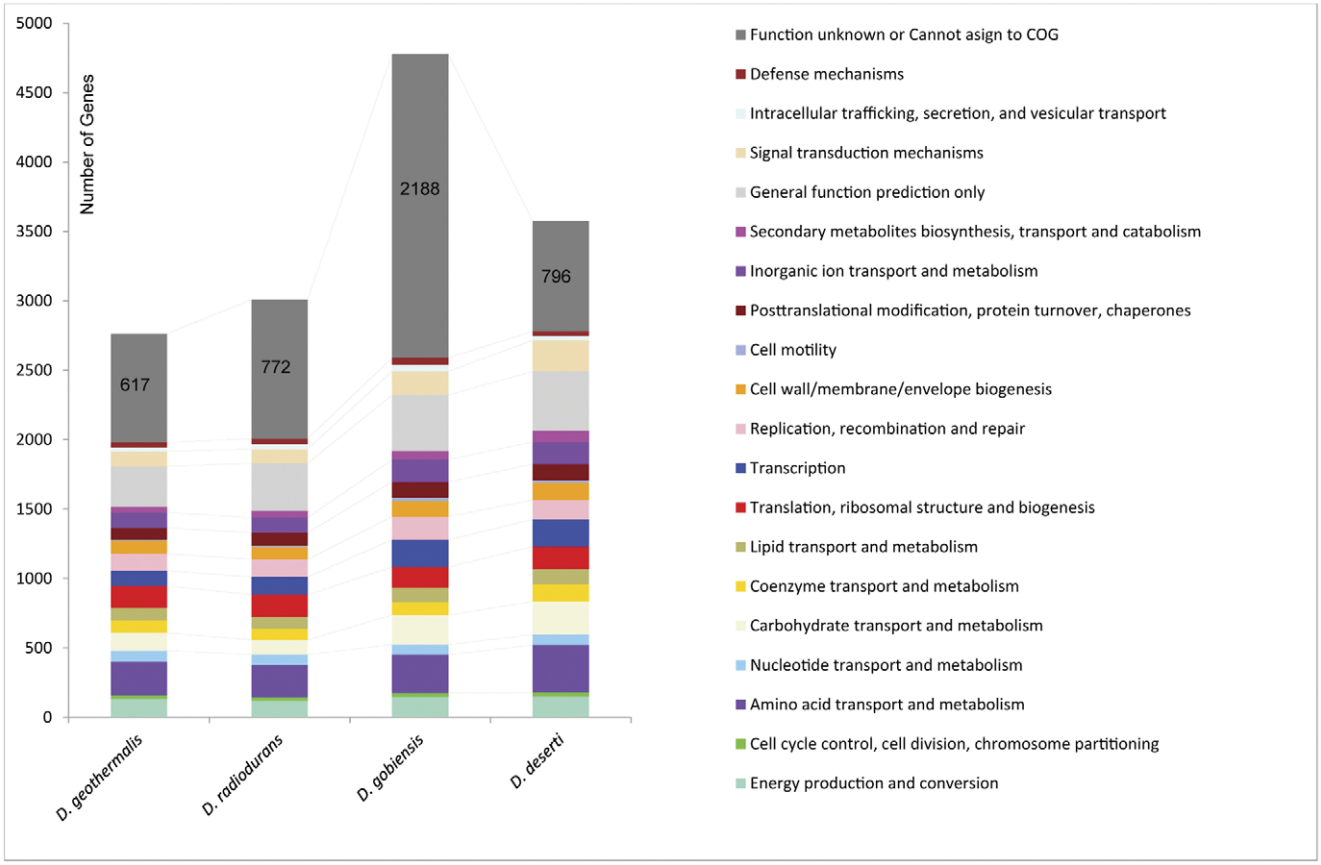

Figure 3. COG functional categories in the four *Deinococcus* species. Standard colors were used to indicate the COG functional categories. The numbers of unassigned and function unknown genes are indicated in the grey areas.
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(TrkG and KdpC) and PO_4^{3-} (PstA and PstC), were induced and 45, including two glycerol transporters and three ribose transporters, were repressed. In addition, we observed strong repression of the *zwf* gene (glucose 6-phosphate dehydrogenase), which is the rate-limiting enzyme of the PP pathway required for removal of reactive oxygen species (ROS). We also found that the two adjacent operons *nuoAB* and *nuoC-N* encoding NADH-quinone oxidoreductase were significantly downregulated, and NADH:quinone oxidoreductase plays a pivotal role in cellular energy production. Also among repressed genes were the *aceB* gene that encodes a malate synthase for the glyoxylic acid shunt, the genes responsible for the synthesis of amino acids (including arginine, ornithine, tryptophan, aspartic acid and lysine), and the genes *fabZ* and *fabG* that encode NADPH-dependent enzymes involved in the synthesis of fatty acids and biotin. This repression can be explained by the induction of *relA*, an inducer of the stringent response involved in ppGpp synthesis. We hypothesize that desert-dwelling bacteria could have specialized mechanisms to reduce their metabolism. This metabolic switch may be a general response for coping with solar UV radiation in a desert environment and could be the subject of further experimental work.

DNA repair and associated systems

The extremely radiation-resistant bacteria must have highly efficient and specialized DNA repair systems [3–6]. *D. gobiensis* contains sets of genes encoding proteins for various DNA repair pathways (Table S7*A*) and, like *D. radiodurans*, *D. gobiensis* has only 15 orthologs of the 31 genes that comprise the LexA-RecA-mediated SOS response to UV in *E. coli* [29]; *D. gobiensis* lacks homologs of the error-prone DNA polymerase V genes *umuC* and *umuD*, which are important for the SOS response in many bacteria [30]. We found, however, many *Deinococcus*-specific genes that are probably involved in DNA repair and extreme resistance. Unexpectedly, most of these genes were not changed in their expression immediately after UV irradiation.

UV radiation generates two major DNA damage products, the cyclobutane pyrimidine dimer and the pyrimidine pyrimidinone dimer. Photoreactivation mediated by photolyase is one of the simplest and oldest repair systems for UV-induced cyclobutane-pyrimidine dimers. The two desert species, *D. gobiensis* and *D. deserti*, contain a homolog (DGo_PA0134 and Deide_3p02150) of the *splB* gene encoding an active spore photoproduct lyase belonging to the radical S-adenosylmethionine superfamily [31], which is absent from both *D. radiodurans* and *D. geothermalis*. Additionally, *D. gobiensis* encodes another photolyase (PhrB, DGo_CA0607) whose closest homolog is from the Archaea. In contrast to photoreactivation, excision repair pathways are much more complex and can be separated into base excision repair (BER) and nucleotide excision repair (NER). The *D. gobiensis* genome contains sets of the excision repair genes, including nine genes for BER and six for NER (Table S7*A*), which may play in important role in UV-induced DNA repair.

A recombinational repair pathway is also operative in various organisms. As a part of the recombinational DNA repair of UV-lesions, *E. coli* RecA protein has a regulatory role in lesion bypass through coprotease activity which includes stimulation of self-cleavage of the repressor LexA. In *D. gobiensis* we observed a two-fold induction of *lexA* by UV irradiation, while *recA* was unchanged. This observation was very different from the response of *E. coli* in which both genes were induced by UV irradiation [16]. RecB is critical for the enzyme activity of the multifunctional exonuclease V (RecBCD) involved in DNA degradation [32]. *D. gobiensis* contains two plasmid-encoded homologs of *recB* (DGo_PB0022 and DGo_PC0098), and the expression of DGo_PC0098 was three-fold induced by UV irradiation. In a previous study, expressing the *E. coli recB* in *D. radiodurans* increased UV resistance [33]. Because the other *Deinococcus* strains lack *recB*, UV irradiation-induced expression of *recB* may contribute to the extreme UV resistance, and it is worth noticing that *recB* is absent in the other three published *Deinococcus* genomes. The two desert species, *D. gobiensis* and *D. deserti*, have a homolog of *polB* encoding DNA polymerase II (DGo_PC0151 and Deide_1p00180), which is essential for resumption of DNA replication after UV exposure [34] and may also be involved in DNA repair. However, *D. radiodurans* and *D. geothermalis* lack *polB*. Further analysis showed that expression of *polB* increased significantly following UV irradiation, whereas *dnaE* encoding the alpha subunit of DNA polymerase III, which is required for misincorporation and bypass during UV mutagenesis, was slightly repressed.

Reactive oxygen species detoxification

The ability to survive acute or chronic exposure to ionizing and UV irradiation and desiccation can be attributed to prevention, tolerance, and repair mechanisms. Scavenging oxygen radicals is an important component of prevention mechanism because reactive oxygen species (ROS) are key intermediates in the damage to cells caused by ionizing and UV radiation and desiccation. Several such prevention gene products are present in the *D. gobiensis* genome, including five catalases, four superoxide dismutases, and several regulatory genes, for example OxyR of the LysR family of proteins that activates the transcription of genes involved in peroxide metabolism and protection (*katG*, *ahpC*, *ahpF*, and *dps*), redox balance (*grxA*, and *trxC*). Genes involved in carotenoid biogenesis have been shown to confer a modest level of radiation resistance by scavenging electrons from ROSs [35]. *D. gobiensis* produces carotenoids, and the carotenoid biosynthetic pathway is similar to that found in *D. radiodurans* [36]. In addition, we observed that genes for secondary metabolite biosynthesis of carotenoids, vitamin B1, vitamin B12, NAD^+ and cytochrome P450 were strongly downregulated after UV irradiation.

D. gobiensis possesses two of the three types of known Mn^{2+} transporters: one from the natural resistance-associated macrophage family and one from the ATP dependent ABC-type transporter family. Interestingly, we observed that *D. gobiensis* (the Mn/Fe ratio of 1.60 ± 0.02) accumulated 1.1 times more Mn and 2.4 times less Fe than *D. radiodurans* R1 (Mn/Fe ratio of 0.60 ± 0.04). Previous studies of stress response systems in *D. radiodurans* demonstrated that the dose-response relationship for desiccation killing in bacteria isolated from desert environments parallels the levels of protein oxidation and the Mn/Fe ratios [37]. A first line of defence against ionizing radiation might be the accumulation of manganese complexes, which can prevent the production of iron-dependent reactive oxygen species [38]. More recently, the quantitative measurement of proteome oxidation (i.e., protein carbonylation) in *D. radiodurans* exposed to ionizing radiation or UVC light has revealed a consistent correlation with cell killing [39]. A comprehensive outlook on *D. radiodurans* strategies of combating oxidative stress suggests that the level of protein damage together with the cellular ROS-scavenging capacity determine the radiation survival of bacteria [12]. Thus, it is likely that in *D. gobiensis*, accumulation of high level of Mn may contribute to the enhanced tolerance to ionizing radiation or UV light.

Discussion

The surface sands of the desert are exposed to intense solar radiation, cycles of extreme temperatures, and desiccation. Such

extreme conditions cause stress-induced damage to DNA and proteins, which is lethal to most organisms. Therefore, desert-dwelling bacteria protect DNA and proteins from damage and/or repair them efficiently. Two striking results of this work came from comparison of *D. gobiensis* with three other sequenced *Deinococcus* species isolated from canned meat, hot springs and the Sahara desert, respectively. Despite their phylogenetic differences, the two desert strains, *D. gobiensis* I-0 and *D. deserti* VCD115, have a large repertoire of similar genes. The two desert strains contain surprisingly large numbers of probably horizontally acquired genes and diverse mobile elements. Many genes shared by the two desert strains are associated with putative mobile elements that aided the parallel evolution of the two desert species. However, *D. gobiensis* and *D. deserti* were isolated from very different deserts: the cold Gobi, and the hot Sahara. Comparative analyses of the two desert strains revealed two distinct gene sets: a core of shared orthologous genes and, species-specific genes. Interestingly, *D. gobiensis* contains 1,541 genes that are missing from *D. deserti*, including genes for a glucose-6-phosphate dehydrogenase, two transketolases, four catalases, two superoxide dismutases, an alkyl hydroperoxide reductase, and a putative glutathione-S-transferase, which are probably involved in adaptation to a cold desert environment. Notably, in *D. gobiensis*, *phrB* and *recB* were induced immediately after UV irradiation, whereas the other *Deinococcus* strains lacked the *phrB* and *recB* genes. This seemed advantageous for *D. gobiensis* to make use of the repair systems associated with *phrB* and *recB*, since *phrB* encodes a photolyase that breaks pyrimidine dimers typically caused by UV exposure [40] and *recBCD* encodes a multifunctional enzyme involved in DNA degradation [32].

Depletion of the stratospheric ozone layer causes increases in UV radiation at the Earth's surface, and the molecular basis of extremely UV radiation-resistant phenotypes is one the intriguing problems of modern biology. The success of *D. gobiensis* in the cold Gobi desert is probably due to its specialized metabolism, complex regulatory mechanisms, and robust repair systems. Indeed, *D. gobiensis* was isolated from the upper sand layers of a cold desert where bacteria are frequently exposed to long-lasting solar UV irradiation, necessitating a specific regulatory response that precedes the cellular recovery after UV irradiation damage. Several studies on UV radiation resistance have been conducted on exponential phase cells recovering from ionizing and UV radiation. In one such study, transcriptome dynamics of *D. radiodurans* recovering from ionizing radiation indicated that the maximum response for most functional gene groups occurred concurrently at approximately three hours post-exposure [11]. UV radiation induces both upregulation of the *nos* gene and cellular nitric oxide (NO) production in *D. radiodurans*, and subsequently NO upregulates *obgE*, a gene for an essential GTPase involved in the regulation of many growth-related processes [18]. These studies have provided important information about cellular recovery after UV irradiation. However, more studies of the transcriptome response immediately after UV irradiation are needed to establish a detailed understanding of the regulatory networks underlying the extreme resistance of deinococci. In the present study, we showed that the expression of most of the previously characterized genes, including *nos* and *obgE*, was not induced immediately after UV irradiation. Notably, the 30 regulatory genes induced immediately after UV irradiation included well-known regulators, such as two transcriptional activators (CarD and PhoR), a glucose-inhibited division protein A (GidA), a cognate response regulator (CitB) and a tryptophan repressor (TrpR), and also two uncharacterized protein kinases and 12 ncRNAs. The *carD* gene encodes an essential regulator of rRNA transcription necessary for the mycobacterial stringent response to oxidative stress, DNA damage, and nutrient limitation [41]. PhoR activates genes of the *E. coli* phosphate regulon in response to phosphate deprivation [42]. The *gidA* gene encodes the glucose-inhibited cell division protein A that controls the posttranscriptional regulation of quorum-sensing genes via RhlR-dependent and RhlR-independent pathways in *Pseudomonas aeruginosa* [43]. These proteins are likely key players in the global transcriptional response immediately following UV irradiation, preceding the cellular recovery of UV irradiation damage (Table 2).

Various DNA repair and stress response-related genes previously identified and many new gene products of potential interest for biotechnological applications were also found in *D. gobiensis* (Table S7). For example, the *D. gobiensis* genome encodes a *Deinococcus*-specific global regulator (DGo_CA2805) that is similar to IrrE, a global regulator from the extremely radiation-resistant *D. radiodurans* that confers enhanced salt tolerance in both *E. coli* and in the plant *Brassica napus* [44]. *D. gobiensis* contains two similar cold shock proteins (DGo_CA1136 and DGo_PA0041), with 65–70% identity to CspA from *E. coli* and CspB from *B. subtilis* that confer abiotic stress tolerance in transgenic plants and improved grain yield in maize under water-limited conditions [45]. Furthermore, approximately 47% of the *D. gobiensis* genes encode proteins of unknown function. We identified a subset of previously uncharacterized genes induced immediately following UV irradiation, suggesting that the organism's extreme resistance phenotype may be attributable to still unknown genes and pathways. It would be intriguing to investigate which of their products are required for the extreme resistance phenotype. To our knowledge, this is the first report of a transcriptome analysis immediately following UV irradiation. Taken together, our results highlight the exceptional ability of *D. gobiensis* to withstand environmental extremes. These findings may have significant potential for biotechnological and agricultural applications. Further investigations will reveal commonalities in the genetic basis of the UV response and provide insight into the molecular mechanisms underlying the extreme resistance phenotype of the genus *Deinococcus*.

Materials and Methods

Bacteria and growth conditions

Cells of *Deinococcus gobiensis* I-0 (=DSM 21396) were grown in TGY broth (1.0% peptone, 0.5% yeast extract, 0.1% glucose) at 30°C. For genome sequencing, cells were harvested at the early stationary phase ($5–10\times10^8$ colony-forming units (CFUs) ml^{-1}). For irradiation, cells were harvested at the late-log phase ($\approx2\times10^8$ CFUs ml^{-1}) and then washed twice with equal volumes of potassium phosphate buffer (100 mM, pH 7.0) as described previously [19]. UV light (254 nm, 200 μW cm^{-2}) was used to irradiate a 20 ml suspension for 5 min in a 9 cm plate with stirring. As a control, an additional non-irradiated suspension was incubated for the same duration. After treatment, cells were harvested by centrifugation at 8,000 rpm for 3 min.

To test the concentrations of Mn and Fe, cells of strains I-0 and R1 were collected from late-log phase TGY cultures and dried by low-temperature vacuum drying. Measurement was performed at the Micro Structure Analytical Lab (Beijing) using Wavelength Dispersive X-Ray Fluorescence (WDXRF).

To test the utilization of aromatic substrates, cells from the TGY 48 h culture were washed twice and subsequently inoculated into Mineral Salt medium (benzoic acid 2 mmol/L, $NaNO_3$ 0.5 g/L, K_2HPO_4 0.65 g/L, KH_2PO_4 0.17 g/L, $MgSO_4$ 0.10 g/L) at a dilution of 1:100.

Table 2. The *D. gobiensis* genes implicated in the immediate global transcriptional response to UV irradiation.

Locus_tag	Gene	Product description	Fold Change**
Regulation			
DGo_CA0550	*carD*	Transcriptional regulator, CarD family	2.2
DGo_CA0552	*ccpA*	Catabolite control protein A	3.4
DGo_CA0357	*citB*	Cognate response regulator	2.0
DGo_CA1040	*ddrI*	Transcriptional regulator, Crp/Fnr family	3.5
DGo_CA0719	*deoR**	DeoR-family transcriptional regulator	2.1
DGo_CA2738	*fliY*	ABC-type amino acid transport/signal transduction system, periplasmic component	2.2
DGo_CA2290	*gidA*	Glucose-inhibited division protein A	2.4
DGo_CA2808	*lspA*	Lipoprotein signal peptidase	4.9
DGo_PC0175	*phoR*	Sensor protein, transcriptional activators	2.7
DGo_CA0725	*sig4*	RNA polymerase sigma factor	2.0
DGo_CA0977	*str*	Streptomycin 3′-kinase	2.1
DGo_PB0002	*trpR**	Tryptophan repressor, LysR family transcriptional regulator	3.4
DNA repair			
DGo_CA2046	*ddrA*	Double-strand break repair protein	1.9
DGo_CA0350	*ddrB*	Single-stranded DNA binding protein	2.2
DGo_CA0002	*dnaN*	DNA polymerase III, beta subunit	2.4
DGo_CA1041	*gyrA*	putative DNA topoisomerase subunit A	2.0
DGo_CA0873	*gyrB*	putative DNA topoisomerase subunit B	2.0
DGo_PC0001	*lexA*	Repressor LexA	1.9
DGo_CA0607	*phrB**	Deoxyribodipyrimidine photo-lyase type II	3.2
DGo_PC0151	*polB*	DNA polymerase II	2.0
DGo_PC0098	*recB**	Predicted nuclease, RecB family	3.0
DGo_CA0376	*yqgF*	Putative Holliday junction resolvase	2.7
Other functions			
DGo_CA0071	*ddrC*	Uncharacterized DNA damage response protein	2.1
DGo_CA0988	*ddrE*	Putative zinc metal lopeptidase	1.9
DGo_CA2239	*ddrP*	Uncharacterized DNA damage response protein	1.9

*Genes that are identified in D. gobiensis but not in other published Deinococcus species.
**Change values are means of values obtained from two independent experiments.
doi:10.1371/journal.pone.0034458.t002

Genomic DNA extraction and whole-genome shotgun sequencing

Total DNA was isolated from *D. gobiensis* I-0 (=DSM 21396) according to a published method described for bacteria [46]. Genome sequencing was performed at Tianjin Research Center for Functional Genomics and Biochip (Tianjin, China) using the Sanger/pyrosequencing strategy described previously [47]. The Roche 454 FLX gene sequencer (454 Life Sciences, Branford, CT) was used to generate 329,480 reads that were assembled into 287 contigs using the Newbler assembler. Artificial 1 kb reads representing the Roche/454 assembly were generated using mktrace in the Consed package (www.phrap.org/) and assembled with 11,444 ABI3730 reads (3.2 kb library) using PhredPhrap (www.phrap.org/). Possible misassemblies were corrected according to the mate-pair relationships of ABI3730 reads; gaps between contigs were closed by editing in Consed, custom primer walks, or PCR amplification.

Genome annotation and analysis

Glimmer3 was initially used to identify putative CoDing Sequences (CDS), and tRNAs were predicted using tRNAscan-SE, and Artemis [48] was used to collate data and facilitate annotation. Function predictions were based on BLASTp similarity searches (E-value $<10^{-5}$) in the non-redundant GenBank protein database (www.ncbi.nlm.nih.gov/protein), the SwissProt protein database (http://www.ebi.ac.uk/swissprot/), the clusters of orthologous groups (COG) database (www.ncbi.nlm.nih.gov/COG) and KEGG database (www.genome.ad.jp/kegg).

Pairwise genome comparisons of *D. gobiensis* with three other *Deinococcus* species were made using nucmer in Mummer 3 [49]. The minimum length of a cluster of matches, break length and maximum gap distance were set to 30 bp, 3 kb and 3 kb, respectively.

To analyze the taxonomic affiliations of *D. gobiensis* proteins, the BLAST hits with at least 95% of the highest score (E-value $<10^{-4}$) to the RefSeq database (www.ncbi.nlm.nih.gov/RefSeq) were collected for each of the *D. gobiensis* proteins. For each query, if the taxonomic affiliations of all hits at the phylum level were the same, the query was considered affiliated with this taxon; otherwise, the taxon affiliation of the query was considered unresolved. For each of the genes belonging to the phylum Deinococcus-Thermus, the query was further assigned to the order Deinococcales or Thermales according to the taxonomic affiliation of the best hit.

