

Table S1. List of bacterial strains used in the study.

Species (No.)	Strain	Obtained from	Notes
<i>B. cereus</i> (11)	ATCC 10872	MIHE institute collection	
	ATCC 10876	The University of Scranton, Pennsylvania, USA	
	ATCC 11778		
	ATCC 13472	The University of Scranton, Pennsylvania, USA	
	ATCC 14579 ^T	The University of Scranton, Pennsylvania, USA	
	ATCC 19637	The University of Scranton, Pennsylvania, USA	
	ATCC 23261	The University of Scranton, Pennsylvania, USA	
	F16959	The University of Scranton, Pennsylvania, USA	
	F17202	The University of Scranton, Pennsylvania, USA	
	F17289	The University of Scranton, Pennsylvania, USA	
	UW85	The University of Scranton, Pennsylvania, USA	
<i>B. thuringiensis</i> (11)	ATCC 33679	MIHE institute collection	
	ATCC 35646	The University of Scranton, Pennsylvania, USA	
	ATCC 10792		
	ATCC 10792 ^T	MIHE institute collection	
	T07-019	The University of Scranton, Pennsylvania, USA	
	T07-128	The University of Scranton, Pennsylvania, USA	
	T07-146		
	T07-151		
	T07-155	The University of Scranton, Pennsylvania, USA	
	T07-202	The University of Scranton, Pennsylvania, USA	
	#35	The University of Scranton, Pennsylvania, USA	
<i>B. anthracis</i> (5)	211	Institute of Veterinary Hygiene in Białystok, field office in Łomża	Isolated from spleen of a cow died of anthrax
	34F2	"Antraphyl" vaccine by Phylaxia-Sanofi	Serial no. 021OE2
	1153		Isolated from a died cow
	1583	The University of Scranton, Pennsylvania, USA	Strain 211 clone
	PZH	National Institute of Public Health - National Institute of Hygiene	
<i>B. mycoides</i> (3)	ATCC 6462		
	ATCC 21929	The University of Scranton, Pennsylvania, USA	
	K184	The University of Scranton, Pennsylvania, USA	
<i>B. sp. Ba 813+</i> (10)	#6 (I/2)	The University of Scranton, Pennsylvania, USA	
	#7 (II/3)	The University of Scranton, Pennsylvania, USA	
	#12 (S8553/2)	The University of Scranton, Pennsylvania, USA	
	#16 (PJ572)	The University of Scranton, Pennsylvania, USA	
	#17 (094)	The University of Scranton, Pennsylvania, USA	
	#21 (T1197-77)	The University of Scranton, Pennsylvania, USA	
	#28 (3)	The University of Scranton, Pennsylvania, USA	
	#30 (1B)	The University of Scranton, Pennsylvania, USA	
	#31	The University of Scranton, Pennsylvania, USA	
	#3403	The University of Scranton, Pennsylvania, USA	
<i>B. subtilis</i>	ATCC 6633	The University of Scranton, Pennsylvania, USA	

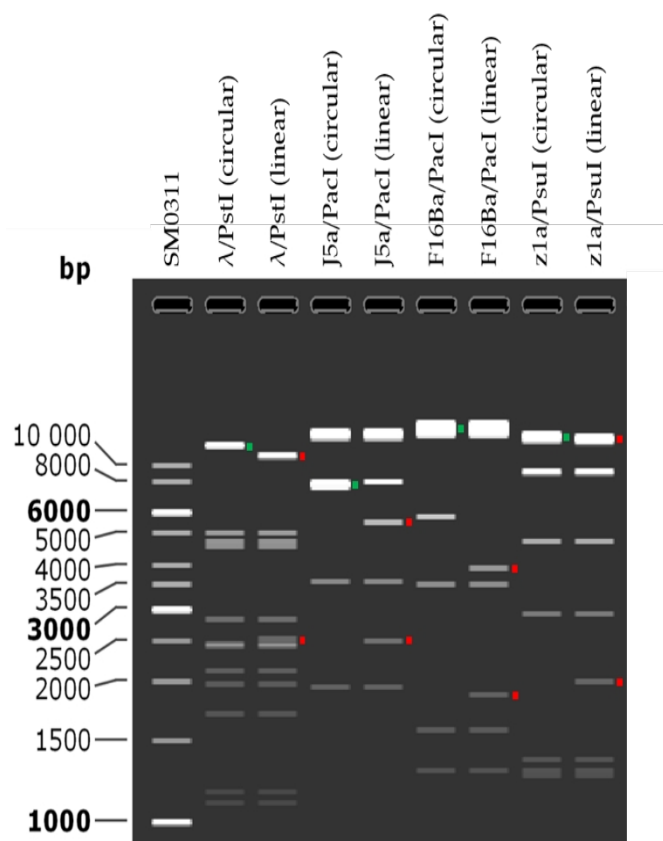


Figure S1. DNA restriction patterns generated *in silico* by SnapGene for Lambda, J5a, F16Ba, and z1a phages, indicating expected differences between restricted DNA untreated (circular forms) and treated with heat (linear forms). DNA ladder used – SM0311 Thermo Scientific GeneRuler 1 kb.

Table S2. Bacteriophage J5a genes and their predicted products. The coverage (in %) and identity (in %) of each protein with its closest homolog from the RefSeq database is as calculated with BLASTp. If no close viral homolog was found bacterial homologs were included. Signal peptides and transmembrane domains are indicated as SP and TMD, respectively.

ORF No.	ORF position (bp)	Length of product (aa)/Predicted molecular mass (kDa)	pI	Predicted function	The closest homolog in GenBank (GenBank acc. no.)	Coverage (%)	Identity (%)	Protein identifier (PHMMER results)
1.	63-548	161/18.43	9.92	Terminase small subunit	<i>B. anthracis</i> phage Gamma (ABB55435.1)	100	98.14	Terminase_4
2.	545-2242	565/65.04	5.03	Terminase large subunit	<i>B. anthracis</i> phage Negev_SA (ARW58459.1)	100	99.47	Terminase_1
3.	2258-3556	432/48.82	6.23	Portal protein	<i>B. anthracis</i> phage Fah (YP_512313.1)	99	97.90	Phage_portal
4.	3519-4139	206/23.68	5.11	Prohead protease	<i>B. anthracis</i> phage Gamma (ABB55432.1)	100	98.06	Peptidase_S78
5.	4178-5356	392/44.42	5.04	Major capsid protein	<i>B. anthracis</i> phage AP631 (AZF88350.1)	100	98.21	Phage_capsid
6.	5374-5664	96/11.15	4.71	Phage head-tail connector protein	<i>B. anthracis</i> phage Carmel_SA (ARW58550.1)	100	98.96	Phage_connect_1
7.	5661-5984	107/12.2	6.57	Head-tail adaptor protein	<i>B. anthracis</i> phage Gamma (ABA46527.1)	100	98.13	Phage_H_T_join
8.	5977-6417	146/16.24	9.62	Hypothetical protein (putative tail-component)	<i>B. anthracis</i> phage Negev_SA (ARW58482.1)	100	100	HK97-gp10_like
9.	6414-6773	119/13.92	5.44	Conserved phage protein (putative structure protein)	<i>B. anthracis</i> phage Gamma (YP_338192.1)	100	98.32	DUF3168
10.	6774-7382	202/22.96	5.17	Major tail protein	<i>B. anthracis</i> phage Negev_SA (ARW58475.1)	100	96.53	
11.	7432-7749	105/11.64	4.46	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58548.1)	100	100	
12.	7761-7955	64/7.81	5.17	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58515.1)	100	98.28	
13.	7972-11823	1283/139.32	8.48	Tail length tape-measure protein	<i>B. anthracis</i> phage Negev_SA (ARW58458.1)	100	97.43	PhageMin_Tail, 3 TMDs

