

Figure S1 A) DNA isolated from *Paenibacillus larvae* 408, 453 and phages 1A-5/A, B) Protein profiles of 1/A-5/A bacteriophages

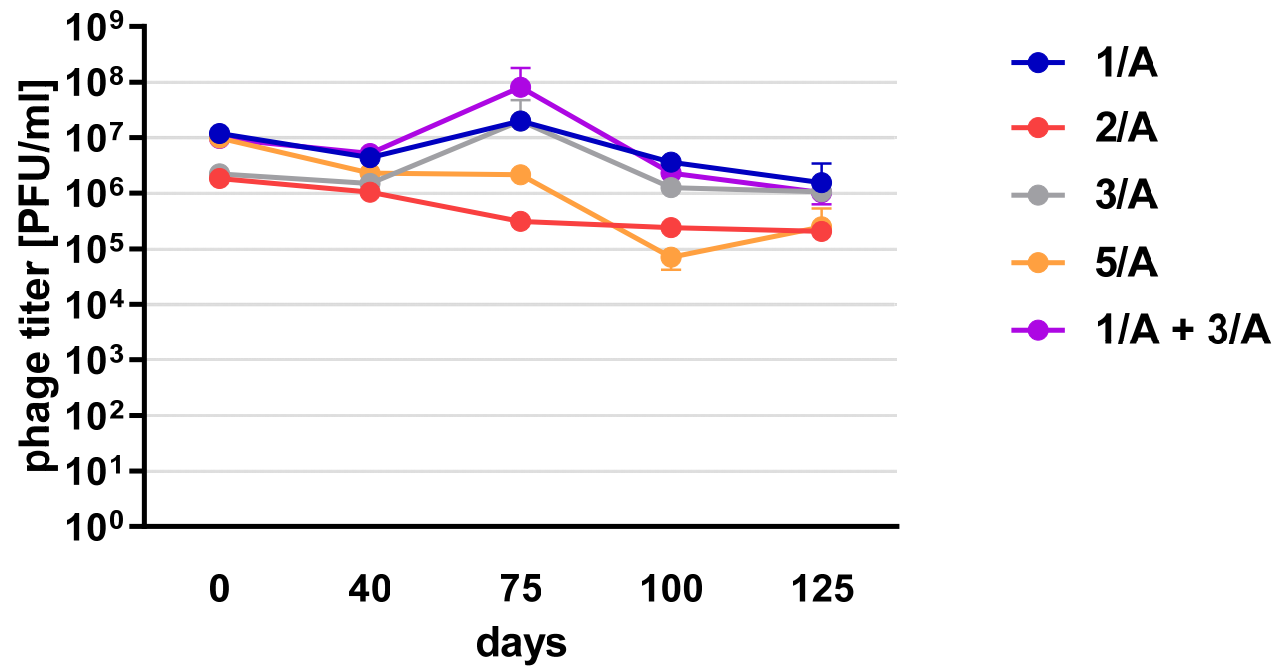
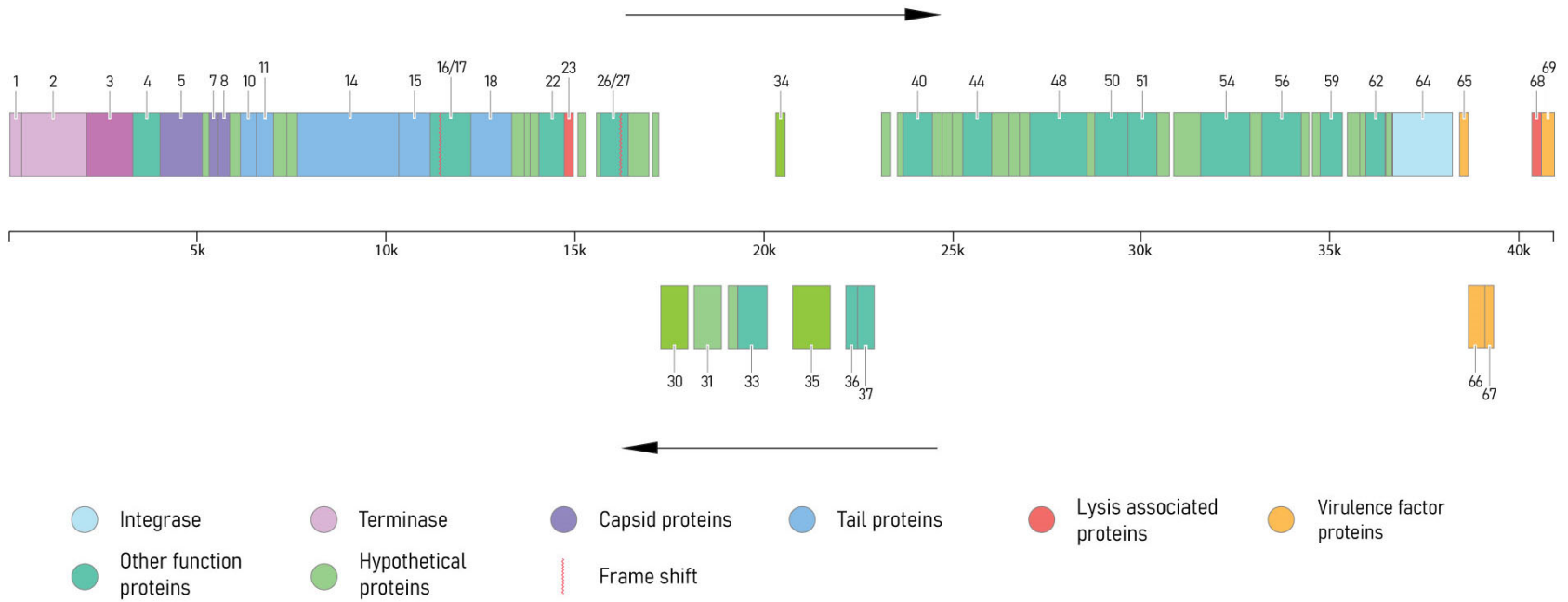
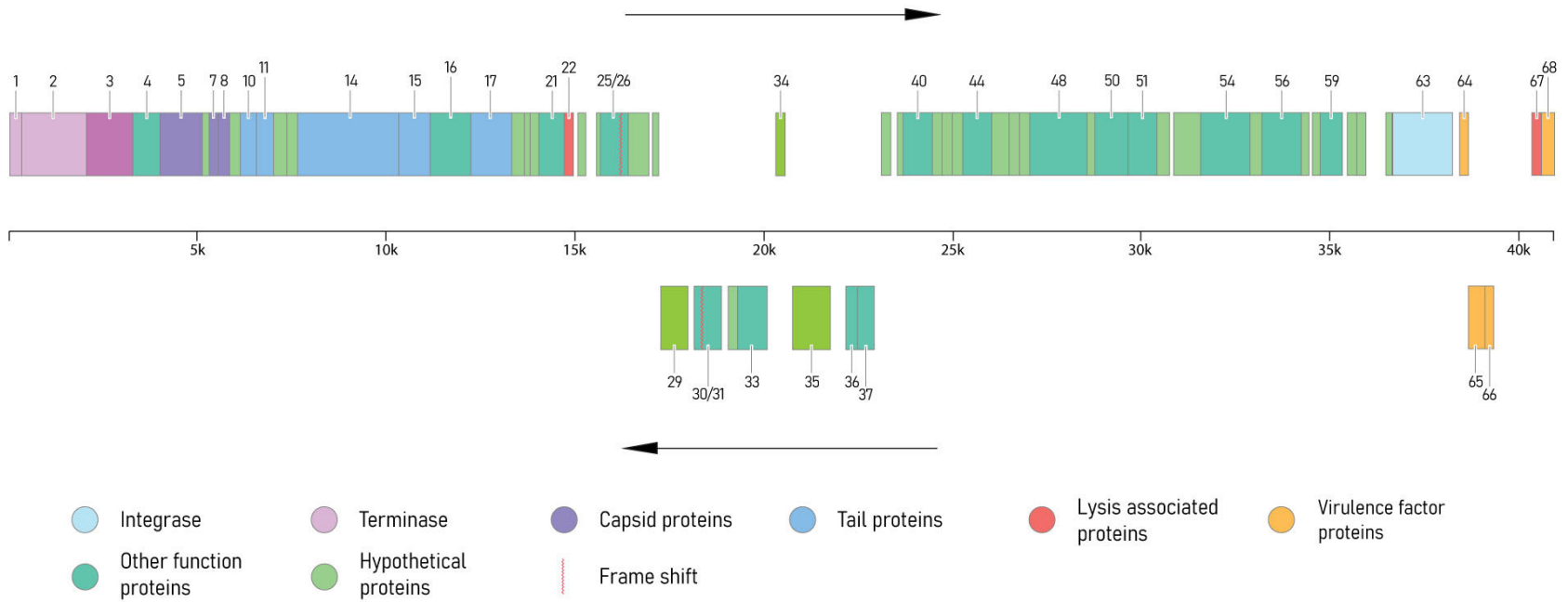