D. gobiensis and another eight publicly available Deinococcus-Thermus genomes from NCBI databases were used in the comparisons. To ensure consistency, the annotations of all genomes were verified based on the similarity with proteins in *D. gobiensis* using tBLASTn [50,51]. The sets of orthologous protein-coding genes were defined as mutual fully transitive reciprocal BLASTp [52] hits (E-value $<10^{-4}$) [53]. The amino acid (for the whole phylum) and nucleic acid sequence (within the order Deinococcales)of each orthologous group was aligned using the CLUSTALW program version 2.0 [54]. For each data set, the phylogenetic relationship was estimated and tested in one thousand bootstrap samples using TREE-PUZZLE version 5.3 (general time reversible (GTR) +Γ4+I model of evolution with a BIONJ starting tree) [55]. The bi-partitions with at least 70% supports in the bootstrap test for each data set were recorded as "0/1" status and used to reconstruct the consensus sequence. The phylogenetic relationship of the consensus sequence was built using SplitsTREE 4 with the BioNJ model [56].

Isolation and enrichment of mRNA, RNA processing and transcriptome sequencing

Bacterial cells were collected and ground into a fine powder in liquid nitrogen. Total RNA was isolated using Trizol reagent (Invitrogen), subsequently purified using RNeasy MinElute Cleanup Kit (Qiagen) and eluted in RNase-free water. Bacterial ribosomal RNAs were removed via a mixed treatment using the MICROB Express kit (Ambion) and the mRNA-ONLY Prokaryotic mRNA isolation Kit (Epeicentre® Biotech.) according to the manufacturer's instructions. Heating at 94°C fragmented the mRNA. First strand cDNA was synthesized with random hexamer primers, and second strand cDNA was synthesized with DNA polymerase. Double strand cDNA was end-repaired, a single adenosine was added, and the Illumina adapters were ligated. Gel-electrophoresis was used to select DNA fragments between 200–250 bp. Libraries were amplified by PCR using Phusion polymerase. Sequencing libraries were denatured with sodium hydroxide and diluted in hybridization buffer for loading onto a single lane of an Illumina GA flow cell. Cluster formation, primer hybridization and pair-end, 101×2 cycle, sequencing were performed using proprietary reagents according to the manufacturers' recommended protocols (https://icom.illumina.com/).

Transcriptomics analysis and qRT-PCR verification

High-throughput cDNA sequencing was performed using the Firecrest, Bustard and GERALD programs [24]. The low quality bases ($Q<5$) at the ends of the reads were trimmed. The reads that were longer than 20 bps were kept and aligned to the *D. gobiensis* genome using Burrows-Wheeler Aligner (BWA) [57]. The reads that were mapped into the rRNA regions were not included in further analysis. A transcript coverage map was calculated based on the alignment of whole transcript reads. For each of the genes, the 5′-end of the translation regions were defined as positions supported by at least 5 reads summarized in both of the samples.

To identify the non-coding RNA, the continuous regions (≥30 bp) with an average sequencing depth of ≥15 times/bp in the intergenic regions were extracted and compared against GenBank using blastx and blastn. Those regions that lacked similarities to known protein coding genes or were similar to known ncRNAs were classified as possible non-coding RNAs.

To compare the different samples, the fragments per kb of CDS per million mapped reads (FPKM) value were used to normalize the data and represent the overall gene expression. The differently expressed genes between the two samples were selected according to their significance in Chi-square tests ($p = 0.05$, with Bonferroni correction) and at least 2-fold differences.

One hundred micrograms of total RNA was then synthesized into cDNA using ProtoScript® M-MuLV First Strand cDNA Synthesis Kit (NEB). The primers were designed by Perlprimer v1.1.19 [58]. The expression levels of the selected genes were determined using the 7500 Real-Time PCR System (Applied Biosystems) according to SYBR® Premix ExTaq™ Kit's manual (Takara) using 20 microliter system.

Supporting Information

Figure S1 Unrooted neighbor-joining phylogenetic tree deduced from the orthologous proteins that occur in all 14 sequenced strains from the phylum Deinococcus-Thermus. *D. gobiensis* and *D. radiodurans* are most closely related. Numbers indicate bootstrap values below 100.
(TIF)

Figure S2 Synteny plots comparing *D. gobiensis* I-0 and the other three *Deinococcus* genomes. The dot plots represent nucmer alignments generated by MUMMER 3 of *D. gobiensis* on the x-axis and three other *Deinococcus* species on the y-axis. Forward matches are shown in red, and reverse matches are shown in blue. *dnaA* isat the bottom left of each plot. The red marks on the horizontal line representing the *D. gobiensis* genome indicate genomic islands.
(TIF)

Table S1 General features of the genomes of Deinococcales species.
(DOC)

Table S2 The qRT-PCR verification.
(XLS)

Table S3 Transcriptional start sites (TSS). First column presents the TSS location; the TSS and its strand are listed in the next two columns.
(DOC)

Table S4 Functional description of 1144 genes induced or repressed after UV-irradiation.
(DOC)

Table S5 Deinococcales-specific genes.
(XLS)

Table S6 Genomic islands in *D. gobiensis*.
(DOC)

Table S7 DNA repair genes (A), stress response-related genes (B) and additional enzymes of possible biotechnological interest genes (C) identified in sequenced deinococci.
(DOC)

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Author Contributions

Conceived and designed the experiments: MC YW ML. Performed the experiments: M. Yuan M. Yang PZ RT XL YH ZZ YZ HY CT. Analyzed the data: M. Yuan MC WZ WL JW YY SP ML. Wrote the paper: M. Yuan ML.

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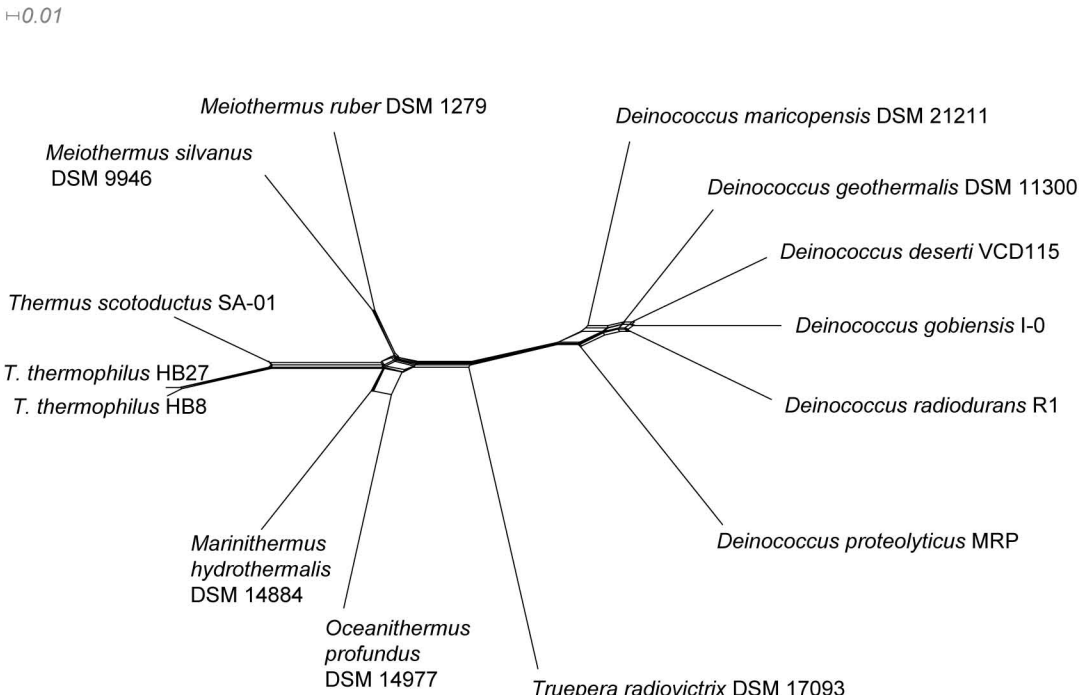
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Meiothermus silvanus DSM 9946
Thermus scotoductus SA-01
T. thermophilus HB27
T. thermophilus HB8
Marinithermus hydrothermalis DSM 14884
Oceanithermus profundus DSM 14977
Truepera radiovictrix DSM 17093
Deinococcus maricopensis DSM 21211
Deinococcus geothermalis DSM 11300
Deinococcus deserti VCD115
Deinococcus gobiensis I-0
Deinococcus radiodurans R1
Deinococcus proteolyticus MRP

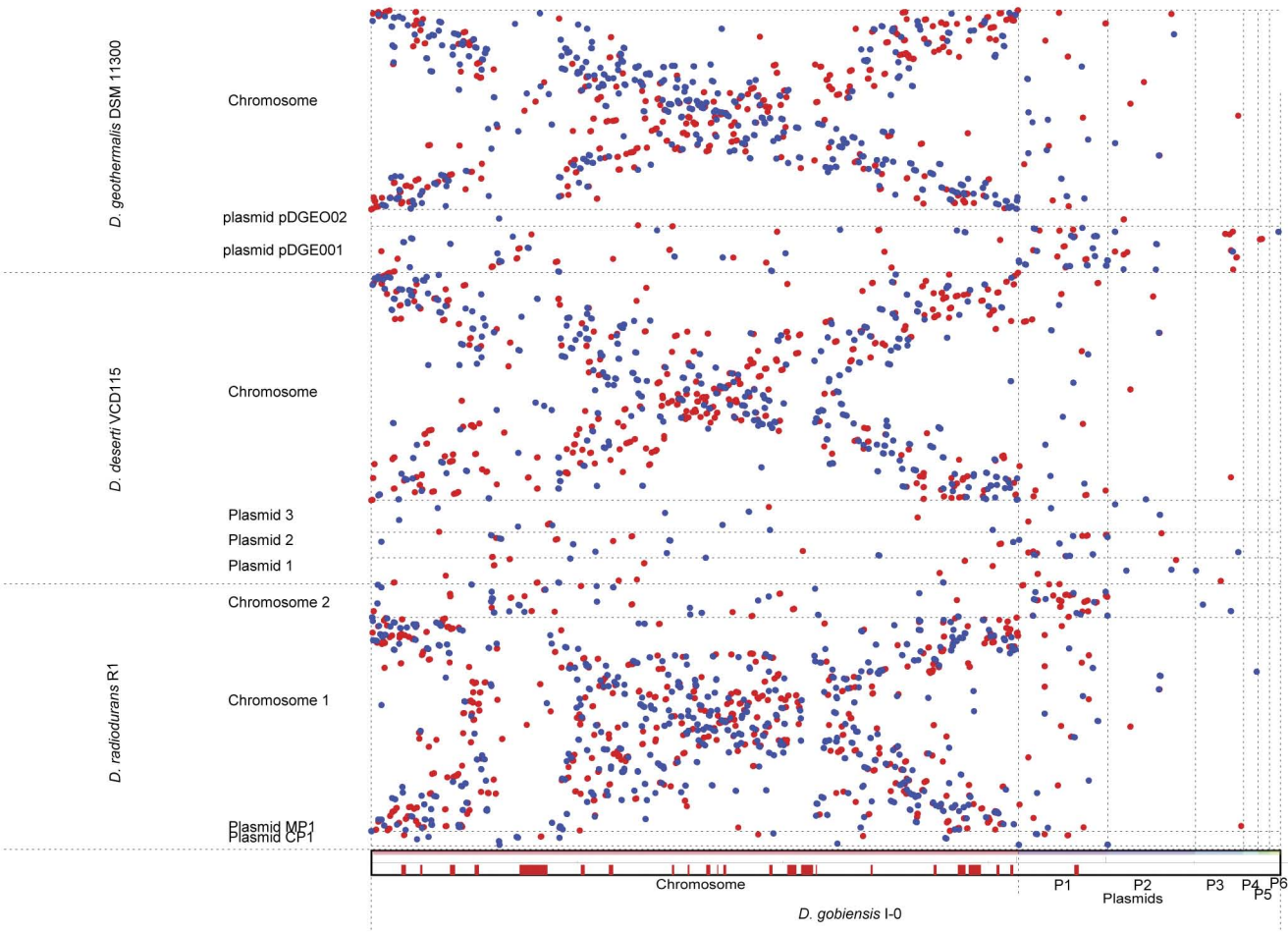
D. geothermalis DSM 11300
Chromosome
plasmid pDGEO02
plasmid pDGE001
D. deserti VCD115
Chromosome
Plasmid 3
Plasmid 2
Plasmid 1
D. radiodurans R1
Chromosome 2
Chromosome 1
Plasmid MP1
Plasmid CP1
Chromosome
P1
P2
P3
P4
P5
P6
Plasmids
D. gobiensis I-0

Table S1 General features of the genomes of Deinococcales species

	D. gobiensis I-0^T	*D. radiodurans* R1^T	*D. deserti* VCD 115^T	*D. geothermalis* DSM11300^T	*D. proteolyticus* MRP	*D. maricopensis* LB-34^T	*Truepera radiovictrix* RQ-24^T
Chromosome (s)	1	2	1	1	1	1	1
Plasmids	6	2	3	2	4	0	0
Size(bp)	4,406,036	3,284,156	3,855,329	3,247,018	2,886,836	3,498,530	3,260,398
GC content (%)	69.15	66.6	62.96	66.47	65.65	69.83	68.14
Coding Density (%)	85.4	90.9	84.31	89.97	(ND)	89.38	87.79
Protein-Coding genes	4340	3187	3455	3062	2656	3,301	2994
(Average length, nt)	(863)	(937)	(ND)	(954)	(ND)	(ND)	(ND)
Pseudo genes	19	ND	ND	ND	83	37	49
tRNAs	46	49	48	48	47	54	46
5S rRNAs	5	3	4	4	3	4	2
16S rRNAs	5	3	4	4	3	4	2
23S rRNAs	5	3	4	4	3	4	2
non-coding RNAs	45	ND	5	ND	2	ND	ND

Table S2 The qRT-PCR verification

Locus_tag	Gene name	Change fold	Change fold (RT-qPCR)	Primer-F	Primer-R
DGo_CA0607	*phrB*	3.16	2.34	CCCTGCTCGAAGAACTGGTC	CTCGTAGCGGTCGTAGTCCG
DGo_PC0098	*recB2*	2.99	2.58	GGGAGGTGTCCGCGTTG	CGAAGAGCGAGGGCTGTG
DGo_PB0002	*trpR*	3.36	2.75	CGCCTTACTGGATGCACTGG	GGGTCTCACTCAGCAAGCG
DGo_CA0719	*deoR*	2.06	2.55	CGCCATCCAGGTCAGTCAG	CAGCCGAACTTGGTGTGGT
DGo_CA2046	*ddrA*	1.95	1.89	CTGGGAATTCAGCGTGGAG	GCAGGTCGTAGAGGTAGC
DGo_PC0151	*polB*	1.99	2.06	AGTTTGACCTAGAGACCACC	TGACCTGAAGGAGAGTGTG
DGo_CA0294	*ruvC*	-1.92	-2.26	GTCGCCATCGAGGACCAG	TCGCCTTGACCATGTAGATCAC
DGo_CA1825	*recD*	-1.59	-2.01	ACAGATCCATCACCCGACAG	ACCACCTGCACCAACTCC
-	16S	-	-	GTTGGAATCGCTAGTAATCGTG	TTACCTTGTTACGACTTCACCC

Table S3. Transcriptional start sites (TSS).

First column presents the TSS location; the TSS and its strand are listed in the next two columns.

Location	Site	Direction
C1	1782	+
C1	3485	+
C1	14106	-
C1	15011	-
C1	16068	-
C1	17352	-
C1	19229	-
C1	19556	+
C1	35587	-
C1	43297	-
C1	43314	+
C1	44133	+
C1	50646	+
C1	51589	+
C1	52478	+
C1	70240	-
C1	76803	-
C1	76995	+
C1	84325	+
C1	88387	+
C1	96681	+
C1	98273	-
C1	100367	+
C1	363295	+
C1	366378	+
C1	114153	+
C1	131979	+
C1	138946	-
C1	139340	+
C1	146891	+
C1	149680	-
C1	151252	-
C1	170962	+
C1	180563	+
C1	189516	-
C1	189763	+
C1	192078	+
C1	202647	-
C1	205031	+
C1	208008	-

C1	212275	+
C1	212511	+
C1	214093	-
C1	216057	-
C1	219656	-
C1	220323	-
C1	221689	-
C1	230080	+
C1	230809	+
C1	231961	-
C1	248472	+
C1	250196	-
C1	258783	+
C1	274648	+
C1	275840	+
C1	279033	-
C1	295367	+
C1	298136	+
C1	300052	+
C1	310389	-
C1	314115	-
C1	315469	+
C1	321597	-
C1	321776	+
C1	323812	-
C1	325246	-
C1	337649	-
C1	338476	-
C1	344952	+
C1	345587	+
C1	349838	+
C1	350962	+
C1	357402	+
C1	361538	+
C1	364436	+
C1	365672	+
C1	369775	-
C1	375210	+
C1	375536	+
C1	376938	+
C1	378618	+
C1	394044	-
C1	407069	+
C1	407924	+
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C1	416290	+
C1	420375	+
C1	423473	+
C1	426292	+
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C1	447329	+
C1	450306	-
C1	451242	-
C1	452346	-
C1	452521	+
C1	456252	-
C1	459013	-
C1	461112	+
C1	471409	+
C1	473947	-
C1	479326	+
C1	484510	+
C1	488708	+
C1	490320	+
C1	493901	+
C1	495998	+
C1	499007	+
C1	499827	+
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C1	578927	-
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C1	589960	-
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C1	662900	+
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C1	682495	+
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C1	703724	-
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C1	727925	+
C1	729183	+
C1	732555	+
C1	738248	+
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C1	754068	+
C1	754509	-
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C1	-460845	+
C1	-363295	+
C1	-366378	+
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C1	914735	-
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C1	956254	+

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C1	994338	+
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C1	1336959	-
C1	1349169	+
C1	1354528	-
C1	1357968	+
C1	1359008	+
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C1	1412083	-
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C1	1831019	-

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C1	1933883	-
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C1	1959969	+
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C1	1989350	+
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C1	2019846	-
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C1	2178631	-
C1	2183403	+
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C1	2191582	-
C1	2194870	+
C1	2198071	-
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C1	2206316	-
C1	2207153	-
C1	2207366	+
C1	2209589	+
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C1	2214179	+
C1	2218459	-
C1	2219492	+
C1	2221417	+
C1	2222460	+
C1	2223477	+
C1	2227643	-
C1	2228243	-
C1	2229297	+
C1	2237082	-
C1	2240926	+
C1	2252823	-
C1	2261275	-
C1	2266230	-
C1	2267753	-
C1	2269368	-
C1	2270138	-
C1	2270361	+
C1	2271545	-

C1	2274000	-
C1	2281478	+
C1	2284355	-
C1	2287436	-
C1	2290237	-
C1	2292279	-
C1	2293807	-
C1	2302857	+
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C1	2320575	+
C1	2338154	-
C1	2339664	-
C1	2343042	-
C1	2344133	-
C1	2345549	-
C1	2346614	-
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C1	2381130	+
C1	2383793	-
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C1	2405252	-
C1	2406757	+
C1	2415684	+
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C1	2431633	+
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C1	2454968	+
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C1	2538428	-
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C1	2628994	-
C1	2629844	+
C1	2634462	-
C1	2637552	-
C1	2637797	+
C1	2640731	-
C1	2641796	-

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C1	2669473	-
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C1	2770769	-
C1	2773852	-
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C1	2779212	-

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C1	2816052	+
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C1	2903638	-
C1	2917767	-
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C1	2956089	+
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C1	2958208	+
C1	2963019	+
C1	2974507	+
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C1	2986362	-
C1	2992177	+
C1	3009084	+
C1	3014028	+
C1	3015312	+
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C1	3017339	+
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P1	3801	+
P1	7230	-
P1	7315	+
P1	8374	+
P1	9491	+
P1	13183	+
P1	18023	+
P1	23543	+
P1	25120	+
P1	46523	+
P1	47508	+
P1	48547	+
P1	61102	-
P1	61528	+
P1	68041	+
P1	69232	+
P1	69648	+
P1	75242	-
P1	76266	+
P1	80388	+
P1	82804	+
P1	87977	+
P1	90533	-
P1	93442	-
P1	93632	+
P1	94815	+
P1	97201	+
P1	100061	+
P1	100642	+
P1	101744	+

P1	112352	-
P1	114166	-
P1	119257	-
P1	119908	+
P1	123857	-
P1	131454	-
P1	131738	+
P1	133444	+
P1	137394	+
P1	140596	+
P1	142105	-
P1	148268	-
P1	148570	+
P1	148793	+
P1	149725	+
P1	157245	+
P1	168605	-
P1	171405	+
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P1	177026	-
P1	184254	-
P1	191620	+
P1	199109	-
P1	201057	-
P1	204081	-
P1	205448	+
P1	206517	+
P1	208773	-
P1	208775	+
P1	214440	-
P1	216611	-
P1	226386	-
P1	229872	-
P1	231323	-
P1	232455	+
P1	236649	+
P1	237274	+
P1	239537	+
P1	241643	-
P1	243576	-
P1	246222	-
P1	246282	+
P1	249532	-
P1	251829	+
P1	252944	+

P1	253706	+
P1	255933	+
P1	257577	+
P1	258029	+
P1	261202	+
P1	261828	+
P1	262967	+
P1	264820	+
P1	266708	+
P1	268394	+
P1	275746	-
P1	276606	-
P1	279225	-
P1	281800	-
P1	285036	+
P1	286769	+
P1	292505	-
P1	297598	-
P1	300384	-
P1	300637	+
P1	303543	+
P1	308076	-
P1	308332	+
P1	311693	+
P1	315319	-
P1	320023	-
P1	323997	-
P1	327317	-
P1	330550	-
P1	331638	-
P1	333358	-
P1	334623	-
P1	337171	-
P1	339167	-
P1	341544	-
P1	341943	+
P1	344217	-
P1	346455	+
P1	355800	+
P1	358020	-
P1	358629	-
P1	360305	-
P1	364628	+
P1	366107	+
P1	367125	+

P1	368248	+
P1	369023	+
P1	369783	+
P1	371333	-
P1	373226	+
P1	380326	-
P1	381173	-
P1	387652	-
P1	388248	-
P1	389520	-
P1	392365	-
P1	393417	-
P1	394273	-
P1	394683	-
P1	396819	-
P1	396827	+
P1	399398	+
P1	405088	+
P1	420059	-
P1	420302	+
P1	422753	-
P1	424724	-
P1	424772	+
P1	426423	+
P2	3719	+
P2	4118	+
P2	19868	+
P2	20471	-
P2	28402	-
P2	30314	-
P2	35964	+
P2	41271	-
P2	47129	+
P2	47961	+
P2	50866	-
P2	51228	+
P2	56334	+
P2	82028	+
P2	83214	+
P2	85152	-
P2	87917	-
P2	90091	+
P2	90878	+
P2	91328	+
P2	96467	-