14.	11838-13328	496/56.98	6.60	Distal tail protein	<i>B. anthracis</i> phage Tavor_SA (ARW58399.1)	100	90.52	Sipho_tail
15.	13325-17254	1309/147.41	5.34	Tal/RBP (Tail lysozyme/receptor-binding protein)	<i>B. anthracis</i> phage Carmel_SA (ARW58514.1)	100	79.87	Peptidase_S74
16.	17293-17529	78/8.67	6.44	XpaF1 protein (hemolysin Xhla1 family protein)	uncultured <i>Caudoviricetes</i> phage (ASN69604.1)	100	93.59	XhlaA, TMD
17.	17529-17768	79/8.38	9.16	Holin	<i>B. anthracis</i> phage Negev_SA (ARW58494.1)	100	93.67	2 TMDs
18.	17765-18820	351/39.33	9.20	N-acetylmuramoyl-L-alanine amidase	<i>B. anthracis</i> phage Tavor_SA (ARW58406.1)	100	95.16	Amidase_2, SP
19.	Complement (18862-19188)	108/12.29	9.70	Hypothetical protein	<i>B. anthracis</i> phage Negev_SA (ARW58500.2)	100	92.59	TMD
20.	Complement (19244-19438)	64/7.26	9.36	Repressor protein	<i>B. anthracis</i> phage Carmel_SA (ARW58551.1)	96	91.94	HTH_3
21.	19598-19900	104/12.73	4.81	Hypothetical protein	<i>Bacillus</i> phage BVE2 (AUG88604.1)	100	94	
22.	19903-20085	60/6.74	9.70	Hypothetical protein	<i>Bacillus</i> phage BVE2 (AUG88603.1)	100	90	2 TMDs
23.	20095-21384	429/49.69	6.78	FtsK/SpoIIIE family protein (cell division protein FtsK)	<i>B. anthracis</i> phage Wbeta (YP_459986.1)	100	95.34	FtsK_SpoIIIE
24.	21311-21943	210/25.18	9.84	Conserved phage protein	<i>B. anthracis</i> phage Wbeta (YP_459987.1)	100	97.62	Replic_Relax
25.	Complement (21977-22213)	78/8.62	6.15	HTH cro/C1-type domain-containing protein (putative transcription regulator)	<i>B. anthracis</i> phage Gamma (YP_338207.1)	100	100	HTH_26
26.	22377-22496	39/45.97	4.23	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338208.1)	100	100	DUF3961, TMD
27.	22509-23372	287/33.38	8.85	Conserved phage protein (HTH domain-containing protein)	<i>B. anthracis</i> phage Gamma (YP_338209.1)	100	97.56	HTH_36
28.	23470-24924	484/57.57	8.96	Site-specific recombinase	<i>B. anthracis</i> phage Tavor_SA (ARW58402.1)	88	96.05	Recombinase
29.	25083-26369	428/49.89	6.15	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58400.1)	100	98.60	

30.	26272-26412	46/52.03	8.25	AimP	<i>B. anthracis</i> phage Tavor_SA (-)	100	97.83	SP, TMD
31.	26518-26673	51/61.08	4.93	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58446.1)	100	94.12	
32.	Complement (26702-27061)	119/13.75	6.17	Hypothetical protein (HTH cro/C1 family protein)	<i>B. anthracis</i> phage Tavor_SA (ARW58421.1)	100	99.16	HTH_3
33.	27223-27450	75/8.75	8.53	Hypothetical protein (HTH cro/C1 family protein)	<i>B. anthracis</i> phage Tavor_SA (ARW58442.1)	100	100	HTH_3
34.	27535-27702	55/6.59	9.15	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58453.1)	98	96.30	
35.	27776-27931	51/5.99	10.45	Hypothetical protein	<i>B. anthracis</i> phage Fah (YP_512340.1)	100	94.12	
36.	27949-28695	248/29.14	5.51	Putative antirepressor	<i>B. anthracis</i> phage Carmel_SA (ARW58528.1)	100	97.98	ORF6C
37.	28762-29415	217/25.81	6.22	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58412.1)	100	83.87	
38.	29544-30464	306/36.04	8.55	Replication initiation protein	<i>B. anthracis</i> phage Negev_SA (ARW58468.1)	100	93.57	Phg_2220_C
39.	30480-31391	303/34.94	8.70	Putative DNA replication protein DnaC	<i>B. anthracis</i> phage Gamma (YP_338216.1)	100	97.69	
40.	31410-31643	77/9.17	7.93	Hypothetical protein	<i>B. anthracis</i> phage Gamma (ABA46469.1)	100	93.51	
41.	31636-32382	248/28.27	6.16	Sigma-70 family RNA polymerase sigma factor (RNA polymerase sporulation specific sigma factor SigF)	<i>B. anthracis</i> phage Negev_SA (ARW58471.1)	100	97.58	Sigma70_r2
42.	32379-32855	158/18.97	9.24	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58419.1)	100	95.57	
43.	32913-33455	180/21.16	5.89	Dimeric dUTPase	<i>B. anthracis</i> phage Carmel_SA (ARW58535.1)	100	95.56	dUTPase_2
44.	33496-33675	59/6.82	8.03	Hypothetical protein	<i>B. cereus</i> AFS001538 (PET50494.1) (Wbeta-like prophage region)	100	98.31	

45.	33847-34017	56/6.05	4.50	Hypothetical protein	<i>B. cereus</i> FSL W8-0268 (KXY22003.1) (Wbeta-like prophage region)	100	98.21	
46.	34047-34649	200/23.67	6.04	Hypothetical protein	<i>B. thuringiensis</i> GBAC46 (PRT13233.1) (Wbeta-like prophage region)	100	97	
47.	34844-35077	77/9.14	5.25	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58441.1)	100	97.40	
48.	35098-35259	53/6.12	9.37	Hypothetical protein	<i>Bacillus</i> virus IEBH (YP_002154356.1)	100	100	
49.	35449-35565	38/43.31	3.96	Hypothetical protein	<i>B. cereus</i> VD045 (EJR26235.1)	100	100	
50.	35601-36041	146/17.47	4.77	Hypothetical protein	uncultured <i>Caudoviricetes</i> phage (ASN69632.1)	48	98.59	
51.	36188-36439	83/10.11	5.42	Hypothetical protein	uncultured <i>Caudoviricetes</i> phage clone 9AX_2 (ASN69632.1)	98	95.12	
52.	36570-36860	96/11.09	10.21	Hypothetical protein	<i>B. thuringiensis</i> 4XX2 (MRA88504.1) (Wbeta-like prophage region)	100	96.88	
53.	36847-37035	62/7.09	4.61	Hypothetical protein	<i>B. anthracis</i> phage Gamma (ABB97503.1)	100	90.32	
54.	37188-37310	40/4.88	11.52	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58455.1)	100	100	DUF3983
55.	37483-37878	131/15.57	6.34	Sigma70_r4 domain- containing protein	<i>B. anthracis</i> phage Wbeta (YP_460009.1)	100	98.47	Sigma70_r4
56.	37998-38222	74/8.52	5.09	Hypothetical protein	<i>B. anthracis</i> phage Gamma (ABA46507.1)	100	86.49	
57.	38229-38450	73/8.21	5.61	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88397.1)	100	97.26	
58.	38456-38785	109/13.4	9.41	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58546.1)	100	92.66	
59.	38786-38977	63/7.14	4.44	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58447.1)	100	100	
60.	38997-39251	84/10.18	9.08	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58435.1)	100	97.62	

61.	39272-39418	48/5.60	8.82	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338234.1)	100	100	
62.	39450-39863	137/15.33	5.55	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88400.1)	89	80.49	
63.	39932-40315	127/15.55	9.49	HNH endonuclease	<i>B. anthracis</i> phage Gamma (YP_338236.1)	100	98.43	HNH

Table S3. Bacteriophage F16Ba genes and their predicted products. The coverage (in %) and identity (in %) of each protein with its closest homolog from the RefSeq database is as calculated with BLASTp. If no close viral homolog was found bacterial homologs were included. Signal peptides and transmembrane domains are indicated as SP and TMD, respectively.

