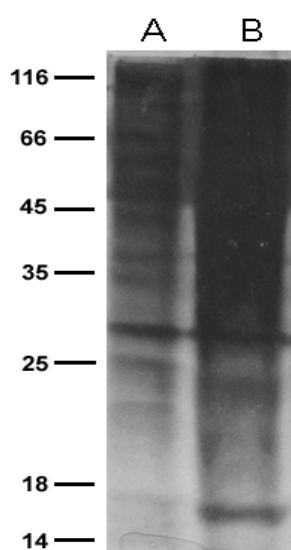
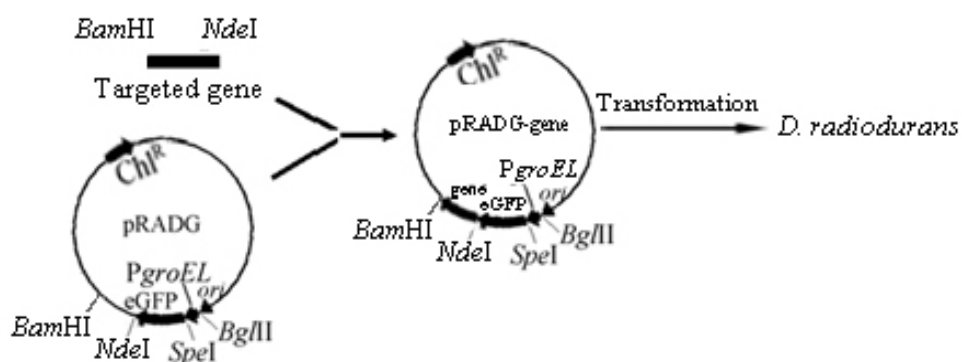


Supporting Information Figure 1. 1-D PAGE of a representative sample of the upper aqueous phase from protein extraction by the temperature-dependent phase partition with Triton X-114 detergent. Proteins were separated by 10% SDS-PAGE and stained with CBB. Lane A and B refer to the cytoplasmic proteins in the aqueous phase and total cell proteins, respectively. Molecular weight markers are indicated on the left (kDa).



Supporting Information Scheme 1. Construction of transformation vectors containing the targeted gene which was fused to eGFP gene. The plasmid pRADG (lab store) containing chloramphenicol resistance gene and the enhanced green fluorescence protein gene (eGFP, BD Clontech, USA), which is under the control of the *groEL* gene promoter (*PgroEL*), was constructed as described previously (see the reference below). Restriction sites relevant for the construction of the vectors were indicated.



Reference:

Gao GuanJun, Fan Lu, Lu HuiMing and Hua YueJin. Engineering *Deinococcus radiodurans* into biosensor to monitor radioactivity and genotoxicity in environment. *Chinese Science Bulletin*, 2008, 53(11): 1675-1681.

**Supplementary Information Table 1. List of identified membrane proteins
of *D. geothermalis***

Accession No.	Gene name	Protein description	Function (COG) ^{a)}	GRAVY value	No. of TMDs	Ortholog in <i>DR</i> or <i>DD</i> ^{b), c)}
Inner membrane						
Metabolism						
gi 94984425	Dgeo_0317	cytochrome c, class I	Energy production and conversion	0.401	5	DR0434 ^c Deide_20670 ^c
gi 94984126	Dgeo_0017	cytochrome c oxidase, subunit I	Energy production and conversion	0.701	13	ND
gi 94984427	Dgeo_0319	cytochrome b/b6-like protein	Energy production and conversion	0.572	8	DR0436 ^c Deide_20650
gi 94984515	Dgeo_0407	cytochrome c oxidase, subunit II	Energy production and conversion	-0.241	3	DR2619 Deide_18320 ^c
gi 94986150	Dgeo_2051	H⁺-transporting two-sector ATPase, C subunit	Energy production and conversion	0.896	3	DR0696^c Deide_00950^c
gi 94986151	Dgeo_2052	V-type ATPase, 116 kDa subunit	Energy production and conversion	0.274	8	DR0695 ^c Deide_00940 ^c
gi 94972172	Dgeo_2705*	cytochrome bd ubiquinol oxidase, subunit I	Energy production and conversion	0.472	9	ND
gi 94986435	Dgeo_2338	pyruvate dehydrogenase (lipoamide)	Energy production and conversion	-0.23	3	DR0029, Deide_23440 ^c , Deide_03910 ^c
gi 94972171	Dgeo_2704*	cytochrome d ubiquinol oxidase, subunit II	Energy production and conversion	0.67	9	ND
gi 94985776	Dgeo_1676	ABC-2 type transporter	Inorganic ion transport and metabolism	0.488	7	DR0926 Deide_15080
gi 94984323	Dgeo_0215	cation diffusion facilitator family transporter	Inorganic ion transport and metabolism	0.426	6	DR1102 Deide_11280
gi 94984757	Dgeo_0650	phosphate ABC transporter, permease protein	Inorganic ion transport and metabolism	0.683	6	DRA0158 Deide_2p01890 ^c

