Table S1. List of primers used in this study.

S.No.	Primer name	Primer sequence	Uses
1	dr0012F	GGAATTC CATATG GTGTCGAAAAAATCTAGCCT	pET28+
2	dr0012R	5'CCGCTCGAG TTATTCCTCGGCCTCGTA3'	pET28+
3	dr0013F	5'GGAATTCCATATGATGACGGACCACGCGGGC3'	pET28+
4	dr0013R	5'CCGCTCGAGCTAGATTTTTTCGACACGTTGCA3'	pET28+
5	Hari12F	5’ CCCCCGAGCTCGTGTCGAAAAAATCTAGCCTG 3’	pDSW209
6	Hari12R	5’ CCCCGGGATCCTTACTCCTCGCGGGAGCCGTAG 3’	pDSW209
7	gfpF	5’ TAGTACTGAGCTCATGAGTAAAGGAGAAGA 3’	pD12GFP
8	ParB1R	5’CCCCTCGAGTTACTCCTCGCGGGAGCCGTAG 3’	pD12GFP
9	Bs1 F	5' CAACCGCTGTTCGCCGCT 3'	*segS1*
10	Bs1 R	5' TCCAACGAAGCGCGCGAA 3'	*segS1*
11	Bs2 F	5' CTTATGCTCGCCCGCTGA 3'	*segS2*
8	Bs2 R	5' CCCCGTTTTCATTTGTCA 3'	*segS2*
9	Bs3 F	5' AGAACCAGCCCGACTGGA 3'	*segS3*
10	Bs3 R	5' ACAGGATGCACTCGTAACT 3'	*segS3*
11	DP1 - F	5' AGCAAGGCGGCCAGCCCGCT 3'	Dp1
12	DP1 - R	5' CTGGCTGTGGCGTCGGT 3'	Dp1
13	Hari 64	5’GGGGTACCCAGCCGTTCCGCAGGAGGA3’	Δ*segN*
14	Hari65	5’ CGGAATTCCGTCAGACGACTTCAAAGCT 3’	Δ*segN*
15	Hari66	5’ GCGGATCCGGGCTCGCCTTTCTTGGTCA 3’	Δ*segN*
16	Hari67	5’CCCCCGAGCTCCCCGCACCCTCATCGCGATGCT 3’	Δ*segN*
17.	CIOF	5’ CG GGATCCATGACGGACCACGCGGGC 3’	pDSW209
18	CIOR	5’ CCCAAGCTTTTATTCCTCGGCCTCGTA 3’	pDSW209
19	CatF	5’GTTAACTGACGGAAGATCACTTCGCA3’	*cat* PCR
20	CatR	5 -GTTAACCACACGGTACATTGCTTCC3’	*cat* PCR
21	XerCF	5’CTAGCTAGCATGACCGATTTACACACCGAT 3’	*xerC* PCR
22	XerCR	CGCGGATTCTTATTTCCCCCGTTTGGCGCG3’	*xerC* PCR

