

		24	82
	<i>Deinococcus radiodurans</i>	499191373	LLGWFDGRAGDLPWRLGDE GRRD PYRVVWAEILLQQTQVARGLGYEERFLEAFPTVQAL
	<i>Deinococcus swuensis</i>	746728251	--A--A-----S-----H-D-----E--
	<i>Deinococcus deserti</i>	502012169	--A--A-----A-V-----IS-V-----T-D--Q-----
	<i>Deinococcus marmoris</i>	1175298040	--A--AS-E-----T-A-----H-D-----S--
Genus <i>Deinococcus</i> (26/26)	<i>Deinococcus reticulitermitis</i>	1094410079	-----V-A-----P-G-----RL-----
	<i>Deinococcus wulumuqiensis</i>	648447004	--A-----E--V-P-A-----V--RM-----
	<i>Deinococcus geothermalis</i>	499848436	--A-----A--V-P-----S-V-----RV-F-----E--
	<i>Deinococcus apachensis</i>	518416424	--S-----P--V-P-----S-V-----RV-F-A-----
	<i>Deinococcus puniceus</i>	1028846678	--T--QH-A-----E-A-----V-----T--S-E--
	<i>Deinococcus aquatilis</i>	517840375	--T--HS-A--A-A-A-----V-----T--S--
	<i>Deinococcus actinosclerus</i>	1011240592	--A--Q-----Q-P-----A--V-----E-H--T--S-V-
	<i>Deinococcus maricopensis</i>	503320979	-----AHA-T--A-A-----S-V-----V-F-A-----
	<i>Deinococcus peraridilitoris</i>	505047897	--A--EHA-----AASP-----S-V-----KV-F--T--D-A--
	<i>Hyphomonas spp.</i>	<i>Hyphomonas adhaerens</i>	916989539
(11/11)	<i>Hyphomonas jannaschiana</i>	916990686	--A--H-----TALG E-----L--M--TIPH-TP-FLT-TQRW--E--
	<i>Acinetobacter dijkshoorniae</i>	1008917059	--N--QH--HDLPWQVAD --K--S-M--KTV-Q-FD--M-R--E--
	<i>Acinetobacter pittii</i>	507073098	--N--QH--HDLPWQVAD --K--S-M--KTV-Q-FD--M-R--E--
	<i>Acinetobacter seifertii</i>	1197250511	--N--QH--HDLPWQVAD --K--S-M--KTV-Q-FD--M-R--E--
	<i>Lactobacillus zymae</i>	951353339	--A-Y-Q-----HDQD --H--S-M--NTVIP--Q--MA--E--
Other bacteria (0/>500)	<i>Muricauda antarctica</i>	1120000780	I-A-YGEHQ-----KTRD --KI-LS-M--R--Q-MP--H--RD-
	<i>Roseivirga seohaensis</i>	921285074	IN-YEENK-----KTRN --I-LS-I--R--Q--P-----I-Q--IHD-
	<i>Peptococcus niger</i>	1086116344	---Y-ANA-A--TSG-- --HI-IS-VM-----TVIP-----E--
	<i>Cesiribacter andamanensis</i>	496488913	--D-Y-Q-NQ-----QTRD --I-LS-VI--R-QQ--P--Q--V-K--E--
	<i>Lactobacillus siliginis</i>	948985388	--D-Y-KE-----KDHD --H--S-M--NTVIP-----MKT--D-
	<i>Oscillibacter valericigenes</i>	503885511	--S-YRANA-----KTRD -----S-M--R--AV--Q--S--S-E--
	<i>Alistipes putredinis</i>	1124923007	--E-YG-E-----RTRD --I-IS-VI--R--Q-MS--H--L--D-A--
	<i>Jeotgalibacillus malaysiensis</i>	748252759	-V--EQEM-----ENQD -----S-M--R-DTVIP--N--M-Q--E--
	<i>Streptococcus rattii</i>	489182032	--A-Y-QEK-----RTKD --I-S-M-----TVIP-----DW--SI-D-
	<i>Porphyromonas levii</i>	517170226	--D--QY--T--GI-D --I-S-I-----VQ-WD--K--I--Y-D-V--
<i>Facklamia hominis</i>	493965538	--A-Y-QN-----RTSD --AI-S-VM-----DTVID--Q--MQ-L-----	
<i>Hymenobacter sedentarius</i>	1056775430	--A-YP-HS-----HTRD --AI-LS-I--R--Q--P--T--A-Y--D-	
<i>Aerococcus urinae</i>	984723132	-FD-Y-E--H--ESKD --I-IS-M-----NTVIP--Q--Q--ED-	

Figure S1. Partial sequence alignment of conserved region of 8-oxoguanine DNA glycosylase (MutY) protein showing a 4 amino acid insertion that is a distinctive characteristic from homologs of *Deinococcus* group of bacteria. This insert is also shared by *Hyphomonas* spp. and it has likely occurred independent in this group.

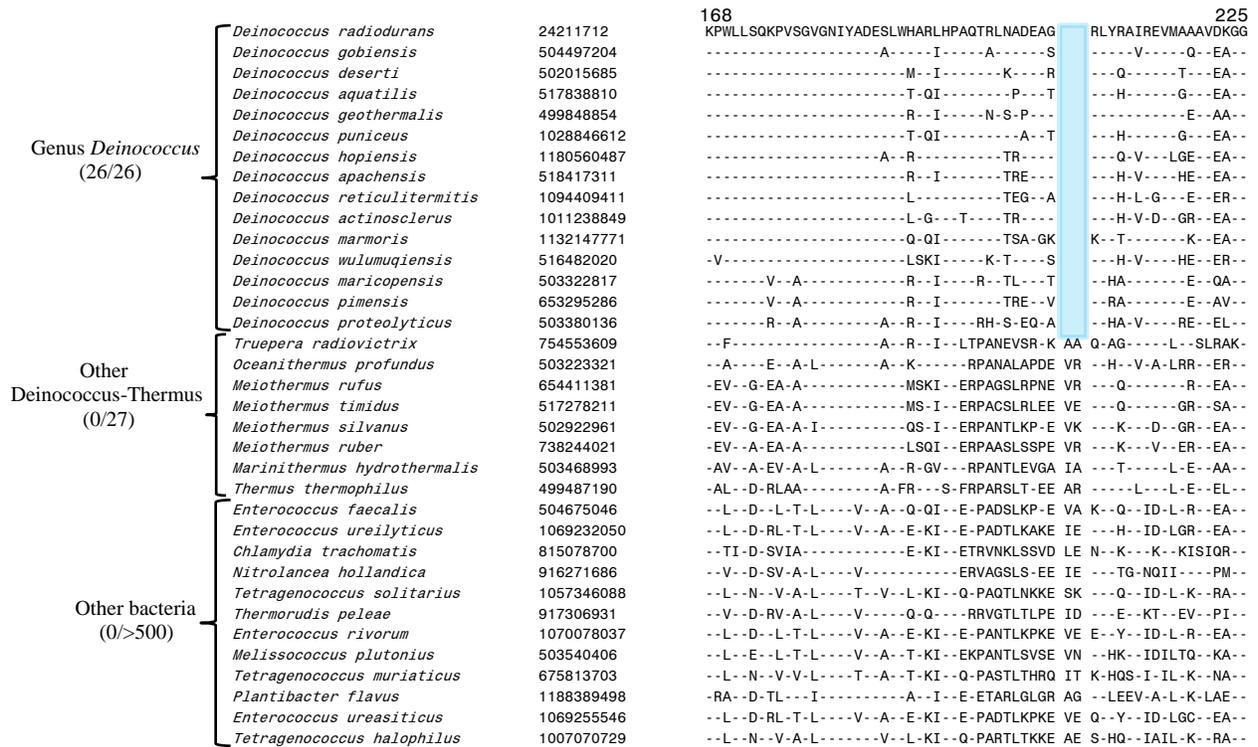


Figure S2. Partial sequence alignment of conserved region of formamidopyrimidine and 8-oxoguanine DNA glycosylase (MutM) protein showing a 2 amino acid deletion that is a distinctive molecular characteristics of *Deinococcus* spp.