P2	102335	-
P2	112047	-
P2	114949	+
P2	121898	+
P2	143419	-
P2	143862	+
P2	147527	-
P2	150897	-
P2	153479	-
P2	153693	+
P2	159473	-
P2	162351	+
P2	164532	-
P2	166138	+
P2	168126	-
P2	174783	+
P2	183581	+
P2	220074	+
P2	220587	+
P2	226131	-
P2	238337	+
P2	242035	-
P2	245808	+
P2	252129	-
P2	254743	-
P2	259205	+
P2	267390	+
P2	277279	-
P2	278075	-
P2	281688	-
P2	285150	+
P2	286225	-
P2	286546	-
P2	286975	-
P2	288627	-
P2	300386	+
P2	301342	+
P2	312251	-
P2	316853	+
P2	321006	+
P2	321764	+
P2	326710	-
P2	327688	-
P2	329386	-
P2	329529	+

P2	334526	+
P2	336202	-
P2	340882	+
P2	341720	+
P2	352933	+
P2	353379	+
P2	359561	+
P2	360702	-
P2	360841	+
P2	379771	-
P2	395451	-
P2	405246	+
P2	407265	+
P2	408769	+
P2	410020	-
P2	410394	-
P2	410767	-
P2	410885	+
P2	413015	+
P2	414236	+
P2	415395	-
P2	424110	-
P3	9961	+
P3	15206	-
P3	22580	+
P3	36855	-
P3	45538	-
P3	48244	+
P3	49016	+
P3	52987	-
P3	53603	-
P3	53844	+
P3	57179	-
P3	62541	+
P3	89372	+
P3	90856	-
P3	91507	-
P3	94843	+
P3	104204	+
P3	115684	+
P3	123821	-
P3	127880	+
P3	136918	+
P3	141625	+
P3	146407	+

P3	149058	-
P3	151486	-
P3	152415	-
P3	153539	+
P3	169867	-
P3	175240	+
P3	175921	+
P3	178187	+
P3	178615	+
P3	196395	+
P3	197713	-
P3	197779	+
P3	200229	+
P3	204099	-
P3	204893	+
P3	206348	-
P3	206604	+
P3	207141	+
P3	208691	-
P3	209649	-
P3	212922	-
P3	215714	+
P3	217328	+
P3	222519	-
P4	1070	+
P4	1891	+
P4	2870	-
P4	3331	+
P4	4219	+
P4	5020	+
P4	6760	-
P4	12792	+
P4	20894	-
P4	22410	-
P4	22564	+
P4	24275	+
P4	24774	-
P4	25373	-
P4	30387	-
P4	32174	+
P4	33096	+
P4	39833	+
P4	42689	+
P4	45417	-
P4	45670	+

P4	49464	-
P4	50003	-
P4	52898	-
P4	55988	-
P4	62203	+
P4	64211	+
P4	69555	-
P5	1772	-
P5	2958	+
P5	3717	+
P5	4090	+
P5	4447	+
P5	5435	+
P5	14894	-
P5	16205	-
P5	17172	-
P5	17279	+
P5	22368	-
P5	23221	-
P5	25375	-
P5	26351	+
P5	28326	+
P5	30284	-
P5	30423	+
P5	30841	+
P5	31703	-
P5	31710	+
P5	32956	-
P5	33709	-
P5	34514	-
P5	36186	-
P5	36455	+
P5	36762	+
P5	39330	-
P5	39441	+
P5	40887	+
P5	43256	+
P5	43964	+
P5	45228	-
P5	45585	+
P5	46975	+
P5	47458	+
P5	50498	-
P5	51383	-
P5	51437	+

P5	53440	+
P6	12801	-
P6	22209	+
P6	34362	+
P6	38612	-
P6	40336	-
P6	44673	-
P6	44815	+
P6	47526	-
P6	48974	+
P6	50272	-

Table S4 Functional description of 1144 genes induced or repressed after UV-irradiation

A. Functional description of 390 genes induced after UV-irradiation

Locus_tag	Type	Name	Description	Fold
DGo_PFnc06	ncRNA		Hypothetical non-coding RNA	>100.0
DGo_CAnc05	ncRNA		Hypothetical non-coding RNA	150.2
DGo_CAnc12	ncRNA		Hypothetical non-coding RNA	57.3
DGo_CAnc03	ncRNA		Hypothetical non-coding RNA	20.1
DGo_PBnc03	ncRNA		Hypothetical non-coding RNA	13.4
DGo_CAnc04	ncRNA		Hypothetical non-coding RNA	12.4
DGo_CAnc13	ncRNA		Hypothetical non-coding RNA	10.5
DGo_PAnc07	ncRNA		Hypothetical non-coding RNA	6.9
DGo_PFnc05	ncRNA		Hypothetical non-coding RNA	5.6
DGo_PDnc01	ncRNA		Hypothetical non-coding RNA	4.1
DGo_PAnc01	ncRNA		Hypothetical non-coding RNA	3.8
DGo_PAnc05	ncRNA		Hypothetical non-coding RNA	3.0
DGo_CAnc15	ncRNA		Hypothetical non-coding RNA	2.2
DGo_CA1805	CDS		Hypothetical protein	>100.0
DGo_PB0291	CDS		Hypothetical protein	>100.0
DGo_PB0445	CDS		Hypothetical protein	25.6
DGo_CA0814	CDS		Hypothetical protein	22.5
DGo_CA2675	CDS		Hypothetical protein	20.4
DGo_PB0147	CDS		Hypothetical protein	14.3
DGo_PB0313	CDS		Hypothetical protein	14.3
DGo_PB0065	CDS		Hypothetical protein	13.7
DGo_PB0263	CDS		Hypothetical protein	13.4
DGo_CA0175	CDS		Hypothetical protein	13.3
DGo_PC0048	CDS		Hypothetical protein	11.5
DGo_PB0290	CDS		Hypothetical protein	11.0
DGo_CA2520	CDS		Acetyltransferase, putative	10.2
DGo_PC0075	CDS		Methyltransferase type 11	8.7
DGo_PB0155	CDS		Hypothetical protein	8.4
DGo_PB0406	CDS		Transposase, IS5 family	8.3
DGo_PB0487	CDS		Hypothetical protein	8.3
DGo_PA0146	CDS		Hypothetical protein	8.0
DGo_PB0359	CDS		Hypothetical protein	8.0
DGo_PB0151	CDS		Hypothetical protein	8.0
DGo_PD0014	CDS		Hypothetical protein	7.9
DGo_PD0052	CDS		Hypothetical protein	7.9
DGo_PF0041	CDS		Hypothetical protein	7.8
DGo_PC0253	CDS		Transposase, IS4	7.6
DGo_PD0062	CDS	*vapB*	SpoVT/AbrB-like	7.5

DGo_PB0405	CDS		IS5 family transposase, orfA	7.5
DGo_CA1616	CDS		Hypothetical protein	7.4
DGo_CA0594	CDS		Hypothetical protein	7.4
DGo_PC0035	CDS		Hypothetical protein	7.4
DGo_PD0024	CDS		Hypothetical protein	7.1
DGo_PD0018	CDS		Hypothetical protein	7.1
DGo_CA0929	CDS		Hypothetical protein	6.8
DGo_PB0171	CDS		Hypothetical protein	6.8
DGo_CA1360	CDS		Hypothetical protein	6.7
DGo_CA2084	CDS		Uracil-DNA glycosylase related enzyme	6.5
DGo_PF0018	CDS		Hypothetical protein	6.5
DGo_PB0479	CDS		Hypothetical protein	6.4
DGo_CA2285	CDS		Glyoxalase/bleomycin resistance protein/dioxygenase	6.4
DGo_PC0059	CDS		Hypothetical protein	6.3
DGo_PC0222	CDS		Hypothetical protein	6.3
DGo_PC0072	CDS		Hypothetical protein	6.0
DGo_CA0381	CDS	*recG*	ATP-dependent DNA helicase RecG	6.0
DGo_CA0897	CDS		Acetyltransferase, GNAT family protein	5.9
DGo_CA1755	CDS		Allophanate hydrolase subunit 1	5.7
DGo_CA1378	CDS		Hypothetical protein	5.6
DGo_CA1217	CDS		Hypothetical protein	5.6
DGo_CA2720	CDS		Hypothetical protein	5.6
DGo_CA2576	CDS	*rpsH*	30S ribosomal protein S8	5.4
DGo_PC0028	CDS		Hypothetical protein	5.4
DGo_PB0337	CDS		Transposase, putative	5.3
DGo_CA1284	CDS		Hypothetical protein	5.2
DGo_CA1240	CDS		Acylphosphatase	5.1
DGo_PD0003	CDS		Hypothetical Membrane Spanning Protein	5.1
DGo_CA0841	CDS		Hypothetical protein	5.0
DGo_PC0063	CDS	*degP*	peptidase S1 and S6, chymotrypsin/Hap	4.9
DGo_PB0279	CDS		Hypothetical protein	4.9
DGo_PC0003	CDS		Transposase, IS4	4.9
DGo_CA2808	CDS	*lspA*	Lipoprotein signal peptidase	4.9
DGo_CA1382	CDS		putative penicillin-binding protein 1B McrB, precursor	4.9
DGo_PA0223	CDS		Permease of the drug/metabolite transporter superfamily	4.8
DGo_CA1944	CDS		Hypothetical protein	4.8
DGo_PA0159	CDS	*ssuC*	taurine transport system permease protein	4.8
DGo_CA0154	CDS		ABC-type sugar transport system, permease component	4.8
DGo_PB0504	CDS		Hypothetical protein	4.7
DGo_PA0350	CDS		Permease of the drug/metabolite transporter superfamily	4.7
DGo_CA2360	CDS		Hypothetical protein	4.7

DGo_CA0585	CDS		alkaline phosphatase	4.7
DGo_CA2869	CDS		Hypothetical protein	4.6
DGo_CA1876	CDS		Hypothetical protein	4.6
DGo_PC0269	CDS		Hypothetical protein	4.6
DGo_PA0303	CDS	*frcA*	ABC transporter, nucleotide binding/ATPase protein	4.5
DGo_PC0158	CDS		Hypothetical protein	4.5
DGo_PC0238	CDS		Phage integrase family protein	4.5
DGo_CA2529	CDS		Hypothetical protein	4.4
DGo_PB0017	CDS		Hypothetical protein	4.4
DGo_PC0031	CDS		Hypothetical protein	4.4
DGo_CA0228	CDS		Serine/threonine protein kinase, putative	4.1
DGo_CA0703	CDS		Hypothetical protein	4.1
DGo_PC0183	CDS		Thioredoxin reductase	4.1
DGo_PB0518	CDS		Hypothetical protein	4.1
DGo_CA1154	CDS	*pstA*	ABC-type phosphate transport system, permease component	4.1
DGo_CA0444	CDS		Phosphoesterase, PA-phosphatase related	4.0
DGo_PB0288	CDS		Hypothetical protein	4.0
DGo_PC0095	CDS		Hypothetical protein	4.0
DGo_PA0133	CDS		Hypothetical protein	4.0
DGo_PC0205	CDS		Transposase, IS4	4.0
DGo_PC0114	CDS		Hypothetical protein	3.9
DGo_CA2802	CDS	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	3.9
DGo_CA0447	CDS	*proS*	Prolyl-tRNA synthetase, bacterial	3.9
DGo_CA0583	CDS		ABC transporter, ATP-binding protein, putative	3.8
DGo_PE0033	CDS		Hypothetical protein	3.8
DGo_PB0495	CDS		Histidine kinase	3.8
DGo_PC0115	CDS		Hypothetical protein	3.8
DGo_CA0205	CDS	*cel*	M42 glutamyl aminopeptidase superfamily	3.8
DGo_CA0687	CDS		Hypothetical protein	3.7
DGo_CA0640	CDS	*gltB*	Glutamate synthase small subunit protein	3.7
DGo_CA2419	CDS		Hypothetical protein	3.7
DGo_PB0056	CDS		Hypothetical protein	3.6
DGo_PC0036	CDS		Hypothetical protein	3.6
DGo_PA0351	CDS		probable transcription regulator	3.6
DGo_CA1233	CDS	*trkG*	K+ transporter Trk	3.5
DGo_CA2390	CDS		Hypothetical protein	3.5
DGo_CA1434	CDS		Hypothetical protein	3.5
DGo_CA1040	CDS	*ddrI*	DdrI, transcriptional regulator, Crp/Fnr family	3.5
DGo_CA0616	CDS		ABC transporter, permease protein, putative	3.5
DGo_CA1441	CDS		Hypothetical protein	3.5
DGo_PB0018	CDS		Hypothetical protein	3.5
DGo_PC0274	CDS		Hypothetical protein	3.5

DGo_PA0251	CDS	*bceK*	Glycosyl transferase group 1	3.5
DGo_PB0329	CDS	*potC*	ABC transporter, membrane spanning protein	3.5
DGo_CA1548	CDS		Hypothetical protein	3.5
DGo_CA0217	CDS		Hypothetical protein	3.5
DGo_CA1652	CDS		Hypothetical protein	3.4
DGo_CA0551	CDS	*iolE*	Xylose isomerase domain protein TIM barrel	3.4
DGo_PB0522	CDS		Hypothetical protein	3.4
DGo_PB0237	CDS		Hypothetical protein	3.4
DGo_PC0138	CDS		Hypothetical protein	3.4
DGo_CA0552	CDS	*ccpA*	Catabolite control protein A, glucose-resistance amylase regulator	3.4
DGo_CA0952	CDS		Hypothetical protein	3.4
DGo_CA1627	CDS		ATP phosphoribosyltransferase	3.4
DGo_PB0002	CDS	*trpR*	LysR family transcriptional regulator	3.4
DGo_PC0279	CDS		Hypothetical protein	3.3
DGo_CA1021	CDS	*ytxJ*	Thioredoxin family protein, general stress protein ytxJ-like protein	3.3
DGo_CA0308	CDS	*folC2*	FolC bifunctional protein	3.3
DGo_PB0338	CDS		Hypothetical protein	3.3
DGo_CA1056	CDS		Beta-lactamase	3.3
DGo_CA1482	CDS		Hypothetical protein	3.3
DGo_CA2179	CDS		Ankyrin domain protein	3.3
DGo_CA0137	CDS		Endoribonuclease L-PSP	3.3
DGo_PB0220	CDS		Peptidase C39	3.3
DGo_PB0175	CDS		Hypothetical protein	3.3
DGo_PA0349	CDS		Hypothetical protein	3.3
DGo_CA2402	CDS		ABC glutamate/glutamine/aspartate/asparagine transporter, ATPase subunit bztD	3.3
DGo_PB0164	CDS		Hypothetical protein	3.2
DGo_CA1552	CDS		Hypothetical protein	3.2
DGo_PB0177	CDS	*pilT*	Tfp pilus assembly protein, pilus retraction ATPase PilT	3.2
DGo_CA2018	CDS	*nrfF*	Formate-dependent nitrite reductase complex, nrfF subunit	3.2
DGo_CA1377	CDS		IG Hypothetical 18565	3.2
DGo_PD0021	CDS		Hypothetical protein	3.2
DGo_PA0053	CDS		Probable transcriptional regulator, MarR family protein	3.2
DGo_PB0384	CDS		Hypothetical protein	3.2
DGo_CA0607	CDS	*phrB*	Deoxyribodipyrimidine photo-lyase type II	3.2
DGo_CA1981	CDS		Hypothetical protein	3.2
DGo_CA2718	CDS		Hypothetical protein	3.2
DGo_PF0026	CDS		Hypothetical protein	3.1
DGo_CA0695	CDS		Glycoside hydrolase, family 43	3.1
DGo_CA0073	CDS	*arsR*	Transcriptional regulator, ArsR family	3.1
DGo_CA1832	CDS		Sugar transporter, putative	3.1

DGo_CA2609	CDS		Trypsin-like peptidase and PDZ domain	3.1
DGo_PC0237	CDS		Phage integrase family protein	3.1
DGo_PD0002	CDS		Hypothetical protein	3.1
DGo_CA0690	CDS		Hypothetical protein	3.1
DGo_CA0548	CDS	*moeZ*	UBA/THIF-type NAD/FAD binding fold	3.1
DGo_CA2789	CDS		Hypothetical protein	3.1
DGo_CA2118	CDS		Hypothetical protein	3.1
DGo_CA0039	CDS		Hypothetical protein	3.0
DGo_PB0420	CDS		Hypothetical protein	3.0
DGo_CA2694	CDS		Hypothetical protein	3.0
DGo_PC0273	CDS		Hypothetical protein	3.0
DGo_PC0098	CDS	*recB2*	Predicted nuclease, RecB family	3.0
DGo_CA1872	CDS	*tauA2*	ABC transporter, periplasmic substrate-binding protein, putative	3.0
DGo_PB0284	CDS		Hypothetical protein	2.9
DGo_CA1849	CDS		Hypothetical protein	2.9
DGo_PB0397	CDS		Hypothetical protein	2.9
DGo_CA1019	CDS		Hypothetical protein	2.9
DGo_PB0412	CDS		Hypothetical protein	2.9
DGo_PB0421	CDS		Acetyltransferase, GNAT family	2.9
DGo_CA1531	CDS		Hypothetical protein	2.9
DGo_CA2839	CDS		Hypothetical protein	2.9
DGo_PA0046	CDS		Putative phosphatase protein	2.9
DGo_CA2057	CDS		DinB/YfiT family metal-binding protein	2.9
DGo_PB0355	CDS		Hypothetical protein	2.9
DGo_PB0139	CDS		Hypothetical protein	2.9
DGo_CA0090	CDS		Mg2+ transporter protein, CorA-like protein	2.9
DGo_PC0143	CDS		Transcriptional regulator with ATPase activity	2.8
DGo_CA1111	CDS	*pepB*	Leucyl aminopeptidase, putative	2.8
DGo_PC0120	CDS		Hypothetical protein	2.8
DGo_CA2860	CDS	*purC*	Phosphoribosylaminoimidazole-succinocarboxamide synthase	2.8
DGo_CA1540	CDS		Hypothetical protein	2.8
DGo_CA1318	CDS		Short-chain dehydrogenase/reductase SDR	2.8
DGo_CA0791	CDS		dTDP-4-dehydrorhamnose reductase and Glycosyl hydrolase family 1	2.8
DGo_CA1653	CDS		Hypothetical protein	2.8
DGo_PF0003	CDS		Hypothetical protein	2.8
DGo_PA0116	CDS		Integrase/recombinase, putative	2.8
DGo_PB0247	CDS		Hypothetical protein	2.8
DGo_CA2761	CDS	*folC*	Folylpolyglutamate synthetase	2.8
DGo_CA0555	CDS		Yellow-related protein	2.8
DGo_CA1850	CDS		Hypothetical protein	2.8
DGo_PB0507	CDS		Hypothetical protein	2.8

DGo_CA0795	CDS		Hypothetical protein	2.8
DGo_CA1589	CDS		Dipeptidase M19	2.7
DGo_CA1804	CDS		Transcriptional regulator, TetR family	2.7
DGo_PC0175	CDS	*phoR*	Sensor protein	2.7
DGo_PC0191	CDS		Hypothetical protein	2.7
DGo_PA0125	CDS		FRG domain protein	2.7
DGo_PB0395	CDS		Hypothetical protein	2.7
DGo_CA0277	CDS		Hypothetical protein	2.7
DGo_CA1165	CDS	*pyrD*	dihydroorotate dehydrogenase 2	2.7
DGo_CA2944	CDS		Hypothetical protein	2.7
DGo_PB0330	CDS		Hypothetical protein	2.7
DGo_CA2242	CDS	*ftsW*	Cell cycle protein	2.7
DGo_CA1782	CDS		HAD superfamily hydrolase	2.7
DGo_CA2366	CDS		Hypothetical protein	2.7
DGo_PB0515	CDS		Hypothetical protein	2.7
DGo_CA0712	CDS		Hypothetical protein	2.7
DGo_PB0264	CDS		Hypothetical protein	2.7
DGo_CA0376	CDS	*yqgF*	Holliday junction resolvase YqgF	2.7
DGo_CA1759	CDS		Hypothetical protein	2.7
DGo_CA2391	CDS		Peptidase S58, DmpA	2.7
DGo_PB0170	CDS		Hypothetical protein	2.7
DGo_PB0292	CDS		Hypothetical protein	2.7
DGo_PB0148	CDS		Hypothetical protein	2.6
DGo_CA2425	CDS		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2.6
DGo_PB0437	CDS		Hypothetical protein	2.6
DGo_CA0682	CDS		Hypothetical protein	2.6
DGo_CA0005	CDS		Mg2+ transporter protein, CorA-like protein	2.6
DGo_PB0106	CDS		Diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor	2.6
DGo_PC0215	CDS		Hypothetical protein	2.6
DGo_CA1142	CDS	*secE*	Preprotein translocase, SecE subunit	2.6
DGo_CA2771	CDS		Hypothetical protein	2.6
DGo_PF0014	CDS		Hypothetical protein	2.6
DGo_CA1005	CDS	*pfkB*	Fructokinase, ScrK	2.6
DGo_CA2438	CDS		Hypothetical protein	2.6
DGo_CA0441	CDS		Hypothetical protein	2.6
DGo_CA2736	CDS		Hypothetical transmembrane protein	2.6
DGo_CA0049	CDS		Hypothetical protein	2.6
DGo_CA2543	CDS		ADP-ribosylglycohydrolase, putative	2.6
DGo_CA0996	CDS	*potA*	Spermidine/putrescine ABC transporter, ATP-binding protein	2.6
DGo_PB0353	CDS		Hypothetical protein	2.6
DGo_PC0044	CDS		Hypothetical protein	2.6

