

Supplementary Material (SM)

Table S1. Spectrophotometer reading (OD_{600nm}) of *B/ 1821L* culture after treatment with the mitomycin C at various concentrations.

Treatments	Time intervals (Hours)					% Decrease in OD _{600nm}
	0	2	4	6	24	
Mitomycin C (1 µg/mL)	1.41	1.44	1.46	1.48	0.71	49.65
Mitomycin C (3 µg/mL)	1.56	1.56	1.57	1.58	0.92	41.03
Control	1.30	1.34	1.47	1.49	1.35	-3.85
*LSD (5%) (Control vs Treated)	0.18	0.15	0.12	0.12	0.37	24.49
LSD (5%) (**MMC1 vs ***MMC3)	0.16	0.14	0.12	0.11	0.34	22.68

Note: *LSD= Least significant digit

**MMC1= Mitomycin C @ 1 µg/mL

***MMC3= Mitomycin C @ 3 µg/mL

Brevibacillus laterosporus 1821L cell free supernatant activity after PEG 8000 precipitation

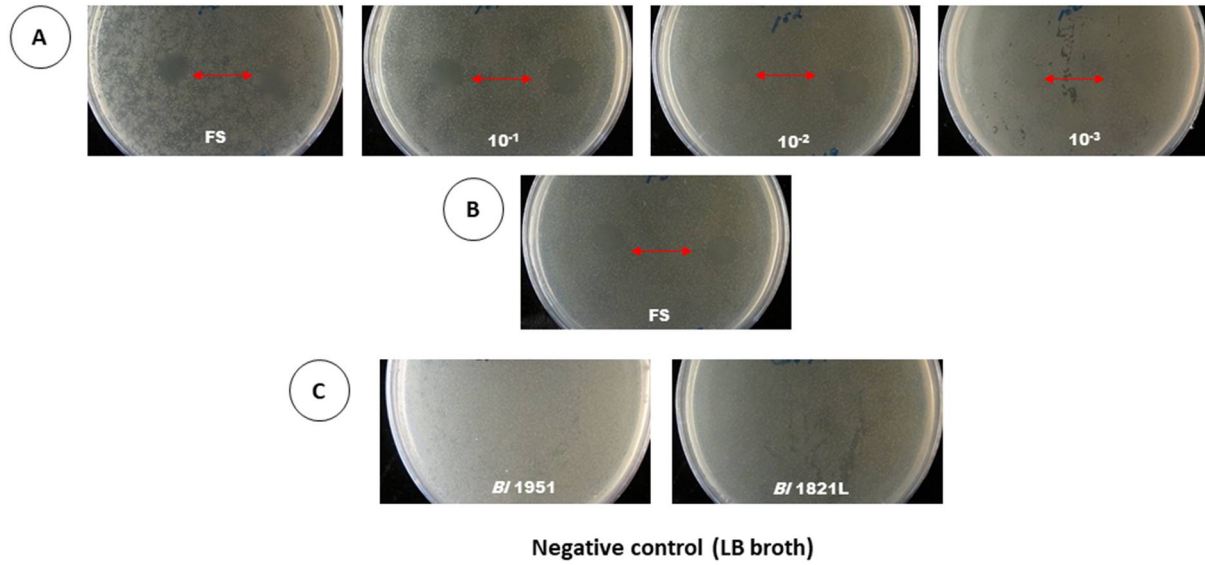


Figure S1. Antibacterial activity of *B/ 1821L* cell free supernatant after PEG 8000 precipitation in the serial dilutions assay test against *B/ 1951* as the host bacterium (A) and *B/ 1821L* as the host bacterium (B). Arrows (red colour) denote the zones of inhibition due to the activity of PEG 8000 precipitated putative antibacterial proteins. LB broth was used as a negative control against both the strains (*B/ 1951* & *B/ 1821L*) (C).

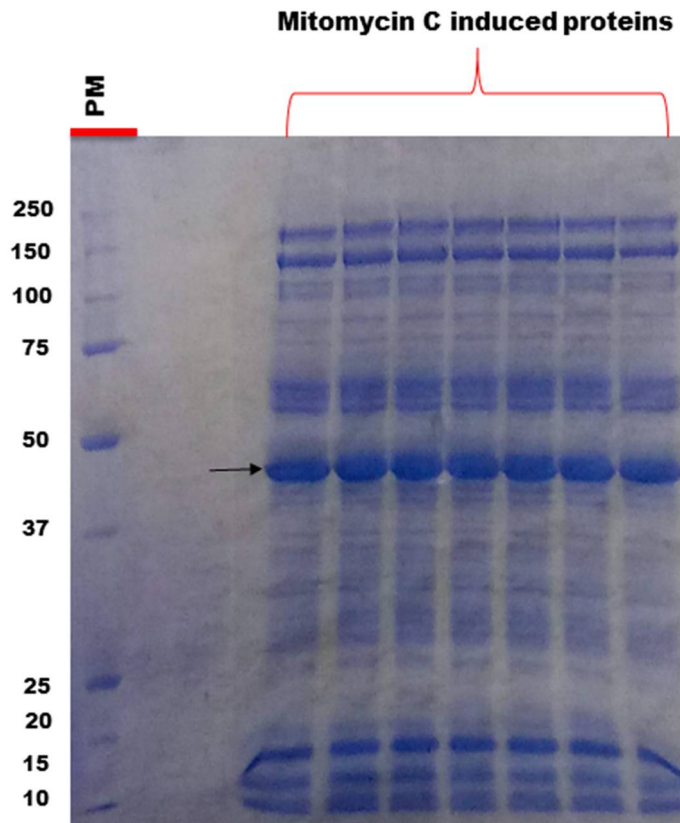


Figure S2. SDS-PAGE of mitomycin C induced culture of *B/ 1821L* showing a prominent band of ~48 kD (shown with dark arrow).

Note: Based on its prominence, ~48 kD protein band was hypothesised to be involved in the putative antibacterial activity. Therefore, the band was excised for preliminary N-terminal sequencing and the resultant short sequence amino acids revealed several hits (covering 70% of the amino acid sequence) to the loci A0A518VEB0 in the *B/ 1821L* genome (NZ_CP033464.1) encoding a predicted defective phage protein, similar to that encoded by the *Bs 168* phage-like element PBSX gene *xkdK*. Furthermore, these findings were authenticated with the subsequent TEM examination, SDS-PAGE, N-terminal sequencing, and bioinformatic analysis of purified ~48 kD protein.

Refer to N-terminal sequencing of ~48 kD crude protein:

(<https://data.lincoln.ac.nz/ndownloader/files/30948223>)

Brevibacillus laterosporus 1821L induced cultures after PEG 8000 precipitation

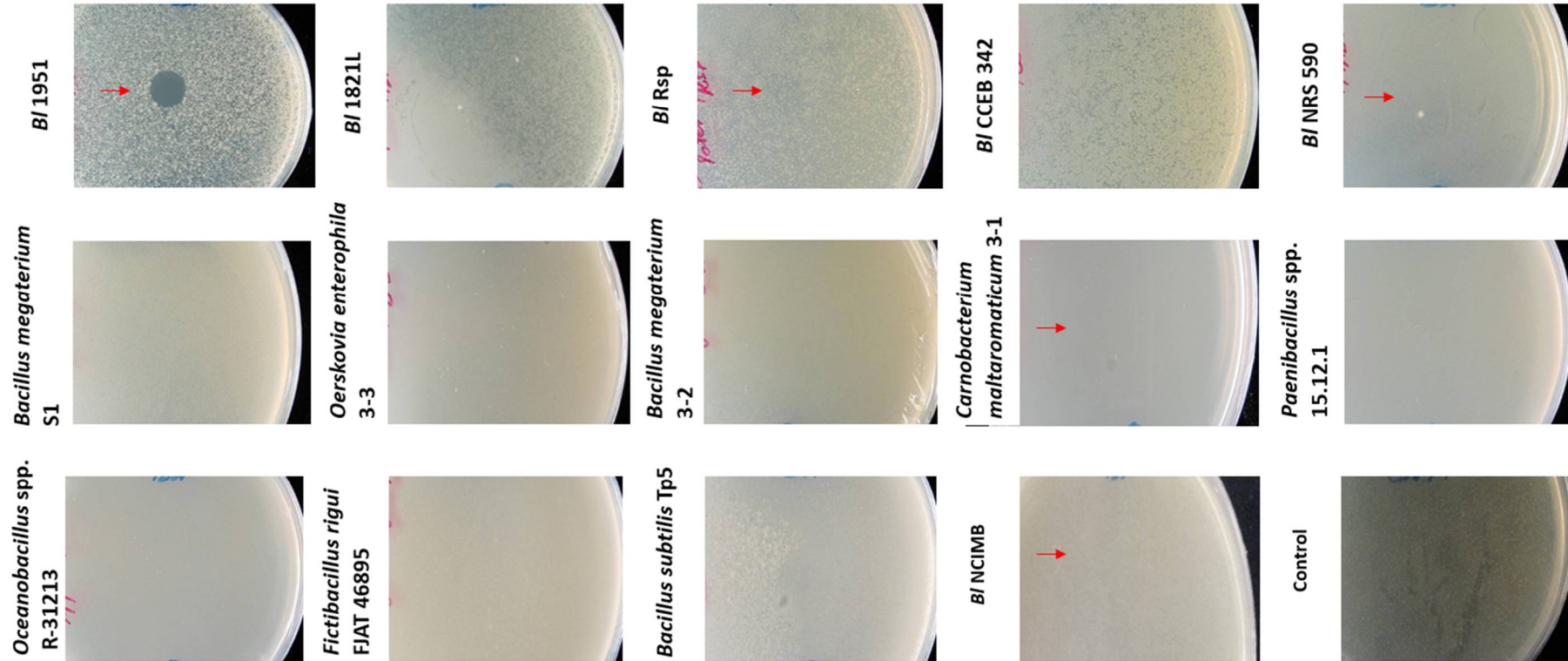


Figure S3. Antibacterial activity of *BI* 1821L induced culture cell free supernatant after PEG 8000 precipitation against various gram-positive bacteria. Arrows (red colour) denote the zone of inhibition due to the activity of PEG 8000 precipitated putative antibacterial proteins.

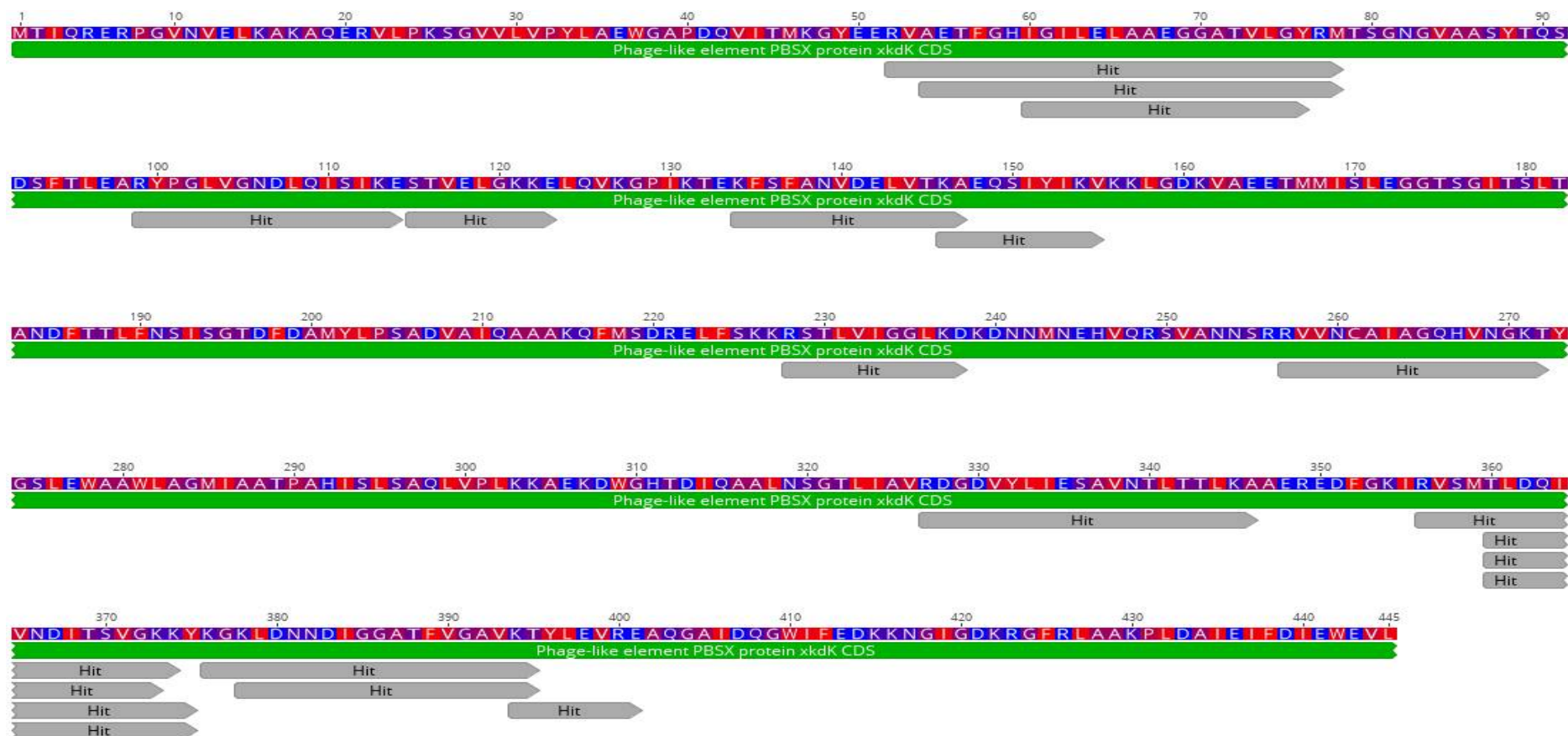


Figure S4. N-terminal sequenced short amino acid match hits to the putative phage tail protein (~48 kD) encoded in *B/ 1821L* genome.

Refer to N-terminal sequencing of ~48 kD purified protein: (<https://data.lincoln.ac.nz/ndownloader/files/30948616>)

Table S2. Similar proteins to the ~48 kD identified putative phage tail protein of *BI 1821L* in the Uniprot database.