		144	228
Genus <i>Deinococcus</i> (26/26)	<i>Deinococcus phoenicis</i>	736331005	GVGMMKTASLLLLFLDARPAIPVENNIHRVAGRLDLIPARWNVLKAERWFDGVLPRD WA ARATFHVSAIRHGRQTCLSQRPRCEVC
	<i>Deinococcus geothermalis</i>	499849194	-----I-----F-S-----E-----L D-----RA----AC-
	<i>Deinococcus apachensis</i>	518415322	-----W-----E-----T-Y-----R-----
	<i>Deinococcus puniceus</i>	1028846869	-----V-----M-DTH-G-I-A-EWV-----AI-V-----E-----S-YG-----E-RA--D-A-
	<i>Deinococcus marmoris</i>	736389575	-----CV-----M-DTH--I-R--E-V-EA--AV-V-----E-----Y-----RARN-A-G--
	<i>Deinococcus maricopensis</i>	503322632	-----A-----M-DGH-D--SK--H--E-----Y-E-----Q-YAY--AT-----E--TRA--NA-
	<i>Deinococcus deserti</i>	613465786	-----I-----L--L-DT--E-I-K-E-V-Q--TPE-V-----A-VR-----E-----AGV----L-RPRD--DQ-
	<i>Deinococcus wulumuqiensis</i>	516480559	---H--VA-V-----R--M-DG-ME-A-K-E-V-A--SH-V---YAE-V-G--E T-FAL-I-GV---D--R-KH-L-PA-
	<i>Deinococcus ficus</i>	760096023	---L-----V-----I--L-DG--E-TLK--EFV-PN-SAERT-----R-VS-E--L L--AL--AGV---H--PRN--PA-
	<i>Deinococcus gobiensis</i>	504498115	---QR-----V-----V--M-DT--A-M-A---V-ET-STNRT-A--GQ-IA--E T-YAL-L-GV---HE--TPR--L-GR-
	<i>Deinococcus radiodurans</i>	499190033	---H--VA-V-----R--M-DG-ME-A-K-E-V-A--SH-V---YAE-M-A--E T-FAL-I-GV---D--R-KH-L-PQ-
	<i>Deinococcus reticulitermitis</i>	1094409371	---H--VA-V-----G-A-M-DG-ME-A-K-E-V--G-SSDRV---Y-EAA---E T-FAL-L-GV---V--RP--L-GE-
	<i>Deinococcus proteolyticus</i>	503380505	---QR-----H-Q-AA-DS--E-LLH--EVV-PG-KADRQ-L-LE---A-AP L-A--RAGV---EI-TRHA--PA-
	<i>Thermorudis peleae</i>	1175339156	---P---ACV--G-G--L-DTHVY--Q-G-L-P-CTSER-HQLLAALV-PE Y-A--LL-----C-HARN--PT-
Other bacteria (0/>500)	<i>Methanosaeta harundinacea</i>	504400110	---P---AVV--AFRM-LL-DTHVN-LSR--GFV--GASIEE--ILEEIT--E KYCS--NL-----AV-RARS-S-GA-
	<i>Ktedonobacter racemifer</i>	495198690	---P---ACV--NMG--LM-IDTHL--LTH--G-GPKVSAOQ-HTI-LKA--PE WAY-L--NL-----TI-HA--K-PQ-
	<i>Anaerolinea thermolimos</i>	1011275067	---P---AIV-V-S-NK--F-DTH-Y--S--IG-R--HLS-EQ-HQYLA--FKP- QY-PG-LNL--L--E--HAR--N-PA-
	<i>Chloroflexi bacterium</i>	1084570780	---P---AIV--S-N--F-DTH-Y--T--IG-R--KMT-EQ-HPYLESF-A- -YYAA-LNI--L--EV-QAR-TM-YK-
	<i>Dehalococcoidia bacterium</i>	931359859	---P---ACV--S-G-SVL--DTHVY-ISR--G-DS-VSPEQ-HQLLEE-V-SQ -LYQ--LNMLA--SI-RA--L-HD-
	<i>Chthonomonas calidirosea</i>	944158928	---P---AIV-C-A-G--V--DTHVF--W--G-EK-VGES--HDLQALV-PE LIYR--AL-E--RV-KAL-----
	<i>Thermogemmatispora onikobensis</i>	1181357612	---P---ACV--A-GW-VM-DTHV--R--G-LGPKVSAEQ-HVLLAQMT-PA WVYAL--NL-----RV-A--PA-
	<i>Anaerolineae bacterium</i>	931423785	---R---IV--SFG--F-DTHV--IS--G-GPKVTAD--HQILENMGDP- TYAM-LNL-----EV-TARN-K-DQ-
	<i>Solirubrobacterales bacterium</i>	1113216706	---R---ACV-I-SWGL-E--DVH--G--G-F--KASLER-HDEMLAIV-PE DAYEL--NL-----TL-RP-K--GG-
	<i>Euryarchaeota archaeon</i>	1197629305	---I-P-SSAVI-N--FDKN-F-DTHVY--TQ--G--NKT-RE--HQILEKQV-SE RMYE--INL-K--TV-KARK-I-SE-
<i>Anaerolineaceae bacterium</i>	1176212619	---P---AIV--SFNL--F-DTHV--SQ--G--GTQVSRE--HSTLETL--PE TYYS--LNL-A--V-HARG--H-	
<i>Anaerolinea thermophila</i>	503323788	---V---IV--S-NK--F-DTHV--S--IG-R-POMSAED-HAYLAQ-FTPE QY-AG-LNL--L--EV-HARK-A-PR-	

Figure S3. Partial sequence alignment of conserved region of Endonuclease III (Nth) protein showing a 2 amino acid insertion that is specific for all *Deinococcus* group of bacteria.

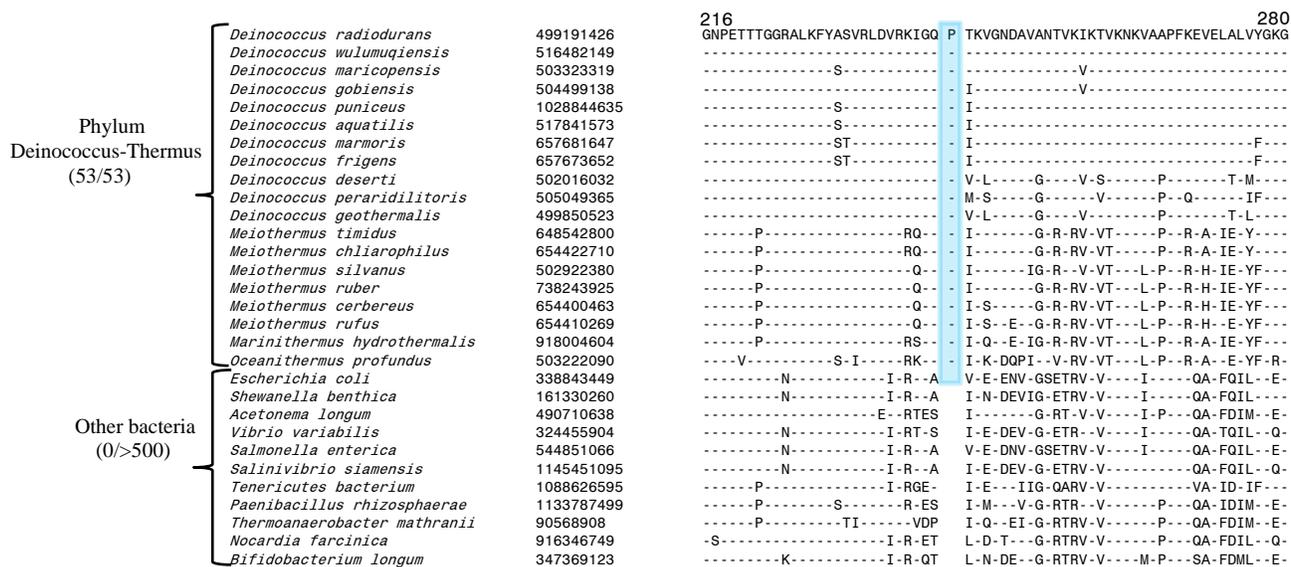


Figure S4. Partial sequence alignment of conserved region of DNA recombination protein RecA showing a 1 amino acid insertion that is specific for all bacteria of Deinococcus-Thermus phylum.

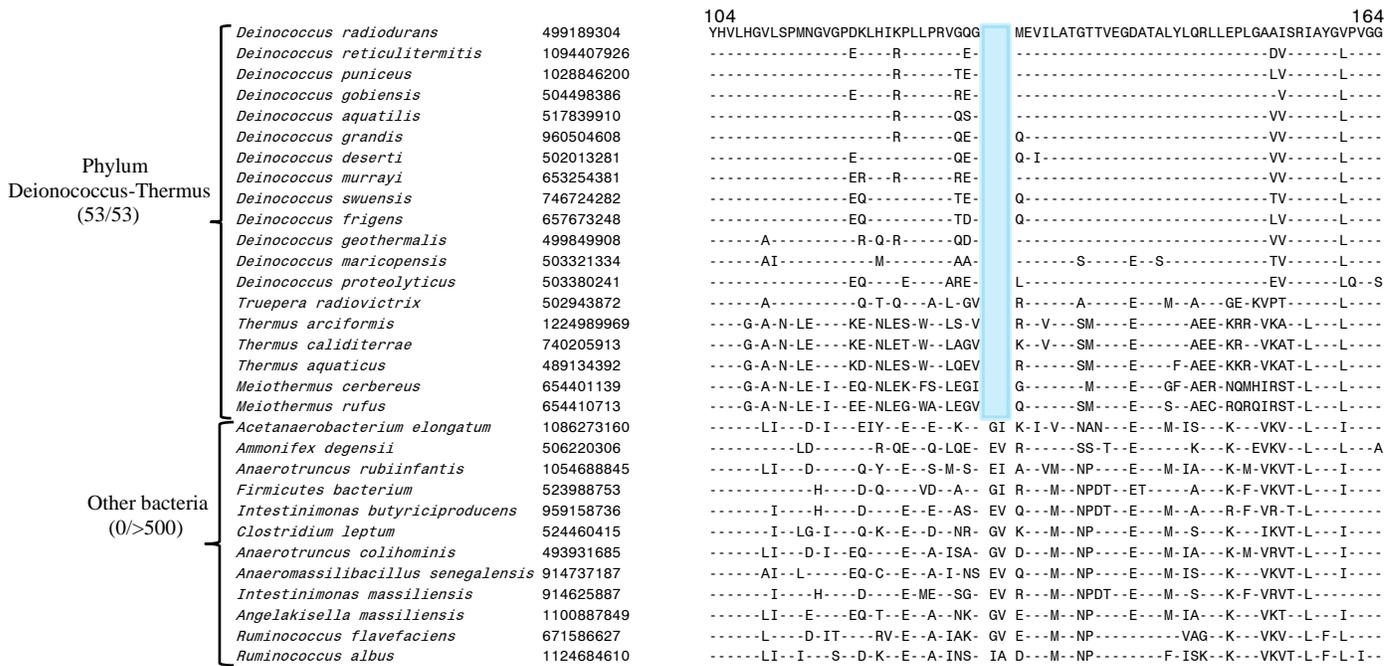


Figure S5. Partial sequence alignment of conserved region of DNA helicase recombination protein RecR showing a 2 amino acid deletion that is a distinctive molecular characteristic of the phylum Deinococcus-Thermus.