DGo_PA0091	CDS		Menaquinol-cytochrome c reductase iron-sulfur subunit	2.5
DGo_CA1745	CDS		putative phosphatase	2.5
DGo_CA1659	CDS		Glycosyl transferase, family 4	2.5
DGo_PB0215	CDS		Hypothetical protein	2.5
DGo_PD0004	CDS		SMI1 / KNR4 family	2.5
DGo_PC0226	CDS		Protein tyrosine phosphatase	2.5
DGo_CA2050	CDS		Hypothetical protein	2.5
DGo_CA0019	CDS		transcriptional regulator	2.5
DGo_PB0198	CDS		Hypothetical protein	2.5
DGo_PF0010	CDS		putative transposase	2.5
DGo_PC0181	CDS		Hypothetical protein	2.5
DGo_CA1591	CDS	*ykfB*	Mandelate racemase-like protein/ muconate lactonizing enzyme-like protein	2.5
DGo_PB0387	CDS		Pentapeptide repeat protein	2.5
DGo_PB0032	CDS		Hypothetical protein	2.5
DGo_CA2038	CDS		Hypothetical protein	2.5
DGo_CA1955	CDS		Hypothetical protein	2.5
DGo_CA1178	CDS		Hypothetical protein	2.5
DGo_CA1542	CDS		Hypothetical protein	2.5
DGo_CA1957	CDS		Hypothetical protein	2.5
DGo_PB0519	CDS		DEAD/DEAH box helicase domain protein	2.5
DGo_CA0794	CDS		YceI-like protein, ycel3	2.4
DGo_PA0246	CDS		Hypothetical protein	2.4
DGo_PB0072	CDS		Hypothetical protein	2.4
DGo_CA2290	CDS	*gidA*	GidA-related protein	2.4
DGo_CA0943	CDS	*relA*	RelA/SpoT domain protein	2.4
DGo_CA2306	CDS		Probable transcriptional regulator	2.4
DGo_PB0189	CDS		Hypothetical protein	2.4
DGo_CA2558	CDS		Hypothetical protein	2.4
DGo_CA0235	CDS		Hypothetical protein	2.4
DGo_CA0186	CDS		Hypothetical protein	2.4
DGo_PB0095	CDS		DNA polymerase	2.4
DGo_PA0373	CDS		Hypothetical protein	2.4
DGo_CA0367	CDS	*ade*	Adenine deaminase	2.4
DGo_CA2479	CDS		50S ribosomal protein L25	2.4
DGo_PC0061	CDS		Hypothetical protein	2.4
DGo_PD0033	CDS		DNA mismatch endonuclease vsr	2.4
DGo_PA0139	CDS		WD40-like repeat/amidohydrolase domain protein	2.4
DGo_CA0017	CDS		Hypothetical protein	2.4
DGo_CA2857	CDS		Low molecular weight protein-tyrosine-phosphatase	2.4
DGo_PF0025	CDS		Phage integrase	2.4
DGo_CA1533	CDS		Putative cation efflux family protein, CzcD-like protein	2.4

DGo_PB0138	CDS		Hypothetical protein	2.4
DGo_CA2821	CDS		Beta-lactamase domain protein	2.4
DGo_CA2079	CDS		GCN5-related N-acetyltransferase	2.4
DGo_CA1628	CDS		Intradiol ring-cleavage dioxygenase	2.4
DGo_CA0002	CDS	*dnaN*	DNA polymerase III, beta subunit	2.4
DGo_CA2172	CDS		Hypothetical protein	2.3
DGo_CA1536	CDS		Zinc finger, DHP-type	2.3
DGo_PC0030	CDS		Integrase/recombinase, putative	2.3
DGo_CA0820	CDS		Hypothetical protein	2.3
DGo_PA0185	CDS		Hypothetical protein	2.3
DGo_PD0031	CDS		Transposase, IS4	2.3
DGo_PB0367	CDS		Transcriptional regulator-like protein	2.3
DGo_CA2114	CDS		Hypothetical protein	2.3
DGo_CA1844	CDS		Hypothetical protein	2.3
DGo_PD0023	CDS		Sulfotransferase domain superfamily	2.3
DGo_PA0136	CDS		DUF790-containing protein	2.3
DGo_CA1334	CDS	*argJ*	Arginine biosynthesis bifunctional protein argJ beta chain	2.3
DGo_CA0534	CDS		3-deoxy-7-phosphoheptulonate synthase	2.3
DGo_CA1181	CDS		Predicted RNA-binding protein associated with RNAse G/E	2.3
DGo_PC0121	CDS		Hypothetical protein	2.3
DGo_CA1335	CDS		HTH transcriptional regulator	2.3
DGo_CA0420	CDS		ABC-type polyamine transport system, ATPase component	2.3
DGo_CA1725	CDS	*miaA*	isopentenylpyrophosphate transferase	2.3
DGo_PA0333	CDS		Probable macrolide-efflux transmembrane protein	2.3
DGo_PB0347	CDS		Hypothetical protein	2.3
DGo_CA2726	CDS		Hypothetical protein	2.3
DGo_PA0192	CDS		Branched-chain amino acid ABC-type transport system, ATPase component	2.2
DGo_PC0102	CDS		Hypothetical protein	2.2
DGo_CA2032	CDS		ABC transporter, ATP-binding protein	2.2
DGo_PE0004	CDS		Hypothetical protein	2.2
DGo_CA0263	CDS		Hypothetical protein	2.2
DGo_CA0550	CDS	*carD*	Transcriptional regulator, CarD family	2.2
DGo_CA2738	CDS	*fliY*	ABC-type amino acid transport/signal transduction system, periplasmic component	2.2
DGo_PB0433	CDS	*parB*	ParB-like nuclease domain family	2.2
DGo_PE0065	CDS		Hypothetical protein	2.2
DGo_CA1678	CDS		Alcohol dehydrogenase, zinc-binding	2.2
DGo_PB0228	CDS		Bifunctional DNA primase/polymerase	2.2
DGo_CA2819	CDS		Hypothetical protein	2.2
DGo_PA0162	CDS		Putative Permease of the major facilitator superfamily	2.2
DGo_PC0236	CDS		Phage integrase family protein	2.2

DGo_PA0309	CDS	*lamB*	LamB/YcsF family protein	2.2
DGo_CA2007	CDS		Hypothetical protein	2.2
DGo_CA0928	CDS		Hypothetical protein	2.2
DGo_PB0212	CDS		Hypothetical protein	2.2
DGo_CA1866	CDS		Transcriptional regulator, TetR family	2.2
DGo_CA0237	CDS		Pilin, type IV, putative	2.2
DGo_PA0115	CDS		Hypothetical protein	2.2
DGo_CA0426	CDS		Epoxide Hydrolase	2.2
DGo_CA0350	CDS	*ddrB*	DdrB, radiation induced single-stranded DNA binding protein	2.2
DGo_CA2354	CDS	*tatC*	Sec-independent protein translocase protein TatC, putative	2.2
DGo_PA0338	CDS	*metI*	ABC transporter, permease protein	2.2
DGo_PB0045	CDS		Hypothetical protein	2.2
DGo_CA1917	CDS		TetR-family transcriptional regulator	2.2
DGo_PC0073	CDS		Hypothetical protein	2.2
DGo_CA1241	CDS	*osmC*	OsmC-like protein	2.1
DGo_CA0647	CDS	*kdpC*	Potassium-transporting ATPase C chain	2.1
DGo_CA1027	CDS		Uncharacterized peroxidase-related	2.1
DGo_CA2029	CDS		Hypothetical protein	2.1
DGo_CA0071	CDS	*ddrC*	DdrC	2.1
DGo_CA0977	CDS	*str*	Streptomycin 3"-kinase	2.1
DGo_PB0267	CDS		Hypothetical protein	2.1
DGo_CA0636	CDS		ABC transporter, permease protein	2.1
DGo_PC0019	CDS		Hypothetical protein	2.1
DGo_CA0920	CDS		SCP/PR1 domain	2.1
DGo_CA1579	CDS		Hydrolase, alpha/beta hydrolase fold family	2.1
DGo_CA2773	CDS		Hypothetical protein	2.1
DGo_CA0956	CDS		Hypothetical protein	2.1
DGo_PB0205	CDS		Hypothetical protein	2.1
DGo_CA0688	CDS		Hypothetical protein	2.1
DGo_PC0240	CDS		Transcriptional regulator, LysR family	2.1
DGo_PA0379	CDS	*manA*	Mannose-6-phosphate isomerase, putative	2.1
DGo_CA1873	CDS		chelatase family protein	2.1
DGo_CA2180	CDS		Luciferase-like protein	2.1
DGo_PB0249	CDS		AAA ATPase	2.1
DGo_CA1763	CDS	*yhfA*	OsmC-like protein	2.1
DGo_CA1726	CDS	*hsp*	Heat shock protein Hsp20	2.1
DGo_CA2102	CDS		Hypothetical protein	2.1
DGo_CA0131	CDS		Phenylacetic acid degradation protein PaaD	2.1
DGo_PE0006	CDS		Hypothetical protein	2.1
DGo_PC0011	CDS	*tniB*	Transposon, transposition helper protein C, putative	2.1
DGo_CA2193	CDS	*alr*	Alanine racemase	2.1
DGo_CA2666	CDS		Hypothetical protein	2.1

DGo_CA2614	CDS		Peptidase M20	2.1
DGo_CA0719	CDS	*deoR*	DeoR-family transcriptional regulator	2.1
DGo_CA0653	CDS		Transcriptional regulator, IclR family	2.1
DGo_CA0312	CDS	*moaC*	Molybdenum cofactor biosynthesis protein C	2.1
DGo_PA0014	CDS		Hypothetical protein	2.1
DGo_CA0335	CDS	*ctaB*	Protoheme IX farnesyltransferase	2.1
DGo_PB0182	CDS		Hypothetical protein	2.0
DGo_PB0081	CDS		Hypothetical protein	2.0
DGo_CA0873	CDS	*gyrB*	putative DNA topoisomerase	2.0
DGo_CA0633	CDS	*argE*	Amidase, hydantoinase/carbamoylase family	2.0
DGo_CA2308	CDS		Hypothetical protein	2.0
DGo_CA2014	CDS		Hypothetical protein	2.0
DGo_CA0725	CDS	*sig4*	RNA polymerase sigma factor	2.0
DGo_CA0843	CDS		HAD-superfamily hydrolase subfamily IA	2.0
DGo_PB0239	CDS		Hypothetical protein	2.0
DGo_PB0413	CDS		Phage protein	2.0
DGo_CA0332	CDS	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.0
DGo_PE0066	CDS		Hypothetical protein	2.0
DGo_CA2368	CDS		Lipase, putative	2.0
DGo_CA0357	CDS	*citB*	response regulator receiver/unknown domain-containing protein	2.0
DGo_CA2138	CDS		Aminotransferase, class V	2.0
DGo_PC0032	CDS		Hypothetical protein	2.0
DGo_PB0396	CDS		Hypothetical protein	2.0
DGo_CA1259	CDS		GGDEF family protein	2.0

B. Functional description of 754 genes that were repressed after UV-irradiation

Locus_tag	Type	Name	Description	Fold
DGo_CAnc10	ncRNA		Hypothetical non-coding RNA	<-100.0
DGo_PBnc01	ncRNA		Hypothetical non-coding RNA	<-100.0
DGo_CAnc16	ncRNA		Hypothetical non-coding RNA	-109.5
DGo_PFnc04	ncRNA		Hypothetical non-coding RNA	-45.9
DGo_PBnc02	ncRNA		Hypothetical non-coding RNA	-32.6
DGo_PAnc04	ncRNA		Hypothetical non-coding RNA	-26.5
DGo_PBnc04	ncRNA		Hypothetical non-coding RNA	-23.3
DGo_PCnc05	ncRNA		Hypothetical non-coding RNA	-20.3
DGo_CAnc06	ncRNA		Hypothetical non-coding RNA	-19.3
DGo_PAnc02	ncRNA		Hypothetical non-coding RNA	-17.9
DGo_PAnc03	ncRNA		Hypothetical non-coding RNA	-17.6
DGo_PFnc01	ncRNA		Hypothetical non-coding RNA	-14.3
DGo_PCnc01	ncRNA		Hypothetical non-coding RNA	-6.4
DGo_PFnc03	ncRNA		Hypothetical non-coding RNA	-6.0
DGo_CAnc02	ncRNA		Hypothetical non-coding RNA	-5.5

DGo_CAnc01	ncRNA		Hypothetical non-coding RNA	-5.5
DGo_PCnc03	ncRNA		Hypothetical non-coding RNA	-3.5
DGo_PCnc02	ncRNA		Hypothetical non-coding RNA	-3.5
DGo_PCnc04	ncRNA		Hypothetical non-coding RNA	-2.9
DGo_PBnc06	ncRNA		Hypothetical non-coding RNA	-2.9
DGo_CAnc07	ncRNA		Hypothetical non-coding RNA	-2.7
DGo_PFnc02	ncRNA		Hypothetical non-coding RNA	-2.2
DGo_CA1065	CDS		Hypothetical protein	<-100.0
DGo_CA1511	CDS		Yfit/DinB family protein	<-100.0
DGo_CA2661	CDS	*nth*	putative endonuclease III	<-100.0
DGo_PB0060	CDS		Hypothetical protein	<-100.0
DGo_PB0425	CDS		Hypothetical protein	<-100.0
DGo_PC0090	CDS		Hypothetical protein	<-100.0
DGo_PC0149	CDS		Hypothetical protein	<-100.0
DGo_PC0178	CDS		Hypothetical protein	<-100.0
DGo_CA0923	CDS		Hypothetical protein	-124.8
DGo_PD0013	CDS		Hypothetical protein	-53.4
DGo_PB0054	CDS	*arsR*	Transcriptional regulator, ArsR family	-51.3
DGo_CA1925	CDS		Signal peptidase I	-45.1
DGo_PB0370	CDS		Transposase, ISMyma01_aa2-like protein	-32.5
DGo_CA1593	CDS	*degV*	DegV family protein	-19.2
DGo_PB0028	CDS		Hypothetical protein	-17.3
DGo_PB0254	CDS		Hypothetical protein	-16.8
DGo_PB0082	CDS		Hypothetical protein	-16.4
DGo_PB0456	CDS		Hypothetical protein	-15.2
DGo_CA1964	CDS		Hypothetical protein	-14.5
DGo_PC0124	CDS		Hypothetical protein	-14.2
DGo_CA1357	CDS		Hypothetical protein	-13.7
DGo_PB0265	CDS		Hypothetical protein	-13.6
DGo_CA0268	CDS		ABC-type branched-chain amino acid transport system, ATPase component	-12.9
DGo_PB0253	CDS		Hypothetical protein	-12.2
DGo_PB0262	CDS		Hypothetical protein	-12.1
DGo_PC0268	CDS		Hypothetical protein	-12.0
DGo_PB0414	CDS		Hypothetical protein	-11.8
DGo_CA1778	CDS		Transcriptional regulator, MarR family	-11.4
DGo_CA1899	CDS		Hypothetical protein	-11.0
DGo_CA2803	CDS	*folB*	Dihydroneopterin aldolase	-10.8
DGo_PB0273	CDS		Hypothetical protein	-10.7
DGo_CA1149	CDS	*rbsC*	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	-10.1
DGo_CA2449	CDS		Glyoxalase/bleomycin resistance protein/dioxygenase	-8.9
DGo_PC0079	CDS		Helicase-like protein	-8.6
DGo_PB0475	CDS		Hypothetical protein	-8.5

DGo_PC0045	CDS		Hypothetical protein	-8.5
DGo_CA0173	CDS		Hypothetical protein	-8.3
DGo_PC0232	CDS		Hypothetical protein	-8.2
DGo_PB0158	CDS	*hofG*	Tfp pilus assembly protein major pilin PilA-like protein	-8.0
DGo_CA1545	CDS	*ccmA*	ABC-type transport system	-7.8
DGo_CA0419	CDS		Acetyltransferase, putative	-7.7
DGo_CA1379	CDS		Putative acetylglutamate kinase-like protein	-7.7
DGo_CA1900	CDS		Hypothetical protein	-7.7
DGo_PC0235	CDS		Hypothetical protein	-7.6
DGo_PB0073	CDS		Transposase IS4 family protein	-7.5
DGo_PB0362	CDS		Hypothetical protein	-7.5
DGo_CA2022	CDS		Hypothetical protein	-7.4
DGo_CA2719	CDS		putative acyltransferase	-7.4
DGo_CA2060	CDS		Sec-C motif containing protein	-7.0
DGo_CA1244	CDS		Transcriptional regulator, AraC family	-7.0
DGo_CA2358	CDS	*crtI3*	Phytoene dehydrogenase, CrtI	-7.0
DGo_CA1906	CDS		Hypothetical protein	-7.0
DGo_PA0347	CDS		Hypothetical protein	-6.9
DGo_PB0453	CDS		Hypothetical protein	-6.9
DGo_CA1702	CDS		Predicted RNA-binding protein	-6.9
DGo_CA1570	CDS		YceI like family protein	-6.8
DGo_CA0906	CDS		Endoribonuclease L-PSP superfamily	-6.8
DGo_PA0359	CDS	*rbsB2*	Ribose ABC transporter, periplasmic ribose-binding protein	-6.8
DGo_PC0018	CDS		Hypothetical protein	-6.8
DGo_CA0105	CDS		Hypothetical protein	-6.8
DGo_PB0092	CDS		Transposase IS4 family protein	-6.8
DGo_CA1602	CDS	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase	-6.7
DGo_PB0033	CDS		Hypothetical protein	-6.7
DGo_PB0084	CDS		Oxidoreductase domain protein	-6.7
DGo_PC0184	CDS		Hypothetical protein	-6.7
DGo_PB0351	CDS		Hypothetical protein	-6.6
DGo_PB0207	CDS		Transposase, IS4	-6.5
DGo_CA0772	CDS		Peptide ABC transporter, permease protein	-6.4
DGo_PB0099	CDS		Hypothetical protein	-6.2
DGo_PC0099	CDS		Hypothetical protein	-6.2
DGo_CA1965	CDS		Terminase small subunit	-6.2
DGo_CA1278	CDS	*clpS*	ATP-dependent Clp protease adaptor protein ClpS	-6.2
DGo_CA1890	CDS		Putative gene transfer agent portal protein	-6.1
DGo_CA1688	CDS		Hypothetical protein	-6.1
DGo_PB0484	CDS		Hypothetical protein	-6.1
DGo_PB0048	CDS		GCN5-related N-acetyltransferase	-6.1
DGo_CA1239	CDS		putative octaprenyl-diphosphate synthase	-6.0

DGo_PC0066	CDS		Hypothetical protein	-6.0
DGo_CA1305	CDS		Response regulator	-5.9
DGo_CA1299	CDS		Maltose ABC transporter, periplasmic maltose-binding protein	-5.9
DGo_PA0106	CDS		Hypothetical protein	-5.9
DGo_CA1654	CDS		Hypothetical protein	-5.8
DGo_CA1989	CDS		Hypothetical protein	-5.8
DGo_PA0178	CDS		Hypothetical protein	-5.8
DGo_CA0745	CDS		Hypothetical protein	-5.7
DGo_CA2031	CDS	*csaA*	T-RNA-binding region	-5.6
DGo_CA0098	CDS		Hypothetical protein	-5.6
DGo_PF0009	CDS		Hypothetical protein	-5.6
DGo_CA1476	CDS	*fabZ*	dehydratase	-5.5
DGo_CA1294	CDS		MutT/nudix family protein	-5.5
DGo_CA2199	CDS		Hypothetical protein	-5.5
DGo_PB0376	CDS		Transposase, putative	-5.5
DGo_PC0146	CDS		Hypothetical protein	-5.4
DGo_PB0071	CDS		Hypothetical protein	-5.4
DGo_CA2389	CDS		Uroporphyrin-III methyltransferase and synthase domains	-5.4
DGo_CA2036	CDS	*alkA*	Putative 3-methyladenine DNA glycosylase	-5.4
DGo_CA0446	CDS		Hypothetical protein	-5.4
DGo_CA1625	CDS		Hypothetical protein	-5.4
DGo_PA0105	CDS		Probable RNA 2'-phosphotransferase	-5.3
DGo_PC0164	CDS		Hypothetical protein	-5.3
DGo_CA2907	CDS	*xseB*	Exonuclease VII small subunit	-5.3
DGo_PB0438	CDS		Hypothetical protein	-5.2
DGo_CA2183	CDS		Isoprenylcysteine carboxyl methyltransferase	-5.2
DGo_CA1728	CDS		Hypothetical protein	-5.1
DGo_CA2530	CDS		Hypothetical protein	-5.1
DGo_CA2399	CDS		amino acid ABC transporter, periplasmic amino acid-binding prote in	-5.1
DGo_CA0750	CDS		Hypothetical protein	-5.0
DGo_CA2807	CDS	*luxS*	S-ribosylhomocysteine lyase	-5.0
DGo_CA1987	CDS		Hypothetical protein	-5.0
DGo_CA2470	CDS	*tolQ*	Biopolymer transport protein, putative	-5.0
DGo_CA1648	CDS		Hydrolase, putative	-4.9
DGo_CA2522	CDS		Cytidine/deoxycytidylate deaminase/nudix/methyltransferase domains protein	-4.9
DGo_PB0156	CDS		Hypothetical protein	-4.8
DGo_CA0478	CDS		putative ATP-binding protein	-4.8
DGo_CA0994	CDS	*potC*	Spermidine/putrescine ABC transporter, permease protein	-4.8
DGo_CA1985	CDS		Hypothetical protein	-4.8
DGo_CA2911	CDS		Ferredoxin	-4.8

DGo_CA2341	CDS		Diguanylate cyclase	-4.8
DGo_CA1973	CDS		Hypothetical protein	-4.8
DGo_PF0032	CDS		Arsenate reductase, ArsC-like protein	-4.7
DGo_CA2428	CDS		Arginine repressor	-4.7
DGo_PA0093	CDS		Hypothetical protein	-4.7
DGo_CA2323	CDS		HAD-superfamily phosphatase subfamily IIIA	-4.6
DGo_CA0979	CDS		Guanyl-specific ribonuclease Sa-like protein	-4.6
DGo_CA0407	CDS	*nrdH*	Glutaredoxin 2	-4.6
DGo_PC0182	CDS		Hypothetical protein	-4.6
DGo_PB0316	CDS		A Chain A, Crystal Structure Of A Protein With Unknown Function From Duf162 Family	-4.6
DGo_PC0067	CDS		Hypothetical protein	-4.6
DGo_CA0740	CDS		Two component transcriptional regulator, winged helix family	-4.6
DGo_CA2173	CDS		Signal transduction diguanylate cyclase	-4.6
DGo_PB0476	CDS		Hypothetical protein	-4.5
DGo_CA1904	CDS		Hypothetical protein	-4.5
DGo_CA2135	CDS	*ompH*	Outer membrane chaperone Skp	-4.5
DGo_PB0310	CDS		Predicted transporter, permease component	-4.4
DGo_CA0196	CDS		RelE/ParE family protein	-4.4
DGo_PB0077	CDS		Hypothetical protein	-4.4
DGo_PB0174	CDS		Hypothetical protein	-4.4
DGo_CA1558	CDS	*ylmE*	UPF0001 protein	-4.4
DGo_CA2322	CDS		UPF0124 protein	-4.4
DGo_PB0398	CDS		Transcriptional regulator, PadR-like family	-4.4
DGo_PB0266	CDS		Hypothetical protein	-4.3
DGo_PA0210	CDS		Acetyltransferase, GNAT family	-4.3
DGo_PB0483	CDS		Hypothetical protein	-4.3
DGo_PA0362	CDS		Oxidoreductase, short chain dehydrogenase/reductase family	-4.3
DGo_CA2528	CDS		Putative kinase protein	-4.3
DGo_CA2291	CDS		Pseudouridine synthase, RluA family	-4.3
DGo_CA1909	CDS		peptidase domain protein	-4.2
DGo_CA1031	CDS		Putative transcriptional regulator	-4.2
DGo_PA0132	CDS		Transcriptional regulator, PadR-like family	-4.2
DGo_CA1255	CDS	*nuoK*	NADH dehydrogenase I subunit K	-4.2
DGo_CA2919	CDS		Acetyltransferase, gnat family	-4.2
DGo_PC0270	CDS		Hypothetical protein	-4.2
DGo_CA0905	CDS		Competence protein ComEC/Rec2, putative	-4.1
DGo_PC0078	CDS		Hypothetical protein	-4.1
DGo_CA2554	CDS		synthase	-4.1
DGo_CA0744	CDS		Transcriptional regulator IclR-like protein	-4.1
DGo_CA1970	CDS		Hypothetical protein	-4.1
DGo_CA1254	CDS	*nuoJ*	NADH-quinone oxidoreductase, J subunit	-4.1