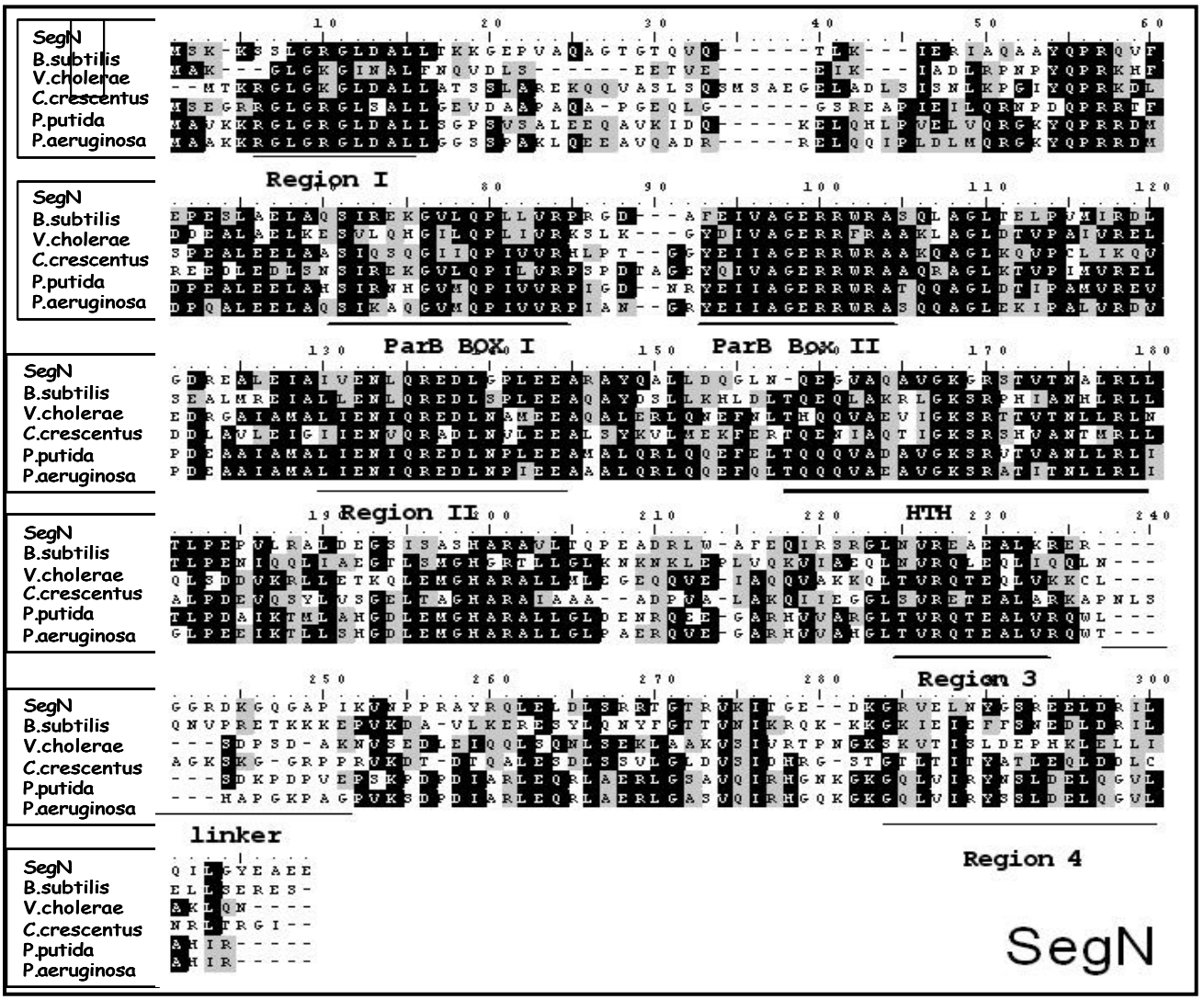

Fig S1 Multiple sequence alignment of ParB (SegN) protein of chromosome 1 with related proteins from other bacteria. The amino acid sequences of putative SegN encoding from DR_0012 ORF of chromosome 1 were subjected to homology search and multiple sequence alignment with related proteins from other bacteria. The SegN showed high similarities with ParBs from other bacteria and showed nearly complete conservation of functional and structural motifs of typical ParB type proteins.