Similar proteins	Organism	Gene name	Length
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	C4A76_07870, C4A77_13935, D5F52_00915	445
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	EX87_06735	445
Phage tail-sheath protein	<i>Brevibacillus laterosporus</i> LMG 15441	BRLA_c036460	462
Uncharacterised protein	<i>Brevibacillus borstelensis</i> GI-9	BLGI_826	445
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	EEL32_11960	445
Phage tail protein	<i>Brevibacillus laterosporus</i> SKDU 10	AYJO8_14030	445
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	EX87_02320	445
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	D5F52_16160	445
Phage tail protein	<i>Brevibacillus laterosporus</i> (<i>Bacillus laterosporus</i>)	C4A76_21720	445

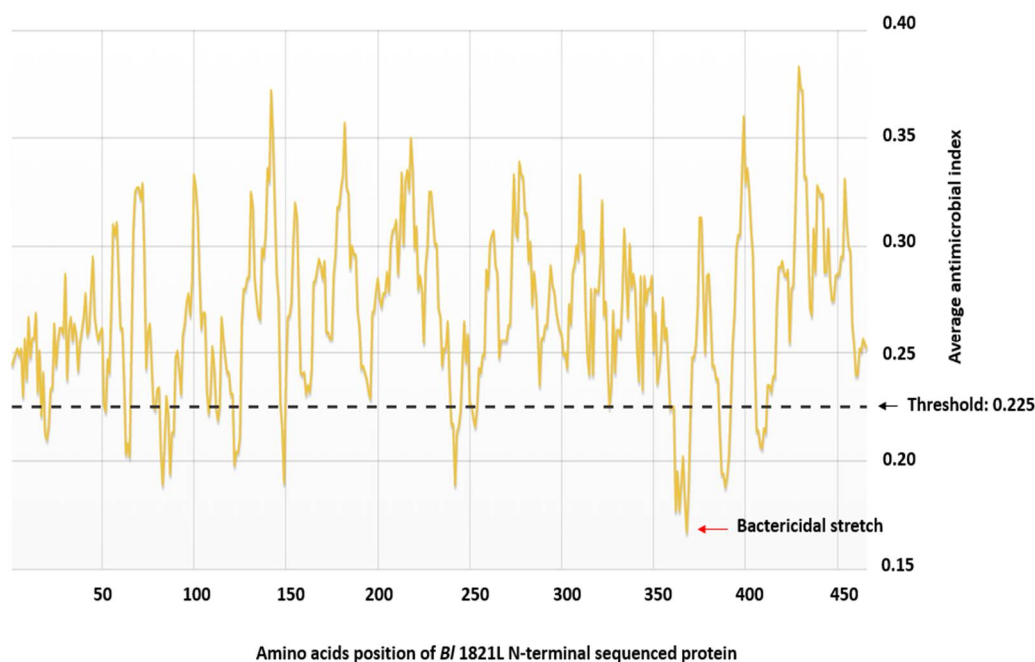


Figure S5. AMPA analysis of identified phage tail-sheath protein of *B/ 1821L*. Identified bactericidal motif is indicated is pointed with red arrow.

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1   MNGGTFTTGKEKERAGIYFNFKTTAQERVLSERGTVALPVASSWGEAKTFVSISSVEDL
61  NKKVGLSIDDPSLLLLREAKKNAKTVLMYRLTEGVRASADIAEGVKATAVYGGTKGNDII
121 IRINQNVLDANSFDVTTYMDESEVDKQTVKKAEELTANGYVFTGTGDLSTIPLTGSEG
181 DTAAETLNASAGIRLSGGTDKAPVNSDYTDFLAAAETESFDVIALPVAEGDQLKATFAAF
241 IKRLRDGQGQKVQGVGTANYAGDYEGIINVTEGVLLLEDGTEVTPDKATAWVAGASAGATN
301 QSLTFVEYEGAVDVLHRLDHDITIVERLGKGFLFTFDARDKSVSVEKDINSLVTFTAEN
361 KKFAKNKIVRVLDAVNNDLTRELKALIKSRKSGSDIPASEDGLQYVKTMITQYMTTLQD
421 AGGITGFDSDEEDITISMNEDRDGFLIDLAVQPVDAAEKFYFNVEVN

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Figure S6. AMPA analysis of identified phage-like element PBSX protein XkdK of *B/ 1821L*. Amino acids (360-373) corresponding to the bactericidal stretch are highlighted in red colour.

Table S3. Effect of crude *B/ 1821L* putative antibacterial proteins (ABPs) on the number of viable cells of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals. Data presents the mean values of four experiments. Values of % decrease/increase in the number of viable cells are calculated from CFUs values of corresponding time intervals.

Time intervals (Hours)	<i>B/ 1821L</i>	<i>B/ 1821L</i> + <i>B/ 1821L</i> crude ABPs	% Decrease/increase in no. of viable cells	<i>B/ 1951</i>	<i>B/ 1951</i> + <i>B/ 1821L</i> crude ABPs	% Decrease/increase in no. of viable cells	*LSD (5%)
1	4.46E+06 (6.650)**	5.56E+06 (6.745)	-24.65	3.18E+06 (6.502)	4.19E+06 (6.622)	-31.89	0.350
3	3.70E+06 (6.568)	3.85E+06 (6.585)	-4.05	3.64E+06 (6.561)	4.93E+06 (6.692)	-35.40	0.281
6	3.58E+06 (6.553)	2.50E+06 (6.398)	30.07	3.74E+06 (6.573)	5.80E+06 (6.763)	-55.18	0.377
12	1.18E+07 (7.071)	1.10E+07 (7.043)	6.36	9.15E+06 (6.961)	1.33E+07 (7.123)	-45.22	0.312
18	1.35E+07 (7.131)	1.67E+07 (7.223)	-23.57	1.05E+07 (7.023)	1.17E+07 (7.068)	-11.03	0.228
24	1.72E+07 (7.236)	1.50E+07 (7.177)	12.71	5.58E+06 (6.746)	7.89E+06 (6.897)	-41.48	0.317

*=Least significant difference

**=The values in parenthesis indicate the converted value of number of viable cells (CFU/mL) into log₁₀ CFU/mL.

Table S4. Effect of crude *B/ 1821* putative antibacterial proteins (ABPs) on the OD_{600nm} reading of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals. Data presents the mean values of four experiments.

Time intervals (Hours)	<i>B/ 1821L</i>	<i>B/ 1821L</i> + <i>B/ 1821L</i> crude ABPs	% Decrease/increase in OD _{600nm} reading	<i>B/ 1951</i>	<i>B/ 1951</i> + <i>B/ 1821L</i> crude ABPs	% Decrease/increase in OD _{600nm} reading	*LSD (5%)
1	1.99	1.99	0.00	1.92	1.90	1.14	0.061
3	1.87	1.85	0.67	1.74	1.73	0.43	0.121
6	1.65	1.63	1.21	1.58	1.55	1.51	0.148
12	1.29	1.26	2.32	1.45	1.39	4.57	0.135
18	1.23	1.21	1.63	1.24	1.25	-0.10	0.227
24	1.25	1.18	5.51	1.29	1.18	8.36	0.237
% Decrease from the start (1 hour) to the end (24 hours) of incubation	37.2%	40.7%		32.8%	37.9%		

*=Least significant difference

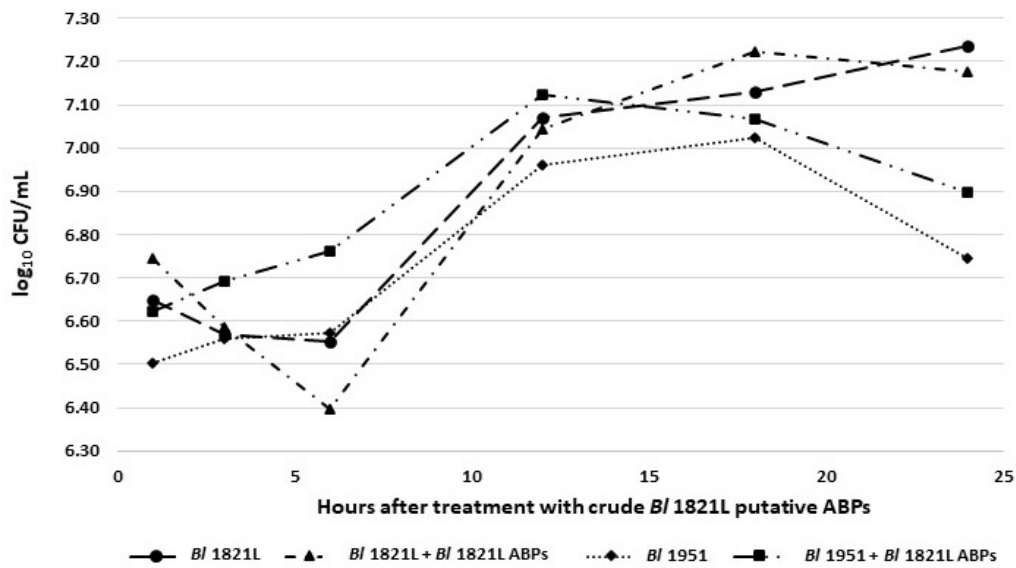


Figure S7. Number of viable cells (log₁₀ CFU/mL) of *B/ 1821L* and *B/ 1951* with/without treatment of crude *B/ 1821L* putative antibacterial proteins (ABPs) after incubation at 30°C over 24 hours.

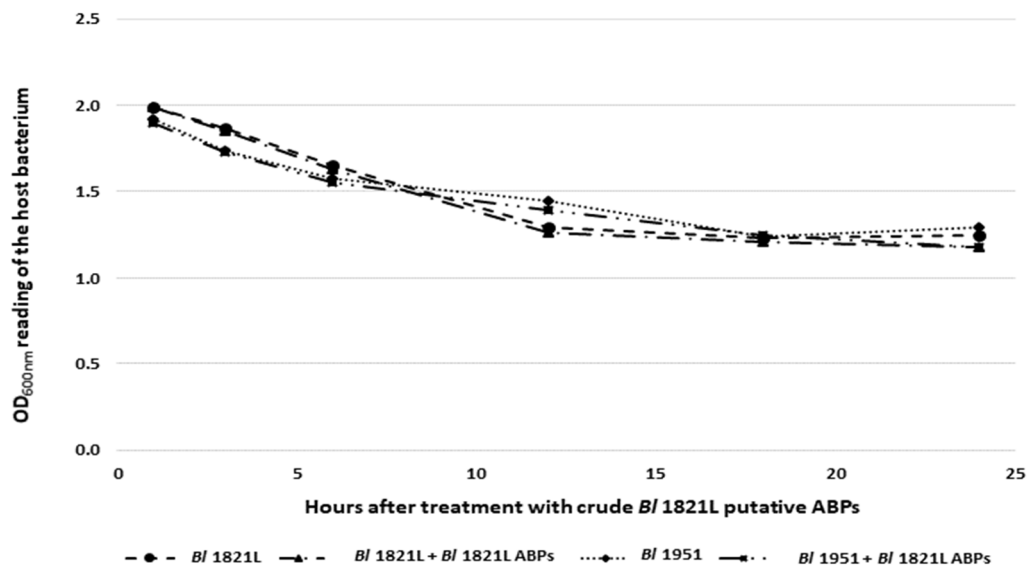


Figure S8. Effect of crude *B/ 1821* putative antibacterial proteins (ABPs) on the OD_{600nm} reading of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals.

Table S5. Effect of purified *B/ 1821L* putative ~48 kD phage tail-like protein (PTLP) on the number of viable cells of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals. Data presents the mean values of one experiment. Values of % decrease/increase in the number of viable cells are calculated from CFUs values of corresponding time intervals .

Time intervals (Hours)	<i>B/ 1821L</i>	<i>B/ 1821L</i> + <i>B/ 1821L</i> PTLP	% Decrease/increase in no. of viable cells	<i>B/ 1951</i>	<i>B/ 1951</i> + <i>B/ 1821L</i> PTLP	% Decrease/increase in no. of viable cells
1	1.74E+07 (7.241)*	2.81E+07 (7.448)	-61.21	9.05E+06 (6.957)	1.66E+07 (7.220)	-83.43
3	2.41E+07 (7.381)	2.16E+07 (7.334)	10.19	6.20E+06 (6.792)	8.80E+06 (6.944)	-41.94
6	1.13E+07 (7.051)	1.64E+07 (7.215)	-45.78	1.17E+07 (7.066)	1.08E+07 (7.031)	7.73
12	2.34E+07 (7.369)	2.14E+07 (7.330)	8.55	2.58E+07 (7.411)	2.01E+07 (7.302)	22.14
18	1.68E+07 (7.224)	2.78E+07 (7.443)	-65.67	2.37E+07 (7.375)	1.56E+07 (7.193)	34.18
24	2.33E+07 (7.366)	2.87E+07 (7.457)	-23.23	1.87E+07 (7.271)	2.03E+07 (7.307)	-8.85

*= The values in parenthesis indicate the number of viable cells (CFUs/mL) converted into log₁₀ CFU/mL.

Table S6. Effect of purified *B/ 1821L* ~48 kD putative phage tail-like protein (PTLP) on the OD_{600nm} reading of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals. Data presents the mean values of one experiment.

Time intervals (Hours)	<i>B/ 1821L</i>	<i>B/ 1821L</i> + <i>B/ 1821L</i> PTLP	% Decrease/increase in OD_{600nm} reading	<i>B/ 1951</i>	<i>B/ 1951</i> + <i>B/ 1821L</i> PTLP	% Decrease/increase in OD_{600nm} reading
1	3.40	3.20	5.88	2.89	2.90	-0.35
3	1.99	1.98	0.50	1.93	1.91	1.04
6	1.70	1.61	5.01	1.76	1.79	-1.70
12	1.26	1.30	-3.59	1.65	1.68	-1.82
18	1.19	1.27	-6.30	1.58	1.59	-0.63
24	1.14	1.21	-6.14	1.43	1.50	-4.90
% Decrease from the start (1 hour) to the end (24 hours) of incubation	66.5%	62.2%			50.5%	48.3%

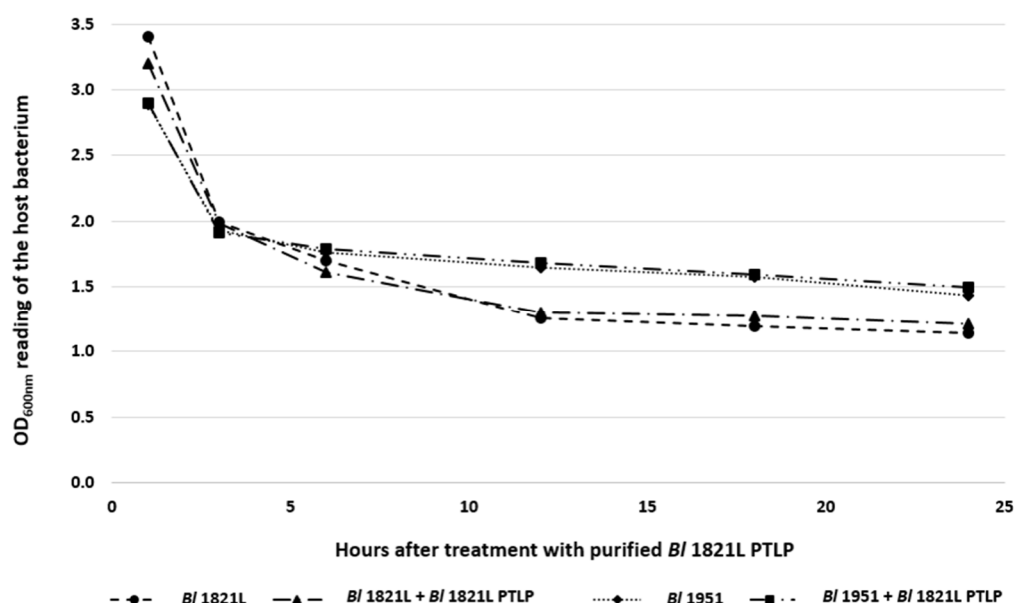


Figure S9. Effect of purified *B/ 1821* putative phage tail-like protein (~48 kD) on the OD_{600nm} reading of *B/ 1821L* and *B/ 1951* after incubation at 30°C for various time intervals.