Figure S2. The stability of lyophilized phages with 10% glucose. Error bars represent standard deviation (\pm SD) of mean phage titer.

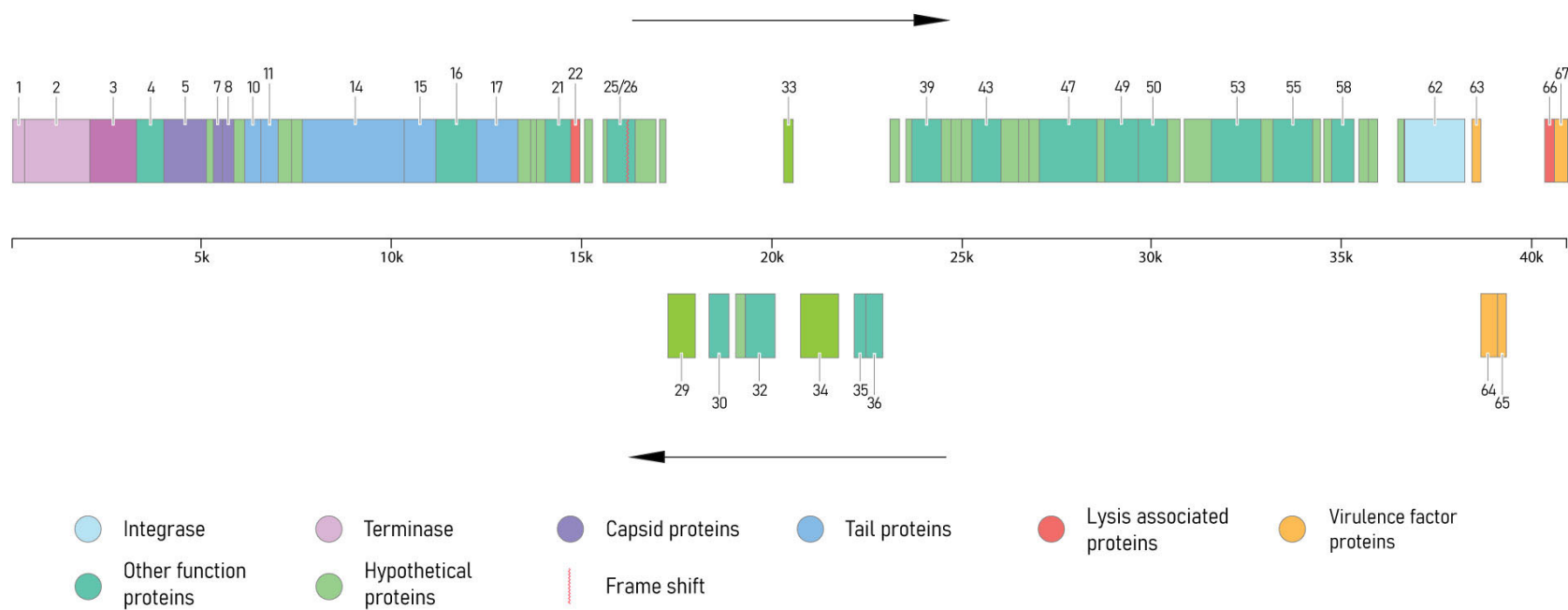
PHAGE 1A



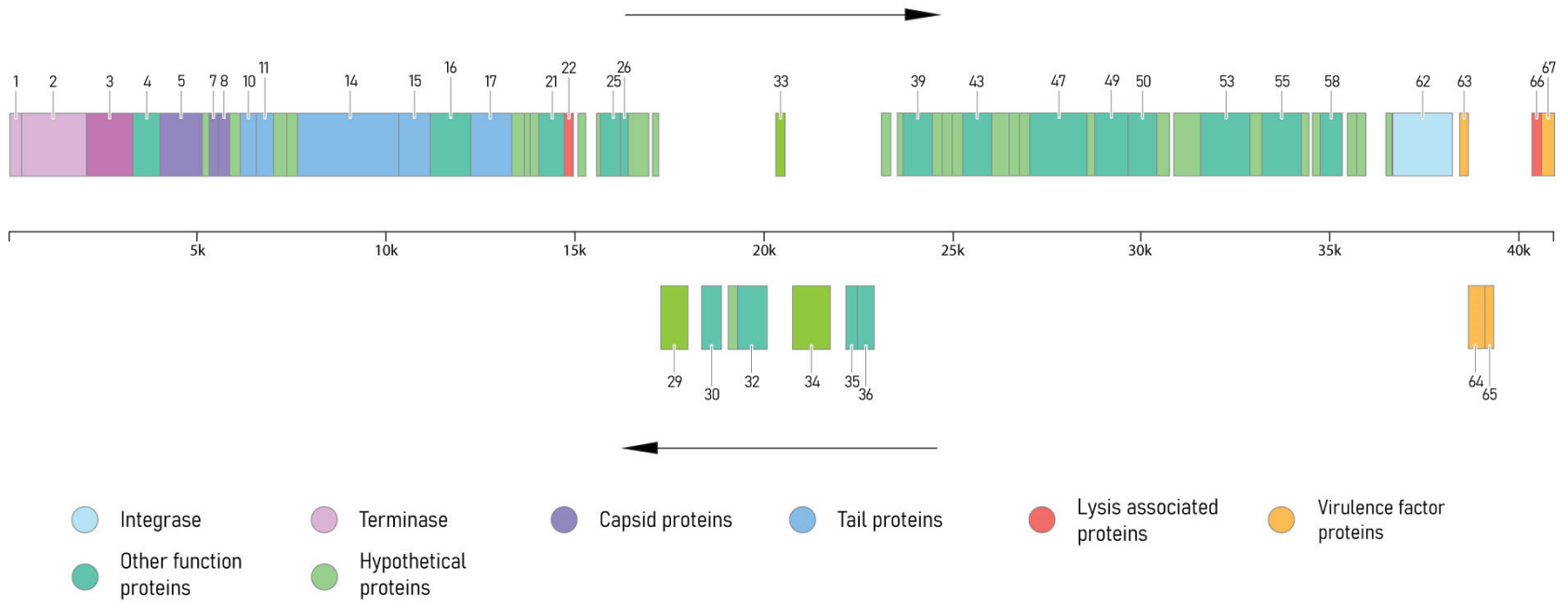
PHAGE 2A



PHAGE 3A



PHAGE 4A



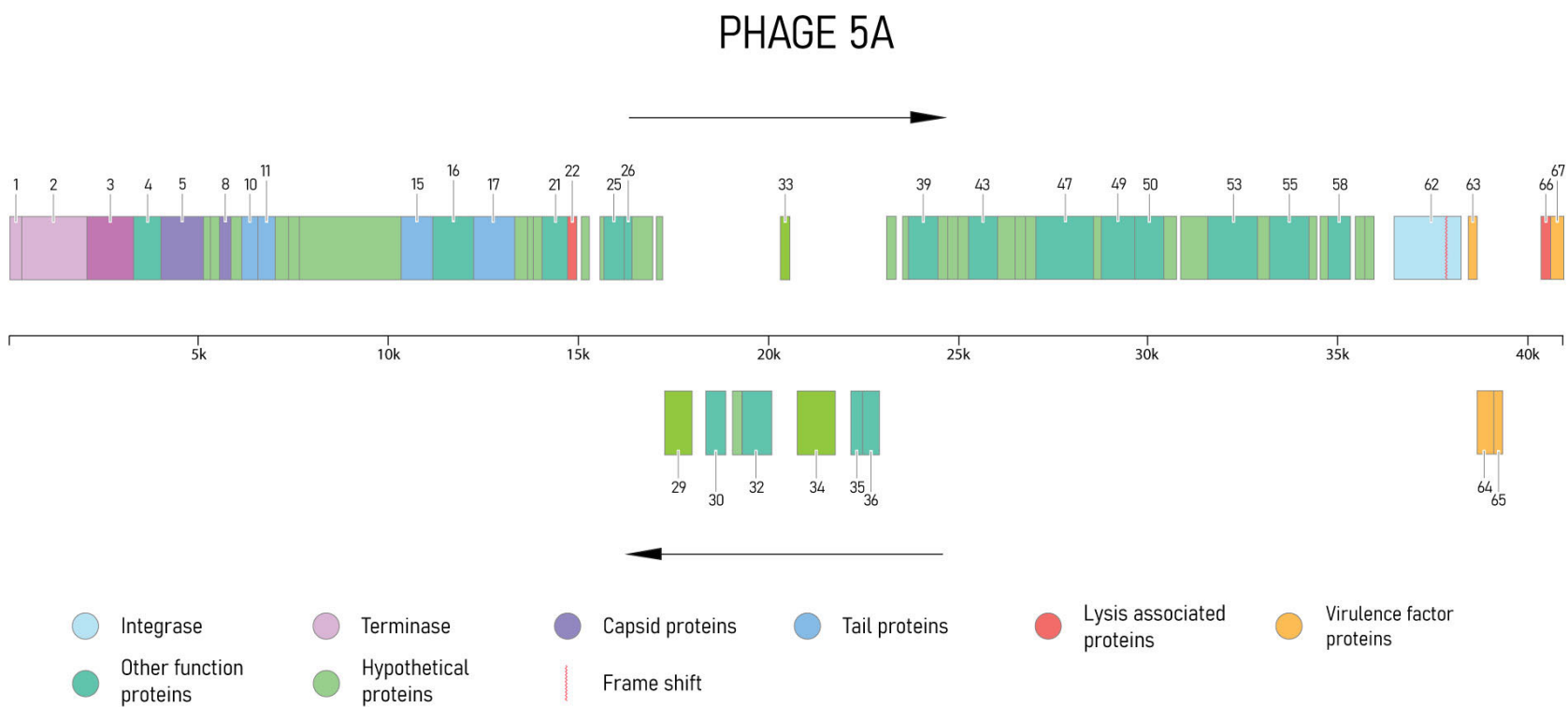


Figure S3. Genomics maps of studied phages 1-5/A

Table S1. Annotation table of phage 1/A

#	Location		Strand	Size		Probable function	Homologue	Comments
	Start	End		nt	aa			
1	45	359	+	315	104	terminase, small subunit	YP_009195191.1	-
2	340	2064	+	1725	574	terminase, large subunit	YP_008320338.1	-
3	2061	3314	+	1254	417	portal protein	YP_009203205.1	-
4	3298	4020	+	723	240	Clp, protease	YP_009203206.1	-
5	4017	5147	+	1131	376	major capsid protein	YP_008320341.1	-
6	5125	5298	+	174	57	hypothetical protein	YP_008320342.1	-
7	5291	5554	+	264	87	head-tail connector protein	YP_008320343.1	-
8	5551	5868	+	318	105	head closure protein	YP_008320344.1	-
9	5868	6128	+	261	86	hypothetical protein	YP_009195199.1	-
10	6138	6578	+	441	146	tail protein	YP_008320346.1	-
11	6580	7017	+	438	145	major tail protein	YP_008320347.1	-
12	7014	7352	+	339	112	hypothetical protein	YP_009195202.1	-
13	7379	7633	+	255	84	hypothetical protein	YP_008320349.1	-
14	7693	10329	+	2637	878	tail tape measure protein	YP_008320350.1	-
15	10326	11177	+	852	283	tail protein	YP_008320351.1	-
16	11180	11440	+	261	86	<i>Siphovirus</i> ReqiPepy6 Gp37-like protein	YP_008320352.1	Potential reading frame shift.
17	11445	12239	+	795	264	<i>Siphovirus</i> ReqiPepy6 Gp37-like protein	YP_008320352.1	