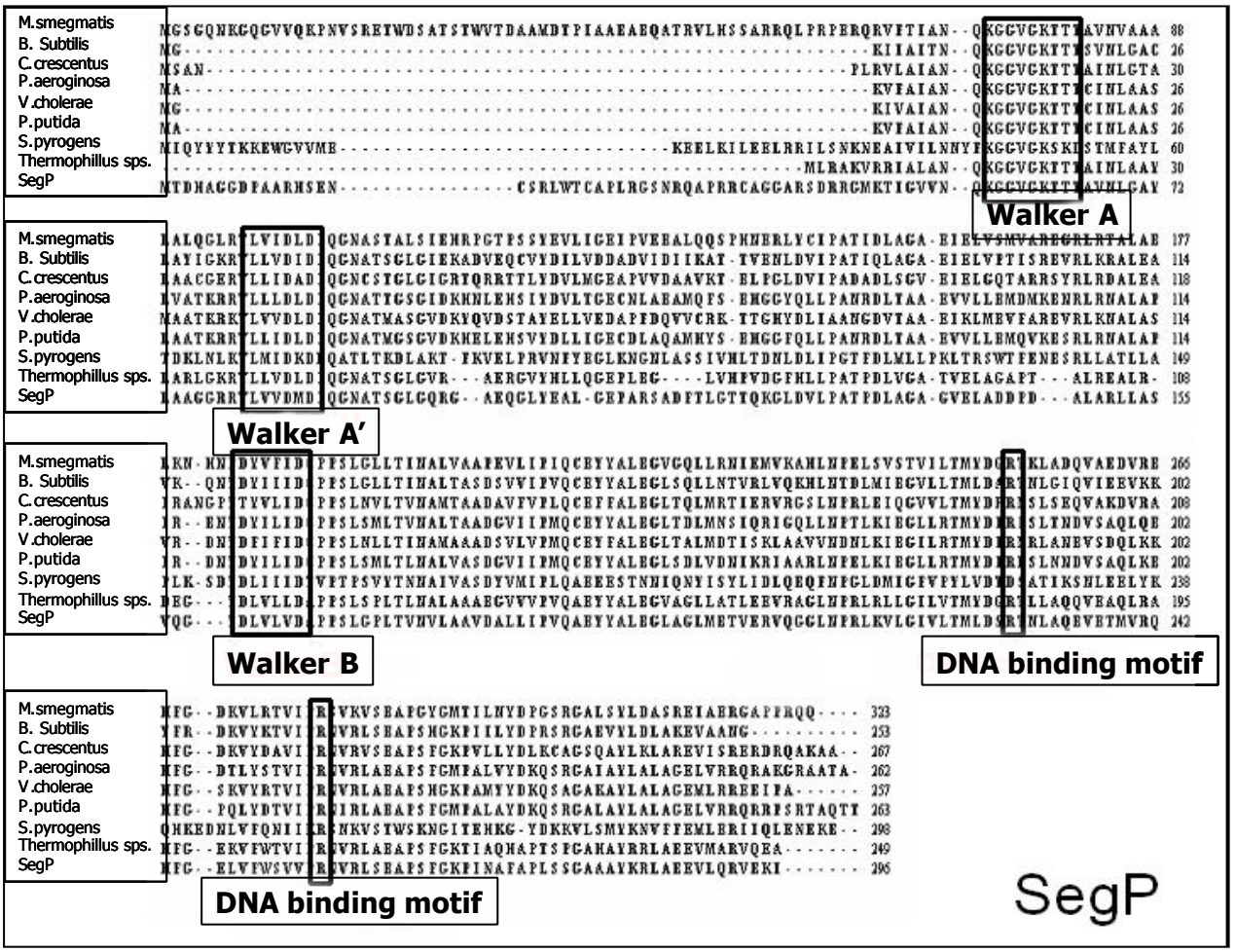

Fig. S2. Multiple sequence alignment of putative ParA (SegP) protein of chromosome 1 with related proteins from other bacteria. The amino acid sequences of polypeptide encoding from DR_0013 were searched for homology with ParAs from other bacteria and the putative SegP sequence was aligned with related proteins. SegP showed both nearly complete conservation of Walker domains and DNA binding domains.