Table S7. Phage-like element PBSX protein XkdK and phage tail-sheath proteins from different gram-positive bacteria.

Accession	Protein name	Organism
A0A0D1WNL8	Phage tail sheath	<i>Aneurinibacillus migulanus</i>
A0A410KN98I	Phage tail sheath	<i>Bacillus aerophilus</i>
R4JQA6	Structural protein	<i>Bacillus</i> phage PBP180
A0A5B0B6Z4	Phage-like element PBSX XkdK	<i>Bacillus</i> sp. ANT_WA51
A0A410QZ71	Phage-like element PBSX XkdK	<i>Bacillus</i> sp. WR11
A0A6H0H1P2	Phage-like element PBSX XkdK	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. SMY
P54331	Phage-like element PBSX XkdK	<i>Bacillus subtilis</i> 168
C0Z5G9	Uncharacterised protein	<i>Brevibacillus brevis</i> (strain 47/JCM 6285/ NBRC 100599)
A0A3M8B733	Phage tail	<i>Brevibacillus gelatini</i>
A0A075R9L5	Phage tail sheath	<i>Brevibacillus laterosporus</i> LMG 15441
Q18BN0	Phage-like element PBSX XkdK	<i>Clostridioides difficile</i> 630
A0A061P351	Phage-like element PBSX XkdK	<i>Geomicrobium</i> sp. JCM 19039

Figure S10. Amino acids alignment of identified *B/* 1821L and *B/* 1951 phage like-element PBSX protein XkdK (A0A518VEB0) with the similar proteins of other gram-positive bacteria (See SM Table 7) using the programme CLUSTALO.

A0A0D1WNL8	A0A0D1WNL8_ANEMI	1	-----MAGGTFQTGERKVRPGFYARFISAAQDRIAVAPRGTVILPLTLNWGRAKE	50
A0A3M8B733	A0A3M8B733_9BACL	1	-----MTIQREPRGVIVELIAKAKERV-VPKSGVVLVPYQAEWGAPDE	42
A0A5B0B6Z4	A0A5B0B6Z4_9BACI	1	-----MNGGFTTTGKEKERAGIYFNFKTTAQERVSLSERGTVALPVASSWGAEKT	50
A0A6H0H1P2	A0A6H0H1P2_BACIU	1	-----MNGGFTTTGKEKERAGIYFNFKTTAQERVSLSERGTVALPVASSWGAEKT	50
A0A061P351	A0A061P351_9BACL	1	-----MNGGTFAPGVEKERAGIYFRFTSAANDRLSVGERGTVALPLELSWGAPKT	50
A0A075R9L5	A0A075R9L5_BRELA	1	MKNKYDNTYLHFEENVSMITIQREPRGVNVELKAKAQERV-LPKSGVVLVPYLAEWGAPDQ	59
A0A410KN98	A0A410KN98_9BACI	1	-----MNGGFTTPGTEKKRPGIYFNFKTTAEQRITLGERGTVALPLVMSWGEPKT	50
A0A410QZ71	A0A410QZ71_9BACI	1	-----MNGGFTTTGKEKERAGIYFNFKTTAQERVSLSERGTVALPVASSWGAEKT	50
A0A518VEB0	A0A518VEB0_BRELA	1	-----MTIQREPRGVNVELKAKAQERV-LPKSGVVLVPYLAEWGAPDQ	42
C0Z5G9	C0Z5G9_BREBN	1	-----MTIQREPRGVIVELIAKAKERV-VPKSGVVLVPYQAEWGAPDE	42
Q18BN0	Q18BN0_CLOD6	1	-----	0
R4JQA6	R4JQA6_9CAUD	1	-----MNGGFTTPGTEKKRPGIYFNFKTTAEQRITLGERGTVALPLVMSWGEPKT	50
P54331	XKDK_BACSU	1	-----MNGGFTTTGKEKERAGIYFNFKTTAQERVSLSERGTVALPVASSWGAEKT	50
A0A0D1WNL8	A0A0D1WNL8_ANEMI	51	FTTIEVEKDTMDKLGVDYNDPEMLLIREARKLAKKVVKYKLNKGEKAKGTFGTT-----	104
A0A3M8B733	A0A3M8B733_9BACL	43	LVKLGSYEERMETTF-----GKVDIVELAAEGGATILAYRMTNGNASKAVYEQA-----	91
A0A5B0B6Z4	A0A5B0B6Z4_9BACI	51	FVSISSEDVLDNKKVGLSIDDPSLLLLREAKKNAKTIVLMYRLTEGVRSADIA-----	102
A0A6H0H1P2	A0A6H0H1P2_BACIU	51	FVSISSEDVLDNKKVGLSIDDPSLLLLREAKKNAKTIVLMYRLTEGVRSADIA-----	102
A0A061P351	A0A061P351_9BACL	51	FVEINGPDDVLKKYGLSVNDSSVLLKKEAMKRSQTVLAYRVNEGSKAETVIGESSGGGGS	110
A0A075R9L5	A0A075R9L5_BRELA	60	VITMKGYEERVAETF-----GQIDILELAAEGGATVVGYRMTNGKSVAAASYSQE-----	108
A0A410KN98	A0A410KN98_9BACI	51	FISVSDMEDLNKKVGLNIDDKSLLLFREAKKKAQTVLLYRLNEGEPAKAEIA-----	102
A0A410QZ71	A0A410QZ71_9BACI	51	FVSISSEDVLDNKKVGLSIDDPSLLLLREAKKNAKTIVLMYRLTEGVRSADIA-----	102
A0A518VEB0	A0A518VEB0_BRELA	43	VITMKGYEERVAETF-----GHIGILELAAEGGATVVGYRMTSGNGVAASYTQS-----	91
C0Z5G9	C0Z5G9_BREBN	43	LVKLGSFEERIAQTF-----GKVDIVELAAEGGATILAYRMTNGTATKAAYEQA-----	91
Q18BN0	Q18BN0_CLOD6	1	-----MAIGLPSINI-----	10
R4JQA6	R4JQA6_9CAUD	51	FISVSDMEDLNKKVGLNIDDKSLLLFREAKKKAQTVLLYRLNEGEPAKAEIA-----	102
P54331	XKDK_BACSU	51	FVSISSEDVLDNKKVGLSIDDPSLLLLREAKKNAKTIVLMYRLTEGVRSADIA-----	102
A0A0D1WNL8	A0A0D1WNL8_ANEMI	105	-----SICTVEALINDGTRGNDITIVSQVNVLDTTKKIVITYVKGROVDKQQTQ	151
A0A3M8B733	A0A3M8B733_9BACL	92	-----DAIRIELALYPGLLGNDLRIVISASTSEPGKKELQVKG-PLQTEKFSF	137
A0A5B0B6Z4	A0A5B0B6Z4_9BACI	103	-----EGVKATAVYGGTKGNDIIIRINQNVLDANSFDVTTYMDESEVDKQTV	149
A0A6H0H1P2	A0A6H0H1P2_BACIU	103	-----EGVKATAVYGGTKGNDIIIRINQNVLDANSFDVTTYMDESEVDKQTV	149
A0A061P351	A0A061P351_9BACL	111	DGDDEEEGASGQSNGLRVAKFGGMKGNDIIRVSENVLDSELDVTTYLNNVAVNRQSV	170
A0A075R9L5	A0A075R9L5_BRELA	109	-----GSIAIQARYPGLVGNELQISIKDSTAEGLKKELQVKG-PIKTEKFSF	154
A0A410KN98	A0A410KN98_9BACI	103	-----ENFVVTANYGGQKGNETIQVAENVLDSTKRDVITYLGTDIVDKQVV	149
A0A410QZ71	A0A410QZ71_9BACI	103	-----EGVKATAVYGGTKGNDIIIRINQNVLDANSFDVTTYMDESEVDKQTV	149
A0A518VEB0	A0A518VEB0_BRELA	92	-----DSFTLEARYPGLVGNELQISIKESTVELGKKELQVKG-PIKTEKFSF	137
C0Z5G9	C0Z5G9_BREBN	92	-----DAIRVELALYPGLVGNELKVTITVSTSEPGKKELQVKG-PLQTEKFSF	137
Q18BN0	Q18BN0_CLOD6	11	-----SFKELAL-----TTVKERSARGIIAMVLKDAKALGLNEIHEKEDI	49
R4JQA6	R4JQA6_9CAUD	103	-----ENFVVTANYGGQKGNETIQVAENVLDSTKRDVITYLGTDIVDKQVV	149
P54331	XKDK_BACSU	103	-----EGVKATAVYGGTKGNDIIIRINQNVLDANSFDVTTYMDESEVDKQTV	149

