Supplemental material

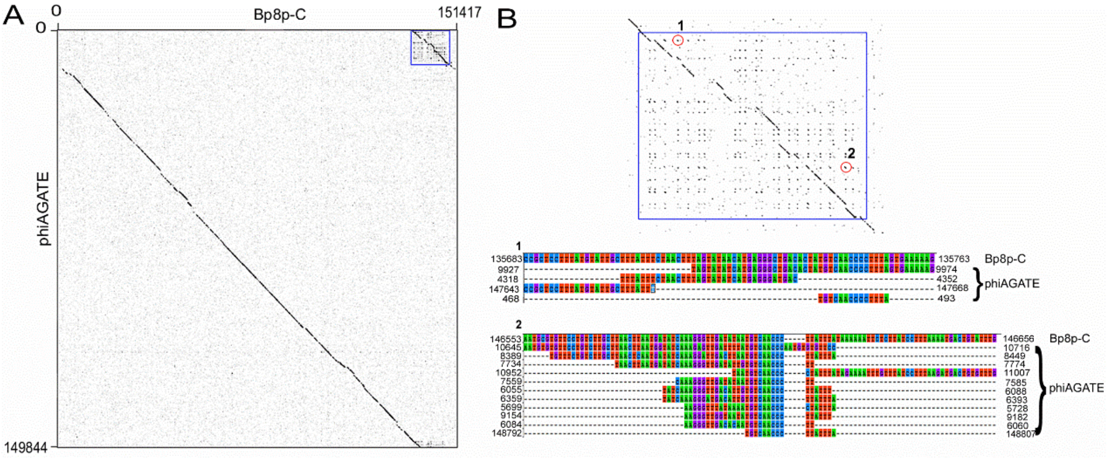

FIG S1 Comparative genomne analysis of Bp8p-C and phiAGATE. (A)Dot plot analysis of Bp8p-C and phiAGATE genomes by using Gepard. The long terminal repeat sequences found in both Bp8p-C and phiAGATE genome were indicated in blue rectangle. (B) The long terminal repeat sequence found by dot plot was analyzed using MEGA 5.0.

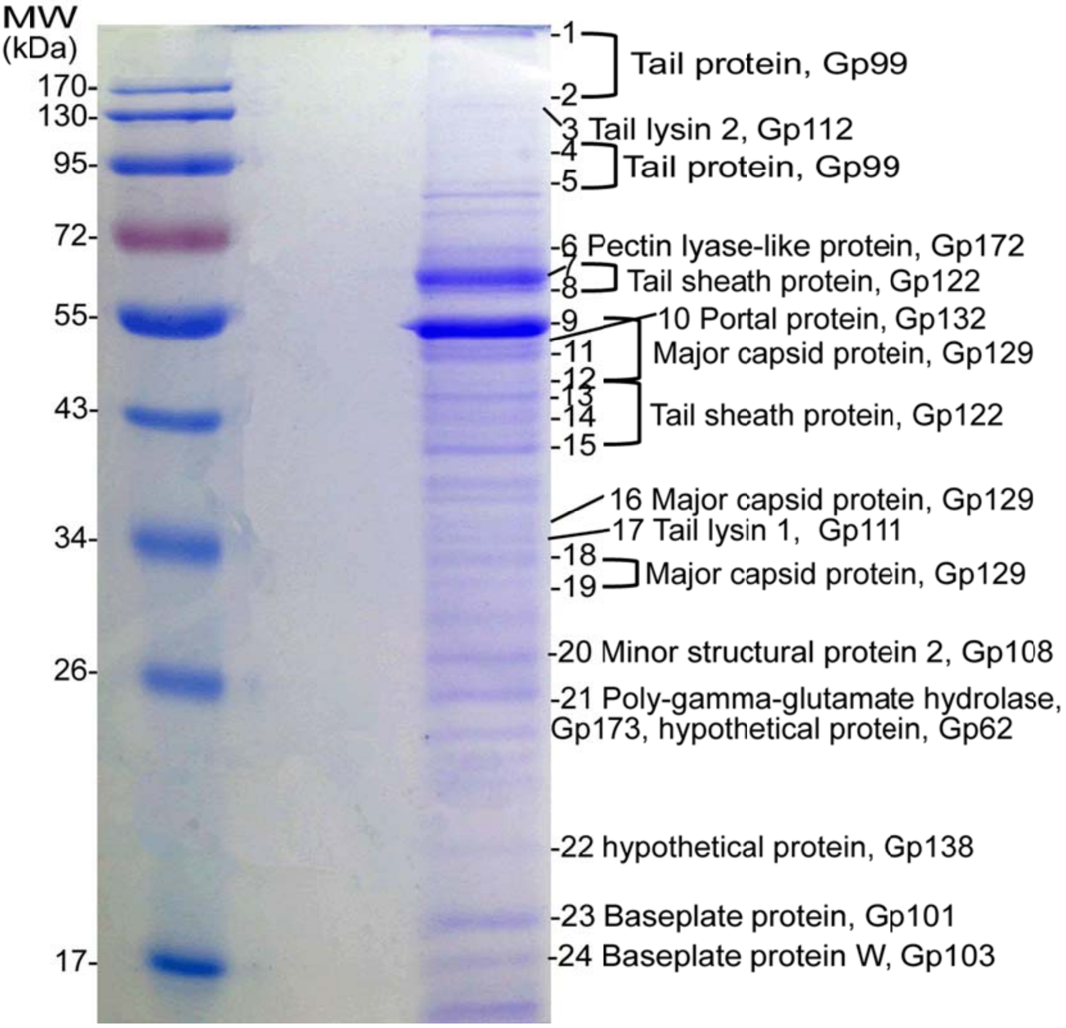

FIG S2 SDS-PAGE analysis of Bp8p-C structural protein. The phage purified by sucrose density gradient centrifugation was analyzed by 12% SDS-PAGE. The molecular weight standard was indicated on the left and the band numbers of the proteins identified by mass spectrometric were also indicated.