18	12236	13318	+	1083	360	tail protein	YP_009201927.1	-
19	13319	13666	+	348	115	hypothetical protein	YP_009201928.1	-
20	13663	13824	+	162	53	hypothetical protein	YP_009197964.1	-

21	13805	14044	+	240	79	hypothetical protein	YP_009197965.1	-
22	14041	14715	+	675	224	N-acetylmuramoyl-L-alanine amidase	YP_009201931.1	-
23	14725	14967	+	243	80	holin	YP_009197967.1	-
24	15101	15292	+	192	63	hypothetical protein	YP_009197968.1	-
25	15574	15684	+	111	36	hypothetical protein	YP_009197969.1	-
26	15681	16202	+	522	173	amidase domain-containing protein	YP_009197970.1	Potential reading frame shift.
27	16199	16387	+	189	62	amidase domain-containing protein	YP_009197970.1	
28	16423	16947	+	525	174	hypothetical protein	YP_009197971.1	-
29	17111	17218	+	108	35	hypothetical protein	YP_009197972.1	-
30	17280	17999	-	720	239	transposase	YP_009201939.1	-
31	18170	18853	-	684	227	helix-turn-helix domain-containing protein	YP_009197974.1	-
32	19339	19542	-	204	67	hypothetical protein	YP_009197976.1	-
33	19544	20092	-	549	182	YolD-like family protein	YP_009197977.1	-
34	20334	20588	+	255	84	transposase	YP_009197978.1	-
35	20786	21475	-	690	229	transposase	YP_009197979.1	-
z	21481	21762	-	282	93	helix-turn-helix transcriptional regulator	YP_009197980.1	-
37	22472	22933	-	462	153	helix-turn-helix domain-containing protein	YP_009197981.1	-
38	23134	23391	+	258	85	hypothetical protein	YP_009201956.1	-
39	23537	23692	+	156	51	hypothetical protein	YP_009201956.1	-
40	23718	24458	+	741	246	antirepressor	YP_009197983.1	-
41	24485	24703	+	219	72	hypothetical protein	YP_009201958.1	-