A0A0D1WNL8	A0A0D1WNL8	ANEMI	152	AEIESL----	VPNEWVTFSGTGAIEA-----	TAGTTL	TGGTNGTVIN	189
A0A3M8B733	A0A3M8B733	9BACL	138	ANADELVEKIGQSVYVRVQKL	GDAA-----	IATAAETN	TGGTSGTVAL	181
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	150	KKAEEL----	TANGYVTFGTGDLSSSTIPLTGSEGD	TAAETLNASAGIR	SGGTDKAPVN	205
A0A6H0H1P2	A0A6H0H1P2	BACIU	150	KKAEEL----	TANGYVTFGTGDLSSSTIPLTGSEGD	TAAETLNASAGIR	SGGTDKAPVN	205
A0A061P351	A0A061P351	9BACL	171	RRSSEL----	QDNDWVSFEQSGRLQE-----	TAGTN	SGGTNSEART	208
A0A075R9L5	A0A075R9L5	BRELA	155	ANMDELVTKAEQSIYIKVKKLGDKA	-----	VEETAMTA	SGGTSGIATL	198
A0A410KN98	A0A410KN98	9BACI	150	KDVKDL----	VKNKYVQFSGEGEAVI-----	TAGAA	SGGKNGVASV	187
A0A410QZ71	A0A410QZ71	9BACI	150	KKAEEL----	TANGYVTFGTGDLSSSTIPLTGSEGD	TAAETLNASAGIR	SGGTDKAPVN	205
A0A518VEB0	A0A518VEB0	BRELA	138	ANVDELVTKAEQSIYIKVKKLGDKV	-----	AEETMMIS	EGGTSGITSL	181
C0Z5G9	C0Z5G9	BREBN	138	ADANELAAKTSQSNYVRVKKLGETA	-----	VTIVPETA	TGAKSGTVAL	181
Q18BN0	Q18BN0	CLOD6	50	PVDLSA----	ENKEYINLALMGVNT-----	PNKL	VYVIEGEADI	86
R4JQA6	R4JQA6	9CAUD	150	KDVKDL----	VKNKYVQFSGEGEAVI-----	TAGAA	SGGKNGVASV	187
P54331	XKDK	BACSU	150	KKAEEL----	TANGYVTFGTGDLSSSTIPLTGSEGD	TAAETLNASAGIR	SGGTDKAPVN	205
				.	. : . *	.	.	
A0A0D1WNL8	A0A0D1WNL8	ANEMI	190	--ADYTD	FMTACETEFFDTIGFLSD-DVTLKTTFVG	FIRRLREDEGRKVKGV	VAGYEADY	246
A0A3M8B733	A0A3M8B733	9BACL	182	AAADATKLFMAVSGADFDAMYL	PFDD-PAVQAAAKQFMSDRRTLGKKLSTL	VIGGKAVED		240
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	206	--SDYTD	FLAAETESFDVIALPVAEGDQLKATFAAFIKRLRD	GGQKQVQGV	TANYAGDY	263
A0A6H0H1P2	A0A6H0H1P2	BACIU	206	--SDYTD	FLAAETESFDVIALPVAEGDQLKATFAAFIKRLRD	GGQKQVQGV	TANYAGDY	263
A0A061P351	A0A061P351	9BACL	209	--WDYTD	FLSAAEHVS YDTIGLPVDDQLKTTFVS	FVKRMRDETGIKITGVLPNFDGDH		266
A0A075R9L5	A0A075R9L5	BRELA	199	SATDFTT	LENSISGVDFDAMYLPSAD-AGIQAAAKQFMVDREL	FSKKRSTLVIGGLPEKD		257
A0A410KN98	A0A410KN98	9BACI	188	--ADYTA	FLAAETESFDVIALPVDNSEQLKATFASFIERLRD	KQGRKQVQGV	VANYAADQ	245
A0A410QZ71	A0A410QZ71	9BACI	206	--SDYTD	FLAAETESFDVIALPVAEGDQLKATFAAFIKRLRD	GGQKQVQGV	TANYAGDY	263
A0A518VEB0	A0A518VEB0	BRELA	182	TANDFTT	LENSISGTDFDAMYLPSAD-VAIQAAAKQFMSDRREL	FSKKRSTLVIGGLKDKD		240
C0Z5G9	C0Z5G9	BREBN	182	ASADSTKLFMAVSGADFDAMYL	PFDD-SAVQAAAKQFMSDRRTQNKLLSTL	VIGGKAADD		240
Q18BN0	Q18BN0	CLOD6	87	--QTALD	FL----ETKEFNLYLCPKA-VEADKTAIKNWI	IKLRDIDKVKVAVLGKVVGNH		140
R4JQA6	R4JQA6	9CAUD	188	--ADYTA	FLAAETESFDVIALPVDNSEQLKATFASFIERLRD	KQGRKQVQGV	VANYAADQ	245
P54331	XKDK	BACSU	206	--SDYTD	FLAAETESFDVIALPVAEGDQLKATFAAFIKRLRD	GGQKQVQGV	TANYAGDY	263
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A0A0D1WNL8	A0A0D1WNL8	ANEMI	247	-----	EGIIINVKNSVKLLDGTETLTKERAVAVVAGAD	AGASITKSN	YQRY	291
A0A3M8B733	A0A3M8B733	9BACL	241	ENMEKHVERSVAQNARFVVN	CAIAGQHNNNGNTYGSLEWAAWVAGMIRAT	PAHESL	TAUVV	300
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	264	-----	EGIIINVTEGVLLDGTETVTPDKATAWVAGAS	AGATFNQSL	TFVEY	308
A0A6H0H1P2	A0A6H0H1P2	BACIU	264	-----	EGIIINVTEGVLLDGTETVTPDKATAWVAGAS	AGATFNQSL	TFVEY	308
A0A061P351	A0A061P351	9BACL	267	-----	EGIIINVTSSVELAER-KLNVAETVAVVAGAS	AGATFNQSL	TFVDY	310
A0A075R9L5	A0A075R9L5	BRELA	258	SNMNEHVDRSAANNSRRVVN	CAIAGQHVNGKTYGSLEWAAWLAGMIRAT	PAHISLS	SAQLV	317
A0A410KN98	A0A410KN98	9BACI	246	-----	EGIIINVTSGVLLDGTETLTPAQTAWVAGAS	AGANFNQSL	TFVEY	290
A0A410QZ71	A0A410QZ71	9BACI	264	-----	EGIIINVTEGVLLDGTETVTPDKATAWVAGAS	AGATFNQSL	TFVEY	308
A0A518VEB0	A0A518VEB0	BRELA	241	NNMNEHVQSVANNNSRRVVN	CAIAGQHVNGKTYGSLEWAAWLAGMIRAT	PAHISLS	SAQLV	300
C0Z5G9	C0Z5G9	BREBN	241	ENMAKHIERSSVAQNARFVVN	SAIAGQHNNNGKTYGSLEWAAWVAGMIRAT	PAHESL	TAUVV	300
Q18BN0	Q18BN0	CLOD6	141	-----	EGIIINFTTEDVLVGEKKYSVDEFTSRVAGLI	AGTPLSQSV	TYTKL	185
R4JQA6	R4JQA6	9CAUD	246	-----	EGIIINVTSGVLLDGTETLTPAQTAWVAGAS	AGANFNQSL	TFVEY	290
P54331	XKDK	BACSU	264	-----	EGIIINVTEGVLLDGTETVTPDKATAWVAGAS	AGATFNQSL	TFVEY	308
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A0A0D1WNL8	A0A0D1WNL8	ANEMI	292	DGAVDIAIPRYTNSEIIEATNKGEFVFNVDG--EQVKVEYDINSLVTTGQDKNSRFKKNRV	349
A0A3M8B733	A0A3M8B733	9BACL	301	PL-KKAQKDWGHSIDILRAIGSGTLVATRDG--DVYIIIESAVNTLSVLGNHEREDYGGIRV	357
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	309	EGAVDVLHRLDHDITIVERLGKGEFLFTFDARDKSVSVEKDINSLVTFTAENKKFAKNKI	368
A0A6H0H1P2	A0A6H0H1P2	BACIU	309	EGAVDVLHRLDHDITIVERLGKGEFLFTFDARDKSVSVEKDINSLVTFTAENKKFAKNKI	368
A0A061P351	A0A061P351	9BACL	311	EGAIGVNEEDLDDEIKERLRNGEFLFHYPDRDRTVSVEKDINSFTSFTAENKRYFSKNLI	370
A0A075R9L5	A0A075R9L5	BRELA	318	PM-KKAQKDWGHTIEIQNALNSGSLIAVRDG--DVYIIIESAVNTLTTLKAAEREDFGKIRV	374
A0A410KN98	A0A410KN98	9BACI	291	EGAVDTLERLDNDQVEYRLSQGEFLFTFDARDRTVSVEKDINSLTSFTVEKNQOMAKNKI	350
A0A410QZ71	A0A410QZ71	9BACI	309	EGAVDVLHRLDHDITIVERLGKGEFLFTFDARDKSVSVEKDINSLVTFTAENKKFAKNKI	368
A0A518VEB0	A0A518VEB0	BRELA	301	PL-KKAQKDWGHTDIIQAALNSGTLIAVRDG--DVYIIIESAVNTLTTLKAAEREDFGKIRV	357
C0Z5G9	C0Z5G9	BREBN	301	PL-KKALKDWGHTDILSAIGSGTLIAVRDG--DVYIIIESAVNTLAVLGHTHEREDYGGIRV	357
Q18BN0	Q18BN0	CLOD6	186	SDVVDI-PKMTKVDAESKVNKGELILIKEA--GAIRIARGVNSLTETAEGEMFQKIKI	242
R4JQA6	R4JQA6	9CAUD	291	EGAVDTLERLDNDQVEYRLSQGEFLFTFDARDRTVSVEKDINSLTSFTVEKNQOMAKNKI	350
P54331	XKDK	BACSU	309	EGAVDVLHRLDHDITIVERLGKGEFLFTFDARDKSVSVEKDINSLVTFTAENKKFAKNKI	368
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A0A0D1WNL8	A0A0D1WNL8	ANEMI	350	MRTLDATHNDIKREIERNYIG-----KMNNDADGQAILKASVIGVLETLOANATQNLQ	403
A0A3M8B733	A0A3M8B733	9BACL	358	SMTLDQIVNDINAVGK-KYKG-----KLGNNDLGGAVFVSANAYMTVREQQGATEPGW	410
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	369	VRVLDVAVNNDLTRELKALIKSRKSGSGSDIPASEDGLQYVKMTITQYMTTLQDAGGITGFD	428
A0A6H0H1P2	A0A6H0H1P2	BACIU	369	VRVLDVAVNNDLTRELKALIKSRKSGSGSDIPASEDGLQYVKMTITQYMTTLQDAGGITGFD	428
A0A061P351	A0A061P351	9BACL	371	VRVLDVAVNNDLTRELKALIKLRKDRGQDIPGSNDGKQIIRSLITVYLNALQEGGAKNFD	430
A0A075R9L5	A0A075R9L5	BRELA	375	SMTLDQIVNDITSVGK-KYKG-----KLGNNDIGGATFVGAVKTYLEVREAQGAIDKGW	427
A0A410KN98	A0A410KN98	9BACI	351	IRVLDVAVNNDLTRELKALIKLRKANGNDIPASDDGVQLVKTLLITQYLTQLQDGGSGITGFN	410
A0A410QZ71	A0A410QZ71	9BACI	369	VRVLDVAVNNDLTRELKALIKSRKSGSGSDIPASEDGLQYVKMTITQYMTTLQDAGGITGFD	428
A0A518VEB0	A0A518VEB0	BRELA	358	SMTLDQIVNDITSVGK-KYKG-----KLGNNDIGGATFVGAVKTYLEVREAQGAIDQGW	410
C0Z5G9	C0Z5G9	BREBN	358	SMTLDQIVNDITSVGK-KYKG-----KLGNNDLGGAVFVSANAYMTVREQQGATDTGW	410
Q18BN0	Q18BN0	CLOD6	243	VDTLDTIHSDIRKVIIDDYIG-----KVTNSYDNKCLLIVATKSYLEELEKSALIES-D	295
R4JQA6	R4JQA6	9CAUD	351	IRVLDVAVNNDLTRELKALIKLRKANGNDIPASDDGVQLVKTLLITQYLTQLQDGGSGITGFN	410
P54331	XKDK	BACSU	369	VRVLDVAVNNDLTRELKALIKSRKSGSGSDIPASEDGLQYVKMTITQYMTTLQDAGGITGFD	428
				. ** : . * : : : : : : * :	
A0A0D1WNL8	A0A0D1WNL8	ANEMI	404	KDADFVIDFVLSV-----DDEVHATIIYQPVDSMEKFFFTILVR	442
A0A3M8B733	A0A3M8B733	9BACL	411	TFTDK-----KNGNGDRRGFQLSAKPLDAIEYFDIDWEVL	445
A0A5B0B6Z4	A0A5B0B6Z4	9BACI	429	SDEDITISMNE-D-----RDGFLIDLAVQPVDAAEKFFYNVEVN	466
A0A6H0H1P2	A0A6H0H1P2	BACIU	429	SDEDITISMNE-D-----RDGFLIDLAVQPVDAAEKFFYNVEVN	466
A0A061P351	A0A061P351	9BACL	431	PSDDIDIVLTD-Q-----EDGFIINLGAQPVDAAEKFFYDTEVR	468
A0A075R9L5	A0A075R9L5	BRELA	428	IFEDK-----KNGIGDKRGFRLLAAKPLDAIEIFDIWEVL	462
A0A410KN98	A0A410KN98	9BACI	411	SETDIVIGLNE-D-----RDGFIIDLAVQPVDAAEKFFYNVEVK	448
A0A410QZ71	A0A410QZ71	9BACI	429	SDEDITISMNE-D-----RDGFLIDLAVQPVDAAEKFFYNVEVN	466
A0A518VEB0	A0A518VEB0	BRELA	411	IFEDK-----KNGIGDKRGFRLLAAKPLDAIEIFDIWEVL	445
C0Z5G9	C0Z5G9	BREBN	411	TFTDK-----KNGIGDRRGFLLSAKPLDAIEYFDIDWEVL	445
Q18BN0	Q18BN0	CLOD6	296	STVEIDFEAQSKSYLKSQGVLSYMTLQEIKEANTGSKVFLKAKIKVLDAMEDIDLSIET-	354
R4JQA6	R4JQA6	9CAUD	411	SETDIVIGLNE-D-----RDGFIIDLAVQPVDAAEKFFYNVEVK	448
P54331	XKDK	BACSU	429	SDEDITISMNE-D-----RDGFLIDLAVQPVDAAEKFFYNVEVN	466
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*Highlighted dark grey color amino acids denote similarity among the aligned phage-like element PBSX protein XkdK.
(Refer to SM Tables S8 & S9)

Table S8. Distance matrices of identified *B/* 1821L and *B/* 1951 phage-like element PBSX protein XkdK (A0A518VEB0) with the similar proteins of other gram-positive bacteria.

Uniprot Accession # (www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)												
	A0A0D1WNL8	A0A3M8B733	A0A5B0B6Z4	A0A6H0H1P2	A0A061P351	A0A075R9L5	A0A410KN98	A0A410QZ71	A0A518VEB0	C0Z5G9	Q18BN0	R4JQA6	P54331
A0A0D1WNL8		1.34	0.8	0.8	0.84	1.4	0.8	0.8	1.33	1.46	1.51	0.8	0.8
A0A3M8B733	1.34		1.44	1.44	1.43	0.38	1.4	1.44	0.36	0.14	1.64	1.4	1.44
A0A5B0B6Z4	0.8	1.44		0	0.56	1.52	0.37	0	1.45	1.45	1.49	0.37	0
A0A6H0H1P2	0.8	1.44	0		0.56	1.52	0.37	0	1.45	1.45	1.49	0.37	0
A0A061P351	0.84	1.43	0.56	0.56		1.42	0.57	0.56	1.45	1.38	1.54	0.57	0.56
A0A075R9L5	1.4	0.38	1.52	1.52	1.42		1.44	1.55	0.1	0.39	1.49	1.44	1.55
A0A410KN98	0.8	1.4	0.37	0.37	0.57	1.44		0.37	1.4	1.37	1.66	0	0.37
A0A410QZ71	0.8	1.44	0	0	0.56	1.55	0.37		1.45	1.45	1.49	0.37	0
A0A518VEB0	1.33	0.36	1.45	1.45	1.45	0.1	1.4	1.45		0.39	1.52	1.4	1.45
C0Z5G9	1.46	0.14	1.45	1.45	1.38	0.39	1.37	1.45	0.39		1.66	1.37	1.45
Q18BN0	1.51	1.64	1.49	1.49	1.54	1.49	1.66	1.49	1.52	1.66		1.66	1.49
R4JQA6	0.8	1.4	0.37	0.37	0.57	1.44	0	0.37	1.4	1.37	1.66		0.37
P54331	0.8	1.44	0	0	0.56	1.55	0.37	0	1.45	1.45	1.49	0.37	

Table S9. Amino acids alignment % of identified *B/* 1821L and *B/* 1951 phage-like element PBSX protein XkdK (A0A518VEB0) with the similar proteins of other gram-positive bacteria.

Uniprot Accession # (www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)												
	A0A0D1WNL8	A0A3M8B733	A0A5B0B6Z4	A0A6H0H1P2	A0A0G1P351	A0A075R9L5	A0A410KN98	A0A410QZ71	A0A518VEB0	C0Z5G9	Q18BN0	R4JQA6	P54331
A0A0D1WNL8		23.9	41.5	41.5	39.8	22.0	42.6	41.5	22.7	23.2	22.0	42.6	41.5
A0A3M8B733	23.9		21.2	21.2	20.7	68.2	20.6	21.2	69.0	86.0	18.4	20.6	21.2
A0A5B0B6Z4	41.5	21.2		100.0	51.8	20.3	64.8	100.0	21.2	20.5	22.4	64.8	100.0
A0A6H0H1P2	41.5	21.2	100.0		51.8	20.3	64.8	100.0	21.2	20.5	22.4	64.8	100.0
A0A0G1P351	39.8	20.7	51.8	51.8		19.0	53.4	51.8	18.8	19.4	20.5	53.4	51.8
A0A075R9L5	22.0	68.2	20.3	20.3	19.0		19.8	20.3	89.1	67.4	19.3	19.8	20.3
A0A410KN98	42.6	20.6	64.8	64.8	53.4	19.8		64.8	20.3	22.0	20.1	100.0	64.8
A0A410QZ71	41.5	21.2	100.0	100.0	51.8	20.3	64.8		21.2	20.5	22.4	64.8	100.0
A0A518VEB0	22.7	69.0	21.2	21.2	18.8	89.1	20.3	21.2		68.1	19.9	20.3	21.2
C0Z5G9	23.2	86.0	20.5	20.5	19.4	67.4	22.0	20.5	68.1		20.2	22.0	20.5
Q18BN0	22.0	18.4	22.4	22.4	20.5	19.3	20.1	22.4	19.9	20.2		20.1	22.4
R4JQA6	42.6	20.6	64.8	64.8	53.4	19.8	100.0	64.8	20.3	22.0	20.1		64.8
P54331	41.5	21.2	100.0	100.0	51.8	20.3	64.8	100.0	21.2	20.5	22.4	64.8	

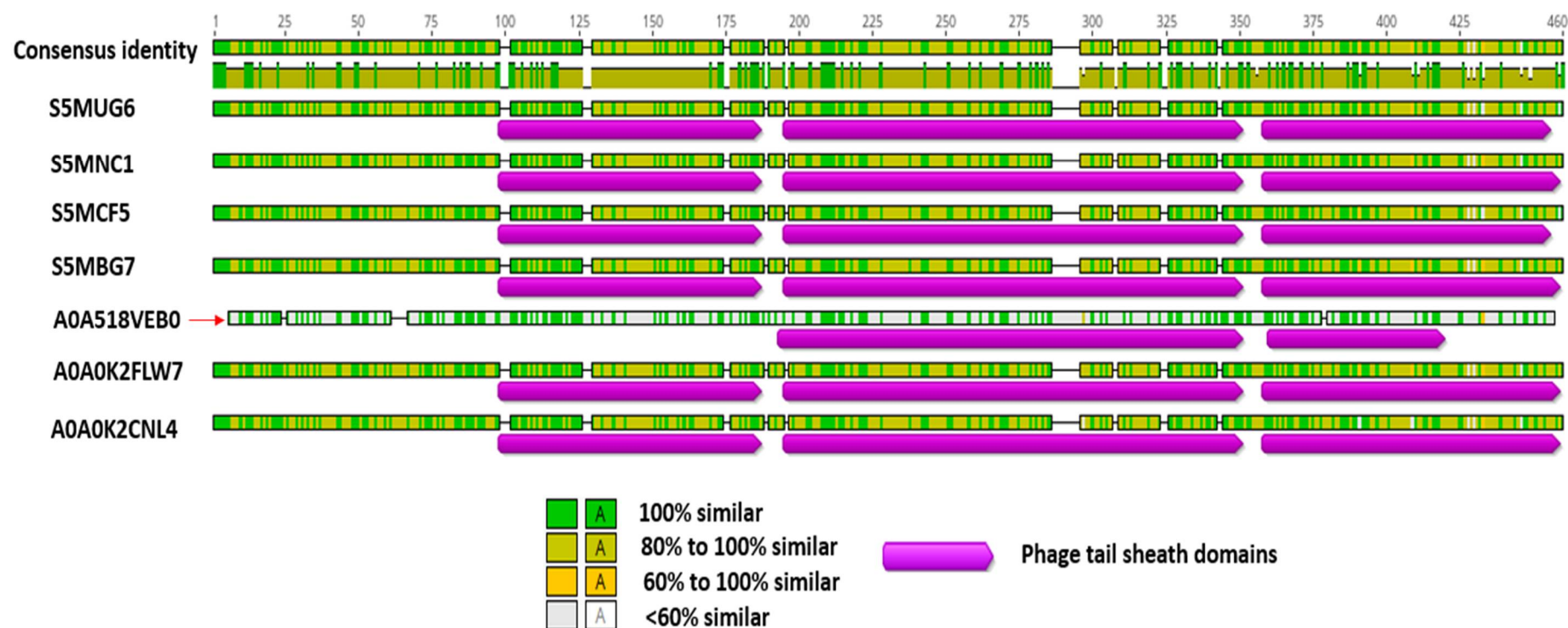


Figure S11. Amino acids alignment and percentage identity of identified putative phage tail-sheath protein (A0A518VEB0, shown with red arrow) of *Bl* 1821L and *Bl* 1951 with similar proteins of different *Bl* phages including Abouo (S5MUG6), Jimmer1 (S5MNC1), Davies (S5MCF5), Jimmer2, (S5MBG7), Powder (A0A0K2FLW7), and Osiris (A0A0K2CNL4) using Geneious basic.