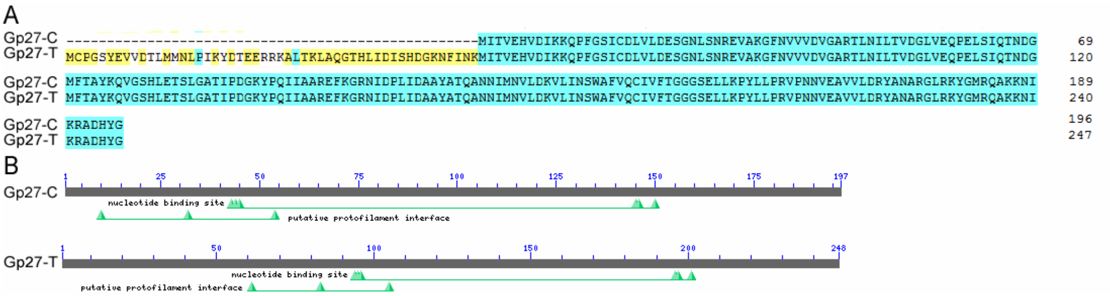

FIG S3 Comparative analysis of Gp27-C and Gp27-T. (A) The alignment of the amino acid sequence of Gp27-C and Gp27-T by using Mega 5.0. (B) The motifs of Gp27-C and Gp27-T were analyzed by searching against the CDD database in NCBI.

Table S1. Host range of phage Bp8p-C and Bp8p-T.

Strain	Species	Bp8p-C	Bp8p-T
X3-1 MGSC B 020607	*Bacillus pumilus*	-	-
3-J	*Bacillus pumilus*	+	+
8-4-Gr31	*Bacillus pumilus*	+	+
4-T	*Bacillus pumilus*	+	+
5	*Bacillus pumilus*	+	+
2-g2-Gr25	*Bacillus pumilus*	-	-
3-t-Gr26	*Bacillus pumilus*	-	-
8-1-Gr29	*Bacillus pumilus*	-	-
8-2-Gr30	*Bacillus pumilus*	+	+
8-3	*Bacillus pumilus*	-	-
1-t-Gr20	*Bacillus pumilus*	-	-
8-5-Gr32	*Bacillus pumilus*	-	-
4-T8	*Bacillus pumilus*	+	+
GR8	*Bacillus pumilus*	+	+
CS-33	*Bacillus thuringiensis*	-	-
168	*Bacillus subtilis*	-	-
411a	*Bacillus cereus*	-	-
63605	*Bacillus anthracis*	-	-

Table S2. General features of the predicted proteins from Bp8p-C genome

ORF name	Position (nt)	ORF length (aa)	Size (kDa(22))	Closest hit (e value)	Accession no. of closest hit	The best match in phages (e value)	Predictive function
1	-/(25..525)	166	19.7(5.30)	Bacillus phage vB_BanS-Tsamsa (1e-55)	AGI11781	Bacillus phage vB_BanS-Tsamsa (1e-55)	hypothetical protein
2	-/(543..737)	64	7.54(4.29)	Bacillus phage Andromeda(8e-21)	YP_007517541.1	Bacillus phage Andromeda(8e-21)	hypothetical protein
3	-/(737..1219)	160	18.0(6.10)	Ceratotherium simum simum (1.1)	XP_004443172.1		hypothetical protein
4	-/(1383..1649)	88	10.2(4.61)	Macaca mulatta (1.8)	EHH20558.1		hypothetical protein
5	-/(1769..1993)	74	8.62(4.94)	Bacillus sp. M 2-6 (2e-23)	WP_008343969.1	Bacillus phage phiAGATE(4e-20)	hypothetical protein
6	-/(2032..2913)	293	33.1(4.76)	Bacillus phage phiAGATE (5e-63)	YP_007349276.1	Bacillus phage phiAGATE (5e-63)	hypothetical protein
7	-/(3037..3357)	106	12.3(6.12)	Bacillus phage phiAGATE (1e-41)	YP_007349277.1	Bacillus phage phiAGATE (1e-41)	hypothetical protein
8	-/(3311..3541)	76	8.43(7.83)	Nostoc punctiforme PCC 73102(6.3)	YP_001866514.1		hypothetical protein
9	-/(3538..4335)	265	30.7(5.32)	Pusillimonas noertemannii](1.7)	WP_017525166.1		hypothetical protein
10	-/(4398..4778)	126	14.6(5.91)	Bacillus phage phiAGATE (4e-70)	YP_007349278.1	Bacillus phage phiAGATE (4e-70)	hypothetical protein
11	-/(4987..5307)	106	12.2(4.69)	Bacillus phage SP10(3e-43)	YP_007003293.1	Bacillus phage SP10(3e-43)	hypothetical protein
12	-/(5309..5821)	170	20.3(4.24)	Bacillus subtilis subsp. subtilis str. 168(1e-09)	NP_389771.1		hypothetical protein
13	-/(5867..5992)	41	4.45(9.82)				hypothetical protein
14	-/(6059..6535)	158	18.4(4.66)	Bacillus phage phiAGATE (3e-100)	YP_007349280.1	Bacillus phage phiAGATE (3e-100)	hypothetical protein
15	-/(6549..7271)	240	27.5(6.04)	Bacillus phage phiAGATE (1e-137)	YP_007349281.1	Bacillus phage phiAGATE (1e-137)	hypothetical protein
16	-/(7821..8051)	76	8.83(6.58)	Bacillus phage phiAGATE (4e-43)	YP_007349282.1	Bacillus phage phiAGATE (4e-43)	putative XRE family transcriptional regulator
17	-/(8074..8361)	90	10.91(5.87)	Bacillus phage phiAGATE (1e-56)	YP_007349283.1	Bacillus phage phiAGATE (1e-56)	hypothetical protein
18	-/(8361..9068)	235	26.71(4.98)	Bacillus phage phiAGATE (3e-39)	YP_007349284.1	Bacillus phage phiAGATE (3e-39)	hypothetical protein
19	-/(9070..9342)	90	11.23(4.39)	Bacillus phage phiAGATE (8e-07)	YP_007349285.1	Bacillus phage phiAGATE (8e-07)	hypothetical protein
20	-/(9356..9568)	70	8.20(6.52)				hypothetical protein