42	24727	24996	+	270	89	hypothetical protein	YP_009201959.1	-
43	24993	25265	+	273	90	hypothetical protein	YP_009201960.1	-

44	25292	26050	+	759	252	antirepressor	YP_009201961.1	-
45	26047	26526	+	480	159	hypothetical protein	YP_009201962.1	-
46	26516	26764	+	249	82	hypothetical protein	YP_009201963.1	-
47	26769	27059	+	291	96	hypothetical protein	YP_009197985.1	-
48	27043	28575	+	1533	510	ATPase	YP_009197986.1	-
49	28562	28759	+	198	65	hypothetical protein	YP_009197987.1	-
50	28762	29664	+	903	300	recombinase RecT	YP_009197988.1	-
51	29677	30435	+	759	252	MBL fold metallo-hydrolase	YP_009197989.1	-
52	30432	30746	+	315	104	hypothetical protein	YP_008320387.1	-
53	30760	31590	+	831	276	hypothetical protein	YP_008320388.1	-
54	31556	32878	+	1323	440	DNA helicase	YP_009197992.1	-
55	32875	33186	+	312	103	hypothetical protein	YP_009201972.1	-
56	33179	34234	+	1056	351	DNA (cytosine-5-)-methyltransferase	YP_009201973.1	-
57	34221	34430	+	210	69	hypothetical protein	YP_009201974.1	-
58	34515	34685	-	171	56	hypothetical protein	-	-
59	34721	35311	+	591	196	resolvase	YP_009838694.1	-
60	35470	35775	+	306	101	hypothetical protein	YP_009201977.1	-
61	35787	35936	+	150	49	hypothetical protein	YP_009838964.1	-
62	35987	36445	+	459	152	transcriptional regulator	YP_009201978.1	-
63	36457	36738	+	282	93	hypothetical protein	YP_009201979.1	-
64	36677	38239	+	1563	520	integrase	YP_009201980.1	-
65	38379	38654	+	276	91	phosphomannomutase	YP_009201981.1	-
66	38683	39093	-	411	136	type II toxin-antitoxin system HicB family antitoxin	YP_009201982.1	-