(Refer to SM Figure S12 & Tables S10 and S11)

Figure S12. Amino acids alignment of identified *Bf* 1821L and *Bf* 1951 putative phage tail-sheath protein (A0A518VEB0) with the phage tail-sheath protein of different *Bf* phages using the programme CLUSTALO.

A0A518VEB0	A0A518VEB0 BRELA	1	-----MTIQEREPGVNVELKAKA-QERVLPKSGVVLVPYLAEWGAPDQVITMKGYEERVA	54
S5MUG6	S5MUG6_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
S5MNC1	S5MNC1_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
S5MCF5	S5MCF5_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
S5MBG7	S5MBG7_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
A0A0K2FLW7	A0A0K2FLW7_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
A0A0K2CNL4	A0A0K2CNL4_9CAUD	1	MMQNWIAQNKVRPGTYVNVVSEAKPQGAISERGTVTMALSLSWGSPSGEVIEIQAGENTLD	60
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A0A518VEB0	A0A518VEB0 BRELA	55	ETF-----GHIGILELAEGGATVLGYRMTSGNGVAASYTQSDSFTLEARYPGILVGNLQ	109
S5MUG6	S5MUG6_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
S5MNC1	S5MNC1_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
S5MCF5	S5MCF5_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
S5MBG7	S5MBG7_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
A0A0K2FLW7	A0A0K2FLW7_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
A0A0K2CNL4	A0A0K2CNL4_9CAUD	61	KLGYDISEPQILLVQEAALKRAKTLILLYRLNTGSKAQ---ASSDNLTVTALYGGVRGNDIT	117
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A0A518VEB0	A0A518VEB0 BRELA	110	TSIKESTVELGKK--ELQVKGPIKTEKFSFANVDELVTKAEQSIYIKVKKLGDKVAEETM	167
S5MUG6	S5MUG6_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
S5MNC1	S5MNC1_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
S5MCF5	S5MCF5_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
S5MBG7	S5MBG7_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
A0A0K2FLW7	A0A0K2FLW7_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
A0A0K2CNL4	A0A0K2CNL4_9CAUD	118	VVVEQNIDDETTFIVKTLVAGSIVDNQLA-----KKIEDLKANKFVTFSGTGALV--ASA	170
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A0A518VEB0	A0A518VEB0 BRELA	168	MTSLLEGGTSGITSLTANDETTTLFNSISGTDFFDAMYLPSADVAIQAAAKQFMSDRELFSSK	227
S5MUG6	S5MUG6_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
S5MNC1	S5MNC1_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
S5MCF5	S5MCF5_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
S5MBG7	S5MBG7_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
A0A0K2FLW7	A0A0K2FLW7_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
A0A0K2CNL4	A0A0K2CNL4_9CAUD	171	GIPITGGTIDGTEIG--VNHTAYREAEELHDFDAMAVPYDDPTIKSVYVAFKRLANQONR	228
			* * * * * . * : : : : : * * * * * : * * : : : . * . : : :	

A0A518VEB0	A0A518VEB0 BRELA	228	RSTLVIGGLKDKNNMNEHVQSVANNRRVVNCAIAGQHVNGKTYGSLEWAAWLAGMIA	287
S5MUG6	S5MUG6_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
S5MNC1	S5MNC1_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
S5MCF5	S5MCF5_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
S5MBG7	S5MBG7_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
A0A0K2FLW7	A0A0K2FLW7_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
A0A0K2CNL4	A0A0K2CNL4_9CAUD	229	FIQIVVPNYAQADDPT-----VISVSNVGVILSNSTVIDAVKATAWVAGATA	274
			::: . : *:	
A0A518VEB0	A0A518VEB0 BRELA	288	ATPAHISLSAQVLVPL-KKAEKDWGHTDIQAALNSGTLIAVRDGDVYLIESAVNTLTTLKA	346
S5MUG6	S5MUG6_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
S5MNC1	S5MNC1_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
S5MCF5	S5MCF5_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
S5MBG7	S5MBG7_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
A0A0K2FLW7	A0A0K2FLW7_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
A0A0K2CNL4	A0A0K2CNL4_9CAUD	275	GANVNQSLTHTAYDDAVAVHGRNLDSQITKALLNGEFLFELHNGKVVEQDINTFTSFSP	334
			::: **:	
A0A518VEB0	A0A518VEB0 BRELA	347	AEREDFGKIRVSMITLDQIVNDIT-SVGKKYKGLDNDIGGATFVGAVKTYLEVREAQGA	405
S5MUG6	S5MUG6_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKGDNDADGRNLYKKECIKISEQYQAMGA	394
S5MNC1	S5MNC1_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKGDNDADGRNLYKKECIKISEQYQAMGA	394
S5MCF5	S5MCF5_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKGDNDADGRNLYKKECIKISEQYQAMGA	394
S5MBG7	S5MBG7_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKGDNDADGRNLYKKECIKISEQYQAMGA	394
A0A0K2FLW7	A0A0K2FLW7_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKGDNDADGRNLYKKECIKISEQYQAMGA	394
A0A0K2CNL4	A0A0K2CNL4_9CAUD	335	DKRKHESKNRVVRTINGITKDWKLAFFDEQYLGKYDNDADGRNLYKKECIKIVEEYQAMGA	394
			:::.* ** *::: *::: . :::: * * *::: * : . * : * **	
A0A518VEB0	A0A518VEB0 BRELA	406	IDQGWIFEDKKN---GIGDKRGFRLAAPLDAIEIFDIEWEVL---	445
S5MUG6	S5MUG6_9CAUD	395	IQN---FDAQKDIAVLPGEDSDSLLTEGYIQAVDSMEKNYLKAVAR	437
S5MNC1	S5MNC1_9CAUD	395	IQN---FDAQKDIIIVSPGNDSDSLLTEGYIQPVDAMEKNYLKAVVR	437
S5MCF5	S5MCF5_9CAUD	395	IQN---FDAQKDIAVLPGEDSDSLLTEGYIQAVDSMEKNYLKAVAR	437
S5MBG7	S5MBG7_9CAUD	395	IQN---FDAQKDIIIVSPGNDSDSLLTEGYIQPVDAMEKNYLKAVVR	437
A0A0K2FLW7	A0A0K2FLW7_9CAUD	395	IQN---FDAQKDIIIVSPGNDSDSLLTEGYIQPVDAMEKNYLKAVVR	437
A0A0K2CNL4	A0A0K2CNL4_9CAUD	395	IQN---FDAQKDIIIVSPGNDSDSLLTEGYIQPVDAMEKNYLKAVVR	437
			*:: *:: *:: *:: . *:: : : : : : :	

*Highlighted dark grey color amino acids denote similarity among the aligned phage tail-sheath like proteins.
(Refer to SM Tables S10 & S11)

Table S10. Distance matrices of identified *B/* 1821L and *B/* 1951 putative phage tail-sheath protein (A0A518VEB0) with the phage tail-sheath proteins of different *B/* phages .

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)						
	S5MUG6	S5MNC1	S5MCF5	S5MBG7	A0A518VEB0	A0A0K2FLW7	A0A0K2CNL4
S5MUG6		0.01	0	0.01	1.56	0.01	0.03
S5MNC1	0.01		0.01	0	1.51	0	0.01
S5MCF5	0	0.01		0.01	1.56	0.01	0.03
S5MBG7	0.01	0	0.01		1.51	0	0.01
A0A518VEB0	1.56	1.51	1.56	1.51		1.51	1.52
A0A0K2FLW7	0.01	0	0.01	0	1.51		0.01
A0A0K2CNL4	0.03	0.01	0.03	0.01	1.52	0.01	

Table S11. Amino acids alignment (%) of identified *B/* 1821L and *B/* 1951 putative phage tail-sheath protein (A0A518VEB0) with the phage tail-sheath proteins of different *B/* phages.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)						
	S5MUG6	S5MNC1	S5MCF5	S5MBG7	A0A518VEB0	A0A0K2FLW7	A0A0K2CNL4
S5MUG6		98.6	100	98.6	21.9	98.6	97.5
S5MNC1	98.6		98.6	100	21.7	100	98.9
S5MCF5	100	98.6		98.6	21.9	98.6	97.5
S5MBG7	98.6	100	98.6		21.7	100	98.9
A0A518VEB0	21.9	21.7	21.9	21.8		21.7	21.7
A0A0K2FLW7	98.6	100	98.6	100	21.7		98.7
A0A0K2CNL4	97.5	98.9	97.5	98.9	21.7	98.9	

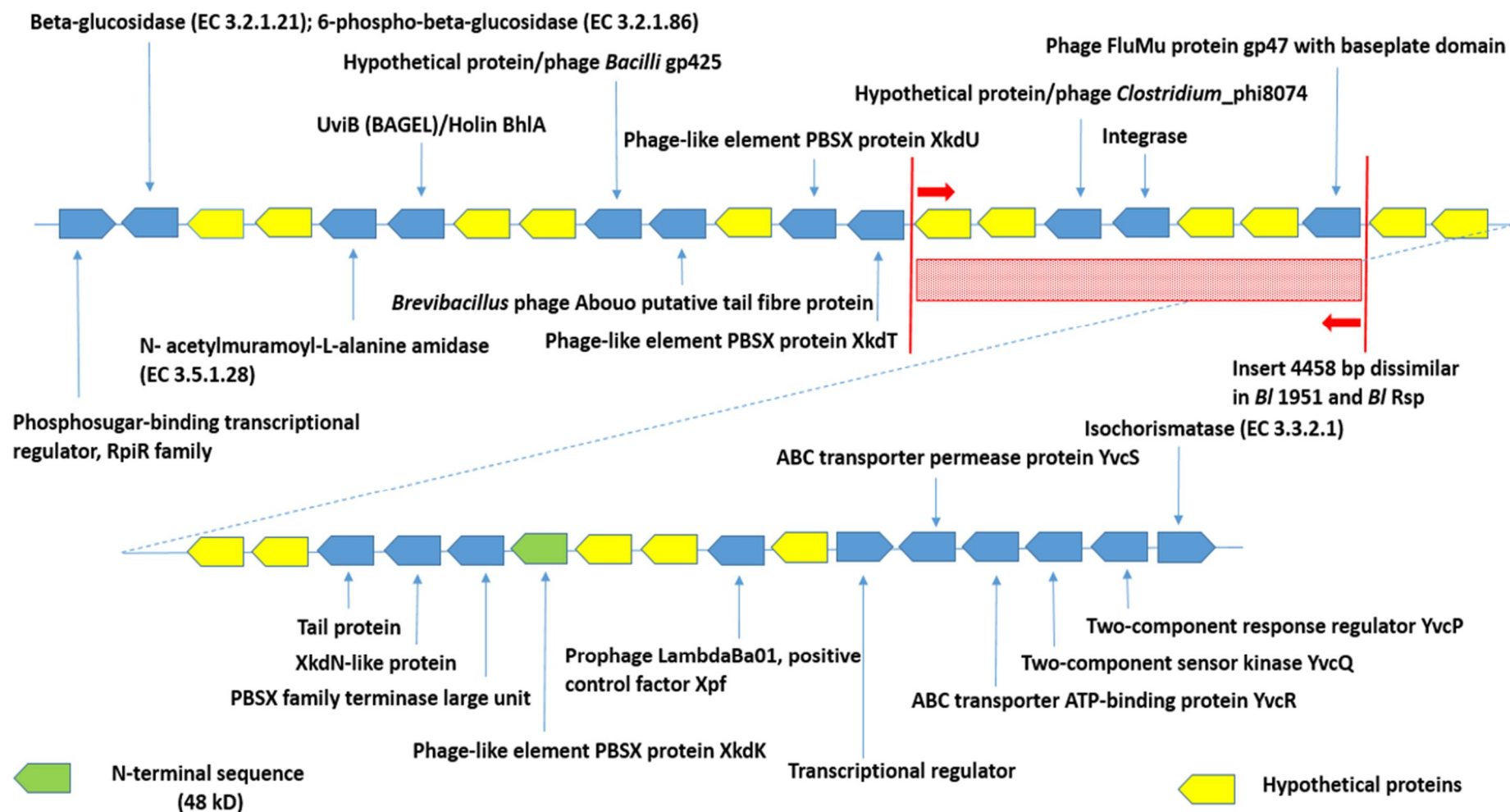


Figure S13. Schematic of the genomic architecture of *B/ 1821L* PBSX-like region encoding the identified gene *xkdK*. The red shaded box denotes *B/ 1951* region absent in *B/ 1821L*.