21	-/(9532..9705)	57	6.23(7.900	Vibrio phage VpV262(3.4)	NP_640273.1	Vibrio phage VpV262(3.4)	hypothetical protein
22	-/(9731..9988)	85	10.21(8.86)	Bacillus phage phiAGATE (0.002)	YP_007349288.1	Bacillus phage phiAGATE (0.002)	hypothetical protein
23	-/(10070..12298)	742	84.09(5.09)	Bacillus phage phiAGATE (0.0)	YP_007349289.1	Bacillus phage phiAGATE (0.0)	putative DNA translocase
24	-/(12418..13779)	453	50.11(10.15)	Bacillus phage phiAGATE (0.0)	YP_007349290.1	Bacillus phage phiAGATE (0.0)	hypothetical protein
25	-/(14427..14975)	182	19.71(6.11)	Bacillus phage phiAGATE (5E-118)	YP_007349293.1	Bacillus phage phiAGATE (5E-118)	putative peptidase M23
26	-/(15108..15440)	110	12.63(5.78)	Bacillus phage phiAGATE (2e-51)	YP_007349294.1	Bacillus phage phiAGATE (2e-51)	hypothetical protein
27	-/(15367..15957)	197	21.63(7.74)	Bacillus phage phiAGATE (5e-134)	YP_007349295.1	Bacillus phage phiAGATE (5e-134)	Putative plasmid segregation protein
28	-/(16543..16974)	143	16.25(8.55)	Bacillus phage phiAGATE (4e-32)	YP_007349296.1	Bacillus phage phiAGATE (4e-32)	hypothetical protein
29	-/(16967..17362)	131	15.09(4.88)	Bacillus phage phiAGATE (2e-41)	YP_007349297.1	Bacillus phage phiAGATE (2e-41)	hypothetical protein
30	-/(17599..17841)	80	9.14(4.00)	Cohnella laeviribosi(0.83)	WP_019003802.1		hypothetical protein
31	-/(17843..18097)	84	9.36(7.81)	Bacillus phage phiAGATE (6e-28)	YP_007349300.1	Bacillus phage phiAGATE (6e-28)	hypothetical protein
32	-/(18124..18312)	62	6.92(4.86)	Bacillus phage phiAGATE (7e-08)	YP_007349301.1	Bacillus phage phiAGATE (7e-08)	hypothetical protein
33	-/(18309..18536)	75	8.79(6.82)	Weeksella virosa DSM 16922(2.4)	YP_004238982.1		hypothetical protein
34	-/(18529..18915)	128	14.15(9.58)	Bacillus phage phiAGATE (1e-28)	YP_007349303.1	Bacillus phage phiAGATE (1e-28)	hypothetical protein
35	-/(18915..19211)	98	11.07(5.17)	Bacillus phage phiAGATE (1e-15)	YP_007349304.1	Bacillus phage phiAGATE (1e-15)	hypothetical protein
36	-/(19214..19402)	62	7.32(10.10)	Leishmania infantum JPCM5 (2.9)	XP_001470126.1		hypothetical protein
37	-/(19557..19925)	122	14.38(10.52)	Erwinia pyrifoliae DSM 12163(0.57)	YP_005801897.1		hypothetical protein
38	-/(20192..20899)	235	27.06(7.73)	Bacillus phage phiAGATE (5e-91)	YP_007349306.1	Bacillus phage phiAGATE (5e-91)	putative RNA polymerase sigma factor SigF 2
39	-/(20935..21714)	259	29.67(5.92)	Bacillus phage phiAGATE (2e-147)	YP_007349307.1	Bacillus phage phiAGATE (2e-147)	putative RNA polymerase sigma factor SigF 1
40	-/(22188..22823)	211	23.91(5.68)	Bacillus phage phiAGATE (1e-119)	YP_007349309.1	Bacillus phage phiAGATE (1e-119)	hypothetical protein
41	-/(22879..23595)	238	27.90(5.61)	Bacillus phage phiAGATE	YP_007349310.1	Bacillus phage	hypothetical protein

				(8e-76)		phiAGATE (8e-76)	
42	-/(23704..24702)	222	24.82(9.19)	Bacillus phage phiAGATE (4e-138)	YP_007349311.1	Bacillus phage phiAGATE (4e-138)	hypothetical protein
43	-/(24468..25322)	284	32.32(5.26)	Bacillus phage phiAGATE (2e-174)	YP_007349312.1	Bacillus phage phiAGATE (2e-174)	hypothetical protein
44	-/(25322..25852)	176	20.07(10.46)	Bacillus phage phiAGATE (2e-105)	YP_007349313.1	Bacillus phage phiAGATE (2e-105)	hypothetical protein
45	-/(25961..26530)	189	21.55(6.20)	Bacillus phage phiAGATE (4e-103)	YP_007349314.1	Bacillus phage phiAGATE (4e-103)	hypothetical protein
46	-/(26627..27349)	240	27.92(8.94)	Bacillus phage phiAGATE (9e-163)	YP_007349315.1	Bacillus phage phiAGATE (9e-163)	hypothetical protein
47	-/(27448..27849)	133	14.75(4.47)	Bacillus phage phiAGATE (3e-40)	YP_007349316.1	Bacillus phage phiAGATE (3e-40)	hypothetical protein
48	-/(27836..28288)	150	16.81(5.40)	Bacillus phage phiAGATE (3e-52)	YP_007349317.1	Bacillus phage phiAGATE (3e-52)	hypothetical protein
49	-/(28292..28552)	86	10.58(5.13)	Bacillus phage phiAGATE (1e-17)	YP_007349318.1	Bacillus phage phiAGATE (1e-17)	hypothetical protein
50	-/(28613..28774)	53	5.61(6.49)	Bacillus phage phiAGATE (2e-10)	YP_007349319.1	Bacillus phage phiAGATE (2e-10)	hypothetical protein
51	-/(29405..29590)	61	7.08(9.99)	Bacillus phage phiAGATE (8e-10)	YP_007349321.1	Bacillus phage phiAGATE (8e-10)	hypothetical protein
52	-/(29556..29768)	70	8.42(5.81)	Bacillus amyloliquefaciens (7e-22)	WP_021493457.1		hypothetical protein
53	-/(29861..30256)	131	14.34(9.22)	Bacillus phage phiAGATE (1e-33)	YP_007349323.1	Bacillus phage phiAGATE (1e-33)	hypothetical protein
54	-/(30299..31639)	446	51.00(6.30)	Bacillus phage phiAGATE (0.0)	YP_007349324.1	Bacillus phage phiAGATE (0.0)	putative metallo-dependent phosphatase 2
55	-/(31658..31939)	93	10.78(4.58)	Bacillus phage phiAGATE (4e-47)	YP_007349325.1	Bacillus phage phiAGATE (4e-47)	hypothetical protein
56	-/(31983..32927)	314	35.40(5.82)	Bacillus phage phiAGATE (0.0)	YP_007349326.1	Bacillus phage phiAGATE (0.0)	hypothetical protein
57	-/(33114..33632)	172	18.62(4.33)	Bacillus phage Grass (4e-35)	AGY47405.1	Bacillus phage Grass (4e-35)	hypothetical protein
58	-/(33652..33972)	106	11.64(6.72)	Bacillus phage phiAGATE (3e-57)	YP_007349328.1	Bacillus phage phiAGATE (3e-57)	Putative holin
59	-/(34015..34587)	190	22.28(5.55)	Bacillus phage phiAGATE (5e-130)	YP_007349329.1	Bacillus phage phiAGATE (5e-130)	hypothetical protein
60	-/(34631..34987)	118	13.37(6.29)	Bacillus phage phiAGATE	YP_007349330.1	Bacillus phage	hypothetical protein