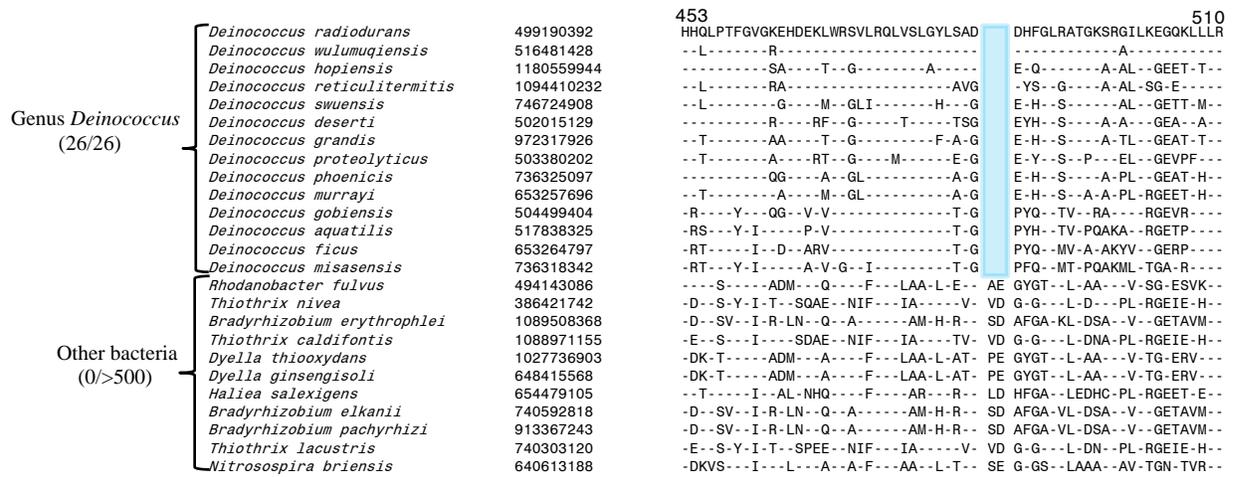


Figure S6. Partial sequence alignment of conserved region of DNA helicase RecQ protein showing a 2 amino acid deletion that is uniquely shared by all *Deinococcus* group of bacteria.

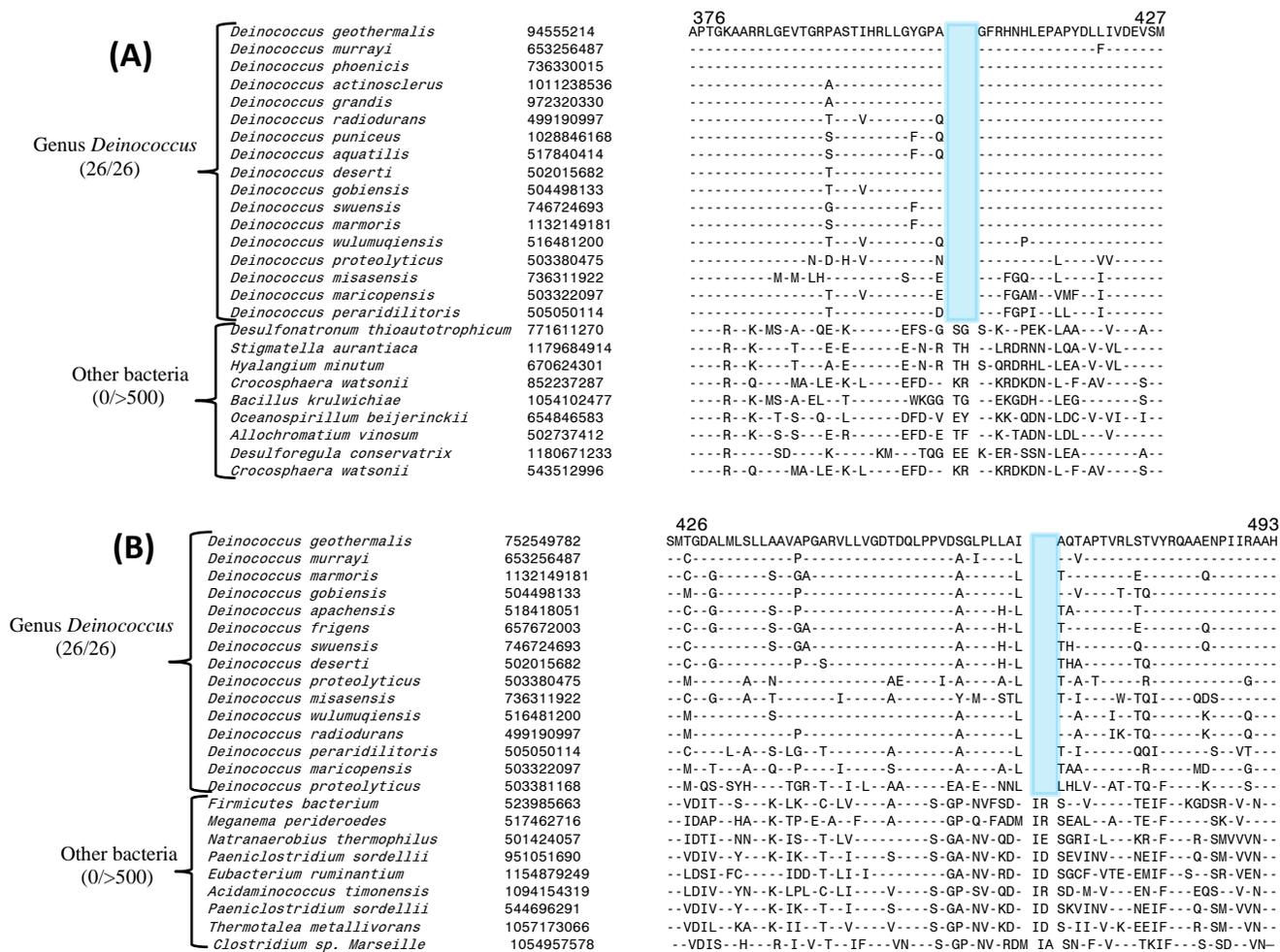


Figure S7. Partial sequence alignments of two conserved regions of helicase RecD protein showing two 2 amino acid deletions that are specific for all *Deinococcus* group of bacteria.

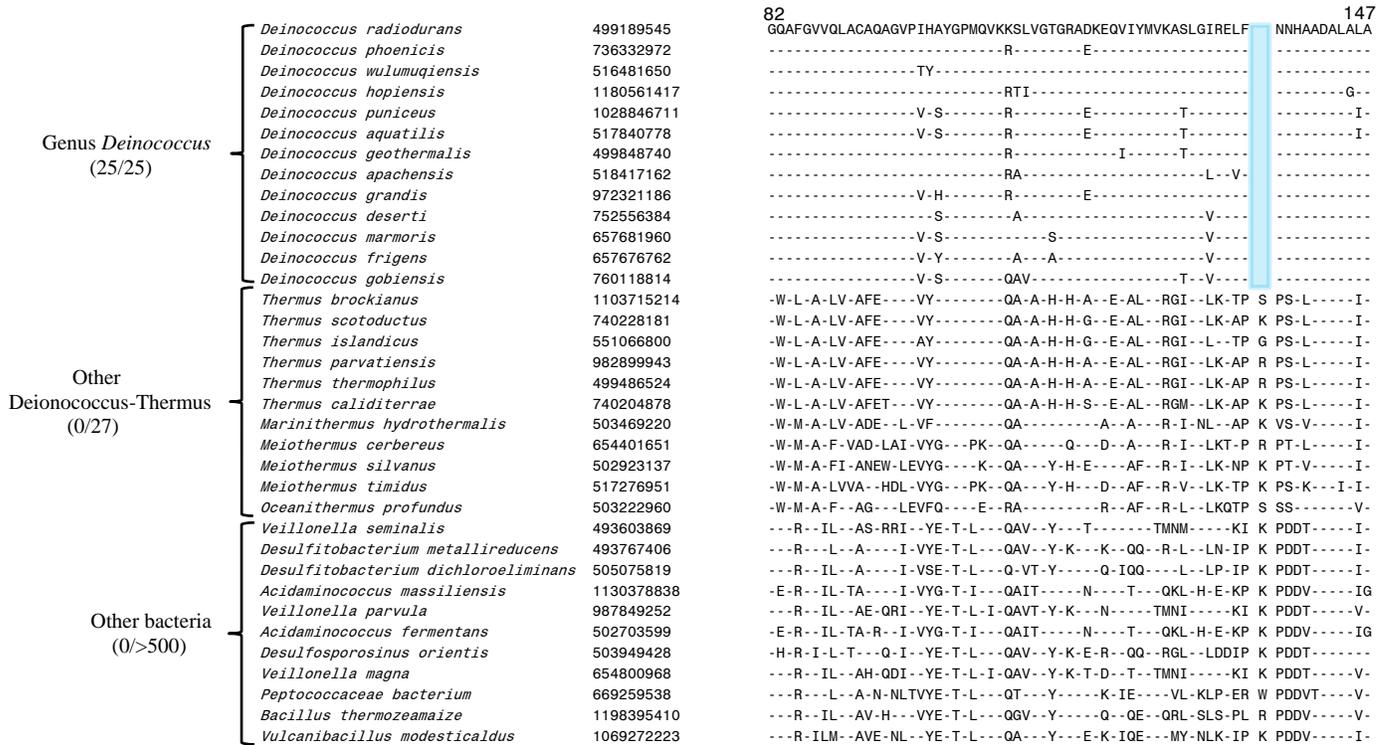


Figure S8. Partial sequence alignment of conserved region of crossover junction endodeoxyribonuclease RuvC protein showing a 2 amino acid deletion that is a distinctive molecular characteristic of *Deinococcus* spp.

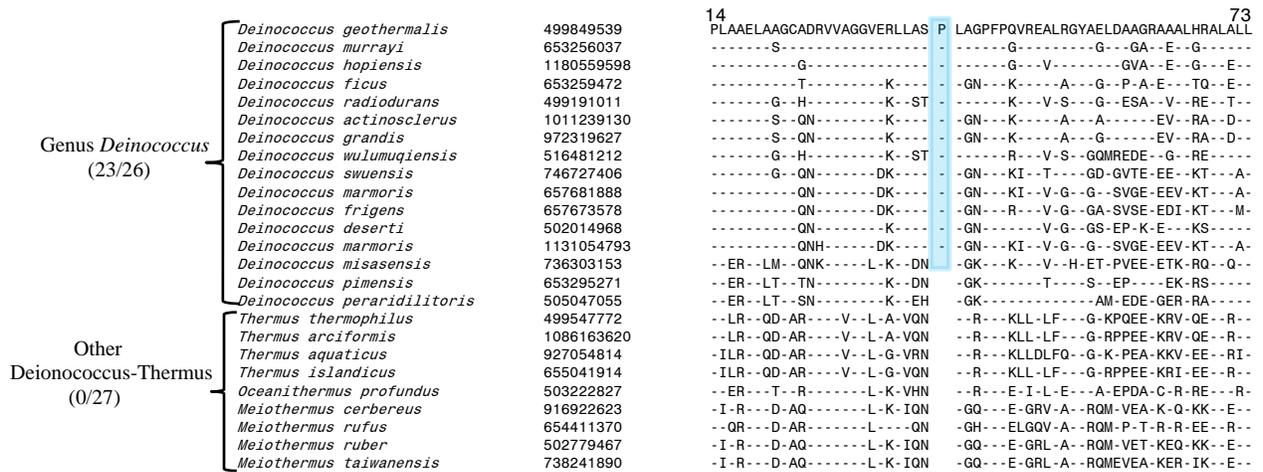


Figure S9. Partial sequence alignment of a conserved region of DNA helicase RecG protein showing a 1 amino acid insertion that is specific for the *Deinococcus* group of bacteria. Three *Deinococcus* spp. do not contain this insertion.