DGo_CA1830	CDS	*cyp*	Cytochrome P450	-4.1
DGo_CA0790	CDS		Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor	-4.1
DGo_CA2404	CDS		FMN-dependent dehydrogenase superfamily	-4.1
DGo_CA1617	CDS		NADH-dependent flavin oxidoreductase, putative	-4.1
DGo_CA0314	CDS		Putative thiol-specific antioxidant related protein	-4.1
DGo_PB0473	CDS	*terL*	Terminase large subunit	-4.0
DGo_CA1082	CDS		Hypothetical protein	-4.0
DGo_PC0223	CDS	*arsR*	Transcriptional regulator, ArsR family	-4.0
DGo_CA1469	CDS		Predicted membrane-bound metal-dependent hydrolase	-4.0
DGo_CA1898	CDS		Hypothetical protein	-4.0
DGo_CA0410	CDS		Hypothetical protein	-4.0
DGo_PA0126	CDS		Hypothetical protein	-3.9
DGo_CA2088	CDS	*recX*	Regulatory protein recX	-3.9
DGo_PC0015	CDS		Hypothetical protein	-3.9
DGo_CA0431	CDS		Hypothetical protein	-3.9
DGo_PA0118	CDS		Probable two-component sensor histidine kinase protein	-3.9
DGo_CA1096	CDS		Methanol dehydrogenase regulatory protein	-3.9
DGo_PA0244	CDS		Hypothetical protein	-3.9
DGo_PB0336	CDS		Hypothetical protein	-3.9
DGo_PA0322	CDS		Hypothetical protein	-3.8
DGo_PC0026	CDS		Hypothetical protein	-3.8
DGo_CA0762	CDS	*ureD*	Urease accessory protein ureD	-3.8
DGo_PD0010	CDS		Hypothetical protein	-3.8
DGo_CA0853	CDS		Hypothetical protein	-3.8
DGo_CA0783	CDS		IclR family transcriptional regulator	-3.7
DGo_CA2281	CDS	*dcd*	dCTP deaminase	-3.7
DGo_CA1066	CDS		Chromosome partitioning protein, ParA family	-3.7
DGo_CA1419	CDS		Transcriptional regulator, Crp/Fnr family	-3.7
DGo_PC0188	CDS		Cell wall hydrolase/autolysin	-3.7
DGo_PF0001	CDS		Hypothetical protein	-3.7
DGo_CA1406	CDS	*deoC*	Deoxyribose-phosphate aldolase	-3.7
DGo_PB0311	CDS		Hypothetical protein	-3.7
DGo_CA2847	CDS		Hypothetical protein	-3.7
DGo_PA0122	CDS		Polyphosphate glucokinase	-3.6
DGo_CA0370	CDS		Zn-finger containing protein	-3.6
DGo_CA1095	CDS		Hypothetical protein	-3.6
DGo_PC0002	CDS		Hypothetical protein	-3.6
DGo_PA0339	CDS		ABC transporter, ATP-binding protein	-3.6
DGo_PF0043	CDS		Hypothetical protein	-3.6
DGo_CA2502	CDS	*nos*	Nitric oxide synthase oxygenase	-3.6
DGo_CA1374	CDS	*minC*	Probable septum site-determining protein minC	-3.6

DGo_CA1908	CDS		Hypothetical protein	-3.5
DGo_CA2217	CDS		Polysaccharide deacetylase, putative	-3.5
DGo_PB0168	CDS		Hypothetical protein	-3.5
DGo_PA0243	CDS		Transposase IS-4	-3.5
DGo_CA0692	CDS		Response regulator receiver:Metal-dependent phosphohydrolase, HD subdomain	-3.5
DGo_PC0193	CDS		Redoxin	-3.5
DGo_PA0166	CDS		ABC-type maltose transport system, periplasmic component, MalE	-3.5
DGo_CA0807	CDS	*cbiG*	Precorrin methylase protein	-3.5
DGo_PA0190	CDS		Hypothetical protein	-3.5
DGo_CA0724	CDS		Hypothetical protein	-3.5
DGo_CA2417	CDS		Hypothetical protein	-3.5
DGo_CA2171	CDS		predicted regulor of amylopullulanase	-3.5
DGo_CA0424	CDS	*lmbE*	LmbE-like protein protein	-3.5
DGo_PA0299	CDS		Hypothetical protein	-3.4
DGo_CA0200	CDS		Thioesterase superfamily	-3.4
DGo_CA1895	CDS		Hypothetical protein	-3.4
DGo_CA1527	CDS		Hypothetical protein	-3.4
DGo_CA1062	CDS		Hypothetical protein	-3.4
DGo_CA0584	CDS		Hypothetical protein	-3.4
DGo_PB0325	CDS		Transcriptional regulator, LacI family	-3.4
DGo_PB0146	CDS		Hypothetical protein	-3.4
DGo_PC0260	CDS		Transposase, IS4	-3.4
DGo_CA0292	CDS		Predicted HD phosphohydrolase family protein	-3.4
DGo_CA1801	CDS		Hypothetical protein	-3.4
DGo_CA1888	CDS		Hypothetical protein	-3.4
DGo_CA1889	CDS		Predicted protein	-3.4
DGo_CA0575	CDS		Hypothetical protein	-3.4
DGo_CA0706	CDS		Putative transcriptional regulator	-3.3
DGo_PB0436	CDS		Hypothetical protein	-3.3
DGo_CA0403	CDS	*moeA*	MoeA-like protein, domain I and II	-3.3
DGo_PB0204	CDS		Hypothetical protein	-3.3
DGo_PB0085	CDS	*mviM*	Oxidoreductase domain protein	-3.3
DGo_CA1807	CDS	*nth*	Endonuclease III, putative	-3.3
DGo_CA0472	CDS		Hypothetical protein	-3.3
DGo_PB0055	CDS		Hypothetical protein	-3.3
DGo_PB0312	CDS	*cyp*	Cytochrome P450 51	-3.3
DGo_CA0747	CDS	*appB*	Peptide ABC transporter, permease protein	-3.3
DGo_CA0954	CDS	*kdtB*	Phosphopantetheine adenylyltransferase	-3.3
DGo_PC0022	CDS		Hypothetical protein	-3.3
DGo_CA1680	CDS	*murM*	Peptidoglycan branched peptide synthesis, doubled GNAT-acetyltrasferase fold	-3.3
DGo_PC0125	CDS		Hypothetical protein	-3.3

DGo_CA1201	CDS		Hypothetical protein	-3.3
DGo_CA1282	CDS		putative acetyltransferase	-3.3
DGo_PB0369	CDS		Probable insertion sequence transposase protein	-3.3
DGo_PA0089	CDS		Hypothetical protein	-3.3
DGo_PB0447	CDS		Hypothetical protein	-3.3
DGo_PB0257	CDS		Hypothetical protein	-3.3
DGo_CA2282	CDS		Hypothetical protein	-3.3
DGo_CA0702	CDS		Lea76/Lea29-like desiccation resistance protein	-3.2
DGo_CA1980	CDS		Hypothetical protein	-3.2
DGo_PB0052	CDS		Arsenite transmembrane pump-like protein	-3.2
DGo_PC0153	CDS		Hypothetical protein	-3.2
DGo_CA1044	CDS		Roadblock/LC7	-3.2
DGo_PB0214	CDS		putative IS1648 transposase	-3.2
DGo_PA0027	CDS	*cynS*	Cyanate lyase, CynS	-3.2
DGo_CA0135	CDS	*mgsA*	Methylglyoxal synthase protein	-3.2
DGo_CA2494	CDS		Serine cycle enzyme, putative	-3.2
DGo_PB0462	CDS		Hypothetical protein	-3.2
DGo_CA1183	CDS		Alpha/beta superfamily hydrolase	-3.2
DGo_PB0417	CDS		Hypothetical protein	-3.2
DGo_CA0978	CDS	*upk*	Undecaprenyl-diphosphatase	-3.2
DGo_PA0165	CDS		Glycosyl hydrolase, family 53-likely arabinogalactan 1,4-beta-galactosidase	-3.2
DGo_CA0227	CDS		Hypothetical protein	-3.2
DGo_PA0150	CDS	*rbsA*	Ribose ABC transporter permease protein RbsD	-3.2
DGo_PC0105	CDS		Hypothetical protein	-3.2
DGo_PA0081	CDS		Hypothetical protein	-3.1
DGo_CA1133	CDS		Hypothetical protein	-3.1
DGo_CA1894	CDS		Hypothetical protein	-3.1
DGo_PA0256	CDS		UDP-galactose-lipid carrier transferase	-3.1
DGo_PB0235	CDS		Hypothetical protein	-3.1
DGo_CA1690	CDS		Hypothetical protein	-3.1
DGo_CA1547	CDS		Alpha/beta hydrolase fold-3	-3.1
DGo_CA1258	CDS	*nuoN*	NADH-quinone oxidoreductase, N subunit	-3.1
DGo_CA2946	CDS		Hypothetical protein	-3.1
DGo_CA2699	CDS		Phenol hydroxylase	-3.1
DGo_CA0742	CDS		Hypothetical protein	-3.1
DGo_PB0190	CDS		Hypothetical protein	-3.1
DGo_CA2090	CDS		Hypothetical protein	-3.1
DGo_CA1363	CDS		ComA like protein, thioesterase superfamily	-3.1
DGo_CA1534	CDS		putative Lipoprotein-releasing system ATP-binding protein lolD; putative ABC transporter, ATP-binding component	-3.1
DGo_PC0108	CDS		Hypothetical protein	-3.1
DGo_CA0015	CDS		Peptidase C39	-3.1

DGo_CA1984	CDS		Hypothetical protein	-3.1
DGo_PC0020	CDS		Hypothetical protein	-3.1
DGo_CA0893	CDS		Hypothetical protein	-3.1
DGo_CA0646	CDS	*kdpD*	Potassium-transporting ATPase, D subunit	-3.1
DGo_CA0300	CDS		Hypothetical protein	-3.0
DGo_CA2853	CDS	*trmH*	RNA methyltransferase, putative	-3.0
DGo_CA2070	CDS		Hypothetical protein	-3.0
DGo_CA0757	CDS		Hydrogenase expression/formation HypB-related protein	-3.0
DGo_CA2044	CDS		Hypothetical protein	-3.0
DGo_PB0008	CDS		Hypothetical protein	-3.0
DGo_CA2613	CDS		Carbonic anhydrase	-3.0
DGo_CA0573	CDS		Response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor	-3.0
DGo_CA0913	CDS	*crt*	Enoyl-CoA hydratase/isomerase	-3.0
DGo_CA2388	CDS	*cysG*	Siroheme synthase	-3.0
DGo_CA1037	CDS	*aacC*	Aminoglycoside N3`-acetyltransferase, type IV	-3.0
DGo_CA0754	CDS		Peptidase M29, aminopeptidase II	-3.0
DGo_CA2450	CDS		putative VanZ like family protein; putative membrane protein	-3.0
DGo_PB0469	CDS		Hypothetical protein	-3.0
DGo_CA0547	CDS		UPF0078 membrane protein	-3.0
DGo_PC0272	CDS		Hypothetical protein	-3.0
DGo_PB0272	CDS		Hypothetical protein	-3.0
DGo_PB0297	CDS		Hypothetical protein	-3.0
DGo_PD0061	CDS		Hypothetical protein	-3.0
DGo_CA1859	CDS		Hypothetical protein	-3.0
DGo_PB0069	CDS		Hypothetical protein	-3.0
DGo_CA2938	CDS		UPF0189 protein	-3.0
DGo_PA0140	CDS		Amidohydrolase family enzyme	-3.0
DGo_CA1516	CDS		Hypothetical protein	-2.9
DGo_PC0192	CDS		Secreted protein	-2.9
DGo_CA1771	CDS	*pcaC*	4-carboxymuconolactone decarboxylase	-2.9
DGo_CA1237	CDS		N-acetylmuramoyl-L-alanine amidase, family 2	-2.9
DGo_CA0025	CDS		Hypothetical protein	-2.9
DGo_CA2734	CDS		putative membrane protein	-2.9
DGo_PC0038	CDS		Diguanylate cyclase and metal dependent phosphohydrolase	-2.9
DGo_CA1251	CDS	*nuoG*	NADH-quinone oxidoreductase	-2.9
DGo_CA0067	CDS		Metallophosphoesterase	-2.9
DGo_CA0119	CDS		Carbohydrate kinase FGGY	-2.9
DGo_CA0253	CDS		Hypothetical protein	-2.9
DGo_CA2752	CDS		Carbohydrate-binding CenC domain protein	-2.9
DGo_CA1975	CDS		Hypothetical protein	-2.9
DGo_CA1795	CDS		Hypothetical protein	-2.9

DGo_CA2249	CDS	*aroC*	Chorismate synthase	-2.9
DGo_PC0278	CDS		Hypothetical protein	-2.9
DGo_CA0100	CDS		Hypothetical protein	-2.9
DGo_CA1067	CDS		Hypothetical protein	-2.9
DGo_PB0418	CDS		Hypothetical protein	-2.9
DGo_CA1993	CDS		Hypothetical protein	-2.9
DGo_PB0187	CDS		Hypothetical protein	-2.9
DGo_CA0013	CDS		Hypothetical protein	-2.8
DGo_CA1286	CDS		Peptidase M29, aminopeptidase II	-2.8
DGo_PB0185	CDS		Hypothetical protein	-2.8
DGo_PB0145	CDS		Hypothetical protein	-2.8
DGo_PC0161	CDS		ParB-like partition protein	-2.8
DGo_PE0049	CDS		Hypothetical protein	-2.8
DGo_CA1574	CDS	*mae*	C4-dicarboxylate transporter/malic acid transport protein	-2.8
DGo_PB0173	CDS		Predicted membrane-bound metal-dependent hydrolase	-2.8
DGo_CA1509	CDS		Hypothetical protein	-2.8
DGo_CA1494	CDS		Metallophosphoesterase	-2.8
DGo_CA1257	CDS	*nuoM*	NADH-quinone oxidoreductase, M subunit	-2.8
DGo_CA2105	CDS		Hypothetical protein	-2.8
DGo_CA0369	CDS	*marR*	Transcriptional regulator, MarR family	-2.8
DGo_CA0855	CDS		Arginase	-2.8
DGo_PC0111	CDS		Hypothetical protein	-2.8
DGo_CA1017	CDS		NAD-dependent aldehyde dehydrogenase	-2.8
DGo_CA2611	CDS	*rpsO*	30S ribosomal protein S15	-2.8
DGo_CA2682	CDS		Hypothetical protein	-2.8
DGo_PA0173	CDS		Hypothetical protein	-2.8
DGo_PA0035	CDS		ABC transporter, permease protein	-2.8
DGo_PB0038	CDS		Hypothetical protein	-2.8
DGo_CA1221	CDS		Putative DNA-binding protein	-2.8
DGo_CA0618	CDS		Glutamine-fructose-6-phosphate transaminase	-2.8
DGo_CA2541	CDS		Thioredoxin	-2.8
DGo_CA2330	CDS		NADH dehydrogenase	-2.7
DGo_CA1703	CDS	*truD*	tRNA pseudouridine synthase D	-2.7
DGo_CA1670	CDS		Hypothetical protein	-2.7
DGo_PB0236	CDS		Hypothetical protein	-2.7
DGo_CA1963	CDS		Hypothetical protein	-2.7
DGo_PC0211	CDS		Glutaredoxin	-2.7
DGo_CA1796	CDS		PBP1 protein; transglycosylase, transpeptidase domain	-2.7
DGo_CA1657	CDS	*bmrU*	Diacylglycerol kinase, catalytic region	-2.7
DGo_CA2862	CDS	*purQ*	Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase domain	-2.7
DGo_CA0465	CDS		Polyferredoxin, putative	-2.7

DGo_PB0268	CDS		Hypothetical protein	-2.7
DGo_CA1256	CDS	*nuoL*	NADH-quinone oxidoreductase, L subunit	-2.7
DGo_PA0012	CDS		Hypothetical protein	-2.7
DGo_CA1464	CDS	*cyp*	Cytochrome P450	-2.7
DGo_CA1626	CDS	*hisZ*	ATP phosphoribosyltransferase, Histidyl-tRNA synthetase-like protein	-2.7
DGo_CA0667	CDS		Miro-like protein	-2.7
DGo_CA1487	CDS		Spermidine synthase	-2.7
DGo_CA0026	CDS		Hypothetical protein	-2.7
DGo_CA0587	CDS		Magnesium chelatase, ChlI subunit	-2.7
DGo_CA1569	CDS	*pdxT*	Glutamine amidotransferase subunit pdxT	-2.7
DGo_CA2141	CDS		Putative transmembrane protein	-2.7
DGo_PB0466	CDS		Hypothetical protein	-2.7
DGo_CA1447	CDS	*trpG*	Glutamine amidotransferase of anthranilate synthase or para-aminobenzoate synthase	-2.7
DGo_CA2495	CDS		Glycosyl transferase, group 1	-2.7
DGo_PB0501	CDS		Hypothetical protein	-2.7
DGo_CA2937	CDS		Hypothetical protein	-2.7
DGo_CA0635	CDS		Permease protein, ABC-type nitrate/sulfonate/taurine/bicarbonate transporter	-2.7
DGo_PA0186	CDS		ABC-type transport system for cytochrome bd biosynthesis, ATPase and permease component	-2.7
DGo_CA0150	CDS		Hypothetical protein	-2.7
DGo_PA0181	CDS		Alpha/beta hydrolase fold	-2.7
DGo_CA0809	CDS	*cobW*	Cobalamin synthesis protein, GTPase of G3E family	-2.7
DGo_CA1741	CDS	*nadE*	NAD synthetase, NH3/glutamine-dependent	-2.7
DGo_CA1760	CDS		TRAP transporter solute receptor, TAXI family	-2.7
DGo_PB0113	CDS		Transposase, IS4	-2.7
DGo_CA0324	CDS		Aminodeoxychorismate lyase	-2.6
DGo_CA1827	CDS	*sbcC*	SbcC, ATPase involved in DNA repair	-2.6
DGo_PA0307	CDS	*ams*	Glycoside hydrolase family 38	-2.6
DGo_CA1267	CDS		multi-sensor signal transduction histidine kinase	-2.6
DGo_PC0247	CDS		Hypothetical protein	-2.6
DGo_PB0192	CDS	*cas2*	Crispr-associated protein cas2	-2.6
DGo_PC0136	CDS		Hypothetical protein	-2.6
DGo_PB0430	CDS		Hypothetical protein	-2.6
DGo_CA1016	CDS	*yqjF*	YqjF	-2.6
DGo_PB0498	CDS		Hypothetical protein	-2.6
DGo_PC0007	CDS		Hypothetical protein	-2.6
DGo_CA0940	CDS		Hypothetical protein	-2.6
DGo_PE0054	CDS		Hypothetical protein	-2.6
DGo_CA0525	CDS		Cation transport system protein, putative	-2.6
DGo_PA0234	CDS		Hypothetical protein	-2.6
DGo_PC0145	CDS		Hypothetical protein	-2.6
DGo_PB0130	CDS		Hypothetical protein	-2.6

DGo_PB0287	CDS		Hypothetical protein	-2.6
DGo_CA0043	CDS		Hypothetical protein	-2.6
DGo_CA0115	CDS		Hypothetical protein	-2.6
DGo_PF0028	CDS		Hypothetical protein	-2.6
DGo_CA1179	CDS		NADH-quinone oxidoreductase subunit 15	-2.6
DGo_CA0612	CDS		TetR family protein transcriptional regulator	-2.6
DGo_PB0304	CDS		Arsenate reductase, ArsC-like protein	-2.6
DGo_CA0637	CDS		ABC transporter, nucleotide binding/ATPase protein	-2.6
DGo_CA0718	CDS	*rbsC*	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	-2.6
DGo_PC0227	CDS		Transposase, IS4 family protein	-2.6
DGo_CA0801	CDS		Hypothetical protein	-2.6
DGo_CA2780	CDS		Hypothetical protein	-2.6
DGo_CA1783	CDS		Hypothetical protein	-2.6
DGo_PA0278	CDS	*pdxY*	Pyridoxamine kinase	-2.6
DGo_CA1236	CDS		Ribonuclease P protein component	-2.5
DGo_PC0156	CDS		Hypothetical protein	-2.5
DGo_PA0318	CDS		Xanthine/uracil/vitamin C permease	-2.5
DGo_CA0743	CDS		cobalt dependent X-Pro dipeptidase	-2.5
DGo_CA1992	CDS		Hypothetical protein	-2.5
DGo_PA0280	CDS		Glycoside hydrolase family 16	-2.5
DGo_PB0015	CDS	*uvrD3*	UvrD/REP helicase	-2.5
DGo_CA0155	CDS	*ugpQ*	Glycerophosphoryl diester phosphodiesterase	-2.5
DGo_CA2672	CDS	*hemC*	Porphobilinogen deaminase	-2.5
DGo_PA0128	CDS		Hypothetical protein	-2.5
DGo_CA2086	CDS		Peptidase M55, D-aminopeptidase	-2.5
DGo_CA0777	CDS		Creatininase subfamily protein	-2.5
DGo_CA2492	CDS		Hypothetical protein	-2.5
DGo_CA1252	CDS	*nuoH*	NADH-quinone oxidoreductase subunit H	-2.5
DGo_PA0156	CDS		Hypothetical protein	-2.5
DGo_PB0454	CDS		Hypothetical protein	-2.5
DGo_PA0134	CDS	*splB*	putative spore photoproduct lyase	-2.5
DGo_CA2584	CDS	*rpsC*	30S ribosomal protein S3	-2.5
DGo_CA2778	CDS		Restriction endonuclease S subunits	-2.5
DGo_CA1775	CDS		Threonyl/alanyl tRNA synthetase, SAD	-2.5
DGo_CA2420	CDS		Peptidase S1 and S6, chymotrypsin/Hap	-2.5
DGo_PB0499	CDS		Histone acetyltransferase HPA10	-2.5
DGo_PB0184	CDS		Hypothetical protein	-2.5
DGo_CA2845	CDS		methyltransferase	-2.5
DGo_PB0153	CDS		Hypothetical protein	-2.5
DGo_PB0160	CDS		Hypothetical protein	-2.5
DGo_PB0136	CDS		Hypothetical protein	-2.5
DGo_CA2849	CDS		Hypothetical protein	-2.5