				(2e-74)		phiAGATE (2e-74)	
61	-/(35034..36245)	403	44.29(5.54)	Bacillus phage phiAGATE (0.0)	YP_007349331.1	Bacillus phage phiAGATE (0.0)	putative DNA recombination and repair protein RecA
62	-/(36326..37549)	407	43.23(4.98)	Bacillus phage phiAGATE (6e-123)	YP_007349332.1	Bacillus phage phiAGATE (6e-123)	hypothetical protein
63	-/(37645..38130)	161	18.83(5.16)	Bacillus phage phiAGATE (7e-98)	YP_007349333.1	Bacillus phage phiAGATE (7e-98)	hypothetical protein
64	-/(38230..40815)	861	99.71(5.95)	Bacillus phage phiAGATE (0.0)	YP_007349336.1	Bacillus phage phiAGATE (0.0)	putative DNA polymerase A.1
65	-/(41596..41992)	108	12.64(6.61)	Bacillus phage phiAGATE (2e-51)	YP_007349337.1	Bacillus phage phiAGATE (2e-51)	putative DNA-binding protein
66	-/(41891..42646)	251	29.80(8.98)	Bacillus phage phiAGATE (1e-166)	YP_007349338.1	Bacillus phage phiAGATE (1e-166)	hypothetical protein
67	-/(42753..43271)	172	20.60(6.99)	Bacillus phage phiAGATE (5e-16)	YP_007349339.1	Bacillus phage phiAGATE (5e-16)	hypothetical protein
68	-/(43308..43610)	100	11.78(6.03)	Bacillus phage phiAGATE (3e-29)	YP_007349339.1	Bacillus phage phiAGATE (3e-29)	hypothetical protein
69	-/(43680..43955)	91	10.47(5.81)	Bacillus phage phiAGATE (2e-38)	YP_007349341.1	Bacillus phage phiAGATE (2e-38)	hypothetical protein
70	-/(43971..44135)	54	6.37(4.42)	Bacillus phage phiAGATE (1e-26)	YP_007349342.1	Bacillus phage phiAGATE (1e-26)	hypothetical protein
71	-/(44328..44564)	78	9.06(5.57)	Bacillus phage phiAGATE (4e-46)	YP_007349343.1	Bacillus phage phiAGATE (1e-26)	hypothetical protein
72	-/(44554..45144)	196	23.02(9.05)	Bacillus phage phiAGATE (4e-135)	YP_007349344.1	Bacillus phage phiAGATE (4e-135)	hypothetical protein
73	-/(45151..45689)	112	12.86(4.81)	Bacillus phage vB_BceM-Bc431v3 (2e-34)	YP_007676980.1	Bacillus phage vB_BceM-Bc431v3 (2e-34)	hypothetical protein
74	-/(45492..45686)	64	7.52(5.19)	Dothistroma septosporum NZE10 (2.6)	EME39600.1		hypothetical protein
75	-/(45785..46222)	145	16.27(4.58)	Bacillus phage phiAGATE (4e-69)	YP_007349345.1	Bacillus phage phiAGATE (4e-69)	hypothetical protein
76	-/(46493..47482)	329	37.58(4.99)	Bacillus phage phiAGATE (0.0)	YP_007349346.1	Bacillus phage phiAGATE (0.0)	putative ribonucleotide reductase of class Ib (aerobic), subunit beta
77	-/(47482..47649)	55	6.43(3.92)	Bacillus phage phiAGATE (2e-20)	YP_007349347.1	Bacillus phage phiAGATE (2e-20)	hypothetical protein
78	-/(47782..49836)	684	78.39(6.00)	Bacillus phage Grass (0.0)	AGY47378.1	Bacillus phage Grass (0.0)	ribonucleotide-diphosphate reductase subunit alpha
79	-/(50389..50667)	92	10.70(4.46)	Bacillus phage phiAGATE (4e-20)	YP_007349352.1	Bacillus phage phiAGATE (4e-20)	hypothetical protein