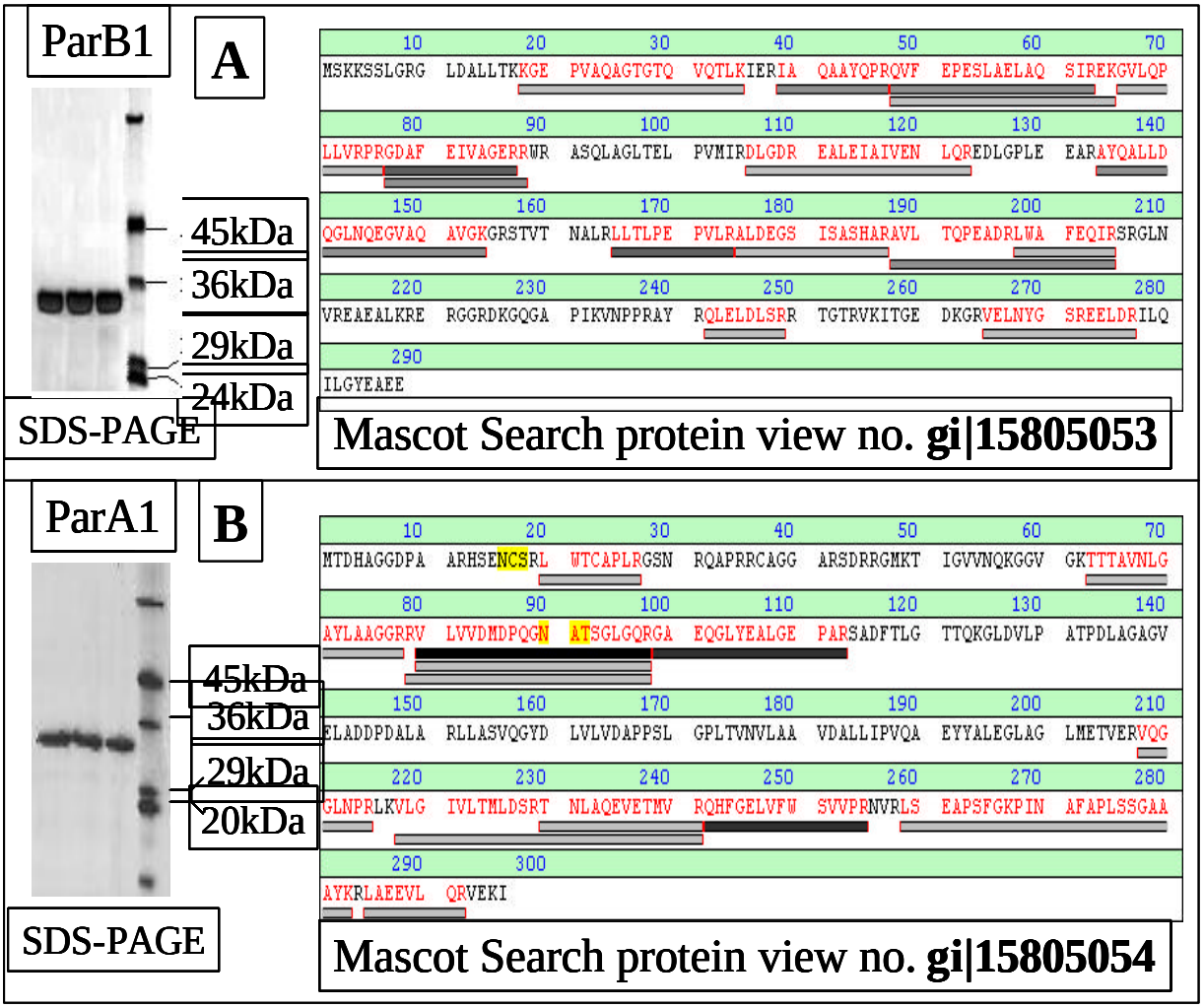

Fig S3. Purification of recombinant ParB1 and ParA1 proteins of *Deinococcus radiodurans* and their identification by mass spectrometry. Transgenic *E. coli* cells expressing recombinant ParB1 and ParA1 were used for purification of these proteins. SDS-PAGE analyses of ParB1 (A) and ParA1 (B) showing the purity of these proteins loaded in triplicates. Coomassie stained protein band was used for MS identification. Peptides detected from MS analysis were analysed using Mascot library. Detailed analyses for both ParB1 and ParA1 are available on-line in protein search accession nos. gi|15805053 and gi|15805054, respectively.