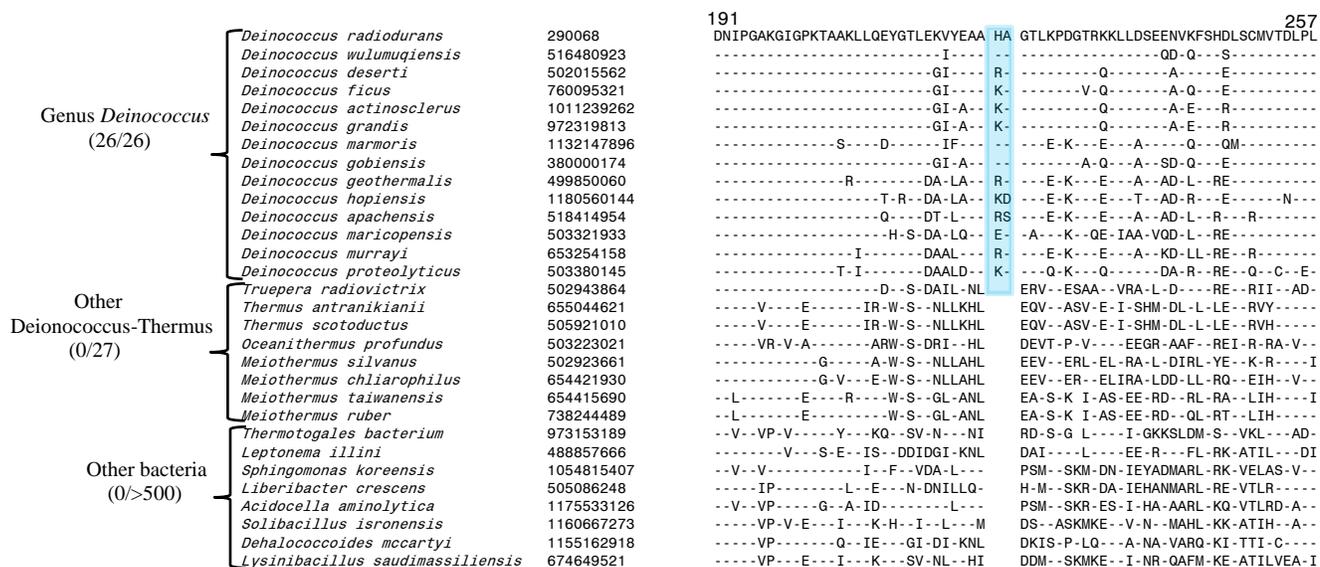


Figure S10. Partial sequence alignment of a conserved region of DNA polymerase I (PolA) protein showing a 2 amino acid insertion that is specific for all *Deinococcus* group of bacteria.

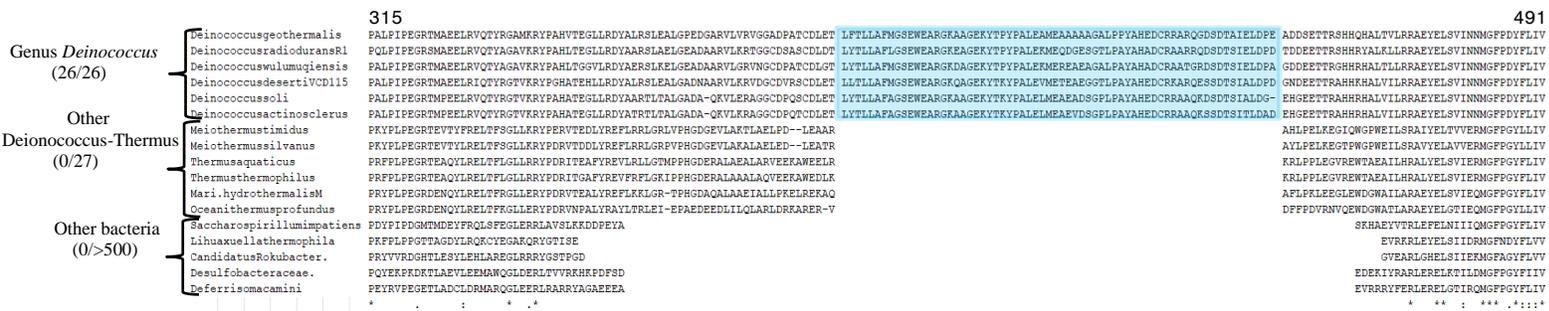


Figure S11. Partial sequence alignment of conserved region of DNA polymerase III alpha (DnaE) protein showing a 65 amino acid insertion that is uniquely shared by all *Deinococcus* group of bacteria.

		499848670	75	131	
Genus <i>Deinococcus</i> (24/26)	<i>Deinococcus geothermalis</i>	499848670	FYNYSQLGVKPILGYEAYV	VP GFGTRRDKKPGVSGEKGIFHLTLLARDFTGYQNL	
	<i>Deinococcus murrayi</i>	653254503	-----M-----	-----E-----	
	<i>Deinococcus ficus</i>	653266326	----TGM-----	---Q---RTR-QD-----E----	
	<i>Deinococcus gobiensis</i>	504498818	----TGM----I-----	---Q---RTR-QD-----E----	
	<i>Deinococcus maricopensis</i>	503320977	----TGM----I-----	---V---ERTR-QD-----E----	
	<i>Deinococcus radiodurans</i>	499189612	----MGME----I-----	-----RSRAQD-----E----	
	<i>Deinococcus actinosclerous</i>	1011240344	----TGM----I-----	---E---RTRAQD-----E----	
	<i>Deinococcus grandis</i>	972312411	----TGM----I-----	---E---RTRAQD-----E----	
	<i>Deinococcus wulumuqiensis</i>	516483568	----MGME----I-----	---M---RSR-QD-----E----	
	<i>Deinococcus deserti</i>	502016316	----QAA----I-----	---Q---RTRAQD-----E----	
	<i>Deinococcus peraridillitoris</i>	505048928	----L-M-----	AA-S-F-R---E---T-----E----	
	<i>Deinococcus pimensis</i>	653296196	----VSM----I-----	AA-S-H-R---E---T-----E----	
	Other Deionococcus-Thermus (0/27)	<i>Thermus brockianus</i>	1103714457	--RK-TE-----	AAES-H-R-R-KGLDG-Y-----K-R----
		<i>Thermus igniterrae</i>	516808234	--RK-TE-----	AAES-H-R-R-KGLDG-Y-----K-R----
<i>Thermus thermophilus</i>		499546976	--KK-TEM-I-----	AAES-F-R-R-KGLDG-Y-----K-----	
<i>Thermus parvatiensis</i>		495906241	--KK-TEM-I-----	AAES-F-R-R-KGLDG-Y-----K-K-----	
<i>Thermus islandicus</i>		551066077	--KK-TEM-I-----	AAES-F-R-R-KGLDG-Y-----K-R-----	
<i>Thermus amyloliquefaciens</i>		740213346	--KK-TSM-----	AAES-Y-R-R-KGLDG-Y-----K-R-----	
<i>Meiothermus chliarophilus</i>		916697201	--K-TEAE----I-----	AADS-F-R-Q-KGLDG-Y-----K-E-----	
<i>Meiothermus rufus</i>		1181339566	--K--EM----I-----	AAES-F-R-Q-KGLDG-Y-----QNMQ-----	
<i>Meiothermus timidus</i>		517277716	--K-TEAE----I-----	AAES-F-R-Q-KGLDG-Y-----K-E-----	
<i>Meiothermus silvanus</i>		908633755	--K-TEAE----I-----	AAES-F-R-Q-KGLDG-Y-----K-E-----	
<i>Meiothermus ruber</i>		738244534	--K-TE----I-----	AA-A-F-PEQ-KGLDG-Y-----QNM-----	
<i>Marinithermus hydrothermalis</i>		503468711	--KK-TAA----I-----	AAES-F-R-M-KGLDG-Y---I--EN-----	
<i>Oceanithermus profundus</i>		503223813	--KK-TAA----I-----	AAES-F-RTMRKGLDG-Y-----K-K-----	
Other bacteria (0/>500)		<i>Chloroflexi bacterium</i>	1125312738	--VA---A----I-V---I	ARQS-F-RD-RIE-HGKP---V---K-----
	<i>Pirellula staleyii</i>	502675500	---K-KA--IN--I-----I	AP-S-FE--DAANSKEASY-----QNRQ-FK--	
	<i>Rhodopirellula baltica</i>	499431723	--RK-KDA-IN--I-----I	AP-S-F--GGAS-SKAASY-----QNR--FK--	
	<i>Opitutaceae bacterium TAV5</i>	918203265	---E-KKA-I--LV-C-L--	AP-S-LE-AGKSEDG-NYY--G---NI-----	
	<i>Clostridium sp. Marseille-P253</i>	1054809256	--RA-KAA-I-----C-V--	AP-S-F--EA-G---DRYY--V---ENDL--H--	
<i>Opitutaceae bacterium TAV1</i>	494601190	---E-KKA-I--LV-C-L--	AP-S-LE-AGKSEDG-NYY--G---NI-----		

Figure S12. Partial sequence alignment of conserved region of DNA polymerase III alpha (DnaE) showing a 2 amino acid insertion that is a distinctive characteristics from homologs of *Deinococcus* group of bacteria. Two *Deinococcus* spp. do not contain this CSI.