80	-/(50867..51259)	130	15.14(10.76)	Bacillus phage phiAGATE (0.80)	YP_007349353.1	Bacillus phage phiAGATE (0.80)	hypothetical protein
81	-/(51275..51562)	95	11.44(10.08)	Bacillus phage phiAGATE (8e-18)	YP_007349353.1	Bacillus phage phiAGATE (8e-18)	hypothetical protein
82	-/(51586..51735)	49	5.59(3.98)	Bacillus marmarensis (1e-06)	WP_022628475.1		hypothetical protein
83	-/(51698..51919)	73	8.76(8.89)	Ktedonobacter racemifer (2.1)	WP_007914275.1		hypothetical protein
84	-/(51960..52142)	60	6.89(8.03)				hypothetical protein
85	-/(52279..52503)	74	8.47(4.55)	Bacillus phage phiAGATE (8e-11)	YP_007349353.1	Bacillus phage phiAGATE (8e-11)	hypothetical protein
86	-/(52503..53066)	187	21.62(6.75)	Bacillus phage phiAGATE (5e-121)	YP_007349362.1	Bacillus phage phiAGATE (5e-121)	putative resolvase
87	-/(53072..53449)	125	14.36(5.26)	Bacillus phage phiAGATE (6e-33)	YP_007349363.1	Bacillus phage phiAGATE (6e-33)	hypothetical protein
88	-/(53442..53762)	106	12.17(4.13)	Bacillus phage phiAGATE (8e-42)	YP_007349364.1	Bacillus phage phiAGATE (8e-42)	hypothetical protein
89	-/(53776..54393)	205	22.52(6.17)	Bacillus phage phiAGATE (2e-111)	YP_007349365.1	Bacillus phage phiAGATE (2e-111)	putative deoxyuridine 5'-triphosphate nucleotidohydrolase
90	-/(54465..55535)	356	40.41(4.84)	Bacillus phage phiAGATE (0.0)	YP_007349366.1	Bacillus phage phiAGATE (0.0)	putative DNA primase
91	-/(55539..56177)	212	24.85(5.49)	Bacillus phage phiAGATE (1e-91)	YP_007349367.1	Bacillus phage phiAGATE (1e-91)	hypothetical protein
92	-/(56174..58078)	634	72.11(5.98)	Bacillus phage phiAGATE (0.0)	YP_007349368.1	Bacillus phage phiAGATE (0.0)	putative recombination related exonuclease
93	-/(58154..58423)	89	10.27(4.79)	Bacillus phage phiAGATE (7e-50)	YP_007349369.1	Bacillus phage phiAGATE (7e-50)	hypothetical protein
94	-/(58420..59475)	351	40.14(5.15)	Bacillus phage phiAGATE (0.0)	YP_007349370.1	Bacillus phage phiAGATE (0.0)	putative recombination exonuclease
95	-/(59477..60736)	419	47.39(5.90)	Bacillus phage phiAGATE (0.0)	YP_007349371.1	Bacillus phage phiAGATE (0.0)	putative helicase
96	-/(60995..62695)	566	65.21(5.80)	Bacillus phage phiAGATE (0.0)	YP_007349372.1	Bacillus phage phiAGATE (0.0)	putative transcriptional regulator
97	-/(62784..65843)	1019	115.89(8.88)	Bacillus phage phiAGATE (0.0)	YP_007349377.1	Bacillus phage phiAGATE (0.0)	putative intein containing helicase/endonuclease protein
98	-/(66101..66274)	57	6.72(8.04)	Bacillus phage phiAGATE (1e-26)	YP_007349375.1	Bacillus phage phiAGATE (1e-26)	hypothetical protein
99	-/(66298..69603)	1101	12.19(4.86)	Bacillus phage phiAGATE (0.0)	YP_007349376.1	Bacillus phage phiAGATE (0.0)	putative tail protein
100	-/(69798..70328)	176	19.92(4.80)	Bacillus phage phiAGATE (3e-119)	YP_007349377.1	Bacillus phage phiAGATE	hypothetical protein

						(3e-119)	
101	-/(70519..71907)	462	52.275.29)	Bacillus phage phiAGATE (0.0)	YP_007349378.1	Bacillus phage phiAGATE (0.0)	Putative baseplate protein
102	-/(71923..72969)	348	39.11（5.37）	Bacillus phage phiAGATE (0.0)	YP_007349379.1	Bacillus phage phiAGATE (0.0)	putative baseplate J family protein
103	-/(72983..73678)	231	25.90(4.67)	Bacillus phage phiAGATE (3e-162)	YP_007349380.1	Bacillus phage phiAGATE (3e-162)	putative baseplate protein W
104	-/(73720..74223)	167	19.23(4.53)	Bacillus phage phiAGATE (1e-99)	YP_007349381.1	Bacillus phage phiAGATE (1e-99)	hypothetical protein
105	-/(74223..74984)	253	28.09(8.50)	Bacillus phage phiAGATE (3e-175)	YP_007349178.1	Bacillus phage phiAGATE (3e-175)	hypothetical protein
106	-/(75046..75360)	104	11.67(4.70)	Bacillus phage phiAGATE (2e-37)	YP_007349179.1	Bacillus phage phiAGATE (2e-37)	hypothetical protein
107	-/(75408..75872)	154	18.02(4.44)	Bacillus phage phiAGATE (8e-62)	YP_007349180.1	Bacillus phage phiAGATE (8e-62)	hypothetical protein
108	-/(75888..78335)	815	87.71(9.57）	Bacillus phage phiAGATE (0.0)	YP_007349181.1	Bacillus phage phiAGATE (0.0)	putative minor structural protein 2
109	-/(78370..82122)	1250	136.69(4.59)	Bacillus phage phiAGATE (0.0)	YP_007349182.1	Bacillus phage phiAGATE (0.0)	putative minor structural protein 1
110	-/(82136..84166)	676	75.07(4.69)	Bacillus phage phiAGATE (0.0)	YP_007349183.1	Bacillus phage phiAGATE (0.0)	putative tail fiber protein
111	-/(84181..86178)	665	73.60(5.25)	Bacillus phage phiAGATE (0.0)	YP_007349184.1	Bacillus phage phiAGATE (0.0)	putative tail lysin 1
112	-/(86427..90164)	1245	131.96(9.02)	Bacillus phage phiAGATE (0.0)	YP_007349185.1	Bacillus phage phiAGATE (0.0)	putative tail lysin 2
113	87451..88041	196	19.24(5.75)				hypothetical protein
114	-/(90215..90805)	196	22.49(4.40)	Bacillus phage phiAGATE (2e-114)	YP_007349186.1	Bacillus phage phiAGATE (2e-114)	hypothetical protein
115	-/(90852..91259)	135	15.78(4.98)	Bacillus phage phiAGATE (2e-69)	YP_007349187.1	Bacillus phage phiAGATE (2e-68)	hypothetical protein
116	-/(91343..91930)	195	22.73(7.79)	Bacillus phage phiAGATE (2e-90)	YP_007349188.1	Bacillus phage phiAGATE (2e-90)	hypothetical protein
117	-/(92039..92647)	202	21.01(9.56)	Bacillus phage phiAGATE (6e-130)	YP_007349189.1	Bacillus phage phiAGATE (6e-130)	putative cell wall-binding, peptidase-related domain protein
118	-/(92801..93202	135	15.08(6.58)	Bacillus phage Grass (3e-59)	AGY47482.1	Bacillus phage Grass (3e-59)	hypothetical protein
119	-/(93216..93563)	115	13.49(4.81)	Bacillus phage phiAGATE (8e-07)	YP_007349190.1	Bacillus phage phiAGATE (8e-07)	hypothetical protein
120	-/(93585..93938)	117	13.45(4.60)	Bacillus phage phiAGATE (3e-09)	YP_007349190.1	Bacillus phage phiAGATE (3e-09)	hypothetical protein