		PstC				
gi 94986310	Dgeo_2211	Mg2+ transporter protein, CorA-like protein	Inorganic ion transport and metabolism	0.039	3	DR2463 Deide_22130
gi 94985848	Dgeo_1748	phosphate transporter	Inorganic ion transport and metabolism	0.865	8	DR0925 Deide_03410
gi 94985443	Dgeo_1343	binding-protein-dependent transport systems inner membrane component	Inorganic ion transport and metabolism	0.583	7	DR1570 ^C Deide_11070
gi 94986222	Dgeo_2123	binding-protein-dependent transport systems inner membrane component	Inorganic ion transport and metabolism	0.672	6	DR0364 ^C Deide_19120 ^C
gi 158421518	Dgeo_3006*	CCC1 related, iron/manganese transporter component, DUF125	Inorganic ion transport and metabolism	0.295	4	ND
gi 94984532	Dgeo_0424	AMP-dependent synthetase and ligase	Secondary metabolites biosynthesis, transport and catabolism	-0.139	1	DR0336, DR2507 Deide_04270 ^C
gi 94985129	Dgeo_1024	tryptophan synthase subunit beta	Amino acid transport and metabolism	-0.066	3	DR0941 Deide_11760
gi 94985291	Dgeo_1189	extracellular solute-binding protein, family 5	Amino acid transport and metabolism	-0.338	1	DR1290^C, DR1712, DR1955^C, DRA0246^C Deide_10250^C, Deide_3p02270^C
gi 94985308	Dgeo_1206	inner-membrane translocator	Amino acid transport and metabolism	1.015	7	DR1037 ^C Deide_12600 ^C
gi 94985168	Dgeo_1064	ABC transporter related	Amino acid transport and metabolism	-0.159	0	DR1648 ^C Deide_07730 ^C
gi 94984433	Dgeo_0325*	binding-protein-d	Amino acid	0.676	6	ND

gi 94985442	Dgeo_1342	dependent transport systems inner membrane component binding-protein-dependent transport systems inner membrane component	transport and metabolism	0.427	6	DR1569 ^C Deide_11080 ^C
gi 94985441	Dgeo_1341	oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein	Amino acid transport and metabolism	-0.1	0	DR1568 ^C Deide_11090 ^C
gi 94985440	Dgeo_1340	oligopeptide/dipeptide ABC transporter, ATP-binding protein-like protein	Amino acid transport and metabolism	-0.077	0	DR1567 ^C Deide_11100 ^C
gi 94985899	Dgeo_1799	major intrinsic protein	Carbohydrate transport and metabolism	1.103	6	DR1929 ^C
gi 94972088	Dgeo_2620*	phosphotransferase system, glucose-specific IIBC component	Carbohydrate transport and metabolism	0.502	12	ND
gi 94985474	Dgeo_1374	Sugar ABC transporter, ATP-binding protein	General function prediction only	-0.058	1	DR0957 ^C Deide_08550 ^C
gi 94985185	Dgeo_1081	6-phosphoglucosate dehydrogenase, NAD-binding	Lipid transport and metabolism	0.293	3	DR0499^C Deide_10300^C
gi 94984254	Dgeo_0146	short chain dehydrogenase	Lipid transport and metabolism	0.195	4	DR0113
gi 94984450	Dgeo_0342	protein-tyrosine kinase	Cellular processes Cell cycle control, mitosis and meiosis	-0.085	1	DRA0033 Deide_20321 ^C