ORF No.	ORF position (bp)	Length of product (aa)/Predicted molecular mass (kDa)	pI	Predicted function	GenBank phage protein sequences with maximal identity	Coverage (%)	Identity (%)	Protein identifier (PHMMER results)
1.	63-548	161/18.47	9.84	Terminase small subunit	<i>B. anthracis</i> phage Gamma (ABB55435.1)	100	97.52	Terminase_4
2.	545-2242	565/65.17	5.10	Terminase large subunit	<i>B. anthracis</i> phage Carmel_SA (ARW58516.1)	100	99.82	Terminase_1
3.	2258-3556	432/48.82	6.21	Portal protein	<i>B. anthracis</i> phage Fah (YP_512313.1)	99	97.90	Phage_portal
4.	3519-4139	206/23.72	5.11	Prohead protease	<i>B. anthracis</i> phage Gamma (YP_338187.1)	100	99.51	Peptidase_S78
5.	4178-5356	392/44.25	5.03	Major capsid protein	<i>B. anthracis</i> phage Gamma (ABB55431.2)	100	99.23	Phage_capsid
6.	5374-5664	96/11.17	4.71	Phage head-tail connector protein	<i>B. anthracis</i> phage Carmel_SA (ARW58550.1)	100	96.88	Phage_connect_1
7.	5661-5984	107/12.19	5.80	Head-tail adaptor protein (phage head-tail joining protein)	<i>B. anthracis</i> phage Gamma (ABA46527.1)	100	99.07	Phage_H_T_join
8.	5977-6417	146/16.24	9.62	Hypothetical protein (putative tail component)	<i>B. anthracis</i> phage Negev_SA (ARW58482.1)	100	100	HK97-gp10_like
9.	6414-6773	119/13.95	5.21	Conserved phage protein (putative structure protein)	<i>B. anthracis</i> phage Gamma (YP_338192.1)	100	98.32	DUF3168

10.	6774-7382	202/22.88	5.16	Major tail protein	<i>B. anthracis</i> phage Tavor_SA (ARW58414.1)	100	99.50	
11.	7433-7750	105/11.68	4.35	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88356.1)	100	100	
12.	7780-7956	58/7.02	5.13	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338195.1)	100	100	
13.	7973-11824	1283/ 139.25	8.35	Tail length tape-measure protein	<i>B. anthracis</i> phage Negev_SA (ARW58458.1)	100	99.06	PhageMin_Tail, 3 TMDs
14.	11839-13329	496/56.91	7.04	Distal tail protein	<i>B. anthracis</i> phage Tavor_SA (ARW58399.1)	100	97.98	Sipho_tail
15.	13326-17393	1355/151.99	5.34	Tal/RBP (Tail lysozyme/receptor-binding protein)	<i>B. anthracis</i> phage Carmel_SA (ARW58514.1)	100	90.29	Peptidase_S74
16.	17432-17668	78/8.70	6.21	XpaF1 protein	uncultured <i>Caudoviricetes</i> phage (ASN69604.1)	100	92.31	XhlA, TMD
17.	17668-17907	79/8.37	9.16	Holin	<i>B. anthracis</i> phage Negev_SA (ARW58494.1)	100	94.94	2 TMDs
18.	17904-18959	351/39.41	9.32	N-acetylmuramoyl-L-alanine amidase	<i>B. anthracis</i> phage Tavor_SA (ARW58406.1)	100	98.29	Amidase_2, SP
19.	Complement (18998-19327)	109/12.36	9.70	Hypothetical protein	<i>B. anthracis</i> phage Negev_SA (ARW58500.2)	100	98.17	TMD
20.	Complement (19395-19988)	197/22.98	5.26	Hypothetical protein	<i>B. anthracis</i> phage Negev_SA (ARW58476.1)	98	96.91	T4SS-DNA_transf
21.	Complement (19985-20182)	65/7.39	8.93	Repressor protein	<i>B. anthracis</i> phage Carmel_SA (ARW58551.1)	100	93.85	HTH_3
22.	20342-20650	102/12.50	5.20	Hypothetical protein	<i>Bacillus</i> phage BVE2 (AUG88604.1)	98	89	
23.	20647-20829	60/6.69	9.70	Conserved phage protein	<i>B. anthracis</i> phage Gamma (ABB72450.1)	100	96.67	2 TMDs
24.	20839-22128	429/49.63	6.54	FtsK/SpoIIIE family protein (cell division protein FtsK)	<i>B. anthracis</i> phage Wbeta (YP_459986.1)	100	95.57	FtsK_SpoIIIE
25.	22055-22687	210/25.20	9.84	Conserved phage protein	<i>B. anthracis</i> phage Wbeta (YP_459987.1)	100	98.10	Replic_Relax

26.	Complement (22721-22957)	78/8.62	6.15	HTH cro/C1-type domain- containing protein (putative XRE family transcriptional regulator)	<i>B. anthracis</i> phage Gamma (YP_338207.1)	100	100	HTH_26
27.	23122-23241	39/45.97	4.23	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338208.1)	100	100	DUF3961, TMD
28.	23254-24117	287/33.37	8.98	Conserved phage protein (HTH domain-containing protein)	<i>B. anthracis</i> phage Gamma (YP_338209.1)	100	99.65	HTH_36
29.	24193-25638	481/56.42	9.16	Site-specific recombinase	<i>B. anthracis</i> phage AP631 (AZF88373.1)	100	99.17	Resolvase
30.	25741-27075	444/51.24	7.45	Hypothetical protein	<i>B. anthracis</i> phage Negev_SA (ARW58462.1)	100	98.87	
31.	26984-27133	49/54.14	9.73	AimP	<i>B. anthracis</i> phage Wbeta (-)	100	100	Kinase domain protein (fragment), SP, TMD
32.	27272-27394	40/47.03	8.77	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88375.1)	100	87.50	
33.	Complement (27416-27772)	118/13.62	6.30	Hypothetical protein (HTH Cro/C1 family protein)	<i>B. anthracis</i> phage Wbeta (YP_459993.1)	100	99.15	HTH_31
34.	27932-28159	75/8.80	8.52	Hypothetical protein (HTH Cro/C1 family protein)	<i>B. anthracis</i> phage Wbeta (YP_459994.1)	100	100	HTH_3
35.	28199-28357	52/6.06	6.23	Conserved phage protein	<i>B. anthracis</i> phage Wbeta (YP_459995.1)	100	100	
36.	28429-28584	51/6.04	10.28	Hypothetical protein	<i>B. anthracis</i> phage Fah (YP_512340.1)	100	98.04	
37.	28602-29348	248/29.17	5.83	Putative antirepressor	<i>B. anthracis</i> phage Carmel_SA (ARW58528.1)	100	96.77	ORF6C
38.	29376-29753	125/14.80	5.10	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58544.1)	100	95.20	
39.	29760-30410	216/25.47	7.65	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58530.1)	100	92.59	
40.	30539-31480	313/36.85	7.74	Replication initiation protein	<i>B. anthracis</i> phage Negev_SA (ARW58468.1)	100	96.17	Phg_2220_C

41.	31496-32407	303/34.92	8.81	Putative DnaC protein (putative replication protein)	<i>B. anthracis</i> phage Wbeta (ABC40434.1)	100	98.68	
42.	32426-32659	77/9.14	7.93	Hypothetical protein	<i>B. anthracis</i> phage Wbeta (ABC40435.1)	100	98.33	
43.	32652-33398	248/28.20	5.72	RNA polymerase sporulation specific sigma factor	<i>B. anthracis</i> phage Tavor_SA (ARW58411.1)	100	100	Sigma70_r2
44.	33395-33871	158/18.97	9.13	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58419.1)	100	99.37	
45.	33929-34471	180/21.17	5.26	Dimeric dUTPase	<i>B. anthracis</i> phage Carmel_SA (ARW58535.1)	100	97.22	dUTPase_2
46.	Complement (34598-35383)	261/31.33	6.79	Beta-galactosidase	<i>B. anthracis</i> phage Carmel_SA (ARW58527.1)	100	92.72	Sulfotransfer_2
47.	35686-35874	62/7.22	4.54	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58563.1)	100	88.71	
48.	36027-36149	40/4.81	10.77	Conserved phage protein	<i>B. anthracis</i> phage Gamma (ABA46517.1)	100	92.50	DUF3983
49.	36322-36717	131/15.60	5.99	Sigma70_r4 domain- containing protein	<i>B. anthracis</i> phage Wbeta (YP_460009.1)	100	97.71	Sigma70_r4
50.	36902-37321	139/16.25	4.78	Hypothetical protein	<i>B. thuringiensis</i> KB1 (KXO02459.1) (Wbeta-like prophage region)	100	94.96	DUF3775
51.	37382-37606	74/8.54	6.58	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58558.1)	100	94.59	
52.	37613-37834	73/8.18	5.86	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58445.1)	100	98.63	
53.	37841-38095	84/10.24	8.97	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58435.1)	100	89.29	
54.	38133-38516	127/15.48	9.46	HNH endonuclease	<i>B. anthracis</i> phage Fah (YP_512360.1)	100	97.64	HNH

Table S4. Bacteriophage z1a genes and their predicted products. The coverage (in %) and identity (in %) of each protein with its closest homolog from the RefSeq database is as calculated with BLASTp. If no close viral homolog was found bacterial homologs were included. Signal peptides and transmembrane domains are indicated as SP and TMD, respectively.