121	-/(94056..94430)	124	13.96(5.15)	Bacillus phage phiAGATE (2e-83)	YP_007349191.1	Bacillus phage phiAGATE (2e-83)	putative structural protein
122	-/(94534..96246)	570	62.09(4.95)	Bacillus phage phiAGATE (0.0)	YP_007349192.1	Bacillus phage phiAGATE (0.0)	putative tail sheath protein
123	-/(96274..96576)	100	11.92(9.79)	Bacillus phage phiAGATE (3e-34)	YP_007349193.1	Bacillus phage phiAGATE (3e-34)	hypothetical protein
124	-/(96506..97192)	228	25.92(4.55)	Bacillus phage phiAGATE (3e-121)	YP_007349194.1	Bacillus phage phiAGATE (3e-121)	hypothetical protein
125	-/(97382..97966)	194	22.59(10.71)	Bacillus phage phiAGATE (1e-132)	YP_007349195.1	Bacillus phage phiAGATE (1e-132)	hypothetical protein
126	-/(98007..98849)	280	31.60(7.63)	Bacillus phage phiAGATE (4e-175)	YP_007349196.1	Bacillus phage phiAGATE (4e-175)	hypothetical protein
127	-/(98863..99510)	215	24.15(5.95)	Bacillus phage phiAGATE (5e-133)	YP_007349197.1	Bacillus phage phiAGATE (5e-133)	hypothetical protein
128	-/(99759..100037)	92	10.30(8.85)	Bacillus phage phiAGATE (5e-21)	YP_007349198.1	Bacillus phage phiAGATE (5e-21)	hypothetical protein
129	-/(100119..101540)	473	52.10(5.18)	Bacillus phage phiAGATE (0.0)	YP_007349199.1	Bacillus phage phiAGATE (0.0)	putative major capsid protein
130	-/(101670..102617)	315	35.10(4.50)	Bacillus phage phiAGATE (1e-87)	YP_007349200.1	Bacillus phage phiAGATE (1e-87)	hypothetical protein
131	-/(102622..103092)	156	17.76(9.18)	Bacillus phage phiAGATE (1e-105)	YP_007349201.1	Bacillus phage phiAGATE (1e-105)	putative prohead protease
132	-/(103532..105187)	551	62.56(5.76)	Bacillus phage phiAGATE (0.0)	YP_007349202.1	Bacillus phage phiAGATE (0.0)	putative portal protein
133	-/(105218..105475)	85	9.76(5.22)	Bacillus phage phiAGATE (7e-41)	YP_007349203.1	Bacillus phage phiAGATE (7e-41)	hypothetical protein
134	-/(105609..105995)	1218	15.05(6.43)	Bacillus subtilis (0.14)	WP_017697671.1		hypothetical protein
135	-/(105988..106359)	123	13.90(5.03)	Bacillus phage phiAGATE (4e-47)	YP_007349205.1	Bacillus phage phiAGATE (4e-47)	hypothetical protein
136	-/(106442..106819)	125	13.85(4.58)	Bacillus macauensis (4e-62)	WP_007201862.1	Streptococcus phage O1205 (2e-43)	hypothetical protein
137	-/(107199..107348)	49	5.50(4.88)	Synechococcus sp. CB0205 (1.4)		WP_010316034.1	hypothetical protein
138	-/(107373..107894)	173	19.945(6.86)	Bacillus phage phiAGATE (7e-109)	YP_007349206.1	Bacillus phage phiAGATE (7e-109)	hypothetical protein
139	-/(107965..108258)	97	11.44(6.83)	Bacillus phage phiAGATE (9e-08)	YP_007349207.1	Bacillus phage phiAGATE	hypothetical protein

						(9e-108)	
140	-/(108346..108639)	97	11.70(5.13)	Bacillus phage phiAGATE (3e-45)	YP_007349207.1	Bacillus phage phiAGATE (3e-45)	hypothetical protein
141	-/(108799..109323)	174	20.47(5.27)	Bacillus amyloliquefaciens LL3 (4e-80)	YP_005546027.1	Bacillus phage SPBc2 (5e-78)	SPBc2 prophage-derived 5'(3')-deoxyribonucleotidase
142	-/(110259..110546)	95	11.11(5.16)	Bacillus phage phiAGATE (9e-34)	YP_007349208.1	Bacillus phage phiAGATE (9e-34)	hypothetical protein
143	112308..112628	106	12.63(6.62)	Bacillus phage phiAGATE (2e-51)	YP_007349210.1	Bacillus phage phiAGATE (2e-51)	putative lambda repressor-like DNA-binding protein
144	112697..112822	41	4.45(6.50)				hypothetical protein
145	-/(112911..113237)	108	12.50(4.93)	Bacillus phage phiAGATE (4e-66)	YP_007349212.1	Bacillus phage phiAGATE (4e-66)	hypothetical protein
146	-/(113264..113614)	116	13.70(5.30)	Bacillus phage phiAGATE (4e-71)	YP_007349213.1	Bacillus phage phiAGATE (4e-71)	hypothetical protein
147	-/(113604..113894)	96	10.55(6.70)	Bacillus phage phiAGATE (2e-46)	YP_007349214.1	Bacillus phage phiAGATE (2e-46)	hypothetical protein
148	114002..117274	90	10.25(10.69)	Bacillus phage phiAGATE (3e-38)	YP_007349215.1	Bacillus phage phiAGATE (3e-38)	hypothetical protein
149	114286..114792	168	19.91(4.11)	Bacillus phage phiAGATE (3e-62)	YP_007349216.1	Bacillus phage phiAGATE (3e-62)	hypothetical protein
150	115063..115479	138	15.17(4.50)	Bacillus phage phiAGATE (2e-74)	YP_007349217.1	Bacillus phage phiAGATE (2e-74)	hypothetical protein
151	115479..117278	599	68.49(6.89)	Bacillus phage vB_BceM-Bc431v3 (0.0)	YP_007676908.1	Bacillus phage vB_BceM-Bc431v3 (0.0)	terminase large subunit
152	117344..118204	286	32.39(5.88)	Bacillus phage phiAGATE (9e-149)	YP_007349221.1	Bacillus phage phiAGATE (9e-149)	hypothetical protein
153	118173..118862	229	25.85(5.02)	Bacillus phage phiAGATE (6e-126)	YP_007349222.1	Bacillus phage phiAGATE (6e-126)	hypothetical protein
154	118855..119190	111	12.65(6.29)	Bacillus phage phiAGATE (1e-61)	YP_007349223.1	Bacillus phage phiAGATE (1e-61)	hypothetical protein
155	119255..120193	312	33.56(9.83)	Bacillus phage phiAGATE (0.0)	YP_007349224.1	Bacillus phage phiAGATE (0.0)	putative N-acetylmuramoyl-L-alanine amidase
156	120522..121241	239	26.82(6.00)	Bacillus phage phiAGATE (3e-164)	YP_007349225.1	Bacillus phage phiAGATE (3e-164)	putative PhoH family protein
157	121241..122248	335	38.03(4.34)	Bacillus phage phiAGATE (5e-66)	YP_007349226.1	Bacillus phage phiAGATE (5e-66)	hypothetical protein
158	122344..123822	492	57.98(7.22)	Bacillus phage phiAGATE (0.0)	YP_007349227.1	Bacillus phage phiAGATE (0.0)	putative PcfJ protein