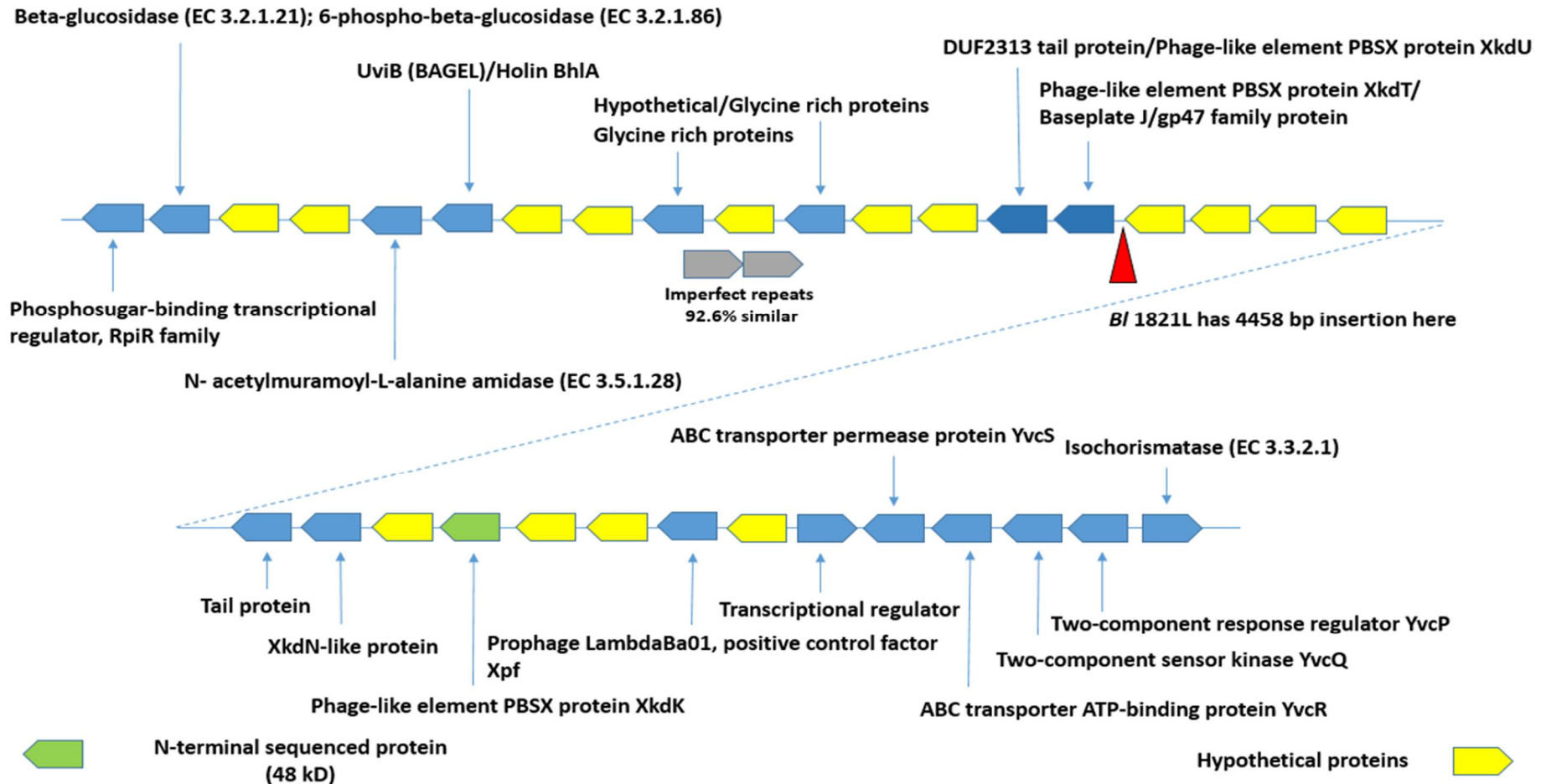


Figure S14. Genomic architecture of *B/ 1951* PBSX-like region encoding the identified gene *xkdK*. The filled red wedge points to the integration of the red shaded region of *B/ 1821L* (Figure 13) in the *B/ 1951* genome.

Table S12. Protein orthologues of *B/* 1821L UviB (BAGEL)/Holin BhIA protein in Uniprot.

Accession	Homologous protein	Organism	% identity
A0A075R9K7	Uncharacterised protein	<i>Brevibacillus laterosporus</i> LMG 15441	100
S5M5U3	Bacteriocin UviB	<i>Brevibacillus</i> phage Emery	92.0
S5M6A1	Uncharacterised protein	<i>Brevibacillus</i> phage Davies	90.8
S5MNE1	Uncharacterised protein	<i>Brevibacillus</i> phage Jimmer 1	90.8
A0A0K2CND1	Uncharacterised protein	<i>Brevibacillus</i> phage Osiris 1	90.8

Figure S15. Amino acids alignment of identified *B/1821L* and *B/1951* phage-like element PBSX protein XkdK (A0A518VEB0) with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 using programme CLUSTALO.

P54331	XKDK_BACSU	279	TEVTPDKATAWVAGASAGATFNQSLT--FVEYEGAVDVLHRLDHTIVERLIGKGEFLFTF	336
AOA518VEB0	AOA518VEB0_BRELA	271	KTYGSLEWAAWLAGMIPATPAHISLSAQLVPLKKA---EKDWGHTDIQAALNSGTLLIAVR	327
R4JQA6	R4JQA6_9CAUD	261	TELTPAQTAWVAGASAGANFNQSLT--FVEYEGAVDTLERLDNDQVEYRLSQGEFLFTF	318
EOU1S9	EOU1S9_BACPZ	279	TEVTPDKATAWVAGASAGATFNQSLT--FVEYEGAVDVLHRLDHTIVERLIGKGEFLFTF	336
			. : **: ** *: : **: : * : * . . : : *..* : : .	
P54331	XKDK_BACSU	337	DARDKSVSVEKDINSLVTFETAEKNKKFAKNKIVRVLDVAVNNDLTRELKALIKSRKSGSD	396
AOA518VEB0	AOA518VEB0_BRELA	328	D--GDVYLIESAVNTLTTLKAAEREDFGKIRVSMITLDQIVNDITSVGKKYKKGK--LDNND	383
R4JQA6	R4JQA6_9CAUD	319	DARDRTVSVEKDINSLSFTVEKNQOMAKNKIIRVLDVINNDLTFELKNLIKLRKANGND	378
EOU1S9	EOU1S9_BACPZ	337	DARDKSVSVEKDINSLVTFETAEKNKKFAKNKIVRVLDVAVNNDLTRELKALIKSRKSGSD	396
			* . :*. :*: :*: : : : .** : **: * ...*	
P54331	XKDK_BACSU	397	IPASEDGLQYVKTMITQYMTTLQDAGGIT-GFDSDEDITISMNEDRDGFLIDLAVQPVDA	455
AOA518VEB0	AOA518VEB0_BRELA	384	I----GGATFVG-AVKTYLEVREAQGAIDQGI-FEDKKNGI-GDKRG--FRLAAKPLDA	434
R4JQA6	R4JQA6_9CAUD	379	IPASDDGVQLVKTLITQYLTQLQDGGGIT-GFNSETDIVIGLNEDRDGFIIDLAVQPVDA	437
EOU1S9	EOU1S9_BACPZ	397	IPASEDGLQYVKTMITQYMTTLQDAGGIT-GFDSDEDITISMNEDRDGFLIDLAVQPVDA	455
			* . * * :. * : : ..* *: * .: *: * : **.:**	
P54331	XKDK_BACSU	456	AEKEYFNVEVN	466
AOA518VEB0	AOA518VEB0_BRELA	435	IEIEDIEWEVL	445
R4JQA6	R4JQA6_9CAUD	438	AEKEYFNVEVK	448
EOU1S9	EOU1S9_BACPZ	456	AEKEYFNVEVN	466
			* * : : **	

*Highlighted dark grey color amino acids denote similarity among the aligned phage-like element PBSX protein XkdK.
(Refer to SM Tables S13 & S14)

Table S13. Distance matrices of identified *B/* 1821L and *B/* 1951 phage-like element PBSX protein XkdK (A0A518VEB0) with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	P54331	A0A518VEB0	R4JQA6	E0U1S9
P54331		1.45	0.37	0.01
A0A518VEB0	1.45		1.40	1.47
R4JQA6	0.37	1.40		0.37
E0U1S9	0.01	1.47	0.37	

(Refer to SM Figure S15)

Table S14. Amino acids alignment (%) of identified *B/* 1821L and *B/* 1951 phage-like element PBSX protein XkdK (A0A518VEB0) with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	P54331	A0A518VEB0	R4JQA6	E0U1S9
P54331		22.9	66.5	98.7
A0A518VEB0	22.9		21.6	22.9
R4JQA6	66.5	21.6		66.5
E0U1S9	98.7	22.9	66.5	

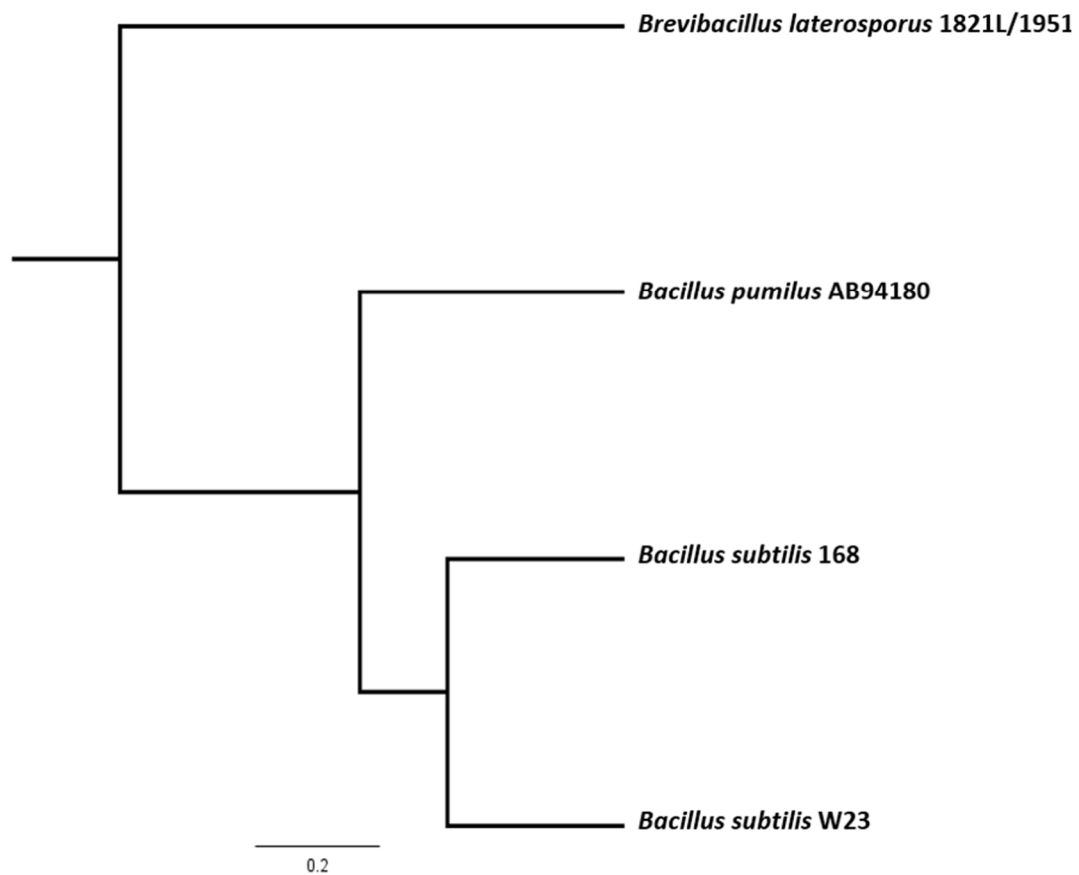


Figure S16. Dendrogram showing alignment of the identified phage-like element PBSX protein XkdK (A0A518VEB0) of *Bl* 1821L and *Bl* 1951 with similar proteins of defective prophages of *Bs* W23 (E0U1S9), *Bs* 168 (P54331), and *Bacillus* phage PBP180 (R4JQA6). Key is 0.2 nt substitutions per site.

Figure S17. Amino acids alignment of tail protein (A0A518VEA0) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 using programme CLUSTALO.

A0A518VEA0	A0A518VEA0 BRELA	1	-----MNNDMVVELLSVQKEMYKVRQGMMEWKRDA--VSL--QVANGQMGRDFLRE	47
EOU1T3	EOU1T3 BACFZ	1	MAKLARFDMEDRVS-----KKLRKVQNGFRALEKYRKMVQRKSAIDIRKDSKITLRT	53
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	1	MAKLARFDELDKVS-----KKLKRIHKGFEVEKKVKTINRQIKISIRAEDQAFY--	51
A0A518VEA0	A0A518VEA0 BRELA	48	TDKMERRIK-----ELHSQKRLGT-----	67
EOU1T3	EOU1T3 BACFZ	54	IDRIQKSLKKKLGSMISISAEDNASAVIQVQTQLQGLPASVSINIGASDQATERFERL	113
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	52	-----	51
A0A518VEA0	A0A518VEA0 BRELA	68	-----	67
EOU1T3	EOU1T3 BACFZ	114	RELVAGFKGFTIIVLSAEDQVSPAVQKIQRYSMETALKNGYSVTIRVIDHVMKTVGRISAGI	173
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	52	-----	51
A0A518VEA0	A0A518VEA0 BRELA	68	----SVQAKLRVTIDDQATQKISQ-----MRSQISQSLVISGGGSSGGSKASVMDPMG	116
EOU1T3	EOU1T3 BACFZ	174	DALTGKDNKLELAINDKVSQKLDLQKRIKIDSMRSGSPDKAAPSAGGNTGDIASMFDPET	233
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	52	-----	51
A0A518VEA0	A0A518VEA0 BRELA	117	DY-----LINSYNDAIPDSQAAAKE-----RGLFMARGKT---ELEGQ---ELD	154
EOU1T3	EOU1T3 BACFZ	234	ILTALDKFASSFMEKVDEIATKFSPETILTDLKFTTSFMNKVDATKFSPEITILTQLD	293
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	52	-----	51
A0A518VEA0	A0A518VEA0 BRELA	155	-----RSVGRMTQINPEM	167
EOU1T3	EOU1T3 BACFZ	294	KFTTSFMSKVDAIATKFSPETILTQLDKFTTSFMSKVDAIATKFSPETILGQLDKFTTSF	353
R4JJ03	R4JJ03_9CAUD	1	-----	0
P54334	XKDO_BACSU	52	-----	51