67	39124	39360	-	237	78	type II toxin-antitoxin system HicA family toxin	YP_009201983.1	-
68	40337	40603	+	267	88	transglycosylase	YP_009201986.1	-
69	40600	40938	+	339	112	HNH endonuclease	YP_009201987.1	-

Table S2. Annotation table of phage 2/A

#	Location		Strand	Size		Probable function	Homologue	Comments
	Start	End		nt	aa			
1	2	304	+	303	100	terminase, small subunit	YP_009195191.1	-
2	285	2009	+	1725	574	terminase, large subunit	YP_008320338.1	-
3	2006	3259	+	1254	417	portal protein	YP_009203205.1	-
4	3243	3965	+	723	240	Clp, protease	YP_009203206.1	-
5	3962	5092	+	1131	376	major capsid protein	YP_008320341.1	-
6	5070	5243	+	174	57	hypothetical protein	YP_008320342.1	-
7	5236	5499	+	264	87	head-tail connector protein	YP_008320343.1	-
8	5496	5813	+	318	105	head closure protein	YP_008320344.1	-
9	5813	6241	+	429	142	hypothetical protein	YP_008320345.1	-
10	6225	6620	+	396	131	tail protein	YP_008320346.1	-
11	6622	7059	+	438	145	major tail protein	YP_008320347.1	-
12	7056	7394	+	339	112	hypothetical protein	YP_009195202.1	-
13	7421	7675	+	255	84	hypothetical protein	YP_008320349.1	-
14	7735	10371	+	2637	878	tail tape measure protein	YP_008320350.1	-
15	10368	11219	+	852	283	tail protein	YP_008320351.1	-

16	11222	12340	+	1119	372	<i>Siphovirus</i> ReqiPepy6 Gp37-like protein	YP_008320352.1	-
17	12337	13419	+	1083	360	tail protein	YP_009201927.1	-
18	13420	13767	+	348	115	hypothetical protein	YP_009201928.1	-
19	13764	13925	+	162	53	hypothetical protein	YP_009197964.1	-
20	13906	14145	+	240	79	hypothetical protein	YP_009197965.1	-
21	14142	14816	+	675	224	N-acetylmuramoyl-L- alanine amidase	YP_009201931.1	-
22	14826	15068	+	243	80	holin	YP_009197967.1	-
23	15202	15393	+	192	63	hypothetical protein	YP_009197968.1	-
24	15675	15785	+	111	36	hypothetical protein	YP_009197969.1	-
25	15782	16303	+	522	173	amidase domain- containing protein	YP_009197970.1	-
26	16300	16488	+	189	62	amidase domain- containing protein	YP_009197970.1	-
27	16524	17048	+	525	174	hypothetical protein	YP_009197971.1	-
28	17212	17319	+	108	35	hypothetical protein	YP_009197972.1	-
29	17381	18100	-	720	239	transposase	YP_009201939.1	-
30	18271	18438	-	168	55	helix-turn-helix domain- containing protein	YP_009197974.1	Potential reading frame shift.
31	18454	18987	-	534	177	helix-turn-helix domain- containing protein	YP_009197974.1	
32	19473	19676	-	204	67	hypothetical protein	YP_009197976.1	-
33	19678	20226	-	549	182	YolD-like family protein	YP_009197977.1	-
34	20468	20722	+	255	84	transposase	YP_009197978.1	-
35	20920	21609	-	690	229	transposase	YP_009197979.1	-
36	21615	21896	-	282	93	helix-turn-helix transcriptional regulator	YP_009197980.1	-

37	22606	23067	-	462	153	helix-turn-helix domain-containing protein	YP_009197981.1	-
38	23268	23525	+	258	85	hypothetical protein	YP_009201956.1	-
39	23671	23826	+	156	51	hypothetical protein	YP_009201956.1	-
40	23852	24592	+	741	246	antirepressor	YP_009197983.1	-
41	24619	24837	+	219	72	hypothetical protein	YP_009201958.1	-
42	24861	25130	+	270	89	hypothetical protein	YP_009201959.1	-
43	25127	25399	+	273	90	hypothetical protein	YP_009201960.1	-
44	25426	26184	+	759	252	antirepressor	YP_009201961.1	-
45	26181	26660	+	480	159	hypothetical protein	YP_009201962.1	-
46	26650	26898	+	249	82	hypothetical protein	YP_009201963.1	-
47	26903	27193	+	291	96	hypothetical protein	YP_009197985.1	-
48	27177	28709	+	1533	510	ATPase	YP_009197986.1	-
49	28696	28893	+	198	65	hypothetical protein	YP_009197987.1	-
50	28896	29798	+	903	300	recombinase RecT	YP_009197988.1	-
51	29811	30569	+	759	252	MBL fold metallo-hydrolase	YP_009197989.1	-
52	30566	30880	+	315	104	hypothetical protein	YP_008320387.1	-
53	30894	31724	+	831	276	hypothetical protein	YP_008320388.1	-
54	31690	33012	+	1323	440	DNA helicase	YP_009197992.1	-
55	33009	33320	+	312	103	hypothetical protein	YP_009201972.1	-
56	33313	34368	+	1056	351	DNA (cytosine-5-)-methyltransferase	YP_009201973.1	-
57	34355	34564	+	210	69	hypothetical protein	YP_009201974.1	-
58	34649	34819	-	171	56	hypothetical protein	-	-
59	34855	35445	+	591	196	resolvase	YP_009838694.1	-
60	35604	36062	+	459	152	hypothetical protein	YP_009201977.1	-
61	36113	36571	+	459	152	hypothetical protein	YP_009201978.1	-