gi 94985754	Dgeo_1654	cell division FtsK/SpolIIE	Cell cycle control, mitosis and meiosis	-0.078	4	DR0400 Deide_15050
gi 94972109	Dgeo_2642	ExoP-related protein	Cell cycle control, mitosis and meiosis	-0.059	0	DRA0033
gi 94985172	Dgeo_1068	peptidoglycan glycosyltransferase	Cell wall/membrane biogenesis	-0.345	1	DR1417 ^C Deide_08370, Deide_18450 ^C
gi 94986065	Dgeo_1966	prolipoprotein diacylglycerol transferase	Cell wall/membrane biogenesis	0.406	7	DR0807 Deide_07510 ^C
gi 94984517	Dgeo_0409	cytochrome oxidase assembly	Posttranslational modification, protein turnover, chaperones	0.838	8	DR2617, Deide_18300
gi 94984581	Dgeo_0474	FeS assembly ATPase SufC	Posttranslational modification, protein turnover, chaperones	-0.169	0	DR2107 Deide_03350^C
gi 94985346	Dgeo_1245	cytochrome c assembly protein	Posttranslational modification, protein turnover, chaperones	0.515	6	DR0348 ^C Deide_08320
gi 94985348	Dgeo_1247	cytochrome c assembly protein	Posttranslational modification, protein turnover, chaperones	0.642	15	DR0346 Deide_08300
gi 94986281	Dgeo_2182	ATP-dependent metalloprotease FtsH	Posttranslational modification, protein turnover, chaperones	-0.172	2	DRA0290 ^C , Deide_01120 ^C , Deide_23310, Deide_18550
gi 94984110	Dgeo_0001	chromosomal replication initiator protein DnaA	Replication, recombination and repair	-0.279	3	DR0002 Deide_00010 ^C
gi 94985370	Dgeo_1269*	sensor, signal transduction histidine kinase	Signal transduction mechanisms	-0.335	0	DR2416 Deide_10780 ^C
gi 94984237	Dgeo_0129*	histidine kinase	Signal transduction mechanisms	-0.143	0	DR2244 Deide_19810
gi 94986195	Dgeo_2096*	multi-sensor, signal	Signal transduction	-0.186	1	ND

gi 94985162	Dgeo_1058*	transduction histidine kinase preprotein translocase subunit SecA	mechanisms Intracellular trafficking and secretion	-0.372	0	DR0575 Deide_17210^C
gi 94985340	Dgeo_1239*	bifunctional preprotein translocase subunit SecD/SecF	Intracellular trafficking and secretion	0.269	11	DR1822 ^C Deide_10360 ^C
gi 94985854	Dgeo_1754	MotA/TolQ/ExbB proton channel	Intracellular trafficking and secretion	0.508	3	DR0456 ^C Deide_03360
gi 94985947	Dgeo_1847*	preprotein translocase subunit SecY	Intracellular trafficking and secretion	0.557	10	DR2116 ^C Deide_18750
gi 94984755	Dgeo_0648	ABC transporter related	Defense mechanisms	0.137	5	DR0096, DR2052 Deide_06140
gi 94986215	Dgeo_2116*	acriflavin resistance protein	Defense mechanisms	0.441	14	DR0740 ^C
gi 94984802	Dgeo_0695	basic membrane lipoprotein	Poorly characterized General function prediction only	-0.096	1	DR2070^C Deide_20440^C
gi 94984810	Dgeo_0703	basic membrane lipoprotein	General function prediction only	0.042	0	DR2070 ^C Deide_20440 ^C
gi 94984645	Dgeo_0538	protein of unknown function UPF0005	General function prediction only	1.129	7	DR0893 Deide_16610 ^C
gi 94984657	Dgeo_0550	peptidase M50	General function prediction only	0.924	5	DR0982 ^C Deide_06230 DR2176, DRB0128, DRB0129,
gi 94985386	Dgeo_1285	protein of unknown function DUF21	General function prediction only	0.126	4	Deide_11960, Deide_3p01910
gi 94985790	Dgeo_1690	inner-membrane translocator	General function prediction only	0.667	14	Deide_3p01900 DR0250 ^C Deide_07820
gi 94985791	Dgeo_1691	inner-membrane translocator	General function prediction only	0.93	9	DR0251 Deide_07810 ^C