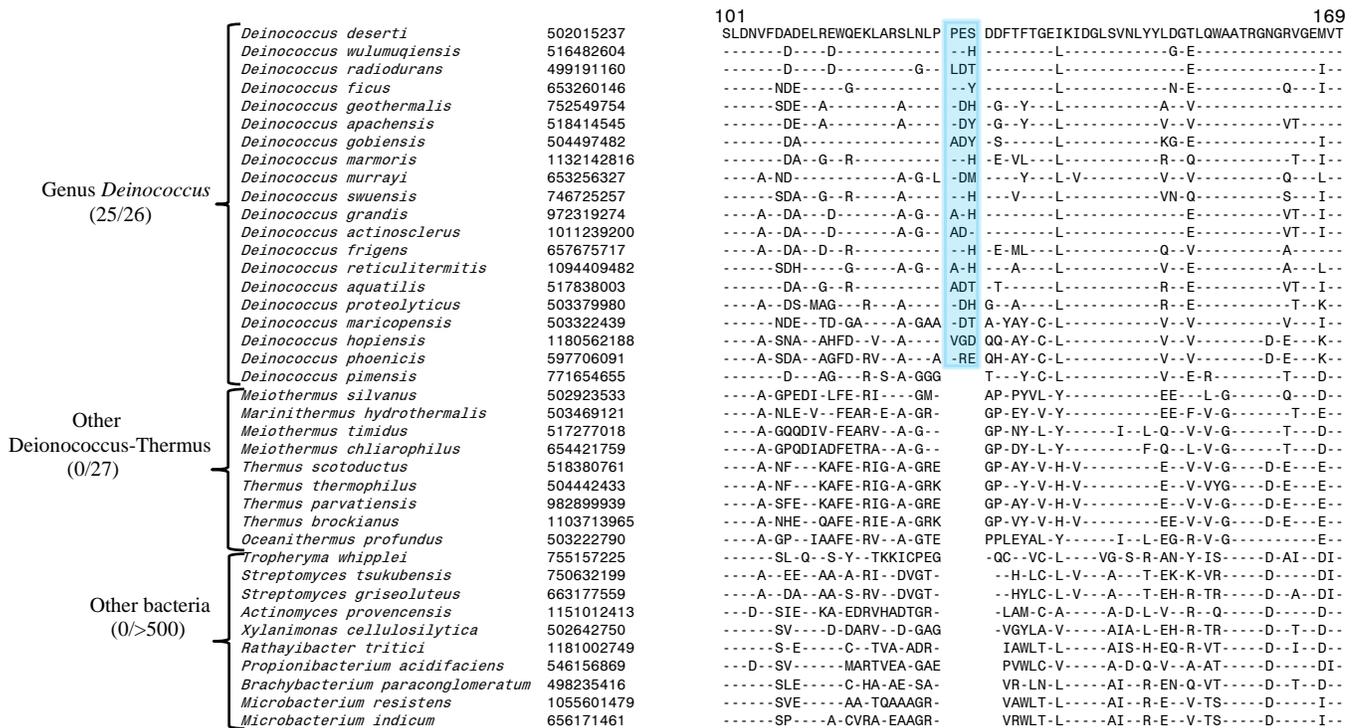


Figure S13. Partial sequence alignment of conserved region of NAD (+)-dependent DNA ligase (LigA) protein showing a 3 amino acid insertion that is uniquely shared by the *Deinococcus* group of bacteria. *Deinococcus pimensis* does not contain this insertion.

		265	341
Genus <i>Deinococcus</i> (26/26)	<i>Deinococcus wulumuquiensis</i>	516481209	NKTNLLQTISAMYKAGKIPDIGALRDESDR K EPVRVIELKRSA AG MGTLVLNQLYKYTLQSSYTVMNLISVNGEP
	<i>Deinococcus radiodurans</i>	499191008	-----S-----D---V---G-L-----F-----
	<i>Deinococcus reticulitermitis</i>	1094409587	-----S-----D---V---G-L-----F-----
	<i>Deinococcus gobiensis</i>	504497349	-----S-----D---V---G-L-----F-----
	<i>Deinococcus geothermalis</i>	499849419	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus murrayi</i>	653256151	---I-----A-----D---V---G-L-----F-----
	<i>Deinococcus aquatilis</i>	517839262	-----S-----D---V---G-L-----F-----
	<i>Deinococcus maricopensis</i>	503322881	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus phoenicis</i>	736330843	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus apachensis</i>	518415676	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus marmoris</i>	1132144081	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus swuensis</i>	746725649	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus deserti</i>	502015264	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus actinoscleris</i>	1011238718	---I-----A-----D---D---G-L-----F-----
	<i>Deinococcus frigens</i>	657674351	---I-----S-----D---V---G-L-----F-----
	<i>Deinococcus peraridilitoris</i>	505047105	---I-----AR-T-----D---V---G-L-----F-----
<i>Deinococcus misasensis</i>	736314419	---S-VS---RQ---S-----R-----D---GT-----	
Other Deinococcus-Thermus (0/27)	<i>Truepera radiovictrix</i>	502943435	---S-I---AAGLVRSKR-E-ANI-----QGM---F---G-HPE-----TFS-N-A-DRS-
	<i>Marinithermus hydrothermalis</i>	503469154	--AH-ISQ-ASLVR-K-E-A-----QGL-A---G-NPDV---F-H-N-T-F-NM-A-D---
	<i>Oceanithermus profundus</i>	503222856	--AS-ISQ-ASLVR-K-LE-SG-----QGM-----G-NPDV---F-Q-N-T-F-INM-A-----
	<i>Thermus igniterrae</i>	516808786	--AS-IAQ-A-LV-K-E-V-----QGL-A---G-NPDV---H-A-T-F-NL-A-----
	<i>Thermus tengchongensis</i>	740198218	--AG-IAQ-A-LV-K-E-V-----QGL-A---G-NPDV---H-A-T-F-NL-A-----
	<i>Thermus scotoductus</i>	740230202	--AG-IAQ-A-LV-K-E-V-----QGL-A---G-NPDV---H-A-T-F-NL-A-----
	<i>Thermus aquaticus</i>	927054606	--AG-IAQ-A-LV-K-E-V-----QGL-A---G-NPDV---H-A-T-F-NL-A-E---
Other bacteria (0/>500)	<i>Thermus thermophilus</i>	499486770	--AS-IAQ-A-LV-K-E-VG-----QGL-A---G-NPDV---H-A-T-F-NL-A-D---
	<i>Ignavibacterium album</i>	504371778	--S-IEK-AELVRE--D-SNI-----DGL-----D-OP-V-----H-M-VTFG-IM-AL-H-V-
	<i>Clostridium colicanis</i>	1008196356	--AK-IES-A-LV-DK-NG-SD-----GM-----D-NANI-----H-KM-D-FGIIM-AL---
	<i>Elusimicrobium minutum</i>	501382623	---IEA-AGLV-DK-VT-ADI-----RGM-L---V-DG-DARV---H---H---T-FS-NM-A-D-R-
	<i>Geoglobus acetivorans</i>	851165112	--A-VEK-AGLARD---EE-KTV-----GI---V---NG-NAGV---R-----TTFGII-AL-DNQ-
	<i>Anaerolinea thermophila</i>	973085201	---T-IER-AELVRSR--E-SD-----TGM--IL-----OPKR---R-----TFGINM-AL-D---
	<i>Gracilimonas tropica</i>	521071534	--ST-I-K-AGLVNDE--TE-SEV-----GI---I-----NAGV-----M-TTFG-I-AL-K-R-
	<i>Rhodohalobacter halophila</i>	1060736857	--AT-I-K-AQLVSDE--T-SEI-----GM---I-----NAGV-----M-QTFG-I-AL-Q-R-
<i>Lachnospiraceae bacterium</i>	1088797531	--A-IKN-ADLV-TK-EG-TD-----GM-----RHD-NANI-----F-H-M-DTFG-IM-L---	
<i>Chloroflexi bacterium</i>	1084617322	---T-IER-AELARK--LD-TD-----RGM-S-IV-----QPRK-----TFGAQM-AL-E---	
<i>Levilinea saccharolytica</i>	1011525517	---T-IER-ADLVRE-R-DA-SD-----KGM-----R-G-EPHK-----P---TFG-NM-AL---	

Figure S14. Partial sequence alignment of conserved region of DNA gyrase A (GyrA) protein showing a 1 amino acid insertion that is uniquely shared by all *Deinococcus* group of bacteria. This sequence alignment also contains a 2 amino acid insertion which is only specific for *Deinococcus radiodurans* and *Deinococcus wulumuquiensis*.