ORF No.	ORF position (bp)	Length of product (aa)/Predicted molecular mass (kDa)	pI	Predicted function	GenBank phage protein sequences with maximal identity	Coverage (%)	Identity (%)	Protein identifier (PHMMER results)
1.	63-548	161/18.52	9.88	Terminase small subunit	<i>B. anthracis</i> phage Carmel_SA (ARW58537.1)	100	99.38	Terminase_4
2.	545-2242	565/65.17	5.07	Terminase large subunit	<i>B. anthracis</i> phage Carmel_SA (ARW58516.1)	100	100	Terminase_1
3.	2258-3556	432/48.78	7.08	Portal protein	<i>B. anthracis</i> phage Gamma (YP_338186.1)	100	97.69	Phage_portal
4.	3519-4139	206/23.7	5.11	Prohead protease	<i>B. anthracis</i> phage Negev_SA (ARW58474.1)	100	98.54	Peptidase_S78
5.	4178-5356	392/44.22	5.04	Major capsid protein	<i>B. anthracis</i> phage Carmel_SA (ARW58522.1)	100	100	Phage_capsid
6.	5374-5664	96/11.15	4.71	Phage head-tail connector protein	<i>B. anthracis</i> phage Carmel_SA (ARW58550.1)	100	100	Phage_connect_1
7.	5661-5984	107/12.28	7.87	Head-tail adaptor protein	<i>B. anthracis</i> phage Carmel_SA (ARW58547.1)	100	97.20	Phage_H_T_join
8.	5977-6417	146/16.24	9.62	Hypothetical protein (putative tail component)	<i>B. anthracis</i> phage Negev_SA (ARW58482.1)	100	100	HK97-gp10_like
9.	6414-6773	119/13.94	5.21	Hypothetical protein (putative structure protein)	<i>B. anthracis</i> phage Carmel_SA (ARW58545.1)	100	97.48	DUF3168
10.	6774-7382	202/22.88	5.27	Major tail protein	<i>B. anthracis</i> phage Gamma (YP_338193.1)	100	97.52	
11.	7431-7748	105/16.67	4.46	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58548.1)	100	99.05	
12.	7760-7954	64/7.68	4.97	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338195.1)	90	93.10	
13.	7971-11822	1283/139.40	7.94	Tail length tape-measure protein	<i>B. anthracis</i> phage AP631 (AZF88358.1)	100	91.58	PhageMin_Tail, 3 TMDs

14.	11837-13327	496/56.84	7.14	Distal tail protein	<i>B. anthracis</i> phage Carmel_SA (ARW58517.1)	100	98.39	Sipho_tail
15.	13324-17250	1308/147.40	5.36	Tal/RBP (Tail lysozyme/receptor-binding protein)	<i>B. anthracis</i> phage Carmel_SA (ARW58514.1)	100	83.76	
16.	17289-17525	78/8.67	6.41	XpaF1 protein	uncultured <i>Caudoviricetes</i> phage (ASN69604.1)	100	92.31	XhlA, TMD
17.	17525-17764	79/8.32	9.52	Holin	<i>B. anthracis</i> phage Tavor_SA (ARW58439.1)	100	100	2 TMDs
18.	17761-18816	351/39.23	9.20	N-acetylmuramoyl-L-alanine amidase	<i>B. anthracis</i> phage Tavor_SA (ARW58406.1)	100	96.58	Amidase_2, SP
19.	Complement (18855-19184)	109/12.39	9.70	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58540.1)	100	99.08	TMD
20.	Complement (19252-19836)	194/22.74	5.28	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58533.1)	100	97.94	T4SS-DNA_transf
21.	Complement (19842-20039)	65/7.40	7.87	Repressor protein	<i>B. anthracis</i> phage Carmel_SA (ARW58551.1)	100	98.46	HTH_3
22.	20199-20507	102/12.48	5.06	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58549.1)	100	98.04	
23.	20504-20686	60/6.70	9.70	Conserved phage protein	<i>B. anthracis</i> phage Gamma (YP_338204.1)	100	96.67	2 TMDs
24.	20696-21985	429/49.43	8.80	Cell division protein FtsK	<i>B. anthracis</i> phage Carmel_SA (ARW58520.1)	100	98.83	FtsK_SpoIIIE
25.	21912-22544	210/25.25	9.84	Conserved phage protein	<i>B. anthracis</i> phage Wbeta (YP_459987.1)	100	98.57	Replic_Relax
26.	Complement (22577-22813)	78/8.65	5.23	Hypothetical protein (putative phage regulatory protein)	<i>B. anthracis</i> phage Carmel_SA (ARW58556.1)	100	100	HTH_26
27.	22977-23096	39/4.63	4.56	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88371.1)	100	84.62	DUF3961, TMD
28.	23112-23975	287/33.50	8.70	Hypothetical protein (HTH domain-containing protein)	<i>B. anthracis</i> phage Tavor_SA (ARW58408.1)	100	94.08	HTH_36
29.	24073-25527	484/57.53	8.90	Site-specific recombinase	<i>B. anthracis</i> phage Tavor_SA (ARW58402.1)	88	97.91	Recombinase

30.	25686-26972	428/50.01	6.33	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58400.1)	100	98.36	
31.	26875-27015	46/50.99	8.25	AimP	<i>B. anthracis</i> phage Tavor_SA (-)	100	91.30	SP, TMD
32.	27077-27280	67/8.10	6.26	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58446.1)	100	94.03	
33.	Complement (27308-27667)	119/13.70	6.21	Hypothetical protein (HTH Cro/C1 family protein)	<i>B. anthracis</i> phage Tavor_SA (ARW58421.1)	100	100	HTH_3
34.	27829-28056	75/8.74	8.55	Hypothetical protein (HTH Cro/C1 family protein)	<i>B. anthracis</i> phage Tavor_SA (ARW58442.1)	100	96	HTH_3
35.	28143-28307	54/6.46	9.15	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58453.1)	100	98.15	
36.	28381-28536	51/5.99	10.35	Hypothetical protein	<i>B. anthracis</i> phage Fah (YP_512340.1)	100	90.20	
37.	28554-29300	248/29.21	5.52	Putative antirepressor	<i>B. anthracis</i> phage Carmel_SA (ARW58528.1)	100	97.98	ORF6C
38.	29328-29705	125/14.94	4.77	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58544.1)	100	99.20	
39.	29712-30362	216/25.60	7.65	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58530.1)	100	95.83	
40.	30491-31459	322/38.04	6.31	Putative phage replisome organizer protein	<i>B. anthracis</i> phage Gamma (ABA46496.1)	100	90.37	Phg_2220_C
41.	31475-32386	303/34.81	8.91	DNA replication protein DnaC (ATP-binding protein)	<i>B. anthracis</i> phage Gamma (YP_338216.1)	100	95.71	
42.	32405-32638	77/9.22	5.84	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88385.1)	100	89.61	
43.	32631-33377	248/28.26	5.90	RNA polymerase sporulation specific sigma	<i>B. anthracis</i> phage Gamma (YP_338218.1)	100	94.76	Sigma70_r2
44.	33374-33850	158/18.86	9.14	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58538.1)	100	96.20	
45.	33909-34451	180/21.18	5.37	Dimeric dUTPase	<i>B. anthracis</i> phage Carmel_SA (ARW58535.1)	100	96.67	dUTPase_2

46.	34489-34887	132/14.65	7.66	Hypothetical protein	<i>Bacillus</i> phage vB_BthS-HD29phi (QDP43463.1)	100	98.48	SP
47.	35281-35469	62/7.18	4.78	Hypothetical protein	<i>B. anthracis</i> phage Gamma (YP_338227.1)	100	85.48	
48.	35622-35744	40/4.91	11.52	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58455.1)	100	97.50	DUF3983
49.	35918-36313	131/15.56	6.01	Sigma70_r4 domain-containing protein	<i>B. anthracis</i> phage Wbeta (YP_460009.1)	100	98.47	Sigma70_r4
50.	36469-36981	170/19.66	5.49	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58536.1)	100	98.82	
51.	37044-37268	74/8.52	7.93	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58558.1)	100	100	
52.	37275-37496	73/8.18	5.87	Conserved phage protein	<i>B. anthracis</i> phage Gamma (YP_338231.1)	100	95.89	
53.	37502-37831	109/13.45	9.41	Hypothetical protein	<i>B. anthracis</i> phage Carmel_SA (ARW58546.1)	98	95.33	
54.	37832-38023	63/7.14	4.44	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58447.1)	100	100	
55.	38043-38297	84/10.13	8.96	Hypothetical protein	<i>B. anthracis</i> phage Tavor_SA (ARW58435.1)	100	98.81	
56.	38294-38464	56/6.49	9.27	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88399.1)	100	89.29	
57.	38496-38909	137/15.47	5.56	Hypothetical protein	<i>B. anthracis</i> phage AP631 (AZF88400.1)	91	79.20	
58.	38978-39361	127/15.60	9.53	HNH endonuclease	<i>B. anthracis</i> phage Fah (YP_512360.1)	100	96.06	HNH