DGo_CA1869	CDS		Hypothetical protein	-2.5
DGo_CA2276	CDS		Thioesterase superfamily	-2.5
DGo_CA1328	CDS		Hypothetical protein	-2.5
DGo_CA2678	CDS	*purK*	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	-2.5
DGo_CA0746	CDS		ABC transporter, substrate binding protein	-2.5
DGo_PB0161	CDS		Hypothetical protein	-2.5
DGo_CA2945	CDS		Hypothetical protein	-2.5
DGo_CA0698	CDS	*ugpB*	ABC-type sugar transport system, periplasmic component	-2.5
DGo_PB0209	CDS		Hypothetical protein	-2.5
DGo_PA0183	CDS	*yjhC*	Oxidoreductase domain protein	-2.5
DGo_CA1897	CDS		Hypothetical protein	-2.5
DGo_PA0022	CDS		Hypothetical protein	-2.5
DGo_PA0114	CDS		Hypothetical protein	-2.5
DGo_PA0059	CDS		ABC transporter, ATP-binding protein, MsbA family	-2.5
DGo_CA2690	CDS		FOG: CheY-like receiver	-2.5
DGo_PD0055	CDS		Resolvase	-2.5
DGo_PA0254	CDS		Hypothetical protein	-2.4
DGo_CA0176	CDS		Hypothetical protein	-2.4
DGo_CA2136	CDS	*ompH*	Cationic outer membrane protein OmpH, putative	-2.4
DGo_CA1332	CDS		Lincosamide nucleotidyltransferase	-2.4
DGo_PB0480	CDS		Hypothetical protein	-2.4
DGo_PA0365	CDS		Alpha/beta hydrolase fold-3 domain protein	-2.4
DGo_PB0486	CDS		Hypothetical protein	-2.4
DGo_CA0141	CDS		Dihydrouridine synthase, DuS	-2.4
DGo_PC0068	CDS		transcriptional regulator	-2.4
DGo_PB0011	CDS		Hypothetical protein	-2.4
DGo_CA2237	CDS		TRAP-T family transporter, periplasmic binding protein	-2.4
DGo_CA1886	CDS		Hypothetical protein	-2.4
DGo_CA2514	CDS		Hypothetical protein	-2.4
DGo_PB0423	CDS		Hypothetical protein	-2.4
DGo_CA0247	CDS		Transcriptional regulator, GntR family/aminotransferase family protein	-2.4
DGo_CA1291	CDS	*yqfG*	Putative metalloprotease	-2.4
DGo_CA1863	CDS		Pyrroline-5-carboxylate reductase	-2.4
DGo_CA0677	CDS		transcriptional regulator, MarR family	-2.4
DGo_PA0006	CDS		Hypothetical protein	-2.4
DGo_CA1563	CDS		Hypothetical protein	-2.4
DGo_PC0271	CDS		Hypothetical protein	-2.4
DGo_CA0672	CDS		Hypothetical protein	-2.4
DGo_PA0267	CDS		Probable amino acid ABC transporter, permease protein	-2.4
DGo_PA0269	CDS		Probable amino acid ABC transporter, substrate-binding protein	-2.4

DGo_CA0372	CDS		Ferric enterobactin esterase-related protein, alpha-beta hydrolase superfamily	-2.4
DGo_CA2581	CDS	*rpsQ*	30S ribosomal protein S17	-2.4
DGo_CA1633	CDS		Glycosyl hydrolase, family 13	-2.4
DGo_PA0340	CDS		Acetyltransferase, GNAT family	-2.4
DGo_PA0219	CDS		Hypothetical protein	-2.4
DGo_PC0220	CDS	*arsR*	Transcriptional regulator, ArsR family	-2.4
DGo_CA2113	CDS		Hypothetical protein	-2.4
DGo_CA1689	CDS		Hypothetical protein	-2.4
DGo_CA1277	CDS		HpaII-like repair protein	-2.4
DGo_CA1580	CDS		Aminotransferase, class V	-2.4
DGo_PB0465	CDS		Hypothetical protein	-2.4
DGo_CA1835	CDS		Protein kinase, ArgK family	-2.4
DGo_CA2441	CDS		Roadblock/LC7	-2.4
DGo_CA2506	CDS		Amylo-alpha-1,6-glucosidase	-2.4
DGo_CA0711	CDS		multi-sensor signal transduction histidine kinase	-2.3
DGo_PA0324	CDS		Xylose isomerase domain protein TIM barrel	-2.3
DGo_PC0263	CDS	*recQ4*	ATP-dependent DNA helicase RecQ	-2.3
DGo_CA1362	CDS		Peptidase M23B	-2.3
DGo_PC0186	CDS		Integrase, catalytic region	-2.3
DGo_PB0424	CDS		Hypothetical protein	-2.3
DGo_PA0336	CDS		Outer membrane protein	-2.3
DGo_CA1273	CDS		Phosphoesterase, RecJ-like protein	-2.3
DGo_CA0393	CDS	*hit*	Histidine triad protein	-2.3
DGo_PC0197	CDS		O-methyltransferase domain protein	-2.3
DGo_CA2109	CDS		transcriptional regulator	-2.3
DGo_PB0451	CDS		Glycoside hydrolase, family 19	-2.3
DGo_CA1821	CDS	*phnP*	Beta-lactamase-like protein	-2.3
DGo_PB0133	CDS		Hypothetical protein	-2.3
DGo_CA2730	CDS		E3 binding	-2.3
DGo_CA1250	CDS	*nuoF*	NADH-quinone oxidoreductase, F subunit	-2.3
DGo_CA2645	CDS	*fabG*	Short-chain dehydrogenase/reductase SDR	-2.3
DGo_CA0261	CDS		Zinc metallohydrolase, glyoxalase II family	-2.3
DGo_PB0179	CDS		Hypothetical protein	-2.3
DGo_CA1194	CDS		Peptidase C39	-2.3
DGo_PC0262	CDS		Hypothetical protein	-2.3
DGo_PB0468	CDS		Hypothetical protein	-2.3
DGo_CA0758	CDS	*hypA*	Probable hydrogenase nickel incorporation protein hypA	-2.3
DGo_PC0085	CDS		Hypothetical protein	-2.3
DGo_CA0418	CDS	*thiN*	Thiamine pyrophosphokinase	-2.3
DGo_PA0062	CDS		Transcriptional regulator, GntR family	-2.3
DGo_PC0173	CDS		Heavy metal translocating P-type ATPase	-2.3
DGo_CA0704	CDS	*aqpZ*	Glycerol uptake facilitator GlpF, MIP/aquaporin	-2.3

			family of transporters	
DGo_CA0739	CDS		sensor histidine kinase, copper metabolism, putative	-2.3
DGo_CA1572	CDS	*lysC*	Aspartokinase	-2.3
DGo_CA1060	CDS		Hypothetical protein	-2.3
DGo_PC0058	CDS		Hypothetical protein	-2.3
DGo_CA1202	CDS	*moaB*	Molybdenum cofactor biosynthesis protein B	-2.3
DGo_PC0023	CDS		UBA/THIF-type NAD/FAD binding protein	-2.3
DGo_PA0229	CDS	*aceB*	Malate synthase	-2.3
DGo_PE0028	CDS		Hypothetical protein	-2.3
DGo_PE0051	CDS		Hypothetical protein	-2.3
DGo_PB0461	CDS		Hypothetical protein	-2.3
DGo_CA1097	CDS		Hypothetical protein	-2.3
DGo_CA2351	CDS	*sigK*	RNA polymerase, sigma-24 subunit, ECF subfamily	-2.3
DGo_CA1701	CDS	*rimM*	Ribosome maturation factor rimM	-2.3
DGo_CA1426	CDS		Hypothetical protein	-2.3
DGo_CA2882	CDS		Hypothetical protein	-2.3
DGo_CA0821	CDS		Hypothetical protein	-2.3
DGo_CA0723	CDS		Lipoprotein	-2.3
DGo_PB0343	CDS		ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein	-2.3
DGo_CA1562	CDS	*ileS*	Isoleucyl-tRNA synthetase	-2.3
DGo_CA2362	CDS		Hypothetical protein	-2.3
DGo_CA0047	CDS		Hypothetical protein	-2.3
DGo_PB0434	CDS		Zn-dependent peptidase	-2.3
DGo_CA1253	CDS	*nuoI*	NADH-quinone oxidoreductase subunit I	-2.3
DGo_CA1195	CDS		Putative membrane protein	-2.3
DGo_PB0295	CDS		Hypothetical protein	-2.3
DGo_PD0069	CDS		Hypothetical protein	-2.2
DGo_CA2680	CDS		Lipid A disaccharide synthase related enzyme	-2.2
DGo_CA2931	CDS		PPC, peptidase containing PKD repeats	-2.2
DGo_CA2852	CDS	*ispF*	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	-2.2
DGo_CA1789	CDS		Amino acid ABC transporter, permease protein	-2.2
DGo_PB0306	CDS		Transposase IS4	-2.2
DGo_CA2951	CDS		Hypothetical protein	-2.2
DGo_PD0017	CDS		Phage integrase family protein	-2.2
DGo_CA1341	CDS		Extracellular solute-binding protein family 1	-2.2
DGo_CA0778	CDS	*apbA*	Ketopantoate reductase ApbA/PanE	-2.2
DGo_CA1032	CDS	*minD*	MinD family ATPase, Mrp	-2.2
DGo_CA0114	CDS		Hypothetical protein	-2.2
DGo_CA0720	CDS	*lacI*	Sugar binding transcriptional regulator, LacI family	-2.2
DGo_CA1926	CDS		Hypothetical protein	-2.2
DGo_PB0354	CDS		Hypothetical protein	-2.2
DGo_CA0674	CDS		Serine phosphatase RsbU, regulator of sigma subunit	-2.2

DGo_PB0058	CDS		Hypothetical protein	-2.2
DGo_CA1186	CDS		Peptidase S1 and S6, chymotrypsin/Hap	-2.2
DGo_PC0133	CDS		Hypothetical protein	-2.2
DGo_CA2455	CDS		Hypothetical protein	-2.2
DGo_PB0517	CDS		Hypothetical protein	-2.2
DGo_PD0070	CDS		Hypothetical protein	-2.2
DGo_CA1230	CDS		Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein	-2.2
DGo_PB0242	CDS		Type IV secretory pathway VirB4 component, ATPase TRAC	-2.2
DGo_CA2633	CDS	*pilT*	Tfp pilus assembly protein, pilus retraction ATPase PilT	-2.2
DGo_CA2788	CDS		Hypothetical protein	-2.2
DGo_PB0410	CDS		Hypothetical protein	-2.2
DGo_CA0206	CDS		Hypothetical protein	-2.2
DGo_PB0096	CDS		Hypothetical protein	-2.2
DGo_CA2435	CDS		Hypothetical protein	-2.2
DGo_CA1523	CDS	*deoD*	Purine nucleoside phosphorylase deoD-type	-2.2
DGo_PA0019	CDS		Hypothetical protein	-2.2
DGo_CA2443	CDS		Hypothetical protein	-2.2
DGo_PB0037	CDS		Integrase, catalytic region	-2.2
DGo_CA0761	CDS	*ureG*	Urease accessory protein ureG	-2.2
DGo_CA0458	CDS		Glucose-6-phosphate 1-dehydrogenase	-2.2
DGo_PB0285	CDS		Hypothetical protein	-2.2
DGo_PA0382	CDS	*cobP*	Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase, CobU	-2.2
DGo_PB0364	CDS		Hypothetical protein	-2.2
DGo_CA1260	CDS		Hypothetical protein	-2.2
DGo_CA2697	CDS		ABC-type multidrug transport system, permease component	-2.2
DGo_CA0589	CDS	*cobN*	Cobaltochelatase, CobN subunit	-2.2
DGo_PA0141	CDS		Trap-t family transporter, periplasmic binding protein	-2.2
DGo_CA2248	CDS		Shikimate kinase	-2.2
DGo_CA1185	CDS		Transcriptional regulator, LuxR family	-2.2
DGo_CA0613	CDS	*rpiR*	Transcriptional regulator, RpiR family	-2.2
DGo_PC0130	CDS		Hypothetical protein	-2.2
DGo_CA2460	CDS		Hypothetical protein	-2.2
DGo_PB0375	CDS		Transposase IS4 family protein	-2.2
DGo_CA2696	CDS		Putative signal transduction histidine kinase	-2.2
DGo_CA1549	CDS		Beta-lactamase-like protein	-2.2
DGo_PB0086	CDS		Xylose isomerase domain protein TIM barrel	-2.2
DGo_PB0383	CDS		Hypothetical protein	-2.2
DGo_PA0321	CDS		ParB-like partition protein	-2.2
DGo_CA2182	CDS		Orotate phosphoribosyltransferase related protein	-2.2
DGo_PC0021	CDS		Hypothetical protein	-2.2

DGo_CA0539	CDS	*oxyR*	Transcriptional regulator, LysR family	-2.2
DGo_PC0162	CDS		Hypothetical protein	-2.2
DGo_PE0027	CDS		Hypothetical protein	-2.2
DGo_CA2572	CDS	*rpmD*	50S ribosomal protein L30	-2.2
DGo_CA2241	CDS		UDP-N-acetylmuramoylalanine--D-glutamate ligase	-2.2
DGo_CA1684	CDS		Hypothetical protein	-2.2
DGo_CA2683	CDS		Hypothetical protein	-2.1
DGo_PA0368	CDS	*appD*	oligopeptide/dipeptide ABC transporter, ATPase subunit	-2.1
DGo_CA1430	CDS		2-oxoacid dehydrogenase	-2.1
DGo_CA0830	CDS		VanW-like protein	-2.1
DGo_CA0435	CDS		5-formyltetrahydrofolate cyclo-ligase	-2.1
DGo_CA1933	CDS		Hypothetical protein	-2.1
DGo_CA0248	CDS	*benE*	Benzoate membrane transport protein, putative	-2.1
DGo_CA0203	CDS		Hypothetical protein	-2.1
DGo_CA2606	CDS	*mntA*	ABC-type Mn2+ transport system, ATPase component	-2.1
DGo_CA2932	CDS		Dipeptidyl peptidase IV-related protein	-2.1
DGo_CA2751	CDS		Hypothetical protein	-2.1
DGo_CA0614	CDS		Periplasmic sugar-binding protein of sugar ABC transporter	-2.1
DGo_PB0439	CDS		Hypothetical protein	-2.1
DGo_PA0383	CDS		Cobyric acid synthase CobQ	-2.1
DGo_CA1302	CDS		Hydroxypyruvate reductase TtuD	-2.1
DGo_PD0015	CDS		Hypothetical protein	-2.1
DGo_CA1936	CDS		Hypothetical protein	-2.1
DGo_CA0697	CDS	*malF*	ABC-type sugar transport system, permease component	-2.1
DGo_CA1340	CDS	*agaL*	Glycoside hydrolase family 4	-2.1
DGo_CA0494	CDS		Hypothetical protein	-2.1
DGo_CA2823	CDS		Hypothetical protein	-2.1
DGo_CA2632	CDS		Phosphotransferase system, fructose IIC component	-2.1
DGo_CA2636	CDS		NIF3 family protein, DUF34	-2.1
DGo_CA0448	CDS		Rhomboid-like protein protein	-2.1
DGo_CA1721	CDS		Acetylornithine and succinylornithine aminotransferase	-2.1
DGo_CA0902	CDS		2-phosphoglycerate kinase, putative	-2.1
DGo_CA2026	CDS		Transcriptional regulator, AsnC family	-2.1
DGo_PA0008	CDS		Hypothetical protein	-2.1
DGo_PB0049	CDS		Hypothetical protein	-2.1
DGo_PC0118	CDS		Hypothetical protein	-2.1
DGo_PA0310	CDS		Allophanate hydrolase subunit 2	-2.1
DGo_PA0142	CDS	*pheA*	prephenate dehydratase	-2.1
DGo_CA2216	CDS		Major facilitator superfamily MFS_1	-2.1
DGo_PA0025	CDS		Putative nitrate ABC transporter	-2.1

DGo_CA0271	CDS		ABC-type branched-chain amino acid transport system, periplasmic component	-2.1
DGo_PE0011	CDS		Hypothetical protein	-2.1
DGo_CA1768	CDS	*lytB*	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	-2.1
DGo_PB0389	CDS		Hypothetical protein	-2.1
DGo_CA0787	CDS	*hupA2*	Signal transduction histidine kinase with CheB and CheR activity	-2.1
DGo_CA1020	CDS		Hypothetical protein	-2.1
DGo_PC0148	CDS		Hypothetical protein	-2.1
DGo_CA1930	CDS		Oxidoreductase, aldo/keto reductase family protein	-2.1
DGo_CA1969	CDS		Hypothetical protein	-2.1
DGo_CA1544	CDS		Hypothetical protein	-2.1
DGo_CA1342	CDS		Putative ABC-type sugar transport system, permease component	-2.1
DGo_PE0063	CDS		Hypothetical protein	-2.1
DGo_CA0656	CDS		Imidazolonepropionase	-2.1
DGo_CA1035	CDS		putative Glutamate--ammonia ligase	-2.1
DGo_CA0037	CDS		Metalloenzyme, phosphoglyceromutase related	-2.1
DGo_CA2625	CDS		GTPase, G3E family	-2.1
DGo_CA0533	CDS		5-formyltetrahydrofolate cyclo-ligase	-2.1
DGo_PA0292	CDS		Peptidase C39	-2.1
DGo_CA0179	CDS	*murE*	UDP-N-acetylmuramyl-tripeptide synthetase	-2.1
DGo_CA1408	CDS		Hypothetical protein	-2.1
DGo_PB0308	CDS		Hypothetical protein	-2.1
DGo_CA1249	CDS	*nuoE*	NADH-quinone oxidoreductase, E subunit	-2.1
DGo_CA0106	CDS		Oxidoreductase, putative	-2.1
DGo_CA0436	CDS		Acetyltransferase-like protein	-2.1
DGo_CA1663	CDS		Predicted Fe-S-cluster containing protein, UPF0153	-2.1
DGo_PB0061	CDS		Hypothetical protein	-2.1
DGo_CA0965	CDS	*glcF*	Glycolate oxidase, iron-sulfur subunit	-2.1
DGo_CA0808	CDS	*cbiJ*	Probable bifunctional: precorrin-3 methyltransferase and precorrin-6x reductase oxidoreductase protein	-2.1
DGo_CA0810	CDS	*yahD*	Putative transcription factor	-2.1
DGo_CA1751	CDS		Hypothetical protein	-2.1
DGo_CA1686	CDS	*smpB*	SsrA-binding protein	-2.1
DGo_CA0600	CDS		Secreted protein	-2.1
DGo_CA0417	CDS		Alpha/beta superfamily hydrolase	-2.1
DGo_CA1907	CDS		Hypothetical protein	-2.1
DGo_CA1107	CDS		Deoxyguanosinetriphosphate triphosphohydrolase-like protein	-2.1
DGo_CA2623	CDS		PaaI-like thioesterase	-2.1
DGo_CA1231	CDS		Hypothetical protein	-2.1
DGo_CA0124	CDS		Transcriptional regulator, MerR family	-2.1
DGo_PA0017	CDS		Methyl-accepting chemotaxis-related protein	-2.1
DGo_PA0088	CDS		Hypothetical protein	-2.1

DGo_CA2056	CDS		Acetyltransferase-like protein	-2.1
DGo_PA0320	CDS		ATPase involved in plasmide/chromosome partitioning, ParA/Soj-like protein	-2.1
DGo_CA0951	CDS		Peptide ABC transporter, periplasmic peptide-binding protein, putative	-2.1
DGo_CA2278	CDS		Hypothetical protein	-2.1
DGo_PD0043	CDS		Superfamily I DNA and RNA helicase	-2.1
DGo_CA1643	CDS		GCN5-related N-acetyltransferase	-2.0
DGo_CA0903	CDS	*tetR*	Transcriptional regulator, TetR family	-2.0
DGo_PC0088	CDS		Hypothetical protein	-2.0
DGo_CA1823	CDS	*hpt*	Hypoxanthine phosphoribosyltransferase	-2.0
DGo_PB0218	CDS		Plasmid replication initiator repA-related protein	-2.0
DGo_PB0271	CDS		Hypothetical protein	-2.0
DGo_CA2787	CDS		RelA/SpoT domain protein	-2.0
DGo_CA2403	CDS		Aminotransferase, putative	-2.0
DGo_CA1477	CDS		Hypothetical protein	-2.0
DGo_PC0008	CDS		Type I restriction-modification deoxyribonuclease, R subunit	-2.0
DGo_CA0040	CDS		Iron dependent repressor, putative	-2.0
DGo_PB0178	CDS		Hypothetical protein	-2.0
DGo_CA2123	CDS		YciI-like protein	-2.0
DGo_PB0446	CDS		Hypothetical protein	-2.0
DGo_PB0090	CDS		ABC ribose transporter, permease component	-2.0
DGo_CA0338	CDS		Methlytransferase, UbiE/COQ5 family	-2.0
DGo_CA2252	CDS	*pilO*	Type IV pilus assembly protein PilO	-2.0
DGo_CA1598	CDS		proline dipeptidase	-2.0
DGo_PD0041	CDS		Helicase domain protein	-2.0
DGo_CA2103	CDS	*rarA*	AAA ATPase, central region	-2.0
DGo_CA1148	CDS		Sugar ABC transporter, permease protein	-2.0
DGo_CA0226	CDS		Hypothetical protein	-2.0
DGo_CA1777	CDS	*pgd*	6-phosphogluconate dehydrogenase	-2.0
DGo_PA0018	CDS		CheA-related protein	-2.0
DGo_CA2863	CDS		Hypothetical protein	-2.0
DGo_CA1685	CDS		Cell wall hydrolase/autolysin	-2.0
DGo_CA1395	CDS		Hypothetical protein	-2.0
DGo_CA1336	CDS		Phosphohydrolase	-2.0
DGo_PB0457	CDS		Hypothetical protein	-2.0
DGo_CA0167	CDS	*ynfL*	Transcriptional regulator, LysR family	-2.0
DGo_PB0322	CDS		Hypothetical protein	-2.0
DGo_PA0137	CDS		Hypothetical protein	-2.0
DGo_CA2124	CDS		Phosphoprotein phosphatase	-2.0
DGo_CA0730	CDS		Two component transcriptional regulator, winged helix family	-2.0
DGo_CA2423	CDS		RNA methyltransferase TrmH, group 3	-2.0
DGo_PF0019	CDS		Ankyrin repeat protein, putative	-2.0

DGo_PC0194	CDS	*noxC*	Uncharacterized oxidoreductase czcO-like	-2.0
DGo_PB0309	CDS		Hypothetical protein	-2.0