62	36583	36864	+	282	93	hypothetical protein	YP_009201979.1	-
63	36803	38365	+	1563	520	integrase	YP_009201980.1	-
64	38505	38780	+	276	91	phosphomannomutase	YP_009201981.1	-
65	38809	39219	-	411	136	type II toxin-antitoxin system HicB family antitoxin	YP_009201982.1	-
66	39250	39486	-	237	78	type II toxin-antitoxin system HicA family toxin	YP_009201983.1	-
67	40462	40728	+	267	88	transglycosylase	YP_009201986.1	-
68	40725	41063	+	339	112	HNH endonuclease	YP_009201987.1	-

Table S3. Annotation table of phage 3/A

#	Location		Strand	Size		Probable function	Homologue	Comments
	Start	End		nt	aa			
1	1	303	+	303	100	terminase, small subunit	YP_009195191.1	-
2	284	2008	+	1725	574	terminase, large subunit	YP_008320338.1	-
3	2005	3258	+	1254	417	portal protein	YP_009203205.1	-
4	3242	3964	+	723	240	Clp, protease	YP_009203206.1	-
5	3961	5091	+	1131	376	major capsid protein	YP_008320341.1	-
6	5069	5242	+	174	57	hypothetical protein	YP_008320342.1	-
7	5235	5498	+	264	87	head-tail connector protein	YP_008320343.1	-
8	5495	5812	+	318	105	head closure protein	YP_008320344.1	-
9	5812	6240	+	429	142	hypothetical protein	YP_008320345.1	-
10	6224	6619	+	396	131	tail protein	YP_008320346.1	-
11	6621	7058	+	438	145	major tail protein	YP_008320347.1	-

12	7055	7393	+	339	112	hypothetical protein	YP_009195202.1	-
13	7420	7674	+	255	84	hypothetical protein	YP_008320349.1	-
14	7734	10370	+	2637	878	tail tape measure protein	YP_008320350.1	-
15	10367	11218	+	852	283	tail protein	YP_008320351.1	-
16	11221	12339	+	1119	372	<i>Siphovirus</i> ReqiPepy6 Gp37-like protein	YP_008320352.1	-
17	12336	13418	+	1083	360	tail protein	YP_009201927.1	-
18	13419	13766	+	348	115	hypothetical protein	YP_009201928.1	-
19	13763	13924	+	162	53	hypothetical protein	YP_009197964.1	-
20	13905	14144	+	240	79	hypothetical protein	YP_009197965.1	-
21	14141	14815	+	675	224	N-acetylmuramoyl-L-alanine amidase	YP_009201931.1	-
22	14825	15067	+	243	80	holin	YP_009197967.1	-
23	15201	15392	+	192	63	hypothetical protein	YP_009197968.1	-
24	15674	15784	+	111	36	hypothetical protein	YP_009197969.1	-
25	15781	16302	+	522	173	amidase domain-containing protein	YP_009197970.1	Potential reading frame shift.
26	16299	16487	+	189	62	amidase domain-containing protein	YP_009197970.1	
27	16523	17047	+	525	174	hypothetical protein	YP_009197971.1	-
28	17211	17318	+	108	35	hypothetical protein	YP_009197972.1	-
29	17380	18294	-	915	304	transposase	YP_009201939.1	-
30	18366	19019	-	654	217	helix-turn-helix transcriptional regulator	YP_009197974.1	-
31	19505	19708	-	204	67	hypothetical protein	YP_009197976.1	-
32	19710	20258	-	549	182	YolD-like family protein	YP_009197977.1	-
33	20500	20754	+	255	84	transposase	YP_009197978.1	-
34	20952	21641	-	690	229	transposase	YP_009197979.1	-

35	21647	21928	-	282	93	helix-turn-helix transcriptional regulator	YP_009197980.1	-
36	22638	23099	-	462	153	helix-turn-helix domain-containing protein	YP_009197981.1	-
37	23300	23557	+	258	85	hypothetical protein	YP_009201956.1	-
38	23703	23858	+	156	51	hypothetical protein	YP_009201956.1	-
39	23884	24624	+	741	246	antirepressor	YP_009197983.1	-
40	24651	24869	+	219	72	hypothetical protein	YP_009201958.1	-
41	24893	25162	+	270	89	hypothetical protein	YP_009201959.1	-
42	25159	25431	+	273	90	hypothetical protein	YP_009201960.1	-
43	25458	26216	+	759	252	antirepressor	YP_009201961.1	-
44	26213	26692	+	480	159	hypothetical protein	YP_009201962.1	-
45	26682	26930	+	249	82	hypothetical protein	YP_009201963.1	-
46	26935	27225	+	291	96	hypothetical protein	YP_009197985.1	-
47	27209	28741	+	1533	510	ATPase	YP_009197986.1	-
48	28728	28925	+	198	65	hypothetical protein	YP_009197987.1	-
49	28928	29830	+	903	300	recombinase RecT	YP_009197988.1	-
50	29843	30601	+	759	252	MBL fold metallo-hydrolase	YP_009197989.1	-
51	30598	30912	+	315	104	hypothetical protein	YP_008320387.1	-
52	30926	31756	+	831	276	hypothetical protein	YP_008320388.1	-
53	31722	33044	+	1323	440	DNA helicase	YP_009197992.1	-
54	33041	33352	+	312	103	hypothetical protein	YP_009201972.1	-
55	33345	34400	+	1056	351	DNA (cytosine-5-)-methyltransferase	YP_009201973.1	-
56	34387	34596	+	210	69	hypothetical protein	YP_009201974.1	-
57	34681	34851	-	171	56	hypothetical protein	-	-
58	34887	35477	+	591	196	resolvase	YP_009838694.1	-