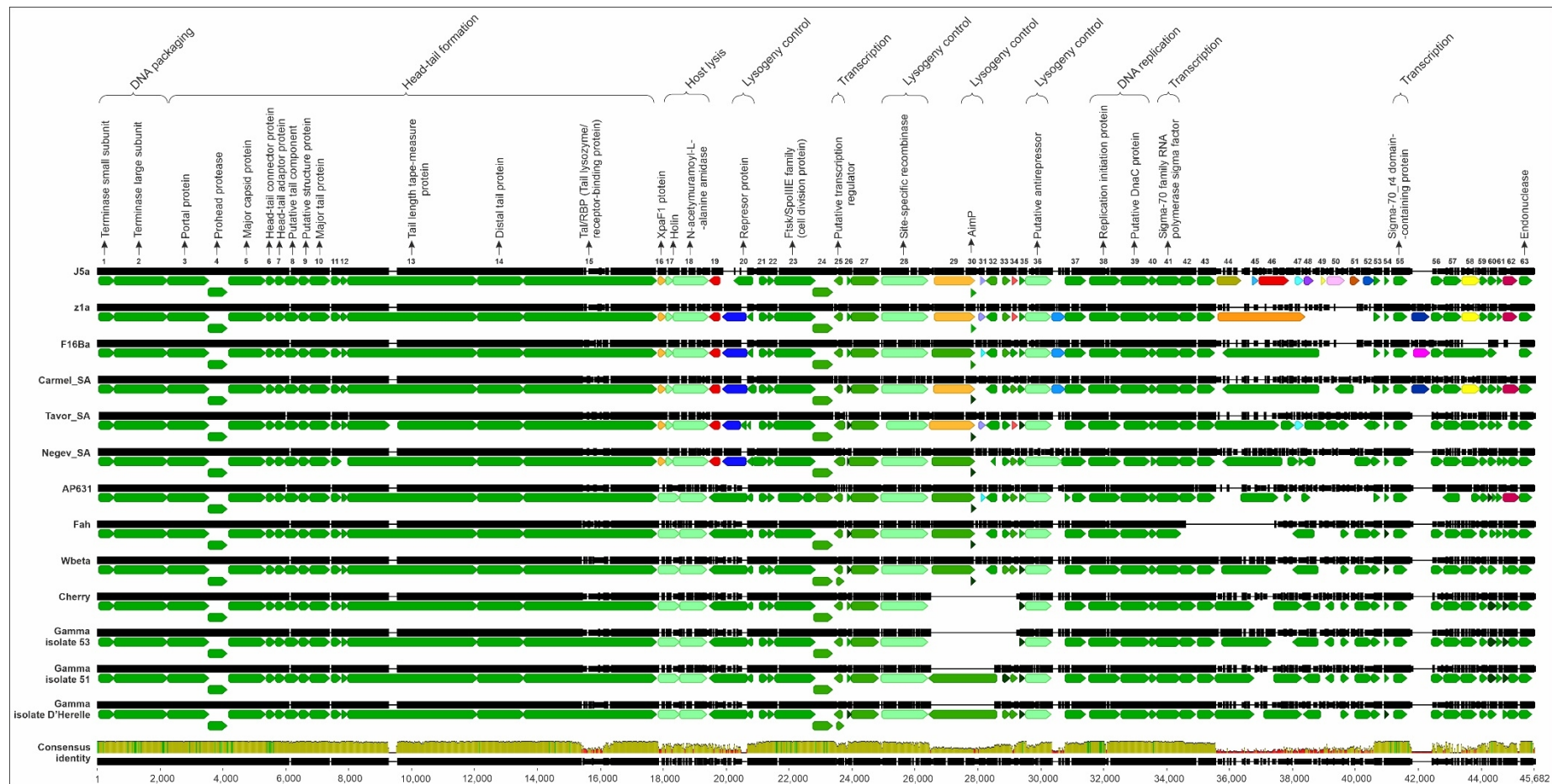


Figure S2. Gene synteny in the genomes of phages J5a, F16Ba, z1a and known or proposed members of *Wbetavirus* genus. The alignment (gapped) was performed with the use of Geneious Prime. Predicted protein-coding genes (CDSs) are color-coded based on the amino acid sequence identity of their products (considered as 70% or higher) or functions. CDSs encoding proteins of J5a, F16Ba and z1a bacteriophages with no homologs among proteins of other *wbetaviruses* are indicated by unique colors. If two to six phages shared a similar sequence of a protein, the adequate CDSs were given a common color. If more than six phages had a similar sequence of a specific protein, the CDSs were left green. Light green indicates CDSs of similar function but no significant sequence similarity in all genomes. Empty regions in the reference phage genomes were screened revealing the presence of previously unidentified open reading frames. The newly identified genes were re-annotated and were marked with a dark green color. The re-annotated genes are listed in a Table S5 (see also Table S8). Their other genes were also additionally verified what revealed a need to alter some coordinates (these ORFs are marked with an asterisk in a Table S8). The scale length corresponds to the consensus sequence including gaps.

Table S5. Coordinates of the newly identified or re-annotated CDSs in the genomes of reference phages.

Carmel_SA (KY963371.1)	Tavor_SA (KY963369.1)	Negev_SA (KY963370.1)	AP631 (MK085976.1)	Fah (DQ150593.1)	Wbeta (DQ289555.1)	Cherry (DQ222851.1)	Gamma isolate 53 (DQ222855.1)	Gamma isolate 51 (DQ222853.1)	Gamma isolate D'Herelle (DQ289556.1)
23,000-23,119	23,449-23,568	22,999-23,115	26,041-26,163	7,770- 7,946	22,202-22,321	24,711- 24,866	24,710- 24,865	24,852-25,079	22,174-22,293
26,898-27,038	28,849-29,004	26,860-27,009		22,037- 22,156	27,510-27,665	35,273- 35,527	36,734- 36,988	25,349-25,504	25,478- 25,633
	27,347-27,487			34,644- 34,766	37,546-37,668	35,726- 35,917	37,187- 37,378	35,911-36,165	34,052- 34,174
				25,899-26,048	26,064-26,213			36,364-36,555	

Table S6. Results of HHpred analysis of selected J5a phage proteins. The best and most relevant hits are shown, including the coordinates of the matching regions, PDB ID and chain identifier, and the HHpred probability (%) in the matched regions. Only proteins HHpred probability results over 80% are presented. Proteins of J5a phage of no homologs among proteins of F16Ba and z1a phages are marked with an asterisk. Corresponding proteins were assessed as those sharing more than 70% sequence identity, according to BLASTp.