A0A518VEA0	A0A518VEA0 BRELA	168	-----MKAETAIYNRSDEVNPTN----KAEYAEFAAKLSMSTGFTSDQSLKMMALL	215
E0U1T3	E0U1T3_BACFZ	354	MSKVDAIATKFSPEITILEQLDKFTTSFMGKVDAIAAKFSPET-ILSQL-DKFTTSFMNKV	411
R4JJ03	R4JJ03_9CAUD	1	-----MKISLEMDEKKLRKFNLSM-----	19
P54334	XKDO_BACSU	52	-----RLRKI-----NDYIILKFAKSLEIKVVL-DDQ---VTSKL	82
			: ..	
A0A518VEA0	A0A518VEA0 BRELA	216	RDSTGVNDPERLANSLOQMST-NMK-----DFSDDFVSSMIKNTSQLGLLMDTPEKMA	267
E0U1T3	E0U1T3_BACFZ	412	DAIATKFSPEITLLKQLDKFTGSFMKKVDEIASKFSPEAFKQLD--KFTGSEFMKKVDDVV	469
R4JJ03	R4JJ03_9CAUD	20	-----RRFSVLMSMKLYQ-----GYRDIR--SLANQLNMIPKQMV	52
P54334	XKDO_BACSU	83	DAIERKL-----KRLPKETKLTVSLVDRTAAAYKK--TKKMIS--NQKLSLLIPDDKV	132
			: .. : : . : . .	
A0A518VEA0	A0A518VEA0 BRELA	268	MLVGEIGN-----M---GIPSNGLPLEA-----LKDIALKMSTQGEMSKV	304
E0U1T3	E0U1T3_BACFZ	470	S-----KFSPEV-IFKQLDKFTGSFMKKVDDVVSKFSP-EAIFKQ	507
R4JJ03	R4JJ03_9CAUD	53	ISIQAQGLDVIKSSIDRLKQSGTSPILLTFKLNDQLSGKMSS-IK-----KSILQL	102
P54334	XKDO_BACSU	133	T-----ST-----VKRIIGYIKKN-----	146
A0A518VEA0	A0A518VEA0 BRELA	305	LQRGYADGKSPFEAKRLATIESKEVTQLLHSDNKSNDQMAMGRIFMNVASIKDDNVRQE	364
E0U1T3	E0U1T3_BACFZ	508	LDKFADSFMMKKVDDIVS-----KFSPTATIFNELDKFADSFMM-KK	545
R4JJ03	R4JJ03_9CAUD	103	MNRYYMRLNMVDQATT-----AI-----QRIKKT-----	127
P54334	XKDO_BACSU	147	LKNGYTVKLKVIDEITK-----TV-----NR-----	167
			... :	
A0A518VEA0	A0A518VEA0 BRELA	365	MLNEVGSGSGK---EILQYLEPLIESAGNI-----SA-----G	394
E0U1T3	E0U1T3_BACFZ	546	VDDVVSKEFSPETIFNELDKFTDSFMKKVDDIVSKFSPDAILTKAEDFLTNIVDKISEKFN	605
R4JJ03	R4JJ03_9CAUD	128	-----KSLTMAKHEI-----RVSVDNAKSKLKKRDQAES	158
P54334	XKDO_BACSU	168	-----LTALRKFEKTYVVKV-----VTKISDKINKKES	198
			* .	
A0A518VEA0	A0A518VEA0 BRELA	395	LNVNKVADDEA-----EKSYQAAKDQNPWFYMQAQNEVRLAMTELAATVAKDL-----	443
E0U1T3	E0U1T3_BACFZ	606	FLNPDKI-----A-----	613
R4JJ03	R4JJ03_9CAUD	159	VVKEKKIKKKP---NATAATKTENKQSWLGNLGNKALKE--IEKYAGDVSDKLKEKLS	213
P54334	XKDO_BACSU	199	LINKETSKESSDKSSDKGSDKNSDKPGWVGKIK-----GWL	235
			..	
A0A518VEA0	A0A518VEA0 BRELA	444	-----APGFKILSNGIANVVQSFNKL-----P-QMARLAIEGVVIAFLAKKAKKS	488
E0U1T3	E0U1T3_BACFZ	614	-----NKAKEFFDNIVSKIAKKFEKFSKDIIIEK-VGFFEKIIKGIAEKLVLNDFGGL	667
R4JJ03	R4JJ03_9CAUD	214	RKFWDEKALPWVETKIDYKQEVIGRISEKIKIN-PEEY-----LDKWFNKGLDLI	264
P54334	XKDO_BACSU	236	KDWWTKSAPWIKDTINEIGAFLLDRFERLIEKLKNDVFDKIID-----KI	283
			. .. : : : . : *	

A0A518VEA0	A0A518VEA0 BRELA	489	QGEQGDSEKNI-----TIKKI-----DVKPKITIKNKVN--VTLQDKKKVIQSCSCG	533
EOU1T3	EOU1T3_BACFZ	668	GGKSSGSGKQKQKASKANTNLSTNSNSNRTKKPSMNQKASGSKSKSGGKGGGAGGCCAG	727
R4JJ03	R4JJ03_9CAUD	265	GPKNQSSNNNTNSSAQNTTETP-----TNPTPTNTQ--QNNRNGKGLFRSSCPCCARG	316
P54334	XKDO_BACSU	284	GPQKKDDSGEN-----S-DTDKKVLN-----RNTGG--NCCDDCEGG	318
			: : *	
A0A518VEA0	A0A518VEA0 BRELA	534	DS DAGGQQRKKKSGSKGKRKGKRSQKQRGPSKNGGKNSGGASKQNRNPSNPSNQKKPNK	593
EOU1T3	EOU1T3_BACFZ	728	ISTGSKKKVKNRNGSSNKGK-----KSNPVNT-----P--	755
R4JJ03	R4JJ03_9CAUD	317	LSRRGSNRTRNRNGRSQRQP-----SNPTATA-----RTE	346
P54334	XKDO_BACSU	319	ISP GTKNNKTYRKKKSPTKA-----PNRTLKV-----PGE	348
			* : : * : *	
A0A518VEA0	A0A518VEA0 BRELA	594	PNSQPKST---KPLNRKGNIPTPAPSKKGLATGFGKLDIGGKAFEGIKNFGGSTWDGL	650
EOU1T3	EOU1T3_BACFZ	756	-----KSAKA-----A--KGG-----GKGFSGL	772
R4JJ03	R4JJ03_9CAUD	347	RYRRPQ-GRGLKLTISAGKIFEK-----VPSGLKKTIGIVAS-----VAGLAGL	389
P54334	XKDO_BACSU	349	VIRRRQSGTPASAPR-----T--SGSK-----LKNWLGG	376
			: *	
A0A518VEA0	A0A518VEA0 BRELA	651	-KNLGGK-G----LGGAKSFGKGLLKIPFVGEAMGLASLATS DNKPM--ELLKLG----	698
EOU1T3	EOU1T3_BACFZ	773	LKTLGESKG----LKGGLKGLKGAAGIPGLGEILSLTDLAGINKDNAGEKVGSGGGGLA	828
R4JJ03	R4JJ03_9CAUD	390	MKGSGGLSGLDVLKNIGKSSQLLRVPIILGNLLSATDLIGTTKENVGEKVGGSGLA	449
P54334	XKDO_BACSU	377	LKSLGKDS-----KL--GKAFRGMGKAVPYVGSALAVFDLAGINKDNAGEKVGSI GGRIA	430
			* * * : * : *	
A0A518VEA0	A0A518VEA0 BRELA	699	GSAGMKAVGTMIGATVGSIVPGLGTAVGGVVGGLGSVGGDFLMDKL----PDWFGWGKE	754
EOU1T3	EOU1T3_BACFZ	829	GAAAG-----AAIGSVVPGVGTAGGVVGG-----IAGTEGGESLKG-----AIDAGA-	871
R4JJ03	R4JJ03_9CAUD	450	GGISGAAI-----GTLIPI-PFVGAAGVGGVAGSIAGTLGGSKL-----GELEDTSKL	496
P54334	XKDO_BACSU	431	GAEAGATAGAEAGATIGSFVGPETAGGAIIGGIGGLVGGIGGEEAGKNIGKMEEDTSKL	490
			* * : : * : : *	
A0A518VEA0	A0A518VEA0 BRELA	755	KPQPPAPV-----P-----PPAPVPPAQPPIPTDFDASQIKPMRRKPQNTLA	797
EOU1T3	EOU1T3_BACFZ	872	-----LNDTWNSITEGAQNAWSAIQGTWGTVSTWFTDNV-----WTPVSSAV	913
R4JJ03	R4JJ03_9CAUD	497	KENISNTLFSEDWWSEKWSVKTSAEKSGLNLSKWKEDIKTASNTLFSNWWAEQAGYI	556
P54334	XKDO_BACSU	491	KESISNSLNFKEWWSGKWSNISDTANGAITWIEDTWSKVSTWFDQYV-----FTPIYNVA	545
			: : *	
A0A518VEA0	A0A518VEA0 BRELA	798	ITPAPPVKPVATNAVNNKESAQNLSTVSTMPITLHADGVLQDVVGMIRLLKDPSVTNEV	857
EOU1T3	EOU1T3_BACFZ	914	MGV---ATSIWSNIVNAWTTIQTIFSTV---STWFMDNVWTPVSSAV-----GV	957
R4JJ03	R4JJ03_9CAUD	557	TGA---LE-----STVFNGEWWSEKWDATK-----DW	580
P54334	XKDO_BACSU	546	VPV---INFIVGLFAYAWDGILAVWNIV---YPWFKDNVWDPISGAVT-----NV	589
		 *	

AOA518VEAO	AOA518VEAO BRELA	858	KRIIETAFVNALETRGGKA-----	876
EOU1T3	EOU1T3_BACFZ	958	ATAIWSKIVNAWTTIKNVFSTVASWFMSNVWGPVKS AVIGAATTIWDKMTGAWTKIKSV-	1016
R4JJ03	R4JJ03_9CAUD	581	TQEKWDGAVEIWNSTIKKLGE--TVFNGEWGGEKWD SVKKWTKEKWDGAVNIWNSTIKGKI	638
P54334	XKDO_BACSU	590	ATTIWTGLCNANTVISGIWSTVSTWFMNDVWNPVSEAVTTAATWIWSKINDAWTIIISNI-	648
:				
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1017	-----FSTVSGWFMDIVWNPVKNTVLDVVGKGISDAFKKAIDTVKNIWKGLSG	1063
R4JJ03	R4JJ03_9CAUD	639	RETVFNKDWGGEKWDVKNWSE-NKWEQSKTIWS-AAKATASSTLFNKNWWTNKWNDVKS	696
P54334	XKDO_BACSU	649	-----WTGVSNNWFYDNVWNPVIVKKVEDIKTSIKEKFDDARKFFEDAWDGIET	695
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1064	WFKKNIQEPLTKVGEAISDAFSKAFGWVKQIWDKAGGVASKVINFTVGGGD-----	1114
R4JJ03	R4JJ03_9CAUD	697	WGKNILG-----DTWDLIKSKGAEVIGRH-----IV--	722
P54334	XKDO_BACSU	696	WFNEHVKDPLVKVSEKIAEK----FQWLFDLKDSVGGFVAKVIHRGEEVTHLKKKPIKKD	751
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1115	-----PNKGKDPDKKATGGYITKPTISWIGEAGKEFVIPV	1149
R4JJ03	R4JJ03_9CAUD	723	-----KFEKGREKGRKDFKPDQKATGGYITQPTLSWIGEAGNEFVIPT	765
P54334	XKDO_BACSU	752	SKEKKTSSKPTTNNIFAQSPSNNMTVFQALDQATGGYITKPTISWIGEAGKEFVIPV	811
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1150	DNNRGRGKMILLSQAASKLGMQVDDMG-AASSSSGNFVSVSGGAASSPLSGSASP-SMDT	1207
R4JJ03	R4JJ03_9CAUD	766	QNNRGRGKMILLAQAASHLGMSVSPSSGAASPVSSSPAPITPNAPAAPTASAGSIGGTVS	825
P54334	XKDO_BACSU	812	DNNRGRGKMILLSQAASKLGMQVDDMG-AASSSGGSPASVSGGAASVPLSGTASP-VMNT	869
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1208	ANLTGQASTLGQQFSEGFGKGISNQPVKMEDWKKKNINTPFTQMISSSQNYGQMVSQGYA	1267
R4JJ03	R4JJ03_9CAUD	826	MNGNIQSASIGEQFNHDFEQGLNQKVSLDQWKQKNIQPFNQMTSDSGKYQQQTVSAFA	885
P54334	XKDO_BACSU	870	ANLTGQASTLGQQFSEGFGKGISDQPVKMEDWKKKNINTPFTQMISASPNYGQMVSQGYA	929
AOA518VEAO	AOA518VEAO BRELA	877	-----	876
EOU1T3	EOU1T3_BACFZ	1268	KGQNGTATGTDGFLQSKVKTPFQATVKNSSSSWGTETVKGFAQQONSTQTGTAQYVSTHVD	1327
R4JJ03	R4JJ03_9CAUD	886	TGQQMTPTGTDSFLQSRVKAPYQQVMTASPTWGSSTVSGFATGQONATSIGTSQYVDQHVK	945
P54334	XKDO_BACSU	930	KGQSGTATGTDGFLQSKVKTPFQATVSKSSSSWGTGTVKGFAQQONSTQTGTAQYVSTHVD	989

A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1268	KGQNGTATGTDGFLQSKVKTPFQATVVKSSSSWGTETVKGFAGQONSTQTGTAYVSTHVD	1327
R4JJ03	R4JJ03_9CAUD	886	TGQQMTPTGTDSFLQSRVKAPYQQVMTASPTWGSSTVSGFATGQNATSIGTSQYVDQHVK	945
P54334	XKDO_BACSU	930	KGQSGTATGTDGFLQSKVKTPFQATVSKSSSSWGTGTVKGFAGQONSTQTGTAYVSTHVD	989
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1328	KPFLRSKDTSSNSWGSVMVGNFVTGMNSKSSEVKQAADMAKRVEQAFREELDIHSPSRVM	1387
R4JJ03	R4JJ03_9CAUD	946	QPFLQAKQESPGWGSMDAFNSGMRKASEVTQAAKEMAKKVEQAFREELDIHSPSRVM	1005
P54334	XKDO_BACSU	990	KPFLRSKDTSSNSWGSGLIGNFVTGMNSKSSEVKQAADMAKRVEQAFREELDIHSPSRVM	1049
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1388	MSLGRFASIGVVKGLGSDVDVKKYAEKQAGSLAAAYSVMGAMSGNVKQWIMAAALMATKTPM	1447
R4JJ03	R4JJ03_9CAUD	1006	MSLGKFASIGVVKGLDSDVDVKKFAENQAGSLIGAFSGMGASGLSVQQWLMAALMATGTSM	1065
P54334	XKDO_BACSU	1050	MSLGRFASVGVVKGLDSDVDVKKYAEKQAGSLAAAYSVMGAVGVGNVQWLMAAIMATKTPM	1109
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1448	SWLPGLMTIAQHESGGNPNAINLWDSNAKAGHPSQGLMQTIPSTFNDHKAPSMGNIKNPI	1507
R4JJ03	R4JJ03_9CAUD	1066	SWLPGLMTIAQHESNGNPNKAINLWDSNAKAGTSPKGLMQTIGPTFHSNKGKGMNDIWNPI	1125
P54334	XKDO_BACSU	1110	SWLSGLMTIAQYESSGNPNINLWDSNAKAGNPSQGLMQTIVPTTFNAHKAPGMGNIKNPI	1169
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1508	HNAAAAIGYIKSRYGSINNVPGIKSLNHGGPYVGYANGGLITKEQIARVGEKNKREWIIP	1567
R4JJ03	R4JJ03_9CAUD	1126	HNAVAAINIYIKGRYGTVFNTPLRSMRRGGPYKGYANGGLITQEVARVGEKNKREWIIP	1185
P54334	XKDO_BACSU	1170	HNAAAAIGYIKSRYGSIDNVPGIKSLKRGGPYVGYANGGLITKEQIARVGEKNKREWIIP	1229
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1568	EERGIRGRYLLQKAAQALGMEVTDPSQSQ-SDLSSGQVSAI-TAGTRQTIHTAGTKEIKI	1625
R4JJ03	R4JJ03_9CAUD	1186	EERGIRGRYLLTQAAKALGMQVYDPSNASAPL-PESQMQQVTSASAGNTTTSNGKQITI	1244
P54334	XKDO_BACSU	1230	EERGIRGRYLLQRAAQALGMEVTDPSQSQSELSSGQVSAV-TSASRPTAAVSGSKEIYI	1288
A0A518VEA0	A0A518VEA0 BRELA	877	-----	876
E0U1T3	E0U1T3_BACFZ	1626	EFNGDQHFHNEQDADSLVAKIKQALLDELQKDINTGTGKVVAFD	1669
R4JJ03	R4JJ03_9CAUD	1245	QFNGDQHFHNGDQDQSLVEKIRQMLVDELEVELQGTGKVVIDG	1288
P54334	XKDO_BACSU	1289	QFNGDQHFHNGQDAESLAAKIKQALIDELQKDINIGTKGVVAFD	1332