gi 94985813	Dgeo_1713	protein of unknown function UPF0118	General function prediction only	0.978	8	DR0252 ^c , DR0898, DR1188, Deide_07790
gi 94984694	Dgeo_0587	ABC transporter related	General function prediction only	-0.312	1	DR2134 Deide_03770 DR1864
gi 94984871	Dgeo_0764	protein of unknown function DUF423	Function unknown	0.962	3	
gi 94985302	Dgeo_1200	protein of unknown function DUF1622	Function unknown	0.31	3	DR1328
gi 94985117	Dgeo_1012	hypothetical protein Dgeo_1012	Function unknown	0.278	5	DR0790 Deide_10450 ^c
gi 94984309	Dgeo_0201	hypothetical protein	Not in COGs	0.326	7	DR0160 ^c Deide_00400 ^c
gi 94984334	Dgeo_0226	TM2	Not in COGs	0.164	3	DR2326 Deide_20790
gi 94984800	Dgeo_0693	hypothetical protein	Not in COGs	0.713	5	DR1770
gi 94984853	Dgeo_0746	hypothetical protein	Not in COGs	0.835	4	ND
gi 94985324	Dgeo_1222	hypothetical protein	Not in COGs	0.329	3	DR1483 ^c
gi 94986094	Dgeo_1995	hypothetical protein	Not in COGs	0.522	4	ND
gi 116247804	Dgeo_1304	glucose-6-phosphate isomerase, gluconeogenesis	Not in COGs	-0.224	3	DR1742 Deide_17080^c
Outer membrane						
Metabolism						
Energy production and conversion						
gi 94984159	Dgeo_0051	phosphate acetyltransferase	Energy production and conversion	0.055	0	DR0073 Deide_23230 ^c
Inorganic ion transport and metabolism						
gi 94972220	Dgeo_2753	periplasmic binding protein	Inorganic ion transport and metabolism	-0.088	0	DRB0125
Cellular processes						
Cell wall						
gi 94984927	Dgeo_0820	hydrolase/autolysin	Cell wall/membrane biogenesis	-0.08	1	Deide_08780 ^c

gi 94985525	Dgeo_1425	surface antigen (D15)	Cell wall/membrane biogenesis	-0.175	0	DR0379^c Deide_08200^c
gi 94986216	Dgeo_2117	secretion protein HlyD	Cell wall/membrane biogenesis	-0.113	0	DR0739
gi 94986217	Dgeo_2118	hypothetical protein	Intracellular trafficking and secretion	-0.057	0	DR0738
gi 94985623	Dgeo_1523	outer membrane efflux protein	Intracellular trafficking and secretion	0.03	0	DR0737 ^c
gi 94985829	Dgeo_1729	type II and III secretion system protein	Intracellular trafficking and secretion	-0.122	0	DR0774 ^c Deide_17640 ^c
			Poorly characterized			
gi 94985743	Dgeo_1643	peptidase M16C associated	General function prediction only	-0.218	1	DR0617 Deide_05430 ^c
gi 94985554	Dgeo_1454	hypothetical protein	Function unknown	-0.86	0	DR1314^c Deide_22640^c
gi 94984223	Dgeo_0115	hypothetical protein	Not in COGs	-0.327	1	DR2527 ^c
gi 94984286	Dgeo_0178	Tetratricopeptide TPR_2	Not in COGs	0.014	4	DR2271 Deide_00230
gi 94984825	Dgeo_0718*	hypothetical protein	Not in COGs	0.127	3	DR0972 Deide_12690 ^c
gi 94985652	Dgeo_1552	hypothetical protein	Not in COGs	0.16	0	DR1371 Deide_09711
gi 94986167	Dgeo_2068	hypothetical protein	Not in COGs	0.285	4	DR0673
gi 94986218	Dgeo_2119	outer membrane efflux protein	Not in COGs	0.127	0	DR0737 ^c
gi 94984261	Dgeo_0153	OstA-like protein, organic solvent tolerance protein	Not in COGs	-0.293	0	DR2319 Deide_22270 ^c
			Periplasmic Metabolism			
gi 94984994	Dgeo_0887	succinate dehydrogenase flavoprotein subunit	Energy production and conversion	-0.296	1	DR0952 ^c Deide_12450 ^c
gi 94985349	Dgeo_1248	thiol:disulfide interchange	Energy production and	0.011	1	DR0189 ^c , DR0345,