ORF	Protein length (aa)	Matched residues (aa)	HHpred best match	PDB ID	Probability(%)
J5a_014	496	190-437	Tail component; bacteriophage infection, <i>Lactobacillus casei</i> , fluorescence microscopy, Carbohydrate Binding Module, sugar binding protein; 1.28A { <i>Lactobacillus</i> phage J-1}	5LY8_A	99.98
		2-196	HYPOTHETICAL PROTEIN 19.1; VIRAL PROTEIN, DISTAL TAIL PROTEIN; 2.95A {BACILLUS PHAGE SPP1}	2X8K_C	99.85
		1-197	Distal tail protein, Receptor-binding protein, Phage baseplate, host adsorption apparatus, genome injection device, VIRAL PROTEIN; 3.8A { <i>Lactococcus</i> phage TP901-1}	4V96_AX	99.77
		1-200	Distal Tail Protein, gp58; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A { <i>Staphylococcus</i> virus 80alpha}	6V8I_BD	99.65
		1-200	LACTOCOCCAL PHAGE P2 ORF15; BASEPLATE, VIRAL PROTEIN; 2.6A { <i>Lactococcus</i> Phage P2}	2WZP_Q	98.21
J5a_015	1309	6-378	Tail-Associated Lysin, gp59; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A { <i>Staphylococcus</i> virus 80alpha}	6V8I_CE	99.94
		3-356	Protein gp18; NP_465809.1, prophage tail protein gp18, Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative; HET: MSE, MLY; 1.7A { <i>Listeria monocytogenes</i> EGD-e}	3GS9_A	99.90
		29-355	Tail protein, 43 kDa; tail protein, structural genomics, PSI, MCSG, Protein Structure Initiative, Midwest Center for Structural Genomics, UNKNOWN FUNCTION; 2.1A { <i>Neisseria meningitidis</i> MC58} SCOP: b.106.1.1	3D37_A	99.08
		1166-1289	Long tail fiber distal subunit; Bacteriophage, Helical sandwich, Tail fiber, polyglycine, VIRAL PROTEIN; HET: MRD, MPD, IMD; 1.70355818561A { <i>Salmonella</i> phage vB_SenMS16}	6F45_B	96.25
		1166-1297	Isoform 2 of Myelin regulatory factor; auto-catalytic protease, protein chaperone. trimeric protein, triple coiled-coil, membrane PROTEIN; HET: MSE; 2.4A { <i>Mus musculus</i> }	7DC3_A	95.93
		1166-1283	Endo-N-acetylneuraminidase; Chaperone, Glycosidase, Hydrolase; HET: TAM, PEG; 2.6A { <i>Enterobacteria</i> phage K1F}	3GW6_B	95.76
		1166-1279	L-SHAPED tail fiber protein; viral protein, bacterial viruses, caudovirales, siphoviridae, infection; HET: FLC; 2.52A {ENTEROBACTERIA PHAGE T5}	4UW8_H	95.19
		1100-1271	Tail spike protein; bacteriophage, tailspike, <i>Acinetobacter baumannii</i> , gp42, VIRAL PROTEIN; HET: MSE; 1.794A { <i>Acinetobacter</i> phage vB_AbaP_AS12}	6EU4_B	87.82
		46-192	Bifunctional autolysin; peptidoglycan, autolysin, amidase, N-acetylmuramoyl-L-alanine amidase, HYDROLASE; HET: IMD, PEG;	4KNK_A	99.76
		45-192	Autolysin; LytA, pneumococci, autolysis, amidase, peptidoglycan complex, antibiotics, hydrolase; HET: NAG, DGL, AMV; 1.05A { <i>Streptococcus pneumoniae</i> serotype 4}	5CTV_A	99.54
J5a_018	351	45-194	Endolysin; amidase-2 domain, HYDROLASE; HET: ZN; 2.27A { <i>Staphylococcus</i> phage GH15}	4OLS_A	99.50
		2-186	N-acetylmuramoyl-L-alanine amidase; amidase, zinc binding, cell wall degradation, endolysine, hydrolase; HET: PO4, GOL; 1.21A { <i>Clostridium intestinale</i> }	6SSC_A	99.41
		26-190	prophage LambdaBa02, N-acetylmuramoyl-L-alanine amidase, family 2; N-acetylmuramoyl-L-alanine amidase, PlyL, E.C.3.5.1.28, HYDROLASE; HET: PO4; 1.86A { <i>Bacillus anthracis</i> } SCOP: d.118.1.1	1YB0_B	99.38
		199-349	L-alanyl-D-glutamate peptidase; listeria, endolysin, cell wall binding domain, bacteriophage, VIRAL PROTEIN; 1.59A { <i>Listeria</i> phage A500}	6HX0_A	98.51
		209-349	putative dipeptidyl-peptidase VI; Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative, PSI-2, HYDROLASE; HET: GOL, CSA, MSE; 1.72A { <i>Bacteroides ovatus</i> }	3NPF_A	97.65
		210-350	Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase; peptidase, NlpC protein, HYDROLASE; 1.2A { <i>Trichomonas vaginalis</i> }	6BIO_A	97.61
		220-351	NLP/P60 family protein; NLPC/P60 FAMILY PROTEIN, STRUCTURAL GENOMICS, JOINT CENTER FOR STRUCTURAL	3H41_A	97.35

		GENOMICS, JCSG, PROTEIN STRUCTURE INITIATIVE, PSI-2, HYDROLASE; HET: PG4, MSE, DGL; 1.79A { <i>Bacillus cereus</i> ATCC 10987}		
J5a_019	108	209-349	Ply protein; alpha/beta hydrolase, multi-domain, hydrolase; 1.8A { <i>Listeria</i> phage PSA} SCOP: c.56.5.6, l.1.1.1, b.34.11.4	1XOV_A 96.61
		73-106	<i>Homo sapiens</i> Transcription initiation factor IIE, alpha subunit; zinc finger	1VD4_A 98.45
		74-106	<i>Thermococcus kodakarensis</i> DNA-directed RNA polymerase subunit P	4QIW_P 98.36
		75-106	<i>Sulfolobus shibatae</i> DNA-directed RNA polymerase; transferase, multi-subunit	4AYB_P 98.23
J5a_024	210	2-81	<i>Mycobacterium tuberculosis</i> (strain ATCC 25618/H37Rv) transcriptional regulator; DNA binding protein	5ZHC_B 97.41
		10-77	<i>Bacteroides thetaiotaomicron</i> uncharacterized protein	2L02_A 97.36
		13-80	<i>Enterobacteria</i> phage T4 transcription regulatory protein MOTA	1BJA_B 97.33
		128-184	Severe fever with thrombocytopenia virus RNA polymerase	6NTV_A 90.09
		128-184	Toscana virus RNA-dependent RNA polymerase	6QW0_B 89.29
J5a_027	287	35-116	<i>Bacillus subtilis</i> DNA replication protein DnaD; primosome, DNA-binding protein	2V79_A 98.49
		35-96	<i>Sulfolobus tokodaii</i> 109aa long hypothetical transcriptional regulator; helix-turn-helix	2D1H_B 98.22
		35-96	<i>Geobacillus kaustophilus</i> HTA426 chromosome replication initiation protein; DnaD	2VN2_C 98.21
J5a_029	428	12-384	<i>Bacillus</i> phage phi3T AimR transcriptional regulator	5ZVV_B 99.97
		9-386	<i>Bacillus</i> phage SPbeta AimR transcriptional regulator; DNA binding protein, peptide binding protein, complex with peptide	5Y24_B 99.97
		7-276	<i>Bacillus thuringiensis</i> transcriptional activator PlcR protein	3U3W_B 99.94
J5a_032	119	1-70	<i>Streptococcus suis</i> 05ZYH33 ComR; <i>Streptococcus</i> , Competence, Quorum sensing, ComR, TRANSCRIPTION REGULATOR	5FD4_B 99.40
		1-108	<i>Streptococcus vestibularis</i> F0396 transcriptional regulator ComR; RNPP family TPR domain HTH domain bacterial signaling peptide binding, TRANSCRIPTION	6HU8_A 99.28
		2-69	<i>Staphylococcus aureus</i> Orf20; SaPI, Repressor, STRUCTURAL PROTEIN	6H49_A 99.20
		1-119	<i>Clostridium difficile</i> 630 putative transposon-related DNA-binding protein	3IVP_B 99.18
J5a_033	75	4-71	<i>Cytophaga hutchinsonii</i> uncharacterized protein	3OMT_B 99.10
		4-72	<i>Streptococcus suis</i> 05ZYH33 ComR; <i>Streptococcus</i> , Competence, Quorum sensing, ComR, TRANSCRIPTION REGULATOR	5FD4_B 99.07
		1-69	<i>Bacillus thuringiensis</i> transcriptional activator PlcR protein	3U3W_B 99.06
J5a_040	77	1-63	<i>Methanococcus maripaludis</i> S2 conserved uncharacterized archaeal protein	2QZG_C 91.42
		2-63	<i>Thermoplasma acidophilum</i> UPF0147 protein Ta0600	2QSB_A 85.94
		12-47	<i>Drosophila melanogaster</i> maternal effect protein oskar; 3'-UTR, dimerization, RNA BINDING PROTEIN	5CD8_B 82.23
		1-41	<i>Bacillus subtilis</i> PROTEIN (SINI PROTEIN); TRANSCRIPTION REGULATOR	1B0N_B 80.87
J5a_044*	59	4-55	<i>Cluyveromyces lactis</i> (strain ATCC 8585/CBS 2359/DSM 70799/NBRC 1267/NRRL Y-1140/WM37) mRNA decay, decapping, Nudix, nucleotide analog, TRANSLATION	6AM0_D 93.80
		5-58	<i>Staphylococcus aureus</i> host factor for Q beta; Hfq, hexamer, RNA binding protein, translational regulator, Sm motif, TRANSLATION	1KQ1_H 91.35
		5-45	<i>Listeria monocytogenes</i> protein hfq; LSm/Sm proteins, RNA chaperone, RNA BINDING PROTEIN	4NL2_C 90.52
J5a_047*	77	10-71	<i>Pyrococcus furiosus</i> DNA double-strand break repair rad50 ATPase; zinc finger, rad50, DNA repair, Recombination	1L8D_A 95.80
		12-62	<i>Saccharomyces cerevisiae</i> Protein PCF11; zinc-binding, mRNA, RNA processing, RNA binding protein	5M9Z_A 95.59
		10-70	<i>Pyrococcus furiosus</i> (strain ATCC 43587/DSM 3638/JCM 8422/Vc1) DNA double-strand break repair Rad50 ATPase; double strand break repair, DNA damage response	6ZFF_B 94.40
J5a_051*	83	12-39	<i>Homo sapiens</i> Myc-binding protein; conserved hypothetical protein	2YY0_D 92.37
		3-44	<i>Escherichia coli</i> cell division protein ZAPB	2JEE_C 91.88
		3-44	<i>Bacillus subtilis</i> 168 initiation-control protein YabA; YabA, DnaA, DnaN,	5DOL_B 91.42