59	35636	36094	+	459	152	hypothetical protein	YP_009201977.1	-
60	36145	36603	+	459	152	hypothetical protein	YP_009201978.1	-
61	36615	36896	+	282	93	hypothetical protein	YP_009201979.1	-
62	36835	38397	+	1563	520	integrase	YP_009201980.1	-
63	38537	38812	+	276	91	phosphomannomutase	YP_009201981.1	-
64	38841	39251	-	411	136	type II toxin-antitoxin system HicB family antitoxin	YP_009201982.1	-
65	39282	39518	-	237	78	type II toxin-antitoxin system HicA family toxin	YP_009201983.1	-
66	40494	40760	+	267	88	transglycosylase	YP_009201986.1	-
67	40757	41095	+	339	112	HNH endonuclease	YP_009201987.1	-

Table S4. Annotation table of phage 4/A

#	Location		Strand	Size		Probable function	Homologue	Comments
	Start	End		nt	aa			
1	1	297	+	297	98	terminase, small subunit	YP_009195191.1	-
2	278	2002	+	1725	574	terminase, large subunit	YP_008320338.1	-
3	1999	3252	+	1254	417	portal protein	YP_009203205.1	-
4	3236	3958	+	723	240	Clp, protease	YP_009203206.1	-
5	3955	5085	+	1131	376	major capsid protein	YP_008320341.1	-
6	5063	5236	+	174	57	hypothetical protein	YP_008320342.1	-
7	5229	5492	+	264	87	head-tail connector protein	YP_008320343.1	-
8	5489	5806	+	318	105	head closure protein	YP_008320344.1	-

9	5806	6234	+	429	142	hypothetical protein	YP_008320345.1	-
10	6218	6613	+	396	131	tail protein	YP_008320346.1	-
11	6615	7052	+	438	145	major tail protein	YP_008320347.1	-
12	7049	7387	+	339	112	hypothetical protein	YP_009195202.1	-
13	7414	7668	+	255	84	hypothetical protein	YP_008320349.1	-
14	7728	10364	+	2637	878	tail tape measure protein	YP_008320350.1	-
15	10361	11212	+	852	283	tail protein	YP_008320351.1	-
16	11215	12333	+	1119	372	<i>Siphovirus</i> ReqiPepy6 Gp37-like protein	YP_008320352.1	-
17	12330	13412	+	1083	360	tail protein	YP_009201927.1	-
18	13413	13760	+	348	115	hypothetical protein	YP_009201928.1	-
19	13757	13918	+	162	53	hypothetical protein	YP_009197964.1	-
20	13899	14138	+	240	79	hypothetical protein	YP_009197965.1	-
21	14135	14809	+	675	224	N-acetylmuramoyl-L-alanine amidase	YP_009201931.1	-
22	14819	15061	+	243	80	holin	YP_009197967.1	-
23	15195	15386	+	192	63	hypothetical protein	YP_009197968.1	-
24	15668	15778	+	111	36	hypothetical protein	YP_009197969.1	-
25	15775	16296	+	522	173	amidase domain-containing protein	YP_009197970.1	Potential reading frame shift.
26	16293	16481	+	189	62	amidase domain-containing protein	YP_009197970.1	
27	16517	17041	+	525	174	hypothetical protein	YP_009197971.1	-
28	17205	17312	+	108	35	hypothetical protein	YP_009197972.1	-
29	17374	18288	-	915	304	transposase	YP_009201939.1	-
30	18344	19012	-	669	222	helix-turn-helix domain-containing protein	YP_009197974.1	-
31	19498	19701	-	204	67	hypothetical protein	YP_009197976.1	-

32	19703	20251	-	549	182	YoID-like family protein	YP_009197977.1	-
33	20493	20747	+	255	84	transposase	YP_009197978.1	-
34	20945	21634	-	690	229	transposase	YP_009197979.1	-
35	21640	21921	-	282	93	helix-turn-helix transcriptional regulator	YP_009197980.1	-
36	22631	23092	-	462	153	helix-turn-helix domain- containing protein	YP_009197981.1	-
37	23293	23550	+	258	85	hypothetical protein	YP_009201956.1	-
38	23696	23851	+	156	51	hypothetical protein	YP_009201956.1	-
39	23877	24617	+	741	246	antirepressor	YP_009197983.1	-
40	24644	24862	+	219	72	hypothetical protein	YP_009201958.1	-
41	24886	25155	+	270	89	hypothetical protein	YP_009201959.1	-
42	25152	25424	+	273	90	hypothetical protein	YP_009201960.1	-
43	25451	26209	+	759	252	antirepressor	YP_009201961.1	-
44	26206	26685	+	480	159	hypothetical protein	YP_009201962.1	-
45	26675	26923	+	249	82	hypothetical protein	YP_009201963.1	-
46	26928	27218	+	291	96	hypothetical protein	YP_009197985.1	-
47	27202	28734	+	1533	510	ATPase	YP_009197986.1	-
48	28721	28918	+	198	65	hypothetical protein	YP_009197987.1	-
49	28921	29823	+	903	300	recombinase RecT	YP_009197988.1	-
50	29836	30594	+	759	252	MBL fold metallo- hydrolase	YP_009197989.1	-
51	30591	30905	+	315	104	hypothetical protein	YP_008320387.1	-
52	30919	31749	+	831	276	hypothetical protein	YP_008320388.1	-
53	31715	33037	+	1323	440	DNA helicase	YP_009197992.1	-
54	33034	33345	+	312	103	hypothetical protein	YP_009201972.1	-
55	33338	34393	+	1056	351	DNA (cytosine-5-)- methyltransferase	YP_009201973.1	-

56	34380	34589	+	210	69	hypothetical protein	YP_009201974.1	-
57	34674	34844	-	171	56	hypothetical protein	-	-
58	34880	35470	+	591	196	resolvase	YP_009838694.1	-
59	35629	36087	+	459	152	hypothetical protein	YP_009201977.1	-
60	36138	36596	+	459	152	hypothetical protein	YP_009201978.1	-
61	36608	36889	+	282	93	hypothetical protein	YP_009201979.1	-
62	36828	38390	+	1563	520	integrase	YP_009201980.1	-
63	38530	38805	+	276	91	phosphomannomutase	YP_009201981.1	-
64	38834	39244	-	411	136	type II toxin-antitoxin system HicB family antitoxin	YP_009201982.1	-
65	39275	39511	-	237	78	type II toxin-antitoxin system HicA family toxin	YP_009201983.1	-
66	40487	40753	+	267	88	transglycosylase	YP_009201986.1	-
67	40750	41031	+	282	93	HNH endonuclease	YP_009201987.1	-