gi 94984661	Dgeo_0554	protein (Redoxin) extracellular solute-binding protein, family 5	conversion Amino acid transport and metabolism	-0.46	0	Deide_08290 ^c DR0986 ^c Deide_06270
gi 94984727	Dgeo_0620	extracellular ligand-binding receptor	Amino acid transport and metabolism	0.117	2	DR0788, DR1038 ^c Deide_12590 ^c Deide_14600 ^c Deide_17040 ^c DR0788, DR1038^c
gi 94985307	Dgeo_1205	extracellular ligand-binding receptor	Amino acid transport and metabolism	-0.049	1	Deide_12590^c Deide_14600^c Deide_17040^c DR0363^c
gi 94986221	Dgeo_2122	extracellular solute-binding protein, family 5	Amino acid transport and metabolism	-0.387	1	Deide_19110 ^c , Deide_06270 ND
gi 94984432	Dgeo_0324*	extracellular solute-binding protein, family 5	Amino acid transport and metabolism	-0.463	1	
gi 94984842	Dgeo_0735	extracellular ligand-binding receptor	Amino acid transport and metabolism	0.013	0	DR2122 ^c Deide_07020 ^c
gi 94985164	Dgeo_1060	extracellular solute-binding protein, family 3	Amino acid transport and metabolism	-0.051	0	DR2154, DRB0078, Deide_05450 ^c Deide_07680 ^c Deide_2p01060 _c Deide_3p00160 _c Deide_3p00200 _c
gi 94986058	Dgeo_1959	extracellular solute-binding protein, family 3	Amino acid transport and metabolism	0.001	0	DR2278
gi 94986288	Dgeo_2189	extracellular solute-binding protein, family 3	Amino acid transport and metabolism	-0.114	1	DR2610, DR1027, Deide_05450 ^c Deide_07680 ^c Deide_3p00160 _c Deide_3p00200 _c

		bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein	Nucleotide transport and metabolism	-0.241	1	DR1736^c Deide_14040^c
gi 94971837	Dgeo_2368	5'-Nucleotidase-like	Nucleotide transport and metabolism	-0.166	0	DR0505 ^c Deide_13330 ^c
gi 94972218	Dgeo_2751	5'-Nucleotidase-like	Nucleotide transport and metabolism	-0.086	1	DRA0018 Deide_2p0058 0^c
gi 94984794	Dgeo_0687	extracellular solute-binding protein, family 1 maltose ABC transporter,	Carbohydrate transport and metabolism	-0.103	0	Deide_10270 ^c
gi 94985600	Dgeo_1500	extracellular solute-binding protein, family 1 glucose dehydrogenase,	Carbohydrate transport and metabolism	-0.114	1	DR0561 ^c Deide_09500 ^c
gi 94985251	Dgeo_1149	Gcd and cytochrome c-like domain	Carbohydrate transport and metabolism	-0.27	1	ND
gi 158421433	Dgeo_2919*	ABC-type sugar transport system, periplasmic component	Carbohydrate transport and metabolism	-0.298	1	ND
gi 94986032	Dgeo_1933	ABC transporter periplasmic binding protein, thiB subfamily	Coenzyme transport and metabolism	-0.129	1	DR0262 Deide_15830 ^c
gi 94984232	Dgeo_0124	hemin ABC transporter, periplasmic binding protein	Inorganic ion transport and metabolism	0.075	0	DRB0014^c
gi 94984756	Dgeo_0649	ABC-type phosphate transporter, periplasmic	Inorganic ion transport and metabolism	-0.054	1	DRA0157 Deide_2p01880 ^c