Table S5 Deinococcales-specific genes

	Genes in D. gobiensis I-0			Expression after UV	Counterpart in the other Deinococcales species					
	Locus_tag	**gene name**	**comments**	**Fold change**	***D. deserti* VCD 115**	***D. maricopensis* LB-34**	***D. proteolyticus* MRP**	***D. geothermalis* DSM11300**	***D. radiodurans* R1**	***T. radiovictrix* RQ-24**
1	DGo_CA0006		Oxidoreductase, short-chain dehydrogenase/reductase family	1.37	Deide_02080	Deima_1960, Deima_2359	Deipr_0808	Dgeo_1140	DR_2595,DR_1700	Trad_2640
2	DGo_CA0065	*pta*	Phosphate acetyltransferase	-1.24	Deide_23230	Deima_2119	Deipr_0245	Dgeo_0051	DR_0073	Trad_1917
3	DGo_CA0166		Fe-S oxidoreductase, NifB/MoaA family containing PDZ domain	1.23	Deide_02230	Deima_3000	Deipr_1174	Dgeo_0304	DR_2521	Trad_1130
4	DGo_CA0261		Zinc metallohydrolase, glyoxalase II family	-2.32	Deide_21210	Deima_3047	Deipr_0747	Dgeo_0280	DR_2264	Trad_0200
5	DGo_CA0263		hypothetical protein	2.24	Deide_21190	Deima_3049	Deipr_0750	Dgeo_0282	DR_2262	Trad_2445
6	DGo_CA0320		Response regulator	-1.23	Deide_19260	Deima_0522	Deipr_0764	Dgeo_2199	DR_2556	Trad_2447
7	DGo_CA0366	*yfhM*	Alpha/beta hydrolase fold	-1.25	Deide_12820	Deima_0402, Deima_0689	Deipr_0144	Dgeo_0419	DR_2549	Trad_2161
8	DGo_CA0451	*crtI*	Phytoene dehydrogenase, CrtI	1.54	Deide_15780	Deima_0890	Deipr_1356	Dgeo_1779	DR_2015,DR_1724	Trad_0676
9	DGo_CA0462	*pys*	Phytoene dehydrogenase and related protein-like protein	1.07	Deide_07600	Deima_2449	Deipr_1663	Dgeo_1398	DR_A0363	Trad_1102

10	DGo_CA0825		hypothetical protein	-1.73	Deide_14640	Deima_0488	Deipr_1160	Dgeo_1640	DR_0638	Trad_0143
11	DGo_CA0865	*yggB*	MscS Mechanosensitive ion channel	-1.22	Deide_18560	Deima_2906	Deipr_2551	Dgeo_1833	DR_1995	Trad_2051
12	DGo_CA0880		histidine kinase	1.44	Deide_05080	Deima_2069, Deima_2899	Deipr_0865	Dgeo_0908, Dgeo_1270	DR_0860	Trad_2606
13	DGo_CA0919	*msrB*	Peptide methionine sulfoxide reductase msrB	-1.56	Deide_04050	Deima_1441	Deipr_1900	Dgeo_2072	DR_1378	Trad_0392
14	DGo_CA0926		Citrate transporter	1.28	Deide_17970	Deima_2592	Deipr_1646	Dgeo_1390	DR_1411	Trad_0190
15	DGo_CA0930		RNA-binding S4	1.42	Deide_05390	Deima_1700	Deipr_0681	Dgeo_1647	DR_1391	Trad_0487
16	DGo_CA0998	*cyp*	Cytochrome P450	1.02	Deide_01550	Deima_1158	Deipr_1131	Dgeo_0143	DR_A0186	Trad_2137, Trad_0092
17	DGo_CA1094	*rpoD*	RNA polymerase sigma factor	1.02	Deide_14380,Deide_03480,Deide_1p00220	Deima_2326	Deipr_1371	Dgeo_0476, Dgeo_1346	DR_0916	Trad_2957
18	DGo_CA1130		hypothetical protein	-1.12	Deide_08531,Deide_16091	Deima_2028	Deipr_2071,Deipr_0460	Dgeo_1470	DR_1312,DR_2483	Trad_2522
19	DGo_CA1215		Protein translocase subunit secA	-1.07	Deide_17210	Deima_1913	Deipr_1341	Dgeo_1058	DR_0575	Trad_0812
20	DGo_CA1233	*trkG*	K+ transporter Trk	-3.54	Deide_03830,Deide_3p00460	Deima_2802	Deipr_0239,Deipr_0387	Dgeo_1583	DR_1667,DR_1668	Trad_0242
21	DGo_CA1234		Putative RNA methylase	1.42	Deide_03840	Deima_2803	Deipr_0075	Dgeo_1582	DR_1669	Trad_0388
22	DGo_CA12		Iron-sulfur binding reductase, putative	-1.08	Deide_12050	Deima_1994	Deipr_1204	Dgeo_0874	DR_2565	Trad_0180

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23	DGo_CA1360		hypothetical protein	-6.69	Deide_09750	Deima_2235	Deipr_1288	Dgeo_1518	DR_0889	Trad_1274
24	DGo_CA1422		Yfit/DinB family predicted metal-dependent hydrolase	1.98	Deide_13680,Deide_13690,Deide_10332	Deima_1987	Deipr_0476	Dgeo_1175, Dgeo_0683	DR_1641,DR_1642,DR_0409	Trad_0032
25	DGo_CA2036,DGo_CA2037	*alkA*	Putative 3-methyladenine DNA glycosylase	-2.43,0.56	Deide_08050	Deima_1135, Deima_0477	Deipr_0812	Dgeo_1660	DR_2074	Trad_2393
26	DGo_CA2056		Acetyltransferase-like protein	2.06	Deide_10333	Deima_0861	Deipr_2537,Deipr_2174	Dgeo_0681	DR_1844	Trad_0677
27	DGo_CA2113		hypothetical protein	-2.37	Deide_11020	Deima_2051	Deipr_1640	Dgeo_1350	DR_1881	Trad_1368
28	DGo_CA2127	*metF*	5,10-methylenetetrahydrofolate reductase-related protein	1.04	Deide_11110	Deima_1940	Deipr_2276	Dgeo_1337	DR_0968	Trad_2518
29	DGo_CA2273		Rieske region	-1.74	Deide_16700	Deima_2259	Deipr_0604	Dgeo_0455	DR_1950	Trad_0260
30	DGo_CA2310		Predicted phosphatase of HAD fold	1.95	Deide_03230	Deima_2109	Deipr_0781	Dgeo_0459	DR_1192	Trad_1218, Trad_1219
31	DGo_CA2459	*pulA*	Type II secretory pathway, pullulanase PulA	-1.48	Deide_16560,Deide_3p01700	Deima_1806	Deipr_0622	Dgeo_0541	DR_0264	Trad_2060
32	DGo_CA2462		Malto-oligosyltrehalose synthase	1.53	Deide_16570	Deima_1804	Deipr_2624	Dgeo_0539	DR_0463	Trad_2079
33	DGo_CA2470	*tolQ*	Biopolymer transport protein, putative	-4.95	Deide_03360	Deima_2267	Deipr_0581	Dgeo_1754	DR_0456	Trad_2383
34	DGo_CA25		hypothetical protein	-1.5	Deide_19060	Deima_0610	Deipr_1321	Dgeo_2115	DR_2596	Trad_1636

	03									
35	DGo_CA2747	*ogt*	S-methyltransferase	-1.07	Deide_22770	Deima_2734	Deipr_2018	Dgeo_2101	DR_0428	Trad_2403
36	DGo_CA2802	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	-3.93	Deide_03051	Deima_0940	Deipr_1894	Dgeo_0398	DR_0170	Trad_1465
37	DGo_CA2826		hypothetical protein	-1.75	Deide_01620,Deide_2p00260,Deide_1p01090	Deima_2844	Deipr_1849	Dgeo_2134	DR_2412,DR_A0207	Trad_0182
38	DGo_PB0021	*hbs*	Histone-like protein DNA-binding protein	-1.71	Deide_2p01940,Deide_3p00060,Deide_00200	Deima_1832, Deima_1042	Deipr_2157,Deipr_2367,Deipr_1664	Dgeo_2501, Dgeo_0175	DR_A0065	Trad_2755

Table S6. Genomic islands in *D. gobiensis*

Islands	Start	Ends	G+C
GI01	DGo_CA0924	DGo_CA0942	74.7%
GI02	DGo_CA1052	DGo_CA1071	74.2%
GI03	DGo_CA1339	DGo_CA1346	69.3%
GI04	DGo_CA1416	DGo_CA1422	72.5%
GI05	DGo_CA1495	DGo_CA1513	71.5%
GI06	DGo_CA1551	DGo_CA1557	71.0%
GI07	DGo_CA1582	DGo_CA1593	72.3%
GI08	DGo_CA1792	DGo_CA1807	72.2%
GI09	DGo_CA1874	DGo_CA1918	66.0%
GI10	DGo_CA1943	DGo_CA2005	65.3%
GI11	DGo_CA2018	DGo_CA2023	73.7%
GI12	DGo_CA2286	DGo_CA2295	74.5%
GI13	DGo_CA2573	DGo_CA2595	65.7%
GI14	DGo_CA2706	DGo_CA2730	71.7%
GI15	DGo_CA2748	DGo_CA2789	68.5%
GI16	DGo_CA2865	DGo_CA2878	68.6%
GI17	DGo_CA2930	DGo_CA2941	67.7%
GI18	DGo_CA0140	DGo_CA0160	72.3%
GI19	DGo_CA0232	DGo_CA0240	63.0%
GI20	DGo_CA0367	DGo_CA0384	68.8%
GI21	DGo_CA0477	DGo_CA0500	70.0%
GI22	DGo_CA0658	DGo_CA0770	69.9%
GI23	DGo_PA0240	DGo_PA0259	48.7%

Table S7 DNA repair genes (A), stress response-related genes (B) and additional enzymes of possible biotechnological interest genes (C) in four deinococci

A. DNA repair genes in four deinococci

1. Main DNA repair genes for Base Excision Repair (BER)

1.1. Monofunctional DNA glycosylases

Gene name	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*		
				D. radiodurans	***D. deserti***	***D. geothermailis***
alkA	DGo_CA2036	3-methyladenine-DNA glycosylaseII	-2.43	DR_2074	Deide_08050	Dgeo_1660
	DGo_CA2905	3-methyladenine-DNA glycosylaseII	-0.41	DR_2584	Deide_02320	Dgeo_0107
mutY	DGo_CA2916	A/8oxoG adenine glycosylase	-0.52	DR_2285	Deide_01970	Dgeo_0019
mug	DGo_CA1116	Removes uracil,thymine or ethenocytosine opposite guanine	0.69	DR_0715	Deide_17530	Dgeo_1718
ung	DGo_CA0399	Uracil-DNA glycosylase	0.01	DR_0689	Deide_00830	Dgeo_2059
	DGo_CA1359		-0.83	DR_1751	-	Dgeo_1556

1.2. Bifunctional DNA glycosylases (displaying also a AP lyase activity)

Gene	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*

name				*D. radiodurans*	*D. deserti*	*D. geothermailis*
mutM	DGo_CA0896	Formamidopyrimidine-DNA glycosylase	-0.09	DR_0493	Deide_16240	Dgeo_0442
nth	-	Endonuclease III; removes ring-saturated or fragmented pyrimidines	-	DR_0289	Deide_01790	Dgeo_0248
	DGo_CA0048		0.97	DR_2438	Deide_23070	Dgeo_2290
	DGo_CA0132		-0.18	DR_2394	Deide_22780	Dgeo_0254

1.3. AP endonucleases

Gene name	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*		
				D. radiodurans	*D. deserti*	*D. geothermailis*
nfi	DGo_CA2027	Endonuclease V	-0.29	DR_2162	-	-
xthA	DGo_CA0439	Exodeoxyribonulease III	-0.38	DR_0354	Deide_03250	Dgeo_0461
				-	Deide_2p01470	Dgeo_2484

2. Main DNA repair genes for Nucleotide Excision Repair (NER)

Gene name	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*		
				D. radiodurans	*D. deserti*	*D. geothermailis*

mfd	DGo_CA0976	transcription-repair coupling factor; helicase	0.70	DR_1532	Deide_06920	Dgeo_0545
uvrA	DGo_CA1010	DNA damage recognition protein UvrA; DNA independent ATPase and DNA binding protein	0.36	DR_1771	Deide_12760	Dgeo_0694
	DGo_CA0556		-0.14	DR_A0188	Deide_2p02060	-
uvrB	DGo_CA0847	DNA damage binding protein UvrB ; helicase	0.44	DR_2275	Deide_03120	Dgeo_1890
uvrC	DGo_CA1577	Excision nuclease	-0.78	DR_1354	Deide_11450	Dgeo_1124
uvrD	DGo_CA1449	DNA helicase II	0.39	DR_1775	Deide_12100	Dgeo_0868
ywjD	DGo_CA0536	UV DNA damage endonuclease UvsE	-0.05	DR_1819	Deide_17800	Dgeo_1819
yejH	DGo_PA0135	DNA or RNA helicase of superfamily II (COG1061); also predicted nuclease	-0.85	DR_A0131	Deide_17320	-

3. Main DNA Repair genes for Mismatch Repair

Gene name	**Locus_tag**	**Product description**	**Log_2Fold**	**Counterpart in the other three *Deioncoccus***		
				D. radiodurans	***D. deserti***	***D. geothermailis***
mutL	DGo_CA0507	DNA mismatch repair protein; ATPase	0.44	DR_1696	Deide_15600	Dgeo_1538
mutS1	DGo_CA2405	DNA mismatch repair protein;	0.05	NoAnnotation	Deide_15540	Dgeo_1537

		ATPase		_610+DR_1039+NoAnnotation_671		
mutS2	DGo_CA2335	DNA mismatch repair protein; ATPase	0.32	DR_1976	Deide_05000	Dgeo_0899
xseA	DGo_CA0092	Exonuclease VII, large subunit	-0.85	DR_0186	Deide_22980	Dgeo_0148
xseB	DGo_CA2907	Exonuclease VII, small subunit	-2.41	DR_2586	Deide_02120	Dgeo_0027

4. Main DNA repair genes for Direct Reversal of DNA damage (DR)

Gene name	**Locus_tag**	**Product description**	**Log_2Fold**	**Counterpart in the other three *Deioncoccus***		
				D. radiodurans	***D. deserti***	***D. geothermailis***
ogt/ ybaZ	DGo_CA2747	O-6-alkylguanine transferase	-0.10	DR_0428	Deide_22770	Dgeo_2101
phrA	DGo_CA1802	photorepair protein PhrA	-0.53	-	-	-
phrB	DGo_CA0607	DNA photolyase	1.66	-	-	-
splB	DGo_PA0134	spore photoproduct lyase	-1.32	-	Deide_3p02150	-
dcd	DGo_CA2281	Deoxycytidine triphosphate deaminase	-1.90	-	Deide_16640	Dgeo_1880
yggV	DGo_CA2488	Xanthosine triphosphate	-0.74	DR_0179	Deide_19360	Dgeo_2209

	pyrophosphatase	

5. Main DNA repair genes for recombinational repair (RER)

Gene name	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*		
				D. radiodurans	***D. deserti***	***D. geothermailis***
recA	DGo_CA2833	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA-and ATP-dependent coprotease	-0.44	DR_2340	Deide_19450, Deide_1p01260,Deide_3p00210	Dgeo_2138
recB	DGo_PB0022, DGo_PC0098	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ss DNA endonuclease	1.58	-	-	-
recD	DGo_CA1825	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ss DNA endonuclease	-0.67	DR_1902	Deide_16210	Dgeo_0826
recD2	DGo_PB0015, DGo_PC0277	Superfamily I DNA and RNA helicases		-	-	-
recF	DGo_CA2190	Recombinational repair protein	-0.72	DR_1089	Deide_14250	Dgeo_1620
recG	DGo_CA1320	Holliday junction-specific DNA helicase; branch migration inducer	-0.04	DR_1916	Deide_09960	Dgeo_1139
	DGo_CA0381	Holliday junction-specific DNA	2.58	-	-	-

		helicase; branch migration inducer				
recJ	DGo_CA0910	ssDNA exonuclease, 5'->3' specific	-0.01	DR_1126+NoAnnotation_611	Deide_07130	Dgeo_1599
recN	DGo_CA1486	Recombination and repair protein	-0.89	DR_1477	Deide_12310	Dgeo_1194
recO	DGo_CA2367	Bacterial recombinational repair protein	-0.43	DR_0819	Deide_13810	Dgeo_0855
recQ	DGo_CA1784,DGo_PB0141	ATP-dependent DNA helicase RecQ	US	DR_1289	Deide_11320	NoAnnotation_505+Dgeo_1226
	DGo_CA2913	ATP-dependent DNA helicase RecQ	-0.77	DR_2444	Deide_02180	Dgeo_0021
recR	DGo_CA2078	Recombination and repair protein	-0.22	DR_0198	Deide_06340	Dgeo_1513
recT	-	Recombinase, DNA renaturation		-	-	-
recX	DGo_CA2088	Regulatory protein, RecX	-1.97	DR_1310	Deide_12350	Dgeo_1433
radA	DGo_CA1836	DNA repair protein RadA	-0.12	DR_1105	Deide_12660	Dgeo_1212
ruvA	DGo_CA1508	Holliday junction helicase subunit A; branch migration	-0.61	DR_1274	Deide_09360	Dgeo_0726
ruvB	DGo_CA2516	Holliday junction helicase subunit A; branch migration	-0.26	DR_0596	Deide_18350	Dgeo_0404
ruvC	DGo_CA0294	Holliday junction endonuclease	-0.94	DR_0440	Deide_20630	Dgeo_0327
yqgF	DGo_CA0376	Putative Holliday junction resolvase	1.42	DR_2509	Deide_04280	Dgeo_0425

sbcC	DGo_CA1827	ATP dependent dsDNA exonuclease	-1.40	DR_1922	Deide_16170	Dgeo_0823
sbcD	DGo_CA1826	ATP dependent dsDNA exonuclease	-0.40	DR_1921	Deide_16180	Dgeo_0824
ssb	DGo_CA0126	Single-stranded DNA-binding protein	0.10	NoAnnotation_542+DR_0099	Deide_00120	Dgeo_0165,Dgeo_2964

6. Other DNA repair related genes

Gene name	Locus_tag	Product description	Log_2Fold	Counterpart in the other three *Deioncoccus*		
				D. radiodurans	***D. deserti***	***D. geothermailis***
dnlJ	DGo_CA1174	DNA ligase, NAD-dependent	-0.07	DR_2069	Deide_12290	Dgeo_0696
gyrA	DGo_CA1041	DNA gyrase subunit A	0.99	DR_1913	Deide_12520	Dgeo_1016
gyrB	DGo_CA0873	DNA gyrase subunit B	1.03	DR_0906	Deide_15490	Dgeo_0546
topA	DGo_CA0471	DNA topoisomerase I	-0.28	DR_1374	Deide_07410	Dgeo_2001
	DGo_CA0400	DNA topoisomerase I	-0.56	DR_0690	Deide_00840	Dgeo_2058
lexA	DGo_PC0001	Transcriptional regulator, repressor of the SOS regulon, autoprotease	0.94	DR_A0344	Deide_1p01870	-
				-	Deide_01180	Dgeo_1366
polA	DGo_CA1437	DNA polymerase I	0.01	DR_1707	Deide_15130	Dgeo_1666
polB	DGo_PC0151	DNA polymerase II	1.00	-	Deide_1p00180	-

dnaE	DGo_CA2511	DNA polymerase III alpha subunit	-0.32	DR_0507	Deide_21950	Dgeo_0255
dnaQ	DGo_CA0849	DNA polymerase III epsilon subunit (3'-5' exonuclease subunit)	0.76	DR_0856	Deide_17790	Dgeo_1818
dnaN	DGo_CA0002	DNA polymerase III beta subunit	1.24	DR_0001	Deide_00020	Dgeo_0003
dnaX	DGo_CA2827	DNA polymerase III tau/gamma subunit	-0.70	DR_2410+DR_2411	Deide_01610	Dgeo_2135
holA	DGo_CA1455	DNA polymerase III delta subunit	-0.67	DR_1244	Deide_10170	Dgeo_0745
dinB	DGo_CA2228	Pol IV, DNA polymerase type-Y family, contains 1 UmuC domain Related to putative Y-family DNA polymerase	0.23	-	-	-
holB	DGo_CA0068	DNA polymerase III delta prime subunit	-0.20	DR_2332	Deide_21710	Dgeo_2262
yshC	DGo_CA0274	DNA polymerase, family X	-0.35	DR_0467	Deide_07030	Dgeo_1609
-	DGo_CA2206	UvrD/REP helicase; COG0210, UvrD, Superfamily I DNA and RNA helicases	0.37	-	Deide_06250	Dgeo_0552
-	DGo_PB0015, DGo_PC0025, DGo_PC0277, DGo_PD0049	UvrD/REP helicase				
ywqA	DGo_CA1433	DNA helicase SNF2/Rad54 family	0.92	DR_1258+DR_1259	Deide_08980	Dgeo_1491

dnaA	DGo_CA0001	Chromosomal replication initiator protein	-0.73	DR_0002	Deide_00010	Dgeo_0001
dnaB	DGo_CA2884	Replicative DNA helicase	0.39	DR_0549	Deide_04710	Dgeo_2037
dnaG	DGo_CA0378	DNA primase	0.57	DR_0601	Deide_04900	Dgeo_1910
priA	DGo_CA2791	Primosomal protein N'	-0.11	DR_2606	Deide_00480	Dgeo_0271
rarA	DGo_CA2103	Replication-associated recombination protein	-1.02	DR_1898	Deide_04980	Dgeo_1401