159	123908..124459	183	21.19(4.96)	Bacillus phage phiAGATE (3e-125)	YP_007349228.1	Bacillus phage phiAGATE (3e-125)	hypothetical protein
160	124684..124797	37	4.49(5.12)	Bacillus phage phiAGATE (5e-18)	YP_007349229.1	Bacillus phage phiAGATE (5e-18)	hypothetical protein
161	125037..125729	230	26.22(6.34)	Bacillus phage phiAGATE (2e-162)	YP_007349230.1	Bacillus phage phiAGATE (2e-162)	putative thymidylate synthase
162	125751..126386	211	24.61(5.54)	Bacillus phage phiAGATE (1e-146)	YP_007349231.1	Bacillus phage phiAGATE (1e-146)	putative adenylate kinase-like protein
163	126401..126886	161	18.93(5.80)	Bacillus phage phiAGATE (2e-115)	YP_007349232.1	Bacillus phage phiAGATE (2e-115)	putative dihydrofolate reductase
164	126903..127700	265	30.68(4.43)	Bacillus phage phiAGATE (1e-172)	YP_007349233.1	Bacillus phage phiAGATE (1e-172)	hypothetical protein
165	128016..128426	136	15.58(4.91)	Bacillus phage phiAGATE (2e-51)	YP_007349234.1	Bacillus phage phiAGATE (2e-51)	hypothetical protein
166	128529..129098	189	22.07(6.01)	Bacillus phage phiAGATE (1e-35)	YP_007349237.1	Bacillus phage phiAGATE (1e-35)	hypothetical protein
167	129088..129606	172	20.07(5.12)	Bacillus phage phiAGATE (4e-80)	YP_007349238.1	Bacillus phage phiAGATE (4e-80)	hypothetical protein
168	129887..130027	46	5.35(4.52)	Bacillus phage phiAGATE (0.99)	YP_007349239.1	Bacillus phage phiAGATE (0.99)	hypothetical protein
169	130020..130280	86	10.12(4.92)	Bacillus phage phiAGATE (2e-40)	YP_007349240.1	Bacillus phage phiAGATE (2e-40)	hypothetical protein
170	130347..130856	169	19.55(5.80)	Bacillus phage phiAGATE (1e-41)	YP_007349241.1	Bacillus phage phiAGATE (1e-41)	hypothetical protein
171	130877..131260	127	14.38(4.68)	Bacillus phage phiAGATE (0.54)	YP_007349241.1	Bacillus phage phiAGATE (0.54)	hypothetical protein
172	131669..133258	529	58.40(5.77)	Bacillus phage phiAGATE (0.0)	YP_007349242.1	Bacillus phage phiAGATE (0.0)	putative Pectin lyase-like protein
173	133368..133967	199	22.07(5.39)	Bacillus phage phiAGATE (1e-118)	YP_007349243.1	Bacillus phage phiAGATE (1e-118)	putative poly-gamma-glutamate hydrolase
174	-/(134412..134756)	114	13.23(4.46)	Bacillus phage phiAGATE (2e-40)	YP_007349244.1	Bacillus phage phiAGATE (2e-40)	hypothetical protein
175	-/(134846..135064)	72	8.78(4.36)	Rhizobium leguminosarum (0.11)	WP_003565261.1	Lactobacillus phage JCL1032 (3.6)	hypothetical protein
176	-/(135155..135394)	79	9.23(5.07)	Bacillus phage phiAGATE (3e-34)	YP_007349245.1	Bacillus phage phiAGATE (3e-34)	hypothetical protein
177	-/(135387..135677)	96	11.06(4.24)	Bacillus phage phiAGATE (1e-47)	YP_007349246.1	Bacillus phage phiAGATE (1e-47)	hypothetical protein