		27	99
	<i>Deinococcus deserti</i>	502015605	GGTGIDGYHQLLTEIIDNGIDELAGFATEVHVIMHADGSATVDDGRG
	<i>Deinococcus reticulitermitis</i>	1094409537	-N-Q-----A-----S-I-E-----
	<i>Deinococcus grandis</i>	972320201	---A-----N---I---L---A---N---
	<i>Deinococcus actinoscleris</i>	1011238675	---A-----N---I---L---A---N---
	<i>Deinococcus geothermalis</i>	499848956	---S-I-K-LE-----A-----N---
	<i>Deinococcus puniceus</i>	1177843460	---A---K-LE-----A-----N---
	<i>Deinococcus radiodurans</i>	499190011	-N-Q-----G-IQIVL-----
	<i>Deinococcus gobiensis</i>	504497181	---H-TM-----V-----RIT-----S
Order <i>Deinococcales</i> (27/27)	<i>Deinococcus aquatilis</i>	517840584	---A---I-K-LE-----A-----N---
	<i>Deinococcus wulumuqiensis</i>	516480581	-N-Q-----N-IEIVL---A---N---
	<i>Deinococcus ficus</i>	916700316	---A-Q-----A-T-VL---T---N---
	<i>Deinococcus swuensis</i>	746727776	---A---K-LE-----V---A---T---D-I-----N---
	<i>Deinococcus marmoris</i>	657680678	---A---K-LE-----V---A---T---D-I-----N---
	<i>Deinococcus apachensis</i>	518414744	-D-SS-I-K-LE-----V---A---G-----N---
	<i>Deinococcus maricopensis</i>	503321958	---Q-I-K-LE-----DTIQ-----I-N---
	<i>Deinococcus phoenicis</i>	736328517	-N-SS-I-K-LE-----V---A---G---D-----N---
	<i>Deinococcus proteolyticus</i>	503380341	---S-I-K-LE-----A-----N-IT-T-E-----N---
	<i>Deinococcus murrayi</i>	653253899	-D-SS-I-K-LE-----A---G---D-----N---
	<i>Deinococcus hopiensis</i>	1180559004	-D-SS-I-K-LE-----A---G---D-----N---
	<i>Deinococcus pimensis</i>	653297875	-N-SS-T-K-LE-----V---A-----T-TF-E-A---N---
	<i>Deinococcus peraridilitoris</i>	505049945	-N-SS-T-K-LE-----M---A---Y-N-T-TF---A-V---N---
	<i>Deinococcus misasensis</i>	736317881	-N-SN-R---LE---E---I-----V---A-----D-T-TL-K---VS---N---
	<i>Truepera radiovictrix</i>	502942889	---S-K-K-LEG---A---A---H-DT-E-VLNP---A-N---
	<i>Enterococcus faecium</i>	816126482	-D-SQ-Q---LE-----I-S-SSE-L-H-VW-V-S---V-----KI---IEK-N-I-I---
	<i>Juglans regia</i>	1098851128	-GS-Q-Q-Q-L-P-----I-S-PR-L-H-VY-L-L-AV-AQ---SKID-L---VSI-N---
	<i>Marinithermus hydrothermalis</i>	503468403	-D-SS-K-K-LEG---A-I-A---T---S-L-AV-A---Y-N-IK-TL---S-E-N---
	<i>Thermoleophilum album</i>	1093218931	-S-Q-T---LE-----I-S---R-L-H-IY-VV-SV-A---CD-IEIVI-P-AV---N---
	<i>Lactobacillus sharpeae</i>	938894560	-D-SQ-Q---LE-----I-S-VQ-L-H-VW-----A---TIN-VEP-N-I-----
	<i>Clostridium botulinum</i>	409742686	-DESQ-Q---LE-----I-S-SLR-L-H-VY-V-S---A---C-HIE-FI-K-N-I-V-----
	<i>Clostridium butyricum</i>	940832684	-DESQ-Q---LE-----I-S-SLR-L-H-VY-V-S---A---C-HIE-FI-K-N-I-V-----
Other bacteria (0/>500)	<i>Enterococcus faecium</i>	695584429	-D-SQ-Q---LE-----I-S-SSE-L-H-VW-V-S---V-----KI---IEK-N-I-I---
	<i>Emiliana huxleyi</i>	551625470	-G-EQ-T---LEP-----I-S-SR-L-H-VF-VV-SV-A---W---N-TI-S-AIS-S-----
	<i>bacterium F16</i>	1202073469	-SGE-K---LE---S-I-D-EA-F-H-VS-VV-S---A---YC-KIE-INE---LS-Q-----
	<i>Hassallia byssoidea</i>	746979532	-S-Q-Q---LEP-----I-T-PK-L-H-VY-VV-SV-A---YC-H-E-EIN---V-----
	<i>Lactobacillus equigenerosi</i>	949563033	-D-SQ-Q---LE-----I-S-TVQ-L-H-VW-V-----A---IN-TVE-N-I---N---
	<i>Vitrella brassicaformis</i>	873225880	---Q-T---LEP-----I-S-VT---H-VW-VV-AV-A---HCNHI-INL-T---VS-S-N---
	<i>Gossypium hirsutum</i>	1029128219	-NSEQ-Q---L-P-----I-S-PR-L-H-VY-L-L-AV-AQ---QID-VL-S---VSI-N---
	<i>Planktothrix agardhii</i>	653002254	-S-Q-Q---LE-----I-S-PR-L-H-VY-VV-A---A---YC-HIEIDFN-N-V-----

Figure S15. Partial sequence alignment of conserved region of DNA gyrase subunit B (GyrB) protein showing a 1 amino acid insertion that is specific for all *Deinococcus* group of bacteria.

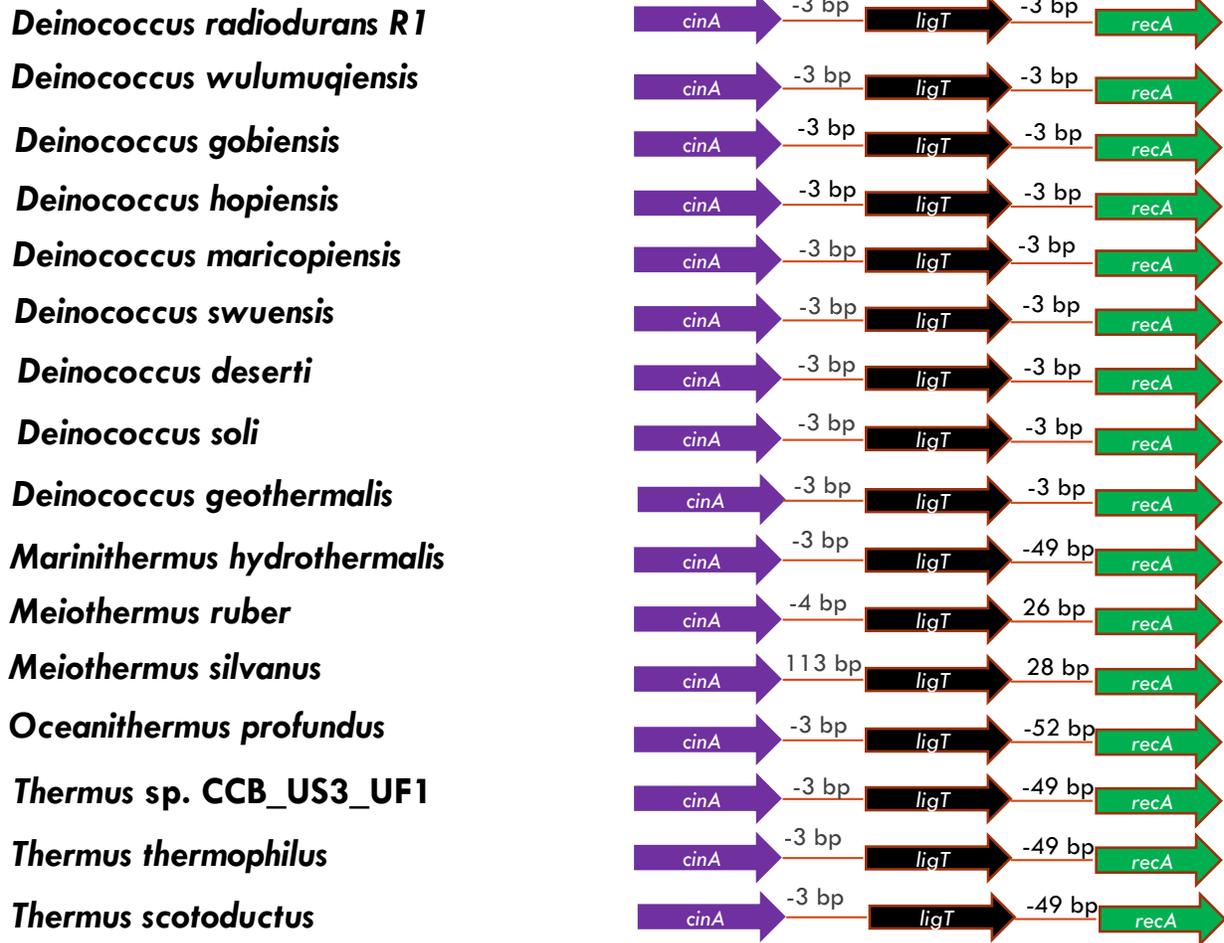


Figure S16. Diagrammatic representation of genomic neighborhood analysis result of DNA recombination protein RecA for representative *Deinococcus*-*Thermus* spp. Gene of RecA protein is present in a genetic linkage with genes of LigT and CinA proteins throughout all *Deinococcus*-*Thermus* spp. The intergenic distance among them is less than 200 bp and is present in the same direction. Genes of RecA, LigT and CinA proteins should be present in same operon among *Deinococcus*-*Thermus* phylum.

(A)

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109      CXXC      131 175      CXXC      191 197      CXXC      229
Deinococcus radiodurans RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACGDCAGIG SEFMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus maricopensis RLLYARVGTPTPIGGRKIERQ FSNFSPYGACGDCAGLG SEYMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus gobiensis RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACPDACAGLG SDFMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus phoenicis RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACPDACAGLG SEFMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus geothermalis RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACSDCAGLG SDFMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus deserti RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACGDCAGLG SEFMREKLEELMELRPPCTCGGTRYKPEILAV
Deinococcus grandis RLLYARVGTPTPIGGRKIEKQ FSNFSPYGACGDCAGLG SDFMREKLEELMELRPPCTCGGTRYKPEILAV
Mycobacterium sp.1465703.0 RLLYARAGTPHCPICGERIARQ FSNFSPYGACPECSGLG SEOMKERYEGFMRDVP CPVCEGTRLKPEILAV
Modestobacter marinus RLLYARAGQPHCPNCGKPISRQ FSNFSPFGACPECTGIG SEFMKDKYEGYMRDVP CPVCHGTRLKPEILAV
Eggerthella lenta RLLFARVGVPHCEGGRVIKQ FSNFNPYGACPDCLGIG SDAQREKLASYFAIVP CPCTGGKRLKPEILAV
Meiothermus timidus RLLFARVGTAFCPHCGRPIERQ FSNFNPYGACPDCSGLG SEGLREAL EAYMTLQCPACSGTRYKKEVLSV
Meiothermus cerbereus RLLFARVGTAYCPHCGRPIERQ FSNFNPYGACPDCSGLG SESLREAL EAYMTLKACPCACGGTRYKREVLVS
Meiothermus ruber RLLFARVGTAYCPHCGRPIERQ FSNFNPYGACPDCSGLG SEGLRETLEAYMTLKACPCACGGTRYKREVLVS
***:***. * ** * * : * ** * : *** : * * * * : : ** * * * * * : ** *
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The other two CXXC motifs in this protein are shown in Figure 8

(B)