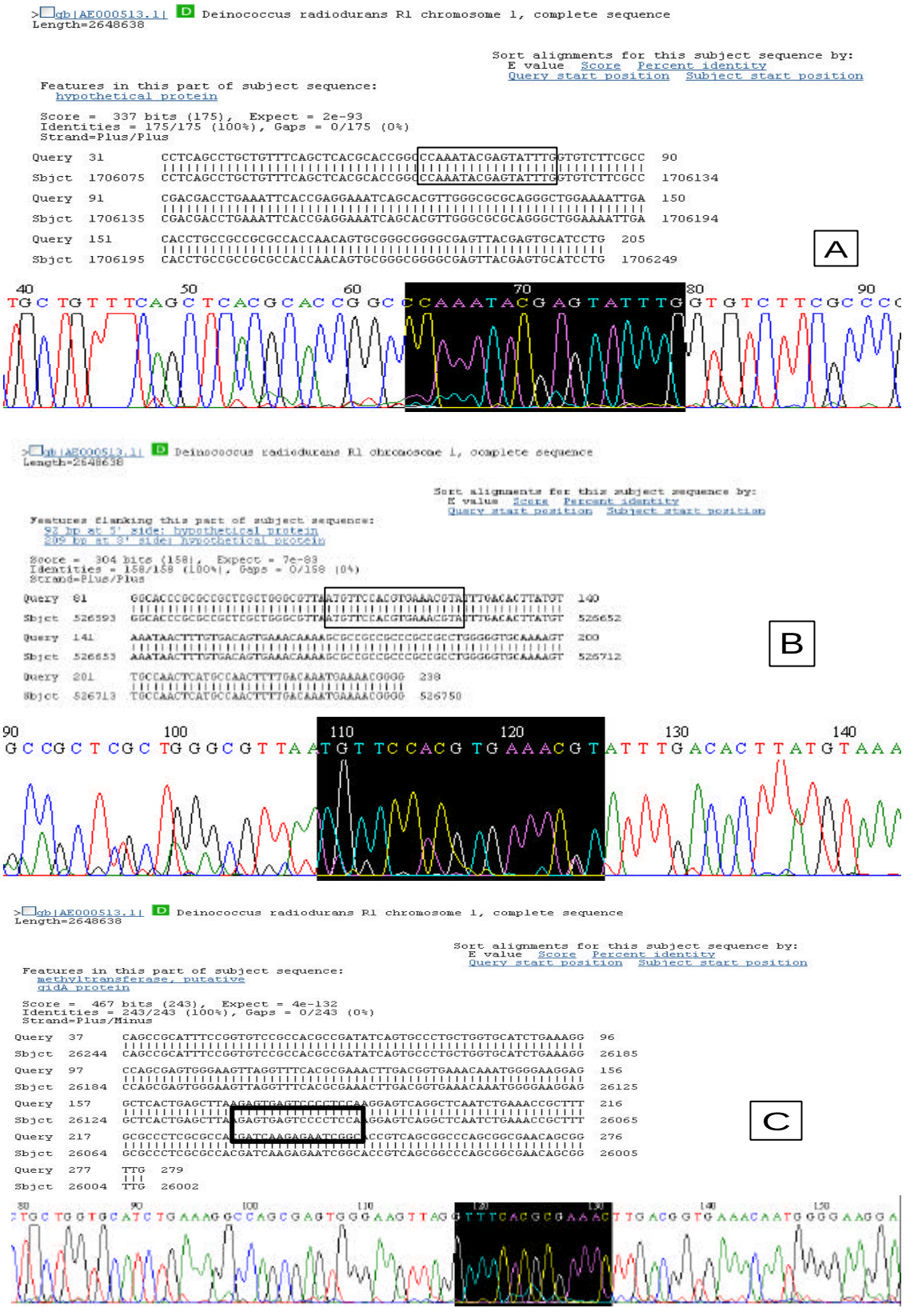

Fig S4. Sequencing of centromeric sequences cloned in mini-F instable plasmid pDAG for checking stability in *E. coli*. The centromeric sequences segS1 (A), segS2 (B) and segS3 (C) cloned in recombinant plasmid pDAGS1, pDAGS2 and pDAGS3 were sequenced directly on plasmid using primers flanking to *segS* elements in these plasmids. Sequences obtained were search for homology search with published sequences.