			Zinc finger, initiation control, replication		
J5a_053	62	12-58	<i>Saccharomyces cerevisiae</i> (strain ATCC 204508/S288c) mediator of RNA polymerase II transcription subunit 4; transcription initiation	5OQM_h	90.44
		1-30	<i>Haloarcula marismortui</i> 50S ribosomal protein LX; 50S ribosomal subunit, ribonucleoprotein, RNA binding, tRNA binding, metal binding	4V9F_6	88.95
		1-30	<i>Escherichia coli</i> bacterial RNA polymerase inhibitor	4LLG_N	88.74
J5a_056	74	1-30	<i>Enterobacteria</i> phage T7 bacterial RNA polymerase inhibitor	2LMC_A	87.03
		2-27	<i>De Novo</i> protein coiled-coil Trimer with Glu:Val:Lys Triad	6Q1W_B	88.30
J5a_059	63	3-35	Bovine Adenovirus 3 assembly intermediate	3ZIF_O	87.40
		35-55	<i>Clostridium botulinum</i> Bot.2110.4; mini-protein binder, inhibitor, TOXIN	5VMR_C	93.20
		30-54	<i>Homo sapiens</i> coiled-coil domain-containing protein 90B, mitochondrial, general control protein GCN4	6H9M_C	91.48
J5a_060	84	12-61	<i>Silicibacter</i> sp. uncharacterized peroxidase-related protein; YP_614459.1	2PFX_A	89.37
		2-66	<i>Homo sapiens</i> general transcription factor IIE subunit 1	5GPY_A	98.90
		2-70	<i>Pyrococcus furiosus</i> transcription factor E	6PLN_A	98.76
J5a_061	48	2-71	<i>Saccharomyces cerevisiae</i> (strain ATCC 204508/S288c) transcription initiation factor IIE subunit alpha	6GYM_W	98.73
		1-42	<i>Thermococcus kodakarensis</i> DNA-directed RNA polymerase subunit P	4QIW_W	97.60
		2-35	<i>Pyrococcus furiosus</i> rubrerythrin; Non heme iron peroxidases, oxidative stress	3PWF_B	96.41
J5a_062	137	1-46	<i>Pyrococcus furiosus</i> hypothetical protein Pf0610; winged-helix like protein with metal binding site	2GMG_A	95.34
		2-45	<i>Thermococcus kodakarensis</i> DNA-directed RNA polymerase subunit P	4QIW_W	96.60
		4-45	<i>Sulfolobus shibatae</i> DNA-directed RNA polymerase	4AYB_P	95.63
J5a_063	127	1-78	HNH endonuclease; Thermophilic bacteriophage, HNH Endonuclease, DNA nicking, HYDROLASE; 1.52A { <i>Geobacillus</i> virus E2}	5HOM_A	99.83

Table S7. Results of HHpred analysis of selected F16Ba and z1a phage proteins of no homologs among proteins of J5a phage. The best and most relevant hits are shown, including the coordinates of the matching regions, PDB ID and chain identifier, and the HHpred probability (%) in the matched region. Only proteins HHpred probability results over 80% are presented. Corresponding proteins are given in parentheses. ORFs unique for a particular phage are marked with an asterisk. Corresponding proteins were assessed as those sharing more than 70% sequence identity, according to BLASTp.

ORF	Protein length (aa)	Matched residues (aa)	HHpred best match	PDB ID	Probability (%)
F16Ba_020 (z1a_020)	197	74-194	<i>Escherichia coli</i> conjugal transfer protein trwb; coupling protein, bacterial conjugation, fl1-atpase-like quaternary structure, ring helicases	1E9R_A	99.52
		75-196	<i>Legionella pneumophila</i> IcmO (DotL); Protein Complex, Secretion, Secretion systems, Gram-negative bacteria, type 4 secretion system, T4SS, coupling protein	6SZ9_A	99.39
		88-197	<i>Thermoanaerobacter pseudethanolicus</i> type IV secretory pathway virb4 components-like protein; hydrolase	4AG6_B	99.04
		57-196	<i>Sulfolobus solfataricus</i> hera; hydrolase, nura, helicase, translocase	4D2I_B	98.96
F16Ba_030 *	444	35-413	<i>Bacillus</i> phage SPbeta AimR transcriptional regulator; DNA binding protein, peptide binding protein	5Y24_A	100
		37-410	<i>Bacillus</i> phage phi3T AimR transcriptional regulator	5ZVV_A	100
		33-299	<i>Bacillus thuringiensis</i> transcriptional activator PlcR protein	3U3W_A	99.92
z1a_046*	132	1-115	<i>Streptococcus pneumoniae</i> lipoprotein; lipocalin, PccL, virulence, transport protein	5CYB_A	97.02
		1-88	<i>Mycobacterium smegmatis</i> MC2 51 superoxide dismutase [Cu-Zn]; Respiratory, Supercomplex, SOD, Mycobacterium, ETC, Lipoprotein, ELECTRON TRANSPORT	6ADQ_Z	96.53
		1-118	<i>Pseudomonas aeruginosa</i> chaperone CupB2; Ig fold, periplasmic chaperone	3Q48_A	93.31

Table S8. Amino acid sequence identity analysis between proteins of J5a bacteriophage and relevant proteins or proteins encoded by similar genome regions of other known or proposed members of *Wbetavirus* genus phages. Asterisks mark ORFs for which their lengths were altered according to their detailed translation analysis. Green color marks newly added ORFs.