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228      CXXC      272
Deinococcus radiodurans DGEQGGFQHSHHVYGRAGQPCDRCGTPIEKIVLQGRGTHFCPVCCQ
Deinococcus misasensis DGNPAYFQFEHMYAREGEPQRCQQPIAKYWLQQRGTHHCPCNCQ
Deinococcus peraridilitoris NGEQGWFRHNVYARKGKACARCGGTIEKIVLQGRGTHFCPECCQ
Deinococcus maricopensis DGLSGLFQQQHNAYARDGEP CARCGTTITKSVLAQRGTHHCPCACQ
Deinococcus geothermalis DGAVGFFQGGHAYVGRGTLGQLCPRCGTPIQKMLVLAQRGTHFCPCACQ
Deinococcus frigens DGVSGLFQHEHHVYKGGQPCPRCGTDIVKTVLAQRGTHFCPKCCQ
Deinococcus deserti DGVSGLFQFSHRAYAREGQPCERCSTSEKIVLQGRGTHFCPCQCQ
Deinococcus soliChaetal.2016 DGLSGLFQHAHVYKGGQPCPRCGTPIEKISVAQRGTHHCPCQCQ
Deinococcus gobiensis DGEQGGFQGRHQAYGRAGQPCARCGTPIAKIVLQGRGTHFCPCQCQ
Deinococcus reticulitermitis DGEQGGFQHAHRVYKAGQPCARCGTPIQKVVLAQRGTHFCPCQCQ
Deinococcus wulumuqiensis DGEQGGYQTRHHAYGKTGQPCERCSTSEKIVLQGRGTHFCPCACQ
Marinithermus hydrothermalisDSM DGALGRFQVQHKVYGRPGAPCVRCTGPIEKIVLQGRGTHFCPCRCQ
Thermus thermophile DGLPGGFQTRHAYVYGRGLGCPACGRPVERRVAGRGTHFCPTCCQ
Thermus scotoductus DGLPGSFQMRHAYVYGRGLGCPVCGTPIAKRVVAGRGTHFCPCRCQ
Morganel lamorganii DGKPGYFAQELFVYQKQGCCANCGQKIEVVVQGRSTFFCPACQ
Streptococcus parasanguinisATCC FGEDGTMQEEHQVYGKTGQPCLCRCGTPIEKIQLGGRGTHFCPHCCQ
Carnobacterium pleistocenium LGEAGTFQMKLAVYKGGIPICRCGTPIEKIKVAQRGTHFCNSCCQ
Enterococcus canis LGEAGFKQLSLNVYQGTGNPCPRCGTPIQKIKVAQRGTHFCPCNCQ
Enterococcus gallinarum LGEAGHFQVSLHVVYQGTGNPCVRCGTPIVKTIVAQRGTHFCPCFCQ
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(C)

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190      CXXC      229
Deinococcus radiodurans NEAVMDLGATICVPKSPACDRCPVSAHCAAYLQGGPDDFP
Deinococcus deserti VCD115 NEALMDLGATICTPRSPRCDQCPVSKYCAFAEGRPAAYP
Deinococcus wulumuqiensis NEAVMDLGATVCPKSPACDRCPVSAHCAAYRLGRPSDFP
Deinococcus hopiensis NEAVMDLGATVCTPKVPKCPDQCPVSLWCAAFQSGQPAAYP
Deinococcus geothermalis DSM1130 NEALMDLGATVCTPKAPKCGECLRRWCAAFQGDPAAFP
Deinococcus phoenicis NEAVMDLGATVCTPKAPKCGACPVSAWCAALGSGEPAAFP
Deinococcus apachensis NEAVMDLGATICTPRAPKCGECPVRAWCAAFASGHPAAFP
Deinococcus aquatilis NEAVMDLGATICTPKAPRCAVCPLAAWCEARASGQPTAFP
Deinococcus marmoris NEAVMDLGATVCTPKAPRCAECLSAHCAAFKRGTPAFP
Deinococcus swuensis NEAVMDLGATVCTPRAPRCECPLAARCAARASGTPAFP
Thermus thermophilus NQALMELGATVCLPKRPRCGACPLGAFCRG--KEAPGRYP
Meiothermus rufus NQALMELGATVCTPRKPNCPGQPLVTFCRG--QGQPERYP
Meiothermus ruber DSM1279 NQALMELGATVCTPONPGCGGCPVAAFCRG--KASPAHYP
Meiothermus taiwanensis NQALMELGATICTPONPGCGGCPVAAFCRG--KASPAHYP
Meiothermus timidus NQAMMELGATLCTPQKPACTSCPLARWCAG--QASPERYP
Lentisphaeria bacterium TMED266 NEALMELGATVCLPQNPSCDVCPSTACQAKLLDDVSRFP
Nitrospina gracilis 3/211 NQSLMELGATLCLPQNPMCLLCPVQHCHEARHQGEPEKFP
Rhodothermus marinus SGO.5JP17-1 NQALMELGATVCTPVQPRCSACLPRRACRAWAMGDPTAFP
Ardenticatena maritima NQALMDVGAIEICTPRSPRCLLCPVQTHCAAAHQHQHDL
Synechococcus sp.PCC8807 NQALMDLGATLCTAKTPACPRCPQNHCTAYLKHQPTDFP
Geitlerinema sp.PCC7105 NQAFMDLGATLCTPONPACLCLCPWRESCQAYNLDLQSEL
Truepera radiovictrix DSM17093 NEALMELGALVCTARAPQCPRCPPVQAHCGAYQGGAVARFP
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(D)

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187
Deinococcus radioduransR1 PV DGNMERA AKRLEL VPA A WNSHKVERWYAEVMPADWETRFALHISGVRHGRDTRCSKHP CXXC 254
Deinococcus geothermalis PIENNIHRVAGRLDLFSPSRWNVKAERWFDEVLPRDWLDRATFHVSAIRHGRQTRCAQRPR CXXC VLR
Deinococcus marmoris PV DTHIHR IARRLEL VPA E A WNAVKVERWFDEVLPREWAARYTFHVSAIRHGRQTRCRANPA CXXC VLR
Deinococcus puniceus PV DTHIGRIAARLEWVPARWNAIKVERWFDEVLPRDWASRYGFHVSAIRHGRETRCAQRPD CXXC VLR
Deinococcus aquatilis PV DTHIGRIAARLEWVPARWNAIKVERWFDEVLPRDWPSRYGFHVSAIRHGRETRCAQRPL CXXC VLR
'Deinococcus soli'Chaetal.2014 PV EGNLDR LARLEWVPDTWTGARVERWFDATVPRTTDR LRLHVAGVRHGREVCLSRHP CXXC VLA
Deinococcus reticulitermitis PV DGNMERA AKRLEL VPA G WSSDRVERWYDEAAPRDWETRFALHLSGVRHGRVTRCPORPL CXXC VLR
Deinococcus wulumuqiensis PV DGNMERA AKRLEL VPA A WNSHKVERWYAEVVPDWDWETRFALHISGVRHGRDTRCSKHP CXXC VLR
Deinococcus ficus PV DGNIER TLKRLEFVPPNWSAERTERWFDVRSREWALRAALHVAGVRHGRHTCLPRNP CXXC VLR
Deinococcusd eserti PV DTHIHR IARRLEL VPA Q RWTPKVERWFDVAVRRDWAERATFHVAGVRHGRHTCRPRDP CXXC VLR
Aminomonas paucivorans PV DTHVAR ICRRLGWVPANLPPHRIQRVMEETVARER - - FQGAHLNLIAHGRAVCRARSPR CXXC VLR
Aminobacterium colombiense PV DTHIHRFSKRIGWAHDKRCKPEEIEGMLQVVP EER - - YLGGHINIITHGRNICLAROPR CXXC SVN
Acetomicrobium thermoterrenum PV DTHVNRLCKRIGWSPKSTPEETQKIMGSVIPSDL - - YWSAHLDIISHGRNICVSRRP CXXC VLR
Actinobacteria bacterium PV DTHVYRVGKRLGIPTKASVEKAHALMDRLVPDDI - - KYRLHVNLDVHGRRIICVARKPK CXXC VLR
Dehalococcoidia bacterium PV DTHVYRVARRLGLVPPRVGAAEHGLLESMLTPDE - - VYPFHMSLIKHGRRICKAQRPL CXXC VLA
Chloroflexi bacterium PV DTHVFRVARRLGLLHKSVAEQAEHILENLIPAGQ - - VYEFHLMVHEGRVKCAQRPR CXXC VLR
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(E)

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734
Deinococcus radiodurans CXXC CLCCGKRT - - - QLQVDHIQSRYAGGTHLDNLQLL CXXC 773
Deinococcus frigens CLCCGKRT - - - RLQVDHIQPRYLGGSDHTENLQTL CXXC VLR
Phormidium ambiguum IAMM-71 CLCCGEDS - - RNVLVIDHIIPRYHGGTHSLDNLQTL CXXC VLR
Methanobacterium congolense CLCCGEEK - - KKLLEVDHINPRYFGGNSIDNLQTL CXXC VLR
Methanobacterium formicicum CLCCGEDH - - KQILEVDHVNPRYMGKDSIENLQTL CXXC VLR
Methanosaeta harundinacea CLCCGTTK - - RSFLQVDHIDPRYLGGSNPENLQTL CXXC VLR
Chondromyces crocatus CLACGSNR - - TLQVDHIIPVYHAGSHEPDNLQTL CXXC VLR
Sorangium cellulosum CLACGTRT - - NLNADHVAVVYGGSNVGNLQTL CXXC VLR
Pseudanabaena biceps PCC7429 CLCCGDH - - RRLQVDHVFPFILGGQTSIDNSQTL CXXC VLR
Desulfosporosinus sp.Tol-M CRCCGRELKGIKLEIDHIVPVKMGQTTLENLQIL CXXC VLR
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(F)