*Highlighted dark grey color amino acids denote similarity among the aligned phage-like element PBSX protein XkdK.
(Refer to SM Tables S15 & S16)

Table S15. Distance matrices of tail protein (A0A518VEA0) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	P54334	E0U1T3	R4JJ03	A0A518VEA0
P54334		0.56	0.85	0.71
E0U1T3	0.56		0.84	1.73
R4JJ03	0.85	0.84		1.79
A0A518VEA0	0.71	1.73	1.79	

Table S16. Amino acids alignment (%) of tail protein (A0A518VEA0) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	P54334	E0U1T3	R4JJ03	A0A518VEA0
P54334		51	37	0
E0U1T3	51.9		37.1	50
R4JJ03	37	37.1		0
A0A518VEA0	0	50	0	

Figure S18. Amino acids alignment of holin protein (A0A075R9K7) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar protein of the defective prophages PBSZ, PBSX, and PBP180 using programme CLUSTALO.

A0A075R9K7	A0A075R9K7_BRELA	1	-----MEESS---VMNALQQGP-----FAAL	18
EOU1U5	EOU1U5_BACFZ	1	MKMFDKGTVIRTVLLLVALLINQTMMLGKSPLDIQEEQVNQLADALYSAGSVIFTIGTTL	60
R4JHG4	R4JHG4_9CAUD	1	MKTFDKGTVIRTVLLLFIALINQTLVMFGQTVLPISEEQVQTAGEALYVAGSTIFTMTAV	60
Q99163	XHLB_BACSU	1	MNTFDKGTVIRTVLLLLIALINQTMMLGKSPLDIQEEQVNQLADALYSAGSIAFTIGTTL	60
			:	
A0A075R9K7	A0A075R9K7_BRELA	19	FVWLLFS--TKKEGRDREALIVKQAQTEAKLMEHNERMVIQLERNTSTLQQIERSLSGL	76
EOU1U5	EOU1U5_BACFZ	61	AAWFKNNYVTEKGKKQORD-LIKENNLTK-----	87
R4JHG4	R4JHG4_9CAUD	61	IAWFKNNYVTEKGQLQKD-ALKQRLTK-----	87
Q99163	XHLB_BACSU	61	AAWFKNNYVTEKGKKQORD-LLRDNNLTK-----	87
			.*: . * * : : * .. * :	
A0A075R9K7	A0A075R9K7_BRELA	77	EMELQELKEKVE	88
EOU1U5	EOU1U5_BACFZ	88	-----	87
R4JHG4	R4JHG4_9CAUD	88	-----	87
Q99163	XHLB_BACSU	88	-----	87

***Highlighted dark grey color amino acids denote similarity among the aligned holin proteins.
(Refer to SM Figure S19 & Tables S17 and S18)**

Table S17. Distance matrices of holin protein (A0A075R9K7) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	A0A075R9K77	E0U1U5	R4JHG4	Q99163
A0A075R9K77		2.41	1.48	1.89
E0U1U5	2.41		0.45	0.08
R4JHG4	1.48	0.45		0.47
Q99163	1.89	0.08	0.47	

Table S18. Amino acids alignment (%) of holin protein (A0A075R9K7) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	A0A075R9K77	E0U1U5	R4JHG4	Q99163
A0A075R9K77		13.6	11.4	13.6
E0U1U5	13.6		64.4	89.8
R4JHG4	11.4	64.4		61.4
Q99163	13.6	89.8	61.6	

Figure S19. Schematic presentation of amino acids alignment of holin protein (A0A075R9K7) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 using programme Geneious basic (A) and CLUSTALO (B).

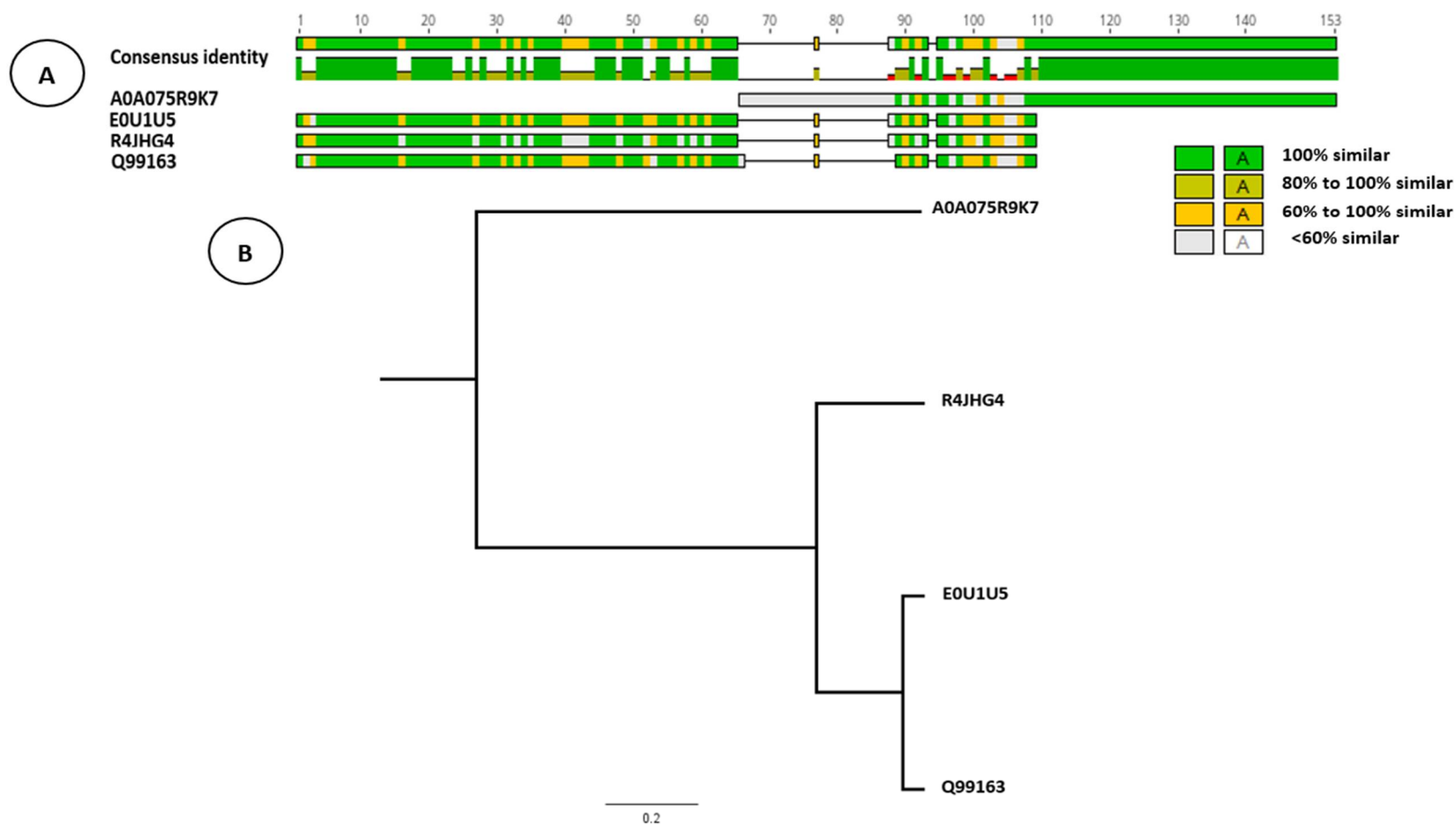


Figure S20. Amino acids alignment of N-acetylmuramoyl-L-alanine amidase protein (A0A518VEA4) encoded in PBSX-like region of *B/ 1821L* and *BI 1951* genome with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 using the programme CLUSTALO.

A0A518VEA4	A0A518VEA4 BRELA	1	-----MEKPIILIDAGHG----GADPGASGNHMQEKDLTLQIGLYQ	37
EOU1U7	EOU1U7_BACFZ	1	MVNIIQDFIPVGANNRPGYAMTEPLYTVHNTANTAAAGADAEAHARYLKNPDTATS-----	55
R4JMV0	R4JMV0_9CAUD	1	MVKIIQALIPKQNRNRPGNRMKEPLYTVHNTSNTGRGADAANHAAFVARASTGVS-----	55
P39800	XLYA_BACSU	1	MVNIIQDFIPVGANNRPGYAMTEPLYTVHNTANTAVGADAAAHARYLKNPDTTTS-----	55
			.*: * . . *** . .: . . .	
A0A518VEA4	A0A518VEA4 BRELA	38	LQRCRELNLPAVITRTIDTTLTSPQRTTLVKQSGATYICISNHINAGGGEGVEAIHSI--F	95
EOU1U7	EOU1U7_BACFZ	56	-----WHFTVDD-----TELYQHL--PLNENGWHAGDGNNGSGNRASIGIE	93
R4JMV0	R4JMV0_9CAUD	56	-----WHFTVDD-----QVLYQHL--PLNENGWHAGDGRGTGNMKSIGIE	93
P39800	XLYA_BACSU	56	-----WHFTVDD-----TELYQHL--PLNENGWHAGDGNNGSGNRASIGIE	93
			. : *	
A0A518VEA4	A0A518VEA4 BRELA	96	TSNKLANAQAQVAAEGQRFRRVYTRVGS DGRDYFMHRETGAVETIIMEYGFIDHVGDA	155
EOU1U7	EOU1U7_BACFZ	94	ICENTDGDFAQATANAQWLKLTLMSEHN-----ISLANVVPHKYWSGKECP	139
R4JMV0	R4JMV0_9CAUD	94	ICENAGANFEQAVKNAQWLIRKLMGDLG-----IPLSNVVPHKHWSGKECP	139
P39800	XLYA_BACSU	94	ICENADGDFAKATANAQWLKLTMAEHN-----ISLANVVPHKYWSGKECP	139
			:: : : * . : : : . : : : . .	
A0A518VEA4	A0A518VEA4 BRELA	156	QKLTNNWKRYAEAVLKAFSSHIGHPYSPALEEPIDDFQMAVDALVQA-----	202
EOU1U7	EOU1U7_BACFZ	140	RKLLDTWDSFKAGIGGGGSQTYVVKQGDTLT SIARAFGVTVAQLREWN NIEDPNVIQVGQ	199
R4JMV0	R4JMV0_9CAUD	140	RKLLNRWDGFKAGIASASTSQMTTAKPVKETS I-----KT	174
P39800	XLYA_BACSU	140	RKLLDTWDSFKAGIGGGGSQTYVVKQGDTLT SIARAFGVTVAQLQEWNNIEDPNLIRVGQ	199
			: ** : * . : . : . . .	
A0A518VEA4	A0A518VEA4 BRELA	203	-----KIITSPDYWKQONAGPNGTVLG	223
EOU1U7	EOU1U7_BACFZ	200	VLIVSAPSYAEPELYPLPDGIIKLTTPYTSGEHVFQVQRALAALYFYFDPKGAVNNGIDG	259
R4JMV0	R4JMV0_9CAUD	175	ISTRSTSKINKVKKTYSLPAGILKVIKPLTKGS AVKAVQALASIYFYFDPKGAINNGIDG	234
P39800	XLYA_BACSU	200	VLIVSAPSAAEKPELYPLPDGIIQLTTPYTSGEHVFQVQRALAALYFYFDPKGAVNNGIDG	259
			: : : : : : . . : *	
A0A518VEA4	A0A518VEA4 BRELA	224	DYAAQLIKNMA-----NHLKAGA-----	241
EOU1U7	EOU1U7_BACFZ	260	IYGPKTADAVARFQSVNGLTADGIYGPATKAKIAAQLS-	297
R4JMV0	R4JMV0_9CAUD	235	YVGPKTANAVSRFQMMHGLTPDGIYGPKTKETLSKVIES	273
P39800	XLYA_BACSU	260	VYGPKTADAVARFQSVNGLTADGIYGPATKEKIAAQLS-	297
			*. : . : : : * . . .	

***Highlighted dark grey color amino acids denote similarity among the aligned N-acetylmuramoyl-L-alanine amidase proteins.
(Refer to SM Figure S21 & Tables S19 and S20)**

Table S19. Distance matrices of N-acetylmuramoyl-L-alanine amidase protein (A0A518VEA4) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 .

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	A0A518VEA4	E0U1U7	R4JMV0	P39800
A0A518VEA4		0.22	1.75	1.40
E0U1U7	0.22		0.55	0.05
R4JMV0	1.75	0.55		0.54
P39800	1.40	0.05	0.54	

Table S20. Alignment (%) of N-acetylmuramoyl-L-alanine amidase protein (A0A518VEA4) encoded in PBSX-like region of *B/* 1821L and *B/* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180.

Uniprot Accession # (https://www.uniprot.org)	Uniprot Accession # (https://www.uniprot.org)			
	A0A518VEA4	E0U1U7	R4JMV0	P39800
A0A518VEA4		15.4	7.7	15.4
E0U1U7	15.4		53.5	95.3
R4JMV0	7.7	53.5		53.9
P39800	15.4	95.3	53.9	

Figure S21. Schematic presentation of amino acids alignment of N-acetylmuramoyl-L-alanine amidase protein (A0A518VEA4) encoded in PBSX-like region of *Bl* 1821L and *Bl* 1951 with the similar proteins of the defective prophages PBSZ, PBSX, and PBP180 using programme Geneious basic (A) and CLUSTALO (B).