178	-/(135765..136193)	142	16.52(4.22)	Bacillus phage phiAGATE (2e-53)	YP_007349247.1	Bacillus phage phiAGATE (2e-53)	hypothetical protein
179	-/(136202..136453)	83	9.62(4.43)	candidate division BRC1 bacterium SCGC AAA252-M09 (0.80)	WP_020249241.1		hypothetical protein
180	-/(136710..137081)	123	13.77(4.58)	Bacillus phage phiAGATE (2e-53)	YP_007349249.1	Bacillus phage phiAGATE (2e-53)	hypothetical protein
181	-/(137506..137718)	70	8.11(4.16)	Comamonas testosteroni CNB-2 (1.0)	YP_003277363.1		hypothetical protein
182	-/(137835..138044)	69	8.35(6.71)	Bacillus thuringiensis HD-789 (2e-09)	YP_006624439.1		hypothetical protein
183	-/(137835..138044)	128	15.38(4.87)	Bacillus phage phiAGATE (2e-09)	YP_007349251.1	Bacillus phage phiAGATE (2e-09)	hypothetical protein
184	-/(138595..138792)	65	7.30(4.28)	Bacteroides (2.5)	WP_007487658.1		hypothetical protein
185	-/(138820..139236)	138	16.28(4.58)	Bacillus phage phiAGATE (3e-72)	YP_007349251.1	Bacillus phage phiAGATE (3e-72)	hypothetical protein
186	-/(139302..139739)	145	17.14(4.37)	Bacillus phage phiAGATE (1e-82)	YP_007349253.1	Bacillus phage phiAGATE (1e-82)	hypothetical protein
187	-/(139743..139913)	56	6.81(7.98)	Prevotella sp. MSX73 (7.4)	WP_007411973.1		hypothetical protein
188	-/(140016..140201)	61	7.37(3.99)	Halorubrum phage GNf2 (0.40)	AGF91265.1	Halorubrum phage GNf2 (0.40)	hypothetical protein
189	-/(140285..140533)	82	9.42(4.66)	Ichthyophthirius multifiliis (1.6)	XP_004036927.1		hypothetical protein
190	-/(140650..140862)	70	8.28(5.00)	Clostridium saccharoperbutylacetonicum N1-4(HMT) (0.75)	YP_007456357.1		hypothetical protein
191	-/(140856..141176)	106	12.29(6.03)	Bacillus phage SPP1 (1e-06)	NP_690744.1	Bacillus phage SPP1 (1e-06)	hypothetical protein
192	-/(141255..141497)	80	9.35(3.74)	Bacillus phage phiAGATE (8e-29)	YP_007349255.1 YP_00734926.1	Bacillus phage phiAGATE (8e-29)	hypothetical protein
193	-/(141578..141979)	133	15.67(3.87)	Bacillus phage phiAGATE (3e-48)	YP_007349257.1	Bacillus phage phiAGATE (3e-48)	hypothetical protein
194	-/(141981..142223)	80	9.07(5.00)	Bacillus phage phiAGATE (2e-43)	YP_007349258.1	Bacillus phage phiAGATE (2e-43)	hypothetical protein
195	-/(142600..143151)	183	21.95(5.31)	Bacillus phage phiAGATE (3e-118)	YP_007349262.1	Bacillus phage phiAGATE (3e-118)	hypothetical protein
196	-/(143213..143509)	98	11.26(4.16)	Ralstonia (0.68)	WP_009239428.1		hypothetical protein
197	-/(143522..143647)	41	4.92(10.12)	Bacillus phage phiAGATE (4e-17)	YP_007349263.1	Bacillus phage phiAGATE (4e-17)	hypothetical protein
198	-/(143724..144281)	185	21.86(4.19)	Bacillus phage phiAGATE (1e-68)	YP_007349264.1	Bacillus phage phiAGATE (1e-68)	hypothetical protein
199	-/(144383..144631)	82	9.32(5.70)	Bacillus phage phiAGATE (7e-45)	YP_007349265.1	Bacillus phage phiAGATE (7e-45)	hypothetical protein

200	-/(144652..144804)	50	5.79(6.01)	Bacillus phage phiAGATE (3e-20)	YP_007349266.1	Bacillus phage phiAGATE (3e-20)	hypothetical protein
201	-/(144828..145079)	83	9.60(6.04)	Lactobacillus buchneri NRRL B-30929 (1.2)	YP_004399033.1		hypothetical protein
202	-/(145115..145627)	170	20.00(3.88)	Bacillus phage phiAGATE (7e-61)	YP_007349267.1	Bacillus phage phiAGATE (7e-61)	hypothetical protein
203	-/(145894..146526)	210	23.49(4.10)	Bacillus phage phiAGATE (2e-55)	YP_007349269.1	Bacillus phage phiAGATE (2e-55)	hypothetical protein
204	-/(146613..146987)	124	14.48(9.63)	Bacillus phage phiNIT1 (1e-39)	YP_008318262.1	Bacillus phage phiNIT1 (1e-39)	hypothetical protein
205	-/(147206..147445)	79	8.81(4.32)	Bacillus cereus (5e-13)	WP_000865212.1		hypothetical protein
206	-/(147505..147903)	132	15.59(4.65)	Bacillus phage phiAGATE (4e-52)	YP_007349271.1	Bacillus phage phiAGATE (4e-52)	hypothetical protein
207	-/(147900..148307)	135	15.91(5.09)	Bacillus phage phiAGATE (2e-52)	YP_007349272.1	Bacillus phage phiAGATE (2e-52)	hypothetical protein
208	-/(148323..148802)	159	18.29(5.40)	Parabacteroides (0.12)	WP_005855820.1		hypothetical protein
209	-/(149139..150254)	371	39.77(5.86)	Bacillus phage phiAGATE (2e-85)	YP_007349274.1	Bacillus phage phiAGATE (2e-85)	putative hexapeptide repeat containing transferase like protein
210	-/(150244..150474)	76	8.75(4.13)	Bacillus phage Grass (1e-05)	AGY47430.1	Bacillus phage Grass (1e-05)	hypothetical protein
211	-/(150576..151064)	162	17.86(4.48)	Flavobacteria bacterium MS024-3C (0.40)	WP_008867922.1		hypothetical protein
212	-/(151051..151413)	120	13.60(5.38)	Paenibacillus polymyxa SC2 (3e-09)	YP_003965746.1		hypothetical protein

Table S3. Feature of predicted tRNA from the genome of phage Bp8p-C

Name	Position	Length	Triple codon	Corresponding amino acid
tRNA^{Met}	-/(106842..106913)	72	CAU	Met
tRNA^{His}	-/(109549..109619)	71	GUG	His
tRNA^{Gly}	-/(109633..109703)	71	UCC	Gly
tRNA^{Phe}	-/(110983..111052)	72	GAA	Phe
tRNA^{Asn}	-/(111434..111505)	72	GUU	Asn

Table S4. Insert sequences found in Bp8p-C genome by using IS Finder

Sequences producing significant alignments	IS Family	Group	Origin	Score (bits)	E (value)
ISSpma1	IS3	IS407	*Sphingopyxis macrogoltabida*	40	0.73
ISNgo3	IS110		*Neisseria gonorrhoeae*	40	0.73
ISSusp4	ISLre2	ISAzba1	*Sulfitobacter sp.*	38	2.9
ISArsp6	Tn3		*Arthrobacter sp.*	38	2.9
ISAcma27	IS630		*Acaryochloris marina*	38	2.9
ISEc8	IS66		*Escherichia coli*	38	2.9
IS231Q	IS4	IS231	*Bacillus thuringiensis*	38	2.9
IS605	IS200/IS605	-	*Helicobacter pylori*	38	2.9

Table S5. Tandem repeats found in Bp8p-C genome by using Tandem Repeat Finder

Indices	Period Size	Copy Number	Consensus Size	Percent Matches	Percent Indels	Score	A	C	G	T	Entropy (0-2)
33141--33178	18	2.1	18	90	0	58	7	21	36	34	1.82
36642--36704	6	11.0	6	90	10	105	0	17	49	33	1.47
135004--135052	24	2.0	24	96	0	89	16	20	6	57	1.60
136688--136741	22	2.5	22	93	0	81	38	12	12	35	1.82
147114--147230	32	3.7	32	100	0	234	27	15	26	30	1.96