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137
Deinococcus radioduransR1 SYKLLGLAGVIPQTAR CXXC CARCGAPDPE - - - HPDPLGGQLL CXXC 182
Deinococcus deserti VCD115 SYKLLGLAGMVPQTAR CXXC CARCGOPDPA - - - HPDPLAGQLL CXXC VLR
Deinococcus gobiensis I-0 SYKLLGLAGIVPQTAR CXXC CARCGEDHPA - - - HPDPLGGQLL CXXC VLR
Deinococcus aquatilis GFKLLGLAGFVAQTAR CXXC CARCGADQPA - - - HPDPLAGQLL CXXC VLR
Deinococcus apachensis SYKLLGLAGFVLQATAR CXXC CARCGAPDPA - - - YPDP LGGQLL CXXC VLR
Deinococcus geothermalis DSM1130 SYKLLGLAGFVPQTGR CXXC CARCGAAAPT - - - HPDPLGGQLL CXXC VLR
Deinococcus sphaenicis SYKLLGLAGFVPQTAR CXXC CARCGTADPA - - - HPDPLGGQLL CXXC VLR
Amycolatopsis pretoriensis FLRAMSYEGWAPALTE CXXC CARCGLPGP - - - VAFSVPAGGSM CXXC VLR
Streptomyces sp.AA4 FLRAMYAGWAPAI TE CXXC CARCGLPGP - - - AAFNVAAGGSM CXXC VLR
Amycolatopsis decaplanina FLRAMYAGWAPAI TE CXXC CARCGLPGP - - - KAFSVSAGGSM CXXC VLR
Herbidospora mongoliensis FLRSLAVAGYAPAL SE CXXC CARCGAEAV - - - RAFAVAGGVCGT CXXC VLR
Nocardioides dokdonensis FR1436 LLRSLSVAGYAPSFDC CXXC CARCGEQGP - - - RWFNPSMGML CXXC VLR
Truepera radiovictrix DSM17093 GWRLLAQGLAPRLAR CXXC CARCGGLEGSSEGRFDVAAGLS CXXC VLR
Deinococcus proteolyticus SYKLLALAGFPQTRM CXXC CARCGAADPQ - - - HPDPFGGQLL CXXC VLR
Deinococcus wulumuqiensis SYKLLGLAGVIPQTAR CXXC CARCGAPEPQ - - - HPDPLGGQLL CXXC VLR
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(G)

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23
Deinococcus radiodurans KSAQRLAFHLFEQPREIERLASALLEAKRDLHV CXXC CFCFNITDAEK CXXC 109
Deinococcus wulumuqiensis KSAQRLAFHLFEQPREIERLASALLEAKRDLHV CXXC CFCFNITDAEK CXXC VLR
Deinococcus frigens KSAQRLAFYLFEQPREIERLAGSLLSAKRDLS CXXC CFCFNITDAER CXXC VLR
Deinococcus geothermalis DSM1130 KSAQRLAFYLFEQPREIERLAGAILLEAKRDLS CXXC CFCFNITDAER CXXC VLR
Deinococcus gobiensis I-0 KSAQRLAFHLFEQPREIERLASALLSAKRDLS CXXC CFCFNITDAET CXXC VLR
Deinococcus murrayi KSAQRLAFHLFEQPREIERLAGALLAASSELHT CXXC CFCFNITDAER CXXC VLR
Deinococcus apachensis KSAQRLAFHLFEQPREIERLAGALLEAKRDLS CXXC CFCFNITDAER CXXC VLR
Deinococcus actinoscleris KSAQRLAFHLFEQPREIERLRSALLEAKRDLS CXXC CFCFNITDAER CXXC VLR
Deinococcus grandis KSAQRLAFHLFEQPREIERLRSALLEAKRDLS CXXC CFCFNITDAER CXXC VLR
Butyricoccus desmolans KTAQRLAFHVLDPKEDAEFRADAI REAKART CXXC CKRCQNLTDTE CXXC VLR
Cald anaerobius fijiensis DSM1791 KTAQRLAFYLLNSPREYVESLARAMEAKNKLKY CXXC CFCFNITDAER CXXC VLR
Alkaliphilus transvaalensis KTAQRLAFHVISLSQEEADQLSSAI ISAKRNKY CXXC CFCFNITDAER CXXC VLR
Defluviitalea phaphyphila KTAQRLAFHINMPDENVENLSSAIMEAKNKY CXXC CFCFNITDAER CXXC VLR
Thermoanaerobacterium thermosac KTAQRLAFYILDMPKDDVINLSNAILEAKNKLKY CXXC CFCFNITDAER CXXC VLR
Caldanaerobacter subterraneus KTAQRLAFFIINMPLDVRSLQAI IEAKELRY CXXC CFCFNITDAER CXXC VLR
Thermoanaerobacter kivui KTAQRLAFFIINMPLDVRSLQAI IEAKELRY CXXC CFCFNITDAER CXXC VLR
Ruminococcus callidus ATCC27760 KSAQRLAYSISRPEEDVERFANALLSAKRD CXXC CFCFNITDAER CXXC VLR
Truepera radiovictrix DSM17093 KSAQRLAFYLFNQPEEDVKSALAEALLNAKGN CXXC CFCFNITDAER CXXC VLR
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(H)

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Deinococcus radiodurans          395  CXXC  442
Deinococcus wulumuqiensis        SEPCGNCDVCLNPPVRDLTREAQMSATIRTNRFGA AHLTDVLLG
Deinococcus actinoscleris        PGPCGNCDLCHTPPQVRDLTREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus deserti VCD115       HGPCGNCDTCLNPPQVRDMTREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus swuensis             REPCGNCDVCLSPPRVQDATREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus marmoris            DEPCGNCDTCLNPPVRDATREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus murrayi             NEPCGNCDTCLNPPVRDATREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus phoenicis           PHPCGNCDVCLAPPRVDRATREAQMSAAIRTNRFGA AHLTDVLLG
Deinococcus apachensis          AEPCGNCDVCLNPPVRDRATREAQMSAAIRTNRFGA AHLTDVLLG
Rhodanobacter sp. Soil772       EKPCGNCDVCLNPPVRDRATREAQMSAAVIRTNRFGA AHLTDVLLG
Nitrosomonas nitrosa            PGPCGHCDNCVAPPKTDATVPAQKALSAVYRTGQRFSGHV IDVLRG
Haliea salexigens               PGRCGGCDNCLNPVDTWDATEAARMALSCVYRTGQRFSGAGH IDVLLG
Methylococcus capsulatusstr.Bat  PQACGNCDTCLPVPVTWDTGTEAARMALSAVYRTGQRFVGNH IDVLRG
Methylobacter luteus            ERPCGNCDNCLNPVQTDWDATEAARKALSCVYRSGQRFGAHYV IDLLLG
Thioalkalivibrio sulfidiphilus  AQPCGNCDTCLPVPVTWDTGLAAQKALSCIYRTEQRFGVNYL IDVLLG
Sulfurifustis variabilis       PEPCCNCDTCLPPEPTWDTVAQKALSCVHRTGQRFVGNHVDVLLG
Thermithiobacillus tepidarius  PRPCGNCDTCLDPPETWDTVPAQKALSCVHRTGQRFVGSYLVDVLLG
                                     PAPCGNCDTCLPVPVTWDTGTEAQMALSCVYRTGQRFVTHLEVLQG
                                     **:*** * . * . *: **: *: :*** :: ::**
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(I)

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Deinococcus radiodurans          450  CXXC  483
Deinococcus grandis              RMEAGLASYSRSHLHEGEP CPLCLQTVHEVPEGES
Deinococcus deserti VCD115       RLEAGLASYSRAHLHVGGDD CPLCGGTVTLPDAPR
Deinococcus ficus                 RLEAGLASHRAHLHVGGDD CPLCGGTVQRLPSAPV
Deinococcus gobiensis            QIDAGVAAYRTHLVHVGEP CPLCAQTVRTLPDTPP
Deinococcus geothermali DSM1130  RLTAGLSAYRAHLHVHVEP CPLCEQTVRVLPQASA
Deinococcus murrayi              RARAGLAAYSRSHLHLGEP CPLCGGAVQTLPPPAE
Meiothermus cerbereus            KLOQGLGLYHAHLKQGEPCPLCGHPVENLPPPKP
Meiothermus ruber                 KLRQGI AHYHPHLVKGEPCPLCGHPVAALPPAQP
Meiothermus taiwanensis          KLRQGI AHYHPHLVKGEPCPLCGHPVAALPPAQP
Thermus amyloliquefaciens        ERRRLGLLAYRDLLRPGEP CPLCGGVVHGLPPAPA
Thermus tengchongensis            ERRRLGLLAYRDLLRPGEP CPLCGSVVHGLPPVLE
Thermus arciformis               ERRRLGLLAYHDLRPGEP CPLCGGVVHRVPERPS
Thermus oshimai                   ERRQGLVAYRDLLQVGAP CPLCGGVVHALPEVPO
                                     . *: : *: * **** * *
```

(J)

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Deinococcus radiodurans          3  CXXC  CXXC  41
Deinococcus wulumuqiensis        KVKTNYICNSCGYQSAKPLGRCPNCGAWNSFEEVPTAS
Deinococcus marmoris             KLKTNYVCTSCGYQSAKPLGRCPNCGAWNSFEEVPTAS
Deinococcus frigens              RVTTKYVCNSCGYTSAPKPLGRCPNCGAWNSFEEVPSVT
Deinococcus deserti VCD115       KVRVGYVCNSCGYQSAKPLGRCPNCGAWNSFEEETPAVA
Truepera radiovictrix DSM17093   KVGTTYVCSECGTHSPVKGRCPRCGTWGSMQAQAPAPA
Meiothermus Silvanus DSM9946     RTSTQYRCTACGYKSVKALGRCPNCGAWDSFKEEAPEAP
Meiothermus rufus                 RASIQYRCIECGYKSVKELGRCPNCGAWDSFKEEAPPPK
Meiothermus cerbereus            KPKSQYRCVECGYRAPKSLGRCPGCGAWGSFLEERSDGG
Oceanithermus profundus DSM14977 MKKADYRCVECGYVTPKPLGRCPGCGAWDSFQRTVPDSP
Marinithermus hydrothermalis DSM MAKAYRCVECGYRTPKPLGRCPGCGAWNSFKEEAPSP
Thermus filiformis                MAKTSYTCVECGYRTPKPLGRCPGCGAWSFQVAPSPR
Thermus scotoductus              KITSKFYCKEAGYSAKWLGCPCGCGAWNSFVEEPVAST
Lachnospiraceae bacterium JC7    KITSKFFCKEAGYSAKWLGCPCGCGAWNSFVEEPVAGT
Oribacterium sp.C9                IKITVFFCQSCGYESAKWGGCCPGCGKEWNSFVEETIKPS
Butyrivibrio sp.WCD2001          KQTSVYFCQSCGYESAKWGGCCPGCGHEWNTFVEEPVKA
Lachnospiraceae bacterium P6A3   : * ** : * : ** * * :
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