7. Other radiation tolerance-associated genes in Locus_tag and other *Deinococcus* spp.

Gene name	**Locus_tag**	**Product description**	**Log2Fold**	**Counterpart in the other three *Deioncoccus***		
				D. radiodurans	***D. deserti***	***D. geo-thermailis***
ddrA	DGo_CA2046	DNA damage response protein DdrA; Rad52/22 double-strand break repair protein	0.96	DR_0423	Deide_09150	Dgeo_0977
ddrB	DGo_CA0350	DdrB, radiation induced single-stranded DNA binding protein	1.12	DR_0070	Deide_02990	Dgeo_0295
ddrC	DGo_CA0071	DdrC	1.09	DR_0003	NoAnnotation_250	Dgeo_0047
ddrD	DGo_CA2608	DdrD	0.43	DR_0326	Deide_01160	Dgeo_2186
ddrE	DGo_CA0988	DdrE; Related to zinc metal lopeptidase	0.96	DR_0194	Deide_11220	Dgeo_1282

ddrH	DGo_CA0299	DdrH	0.16	DR_0438	NoAnnotation_335	NoAnnotation_ 431
ddrI	DGo_CA1040	DdrI; Transcriptional regulator, Crp/Fnr family	1.82	DR_0997	Deide_12530	Dgeo_1015
ddrN	DGo_CA0142	DdrN	-0.17	DR_2441	Deide_02930	Dgeo_0078
ddrO	DGo_CA0310	DdrO, transcriptional regulator, HTH_3 family	0.19	DR_2574	Deide_20570,Deide_3p 02170	Dgeo_0336
ddrP	DGo_CA2239	DdrP	0.93	DR_B0100	-	-
frnE	DGo_CA0380	predicted dithiol-disulfide isomerase		DR_0659	Deide_00690	Dgeo_2073
hicB	-	HicB		DR_B0141	-	-
irrE	DGo_CA2805	IrrE, regulator of recA expression in D. radiodurans	0.05	DR_0167	Deide_03030	Dgeo_0395
irrI	-	IrrI		DR_0171	-	-
pprA	DGo_PA0354	DNA damage repair protein PprA	0.11	DR_A0346	Deide_2p01380	Dgeo_2628
pprM	DGo_CA1136	PprM	0.66	DR_0907	Deide_2p00490	Dgeo_0638
	DGo_PA0041		0.20	-	Deide_3p00840	-

B. Stress response-related genes in four deinococci.

Stress	Gene name	Locus_tag	Product description	Log_2Fold er)	Counterpart in the other three *Deioncoccus*		
					D. deserti	***D. radiodurans***	***D.***

							geothermaili s
Desiccation	-	DGo_CA1605	Desiccation-related protein, LEA 14 family	0.06	Deide_09710	DR_1372	Dgeo_1551
	-	DGo_CA1631	LEA76 family desiccation resistance protein	0.46	Deide_08510	DR_1172	Dgeo_1473
	-	DGo_CA1742	Desiccation-related protein	0.68	Deide_08080	-	Dgeo_1323
	-	DGo_CA2349	Desiccation-related protein	0.06	Deide_07540	DR_B0118	Dgeo_0097
General&Hot	*ytxJ*	DGo_CA1021	Thioredoxin-like	1.74	Deide_14700	DR_1832	Dgeo_1464
	clpA	DGo_CA1279	ATPase subunits of Clp protease	-0.74	Deide_08490	DR_0588	Dgeo_1475
	clpB	DGo_CA1752	ATPase subunits of Clp protease	0.14	Deide_12640	DR_1046	Dgeo_1210
	clpC	DGo_CA1460	ATPase subunits of Clp protease	-0.34	Deide_12680	DR_1117	Dgeo_1215
	clpP	DGo_CA0282	ATP-dependent protease with chaperone activity	-0.66	Deide_07080	DR_0078	Dgeo_1604
	clpQ	-	ATP-dependent protease HslV	-	-	-	-
	clpX	DGo_CA2328	ATPase subunit of Clp protease	0.02	Deide_19580	DR_1973	Dgeo_2152
	-	DGo_CA0852	GTPase, protease modulator	0.81	Deide_18500	DR_0646	Dgeo_1825
	dksA	-	DnaK suppressor protein	-	-	-	-
	dnaJ	DGo_CA0461	Hsp70, chaperone cofactor	0.45	Deide_07590	DR_1424	Dgeo_0451
		DGo_CA1008		-0.92	Deide_12740	DR_0753	Dgeo_0692
	dnaK	DGo_CA2644	Hsp70, molecular chaperone	0.04	Deide_21970	DR_0129	Dgeo_2076
	ftsH	-	ATP-dependent Zn protease	-	Deide_01120	DR_A0290	Dgeo_2182
		DGo_CA2394		0.18	Deide_18550	DR_1020	Dgeo_1832
		DGo_CA2646		-0.24	Deide_23310	DR_0583	Dgeo_2075
	groL	DGo_CA2525	Hsp10, molecular chaperone	0.20	Deide_22590	DR_0607	Dgeo_2231
	groS	DGo_CA2524	Hsp60, molecular chaperone	-0.17	Deide_22580	DR_0606	Dgeo_2230
	grpE	DGo_CA2643	Hsp20, molecular chaperone	-0.26	Deide_21980	DR_0128	Dgeo_2077
	hflX	DGo_CA2820	GTPase, protease modulator	0.73	Deide_19040	DR_0139	Dgeo_2006
	hit	DGo_CA0393	Diadenosine tetraphosphate (Ap4A) hydrolase, HIT family, cell cycle regulation	-1.23	Deide_12650	-	Dgeo_2064
		DGo_CA1744		0.02	Deide_15190	DR_1621	Dgeo_1329
	hslJ	DGo_CA0947	Related to heat shock protein	0.54	Deide_07610	DR_1940	-

htpG	-	Hsp90, molecular chaperone	-	-	-	-
htpX	DGo_CA0938	Predicted Zn-dependent proteases (possible chaperone)	-0.34	Deide_21060	-	-
	DGo_CA0988		0.96	Deide_11220	DR_0194	Dgeo_1282
htrA	DGo_CA0185	Do serine protease, with PDZ domain	0.43	Deide_21550	DR_0300+NoAnnotation_835	Dgeo_0103
	DGo_CA1376		0.24	Deide_10420	DR_1756	Dgeo_0676
	DGo_CA1644		0.83	Deide_12870	DR_1703	Dgeo_0795
	DGo_CA1790		-0.02	Deide_07680	DR_2154	Dgeo_1060
	DGo_CA1941		-0.41	-	DR_1599+DR_1600	-
	DGo_CA2420		-1.32	Deide_04820	DR_0745	Dgeo_2025
ibpA/ibpB	DGo_CA1726	Small heat shock protein	1.06	Deide_11290	DR_1691	Dgeo_0859
	DGo_CA2067		0.40	Deide_18090	DR_1114	Dgeo_0505
lon	DGo_CA1831	ATP-dependent Lon Serine protease	-0.58	-	DR_0394	Dgeo_2485
***lo**nA*	DGo_CA2327	ATP-dependent Lon Serine protease	-0.08	Deide_19590	DR_1974	Dgeo_2153
prc	DGo_CA1196	Tail-specific periplasmic serine protease	-0.30	Deide_10700	DR_1551	Dgeo_1479
	DGo_CA1459		-0.11	Deide_12780	DR_1491	Dgeo_1216
	DGo_CA2561		0.68	Deide_21230	DR_1308	Dgeo_0277
radA	DGo_CA1836	ATP-dependent serine protease COG1066 / DNA repair protein	-0.12	Deide_12660	DR_1105	Dgeo_1212
sugE	DGo_CA2538	Small multidrug resistance membrane protein	0.56	-	-	Dgeo_1956
	DGo_CA2539		-0.08	-	-	Dgeo_1957
	DGo_CA2790		0.14	Deide_20500	DR_1004,DR_1005	Dgeo_2170
thiJ	DGo_CA0475	Protease I, related to general stress protein 18, ThiJ superfamily protein	0.65	Deide_04910	DR_1199	Dgeo_0863
uspA	-	Universal stress protein, nucleotide-binding	-	Deide_08840	DR_2132	Dgeo_1279
	DGo_CA0010		-0.11	Deide_22300	DR_2363	Dgeo_0155
yaeL	DGo_CA1846	Membrane-associated Zn-dependent protease I	-0.77	Deide_13240	DR_1507	Dgeo_1043
yebL	-	Zn-binding (lipo)protein of the ABC type Zn	-	Deide_2p01321,D	-	-

			transport system (surface adhesin A)		eide_3p02720		
		DGo_CA2604		-0.80	Deide_07330	DR_2523+NoAnnotation_871	Dgeo_0534
Osmotic	*aqpZ*	-	Major intrinsic protein (aquaporin Z and glycerol uptake facilitator)	-	Deide_1p01582,Deide_3p02450	-	Dgeo_0516
		DGo_CA0704		-1.20	-	-	Dgeo_1799
	glpF	DGo_CA2316	Major intrinsic protein (aquaporin Z and glycerol uptake facilitator)	-0.51	Deide_2p00230	DR_1929	Dgeo_2523
	kdpD	DGo_CA0646	Osmosensitive K+ channel histidine kinase sensor domain	-1.61	-	DR_B0088	Dgeo_2852
	mscL	DGo_CA2713	Large conductance mechano-sensitive channel	0.45	Deide_02220	DR_2422	Dgeo_0305
	otsA	-	Trehalose-6-phosphatase synthase	-	Deide_21370	-	Dgeo_0059
	otsB	-	Trehalose-6-phosphatase Maltooligosyltrehalose trehalohydrolase TreZ	-	Deide_21360	-	Dgeo_0060
		DGo_CA2461		0.22	Deide_2p01290	DR_0464	Dgeo_0540
		DGo_CA2462		-0.61	Deide_16570	DR_0463	Dgeo_0539
		DGo_CA2600		-0.35	Deide_07350	DR_2036	Dgeo_0537
	proV	-	Proline/glycine betaine ABC-type transport, ATPase subunit	-	Deide_00170	DR_A0137	Dgeo_0172
	proW	-	Proline/glycine betaine ABC-type transport, permease subunit	-	Deide_00180	DR_A0136	Dgeo_0173
		DGo_CA2785		-0.83	Deide_20480	DR_0283	Dgeo_2168
	trkA	-	Potassium uptake system, NAD-binding component	-	-	-	-
	trkH/trkG	-	Potassium uptake component	-	Deide_3p00460	DR_1668	Dgeo_1583
		DGo_CA1233		1.83	Deide_03830	DR_1667	-
	yehZ	DGo_PA0197	ABC-type proline/glycine/betaine transport system, periplasmic component		DR_A0135	Deide_00190	Dgeo_0174
	yehY	DGo_PA0198	ABC-type proline/glycine/betaine transport system, permease component		DR_A0136	Deide_00180	Dgeo_0173
	yehW	DGo_PA0199	ABC-type proline/glycine/betaine transport		DR_A0137	Deide_00170	Dgeo_0172

	2		system, ATPase component				
	yehW	DGo_PA0200	ABC-type proline/glycine/betaine transport system, permease component		DR_A0138	Deide_00160	Dgeo_0171
	yggB	DGo_CA0865	Membrane protein	-0.29	Deide_18560	DR_1995	Dgeo_1833
Other	*arsC*	-	Arsenate oxidoreductase (ArsC-like Rodanese protein)	-	Deide_3p02440	-	Dgeo_2768
		-		-	-	DR_A0123	Dgeo_0756, Dgeo_2548
		DGo_CA2817		0.25	Deide_18400	DR_0136	Dgeo_0403
	BS_yloU/BS_yqhY	DGo_CA1110	Alkaline shock protein, function unknown	-0.16	Deide_17570	DR_0389	Dgeo_1721
		DGo_CA1175		-0.85	Deide_12280	DR_2068	Dgeo_0697
	pprM	DGo_PA0041	Cold shock protein, OB fold nucleic acid binding protein	-	Deide_09930	-	Dgeo_1006
		DGo_CA1136		0.66	Deide_2p00490,Deide_3p00840	DR_0907	Dgeo_0638
	hupA	DGo_CA0549	Histone-like nucleoid DNA-binding protein	0.03	Deide_2p01940	DR_A0065	Dgeo_2501
		DGo_CA0787		-1.07	Deide_1p00200,Deide_2p00460	-	-
	pspA	DGo_CA1515	Phage shock protein A, controls membrane integrity	-0.02	Deide_09450	DR_1473	Dgeo_0996
Oxidative& detoxication	-	-	Fe dependent peroxidase	-	-	-	-
	-	-	Mn-containing catalase	-	-	-	-
	cyp	-	Cytochrome P450	-	-	DR_C0001	-
		DGo_PB0312		-	-	-	-
		DGo_PB0521		-	-	-	-
		-		-	Deide_22920	DR_2538	-
		DGo_CA0998		0.03	Deide_01550	DR_A0186+No Annotation_878	Dgeo_0143
		DGo_CA1464		-1.44	-	DR_1723	-

	DGo_CA1830		-2.03	Deide_08170	-	Dgeo_0944
	DGo_CA2870		-0.02	-	DR_2473	-
ahpC/ ahpE-like	DGo_CA2657	Thioredoxin reductase/alkyl hydroperoxide reductase	0.63	Deide_02430	DR_2242	Dgeo_0122
ahpf/trxB	-	Thiol-alkyl hydroperoxide reductase	-	Deide_3p01180	DR_B0033	-
	DGo_CA0078		-0.39	Deide_23360	DR_2623	Dgeo_2331
	DGo_CA1038		-0.11	Deide_12541	-	Dgeo_1013
	DGo_CA2053		0.63	Deide_09090	DR_0412	Dgeo_0975
	DGo_CA2339		-0.21	Deide_05800	DR_1982	Dgeo_1576, Dgeo_2772
bcp	DGo_CA1364	Peroxiredoxin, bacterioferritin comigratory protein, antioxidant protein	0.71	Deide_10900	DR_0846	NoAnnotation_481
	DGo_CA1403		0.76	Deide_09051	DR_1209	Dgeo_0990
BS_yceH	DGo_CA1262	Toxic anion resistance protein, possibly tellurite resistance	-0.52	Deide_05270	DR_1127	Dgeo_0931
fur	-	Ferric uptake regulation protein	-	Deide_2p00340	-	Dgeo_2727
	DGo_CA0886		0.80	Deide_16041	DR_0865	Dgeo_0519
	DGo_CA2836		0.06	Deide_19480	NoAnnotation_640+NoAnnotation_586	Dgeo_2141
grxA	-	Glutaredoxin	-	-	DR_A0072	Dgeo_2583
	DGo_CA2073		0.61	Deide_06390	DR_2085	Dgeo_1508
katA	DGo_CA2912	Catalase; Eukaryotic type	0.25	-	DR_A0146	-
katE	DGo_CA1736	Catalase	-0.15	Deide_2p00330	DR_1998	Dgeo_2728
katG	DGo_PA0127	Catalase (peroxidase)	-	-	-	-
katX	DGo_PA0314	Catalase X		DR_1998	Deide_2p00330	Dgeo_2728
msrA	DGo_CA1541	Peptide methionine sulfoxide reductase A	0.47	Deide_10980	DR_1849	Dgeo_0843

	msrB	DGo_CA0919	Peptide methionine sulfoxide reductase B	0.64	Deide_04050	DR_1378	Dgeo_2072
	nrdH	DGo_CA0407	Glutaredoxin	-2.21	Deide_13741	DR_0057	Dgeo_0729
	osmC	DGo_CA0901	Protein involved in alkylperoxide and oxidative stress response, osmotically induced protein	0.53	-	DR_1857	Dgeo_0446
		DGo_CA1241		1.10	Deide_16090	DR_1538	Dgeo_0526
	oxyR	-	Transcriptional regulator, LysR family	-	Deide_3p01240	-	Dgeo_2711
		DGo_CA0172		0.00	Deide_16400	-	Dgeo_1692
		DGo_CA0539		-1.12	Deide_03130	DR_0615	Dgeo_1888
		DGo_CA1575		-0.63	-	-	Dgeo_2840
	sodA	DGo_CA2200	Superoxide dismutase Mn or Fe dependent	0.12	Deide_07760	DR_1279	Dgeo_0830
	sodC	-	Superoxide dismutase Cu/Zn dependent	-	Deide_19880	DR_1546	-
		DGo_CA1102		0.08	Deide_1p00740	DR_A0202	-
	soxR	-	Transcriptional regulator, MerR family	-	Deide_3p02530	DR_2306	Dgeo_2202
		-		-	Deide_04091	DR_1111	-
		DGo_CA0538		-0.06	Deide_2p01800	DR_2448	Dgeo_1424
	tlp	DGo_CA2017	Peroxiredoxin, disulfide reductase	0.68	Deide_08290	DR_0189	Dgeo_1248
	trx	-	Thioredoxin	-	Deide_01140	DR_A0164	Dgeo_2518
		DGo_CA0861		0.74	Deide_18600	DR_0944	Dgeo_1837
	yhfA	DGo_CA1763	Protein involved in alkylperoxide and oxidative stress response, osmotically induced protein	1.06	Deide_10790	DR_1177	Dgeo_1268
Starvation	cstA	-	Carbon starvation-induced protein, membrane	-	-	-	-
	dps	DGo_CA0262	Starvation inducible DNA-binding protein	0.55	Deide_21200	DR_2263	Dgeo_0281
		DGo_CA0741		-0.23	-	DR_B0092	-
	mazE	-	Regulatory protein, MazF antagonist	-	-	-	-
	mazF	-	ppGpp regulated growth inhibitor	-	-	DR_0417	Dgeo_1937
	ppx	-	Phosphatase of ppGpp	-	Deide_01820	DR_A0185	-
	spoT	DGo_CA1014	Guanosine polyphosphate (ppGpp) pyrophosphohydrolase/synthetase	0.25	Deide_14760	DR_1838	Dgeo_1308

Table S6C. Additional enzymes of possible biotechnological interest

Class / pathway	Locus tag	function
DNA / RNA processing enzymes	DGo_CA1437	DNA polymerase I
	DGo_PC0151	DNA polymerase II
	DGo_CA0002, DGo_CA0068, DGo_CA0849, DGo_CA1455, DGo_CA2511, DGo_CA2827, DGo_PB0516	DNA polymerase III
	DGo_CA0274	DNA polymerase X
	DGo_PB0095	DNA polymerase
	DGo_CA2228	Nucleotidyltransferase/DNA polymerase involved in DNA repair
	DGo_CA1174, DGo_PB0078, DGo_PD0007	DNA ligase
	DGo_CA0381, DGo_CA1320, DGo_CA1433, DGo_CA1449, DGo_CA1508, DGo_CA1784, DGo_CA1885, DGo_CA2516, DGo_CA2884, DGo_PA0147, DGo_PB0141, DGo_PB0482, DGo_PC0263, DGo_PD0043, DGo_PF0017	DNA helicase
	DGo_CA0400, DGo_CA0471, DGo_CA0873, DGo_CA1041, DGo_CA2574, DGo_PB0093, DGo_PC0276	DNA topoisomerase
	DGo_CA0710, DGo_CA0792, DGo_CA1063, DGo_PB0079, DGo_PB0343, DGo_PC0210, DGo_PE0056	DNA gyrase
	DGo_CA0048, DGo_CA1807, DGo_CA2661	endonuclease III
	DGo_CA0165	endonuclease IV
	DGo_PA0054	endonuclease V
	DGo_CA2778, DGo_PC0006	Restriction endonuclease S-submit

	DGo_CA0536	UV endonuclease
	DGo_CA0294	Crossover junction endodeoxyribonuclease ruvC
	DGo_PD0033	mismatch endonuclease
	DGo_CA2841, DGo_PB0373, DGo_PB0497, DGo_PE0071	HNH endonuclease
	DGo_CA0439	Exodeoxyribonuclease III
	DGo_CA0092, DGo_CA0092	Exodeoxyribonuclease VII
	DGo_PC0008, DGo_CA2781	Type I restriction-modification deoxyribonuclease
	DGo_CA2027	Deoxyinosine 3'endonuclease
	DGo_CA0024	Ribonuclease II
	DGo_CA2497	Ribonuclease BN
	DGo_CA0972, DGo_CA2741	Ribonuclease H
	DGo_CAnc18	Ribonuclease P
	DGo_CA0433	Ribonuclease PH
	DGo_CA0440	Ribonuclease R
	DGo_CA0276	Ribonuclease Z
	DGo_CA2271	Ribonuclease
	DGo_CA0979	Guanyl-specific ribonuclease
polymerdegrading/modifying enzymes	DGo_CA1058	putative pullulanases
	DGo_CA1633	alpha-glucosidases

	DGo_PA0281	beta-glucosidase
	DGo_CA1180	maltodextrin glucosidase
	DGo_CA1339	alpha-galactosidase
	DGo_CA1498	amylomaltase
	DGo_CA1773	alpha-glucan phosphorylase
	DGo_CA1724, DGo_CA2610, DGo_CA2433, DGo_CA1210	glycogen biosynthesis
	DGo_CA0878, DGo_CA2665, DGo_CA2647	esterases (lipases)
	DGo_CA2548	polyphosphate kinase
Press resistance	DGo_CA2805	irrE
	DGo_CA1136, DGo_PA0041	Cold shock proteins
antibiotics resistance	DGo_CA0099, DGo_CA0213, DGo_CA0317, DGo_CA0631, DGo_CA0789, DGo_CA1056, DGo_CA1075, DGo_CA1264, DGo_CA1274, DGo_CA1549, DGo_CA1821, DGo_CA2266, DGo_CA2383, DGo_CA2648, DGo_CA2821, DGo_PB0301, DGo_PB0390, DGo_PC0037	putative β-lactamases

	DGo_CA0368, DGo_CA0452, DGo_CA0676, DGo_CA0786, DGo_CA0941, DGo_CA1145, DGo_CA1323, DGo_CA1521, DGo_CA2296, DGo_CA2465, DGo_CA2697, DGo_CA2698, DGo_CA2707, DGo_PA0223, DGo_PA0350, DGo_PB0098, DGo_PD0060	drug efflux proteins
	DGo_CA2225	putative resistance to florfenicol
	DGo_CA2181	putative resistance to fosmidomycin
	DGo_CA0978, DGo_PC0199	putative resistance to bacitracin
	DGo_CA0830	putative resistance to vancomycin
vitamin/cofactor synthesis	DGo_CA2761	folylpolyglutamate synthase
	DGo_CA2804	dihydropteroate synthase
	DGo_CA0403, DGo_CA0548	molybdopterin biosynthesis
	DGo_CA0131, DGo_CA0195, DGo_CA0561, DGo_CA0562, DGo_CA0563, DGo_CA1832, DGo_CA2498, DGo_CA2825, DGo_CA2891, DGo_CA2892, DGo_PA0212	thiamine biosynthessis
	DGo_CA0162, DGo_CA0164	riboflavin synthase

	DGo_CA0586, DGo_PA0002, DGo_PA0380, DGo_PA0381, DGo_CA0804, DGo_CA0806, DGo_CA0808, DGo_CA0803, DGo_CA2389, DGo_CA0839, DGo_PA0001, DGo_PA0383	B12 biosynthesis
	DGo_CA0451, DGo_CA0881, DGo_CA0882, DGo_CA0913, DGo_CA2358, DGo_CA2369, DGo_CA2871, DGo_CA2876, DGo_CA2878	Carotenoid biosynthesis
other	DGo_CA0607, DGo_PA0134, DGo_PB0391	photolyase
	DGo_CA0998, DGo_CA1464, DGo_CA1830, DGo_CA2870, DGo_PA0179, DGo_PB0312	Cytochrome P450
	DGo_CA0240	Mercuric reductase
	DGo_CA1190	2-nitropropane dioxygenase
	DGo_PB0053,DGo_PB0304,DGo_PC0224,DGo_PF0032	Arsenate reductase