gi 94985470	Dgeo_1370	binding protein iron ABC transporter, periplasmic binding protein	Inorganic ion transport and metabolism	-0.126	1	DRB0125 Deide_17140 ^c
gi 94971832	Dgeo_2363	putative high-affinity iron ion transporter, periplasmic binding protein	Inorganic ion transport and metabolism	-0.032	1	DRB0007 ^c Deide_2p01550 ^c
gi 94971967	Dgeo_2499	molybdenum ABC transporter	Inorganic ion transport and metabolism	0.055	1	DRA0169 ^c
gi 94972224	Dgeo_2757*	ABC-type Fe ³⁺ -siderophore transport system, periplasmic binding protein	Inorganic ion transport and metabolism	-0.075	2	Deide_2p00380 ^c
gi 94984134	Dgeo_0025	iron ABC transporter, periplasmic binding protein	Inorganic ion transport and metabolism	-0.003	1	DR2588 ^c Deide_02140 ^c
gi 94972221	Dgeo_2754	Iron ABC transporter, periplasmic binding protein	Inorganic ion transport and metabolism	0.015	1	DRB0125
Cellular processes						
gi 94984211	Dgeo_0103	peptidase S1 and S6, chymotrypsin/Hap	Posttranslational modification, protein turnover, chaperones	0.04	0	DR0300 Deide_21550 ^c
gi 94984659	Dgeo_0552	peptidase S1 and S6, chymotrypsin/Hap	Posttranslational modification, protein turnover, chaperones	0.001	1	DR1756 ^c DR0984, Deide_06250
Poorly characterized						
gi 94985232	Dgeo_1130	copper resistance protein CopC	General function prediction only	0.373	1	DRA0299, Deide_3p01290 ^c

Proteins are grouped by their subcellular locations and molecular functions.
Previously identified membrane proteins from the cell envelope fraction of *D.*

geothermalis E50051 (Hambi 2411) by 2-D MALDI-TOF analysis were shown in bold fonts [1]. The cell culture was grown in the oligotrophic R2 medium where glucose was replaced by starch.

The membrane proteins discussed in this study were indicated with superscript *.

a) COG functional class (www.ncbi.nlm.nih.gov/COG).

b) Orthologs in *D. radiodurans* or *D. deserti* [2, 3].

c) Previously identified proteins in *D. radiodurans* and *D. deserti* [3, 4]. ND, not found.

Reference:

[1] Liedert, C., Bernhardt, J., Albrecht, D., Voigt, B., *et al.*, Two-dimensional proteome reference map for the radiation-resistant bacterium *Deinococcus geothermalis*. *Proteomics* 2010, 10, 555-563.

[2] Makarova, K. S., Omelchenko, M. V., Gaidamakova, E. K., Matrosova, V. Y., *et al.*, *Deinococcus geothermalis*: the pool of extreme radiation resistance genes shrinks. *PLoS One* 2007, 2, e955.

[3] de Groot, A., Dulermo, R., Ortet, P., Blanchard, L., *et al.*, Alliance of proteomics and genomics to unravel the specificities of Sahara bacterium *Deinococcus deserti*. *PLoS Genet* 2009, 5, e1000434.

[4] Blonder, J., Goshe, M. B., Moore, R. J., Pasa-Tolic, L., *et al.*, Enrichment of integral membrane proteins for proteomic analysis using liquid chromatography-tandem mass spectrometry. *J Proteome Res* 2002, 1, 351-360.

Supporting Information Table 5. Primers used in this study

Gene name	Primers	Sources
Dgeo_3006	5' <u>CATATG</u> CCCCAGACCCCCAC 3' (<i>NdeI</i>)	This work
Dgeo_3006	5' <u>GGATCC</u> CTACGCCACCCCAGGCC 3' (<i>Bam</i> HI)	This work
Dgeo_0695	5' <u>CATATG</u> AAAAAAGGCCTAACCC 3' (<i>NdeI</i>)	This work
Dgeo_0695	5' <u>GGATCC</u> TTACTTGCTGGGCACCTG 3' (<i>Bam</i> HI)	This work
Dgeo_1754	5' <u>CATATG</u> AACCTTCTGGCGCTGATCC 3' (<i>NdeI</i>)	This work
Dgeo_1754	5' <u>GGATCC</u> TCACCGTGCCGCCCA 3' (<i>Bam</i> HI)	This work

Restriction sites are underlined and restriction enzymes are indicated in parenthesis.