Table S5. Annotation table of phage 5/A

#	Location		Strand	Size		Probable function	Homologue	Comments
	Start	End		nt	aa			
1	1	303	+	303	100	terminase, small subunit	YP_009195191.1	-
2	284	2008	+	1725	574	terminase, large subunit	YP_008320338.1	-
3	2005	3258	+	1254	417	portal protein	YP_009203205.1	-
4	3242	3964	+	723	240	Clp, protease	YP_009203206.1	-
5	3961	5091	+	1131	376	major capsid protein	YP_008320341.1	-

6	5069	5242	+	174	57	hypothetical protein	YP_008320342.1	-
7	5257	5427	+	171	56	hypothetical protein	YP_008320343.1	Potential reading frame shift.
8	5506	5823	+	318	105	head closure protein	YP_008320344.1	-
9	5823	6251	+	429	142	hypothetical protein	YP_008320345.1	-
10	6235	6630	+	396	131	tail protein	YP_008320346.1	-
11	6632	7069	+	438	145	major tail protein	YP_008320347.1	-
12	7066	7404	+	339	112	hypothetical protein	YP_009195202.1	-
13	7431	7685	+	255	84	hypothetical protein	YP_008320349.1	-
14	7745	10282	+	2538	845	hypothetical protein	YP_008320350.1	Potential reading frame shift.
15	10279	11130	+	852	283	tail protein	YP_008320351.1	-
16	11133	12251	+	1119	372	Siphovirus ReqiPepy6 Gp37-like protein	YP_008320352.1	-
17	12248	13330	+	1083	360	tail protein	YP_009201927.1	-
18	13331	13678	+	348	115	hypothetical protein	YP_009201928.1	-
19	13675	13836	+	162	53	hypothetical protein	YP_009197964.1	-
20	13817	14056	+	240	79	hypothetical protein	YP_009197965.1	-
21	14053	14727	+	675	224	N-acetylmuramoyl-L-alanine amidase	YP_009201931.1	-
22	14737	14979	+	243	80	holin	YP_009197967.1	-
23	15113	15304	+	192	63	hypothetical protein	YP_009197968.1	-
24	15586	15696	+	111	36	hypothetical protein	YP_009197969.1	-
25	15693	16214	+	522	173	amidase domain-containing protein	YP_009197970.1	-
26	16211	16399	+	189	62	amidase domain-containing protein	YP_009197970.1	-
27	16435	16959	+	525	174	hypothetical protein	YP_009197971.1	-
28	17123	17230	+	108	35	hypothetical protein	YP_009197972.1	-

29	17292	18011	-	720	239	transposase	YP_009201939.1	-
30	18182	18865	-	684	227	helix-turn-helix domain-containing protein	YP_009197974.1	-
31	19351	19554	-	204	67	hypothetical protein	YP_009197976.1	-
32	19556	20104	-	549	182	YolD-like family protein	YP_009197977.1	-
33	20346	20600	+	255	84	transposase	YP_009197978.1	-
34	20798	21487	-	690	229	transposase	YP_009197979.1	-
35	21493	21774	-	282	93	helix-turn-helix transcriptional regulator	YP_009197980.1	-
36	22484	22945	-	462	153	helix-turn-helix domain-containing protein	YP_009197981.1	-
37	23146	23403	+	258	85	hypothetical protein	YP_009201956.1	-
38	23549	23704	+	156	51	hypothetical protein	YP_009201956.1	-
39	23730	24470	+	741	246	antirepressor	YP_009197983.1	-
40	24497	24715	+	219	72	hypothetical protein	YP_009201958.1	-
41	24739	25008	+	270	89	hypothetical protein	YP_009201959.1	-
42	25005	25277	+	273	90	hypothetical protein	YP_009201960.1	-
43	25304	26062	+	759	252	antirepressor	YP_009201961.1	-
44	26059	26538	+	480	159	hypothetical protein	YP_009201962.1	-
45	26528	26776	+	249	82	hypothetical protein	YP_009201963.1	-
46	26781	27071	+	291	96	hypothetical protein	YP_009197985.1	-
47	27055	28587	+	1533	510	ATPase	YP_009197986.1	-
48	28574	28771	+	198	65	hypothetical protein	YP_009197987.1	-
49	28774	29676	+	903	300	recombinase RecT	YP_009197988.1	-
50	29689	30447	+	759	252	MBL fold metallo-hydrolase	YP_009197989.1	-
51	30444	30758	+	315	104	hypothetical protein	YP_008320387.1	-
52	30772	31602	+	831	276	hypothetical protein	YP_008320388.1	-
53	31568	32890	+	1323	440	DNA helicase	YP_009197992.1	-

54	32887	33198	+	312	103	hypothetical protein	YP_009201972.1	-
55	33191	34246	+	1056	351	DNA (cytosine-5-)-methyltransferase	YP_009201973.1	-
56	34233	34442	+	210	69	hypothetical protein	YP_009201974.1	-
57	34527	34697	-	171	56	hypothetical protein	-	-
58	34733	35323	+	591	196	resolvase	YP_009838694.1	-
59	35482	35940	+	459	152	hypothetical protein	YP_009201977.1	-
60	35991	36449	+	459	152	hypothetical protein	YP_009201978.1	-
61	36681	37061	+	381	126	integrase	YP_009201980.1	Potential reading frame shift.
62	37064	38347	+	1284	427	integrase	YP_009201980.1	
63	38487	38762	+	276	91	phosphomannomutase	YP_009201981.1	-
64	38791	39201	-	411	136	type II toxin-antitoxin system HicB family antitoxin	YP_009201982.1	-
65	39232	39468	-	237	78	type II toxin-antitoxin system HicA family toxin	YP_009201983.1	-
66	40444	40710	+	267	88	transglycosylase	YP_009201986.1	-
67	40707	41045	+	339	112	HNH endonuclease	YP_009201987.1	-