J5a ORF no.	No. of amino acid residues	Known or predicted function	z1a	F16Ba	Carmel_SA	Tavor_SA	Negev_SA	AP631	Fah	Wbeta	Cherry	Gamma isolate 53	Gamma isolate 51	Gamma isolate D'Herelle
1.	161	Terminase small subunit	154/161	158/161	153/161	159/161	159/161	158/161	158/161	158/161	158/161	158/161	158/161	158/161
2.	565	Terminase large subunit	556/565	555/565	556/565	562/565	562/565	561/565	560/565	559/565	558/565	559/565	558/565	558/565
3.	432	Portal protein	424/432	425/432	425*/432	423*/432	422*/432	424/432	424*/432	424/432	424/432	424/432	424/432	424/432
4.	206	Prohead protease	202/206	203/206	203*/206	202/206	202/206	203/206	203/206	203/206	203/206	203/206	203/206	203/206
5.	392	Major capsid protein	385/392	378/392	379/392	385/392	379/392	385/392	379/392	379/392	379/392	379/392	379/392	379/392
6.	96	Head-tail connector protein	95/96	94/96	95/96	95/96	95/96	95/96	95/96	95/96	95/96	95/96	95/96	95/96
7.	107	Head-tail adaptor protein	101/107	104/107	100/107	96/107	105/107	104/107	105/107	105/107	105/107	105/107	105/107	105/107
8.	146	Hypothetical protein	146/146	146/146	145/146	111/145	146/146	115/145	145/146	145/146	145/146	145/146	145/146	145/146
9.	119	DUF3168 domain protein	114/119	117/119	114/119	104/119	117*/119	115/119	118/119	118/119	118/119	118/119	118/119	118/119
10.	202	Major tail protein	197/202	194/202	177/202	195/202	195/202	176/202	195/202	195/202	195/202	195/202	195/202	195/202
11.	105	Hypothetical protein	104/105	75/105	105/105	77/105	75/105	75/105	75/105	75/105	75/105	75/105	75/105	75/105
12.	64	Hypothetical protein	63/64	53/58	57/58	46/58	-	33/37	53/58	53/58	53/58	53/58	53/58	53/58
13.	1283	Tail length tape-measure protein	1192/1283	1251/1283	1219/1283	800/845 + 394/438	1250/1283	1219/1283	1203/1283	1203/1283	1203/1283	1203/1283	1203/1283	1203/1283
14.	496	Distal tail protein	444/496	447/496	441/496	450/496	448/496	445/496	444/496*	443/496	444/496*	443/496*	444/496*	444/496
15.	1309	Tal/RBP (Tail lysozyme/receptor-binding protein)	1155/1308	1083/1355	1075/1321	1076/1332	1036/1332	1095/1309	1024/1288	1057/1331	1023/1288	1025/1288	1025/1288	1057/1331
16.	78	XpaF1 protein (hemolysin of Xhla1 protein family)	72/78	72/78	71/78	71/78	71/78	-	-	-	-	-	-	-
17.	79	Holin	73/79	78/79	73/79	73/79	74/79	-	-	-	-	-	-	-
		Holin						unrelated (141 aa)	unrelated (141 aa)	unrelated (141 aa)	unrelated (141 aa)	unrelated (141 aa)	unrelated (141 aa)	unrelated (141 aa)
18.	351	N-acetylmuramoyl-L-alanine amidase	334/351	331/351	332/351	334/351	333/351	-	-	-	-	-	-	-
		N-acetylmuramoyl-L-alanine amidase						unrelated (233 aa)	unrelated (233 aa)	unrelated (233 aa)	unrelated (233 aa)	unrelated (233 aa)	unrelated (233 aa)	unrelated (233 aa)
19.	108	Hypothetical protein	103/109	99/109	102/109*	86/109*	100/109	-	-	-	-	-	-	-
		Predicted lipoprotein						unrelated (163 aa)	unrelated (165 aa)	unrelated (165 aa)	unrelated (163 aa)	unrelated (165 aa)	unrelated (165 aa)	unrelated (165 aa)

			unrelated (194 aa)	unrelated (197 aa)	unrelated (197 aa)	unrelated (163 aa)	unrelated (194 aa)							
		Hypothetical protein, partly similar to J5a ORF033				(60 aa)								
20.	64	Repressor protein	58/65	57/65	57/65*	22/67*	51/65	22/70	22/70	22/70	22/70	22/70	22/70	22/70
21.	100	Hypothetical protein	88/102	91/102	87/102	86/102	86/102*	93/102	93/102	93/102	93/102	93/102	93/102	93/102
22.	60	Hypothetical protein	54/60	55/60	55/60	55/60	54/60	55/60	55/60	55/60	55/60	55/60	55/60	55/60
23.	429	FtsK/SpoIIIE family protein (cell division protein FtsK)	405/429	424/429	407/429	407/429	405/429 *	376/397 + 38/65	409/429	409/429	409/429*	409/429*	409/429*	409/429
24.	210	Conserved phage protein	206/210	209/210	204/210*	205/210*	203/210*	204/210*	205/210*	205/210	205/210*	204/210*	205/210*	205/210
25.	78	HTH cro/C1-type domain- containing protein (putative transcription regulator)	75/78	78/78	75/78	-	-	-	78/78	78/78	78/78	78/78	78/78	78/78
		Putative transcriptional regulator of Xre family, putative phage repressor				unrelated (72)	unrelated (72)	unrelated (72)						
26.	39	Hypothetical protein	29/39	39/39	29/39	26/39	25/39	26/39	39/39	39/39	39/39	39/39	39/39	39/39
27.	287	Conserved phage protein (HTH cro/C1-type domain- containing protein)	269/287	281/287	263/287	275/287	269/287	263/287	280/287	280/287	280/287	280/287	280/287	280/287
28.	484	Site-specific recombinase	469/484	262/481	260/480	467/484*	263/481	259/481	261/481	261/481	261/481	261/481	261/481	261/481
29.	428	Transcriptional regulator (AimR family lysis-lysogeny pheromone receptor)	425/428	215/414	339/428	422/428	217/414	218/414	215/414	215/414	-	-	-	-
30.	46	AimP	44/46	14/46	32/46	45/46	14/46	17/46	14/46	14/46	-	-	-	-
31.	51	Hypothetical protein	46/51			48/51								
32.	119	Hypothetical protein (HTH Cro/C1 family protein), transcriptional regulator of Xr	118/119	90/117	91*/117	118/119	90/117*	91/117*	90/118	90/118	-	-	28/36	28/36
33.	75	Hypothetical protein (HTH Cro/C1 family protein)	72/75	61/75	61/75	75/75	61/75	61/75	61/75	61/75	-	-	61/75	61/75
34.	55	Hypothetical protein	54/55*	16/52	16/52	53/55*	16/52	15/52	16/52	16/52*	16/52	16/52	16/52	16/52*
35.	51	Hypothetical protein	47/51	48/51	43/53	48/51	42/51	48/51	48/51	48/51	48/51	48/51	48/51	48/51
36.	248	Putative antirepressor	245/248	242/248	243/248	147/275	23/227	146/275	145/271	145/271	145/271	145/271	145/271	145/271
		Hypothetical protein	unrelated (125)	unrelated (125)	unrelated (125)									
37.	217	Hypothetical protein	117/216	121/216	119/216	188/217*	127/216*	166/175 50/55	188/217	188/217	188/217	188/217	188/217	188/217
38.	306	Replication initiation protein	283/322	277/313	286/316*	277/323*	291/311*	288/305	276/306*	294/315	294/315*	286/315*	294/315*	294/315

[illegible]

		phages, present in many strains of <i>B. thuringiensis</i> and other bacteria, putative glucose epimerase (HHpred 7740054)												
47.	77	Hypothetical protein, only in J5a and Tavor_SA among wbetaviruses; identical or nearly identical proteins are encoded by several <i>Bacillus</i> strains	-	-	-	75/77	-	-	-	-	-	-	-	-
48.	53	Hypothetical protein, only in J5a among wbetavirus phages, present in 12 other phages; identical or nearly identical protein is encoded by many strains of various <i>Bacillus</i> species	-	-	-	-	-	-	-	-	-	-	-	-
49.	38	Hypothetical protein, only in J5a among phages	-	-	-	-	-	-	-	-	-	-	-	-
50.	146	Hypothetical protein, only in J5a among wbetavirus phages, nearly identical in N-terminal moiety to the N-terminal moiety of an uncultured phage protein 9AX2_46; identical or nearly identical protein in their N-terminal moieties are encoded by many strains of various <i>Bacillus</i> species	-	-	-	-	-	-	-	-	-	-	-	-
51.	83	Hypothetical protein; only in J5a among wbetavirus phages, nearly identical in N-terminal moiety to the C-terminal moiety of an uncultured phage protein 9AX2_46	-	-	-	-	-	-	-	-	-	-	-	-
52.	96	Hypothetical protein; only in J5a among wbetavirus phages, nearly identical to a <i>B. thuringiensis</i> protein	-	-	-	-	-	-	-	-	-	-	-	-
53.	62	Hypothetical protein; putative inhibitor of RNA polymerase (HHpred 5227104; E=0.025, Probability 96.15)	55/62	57/62	54/62	56/62	56/79	54/62	56/79	56/79	56/79	56/79	56/79	56/79
54.	40	Hypothetical protein	39/40	38/40	38/40	40/40	40/40	36/40	39/40	39/40	39/40	39/40	39/40	39/40
55.	131	RNA polymerase sigma factor,	127/131	128/131	127/131	127/131	129/131	129/13	129/131*	129/131*	129/131	129/131	129/131	129/131*

[illegible]

00037199.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVALLQQNLVLKEVRDGRIVPYVITET	80
00037255.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
ARW58514.1	1	MSTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
ARW58396.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
AZF88360.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
YP 459979.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
00037148.1	1	MRTPSGILHVDFKTDQIIAAIQPDYWDKRWHELKNNVMDLDTAFDGDSDSATLQQNLVLKEVRDGRIVPYVITET	80
ARW58457.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNVMDLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
ABA46383.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNIDMLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
YP 338198.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNIDMLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
YP 512324.1	1	MRTPSGILHVDFKTDQIVAAIQPEDYWDKRWHELKNNIDMLDTAFDGDTHAVTLQQNLVLKEVRDGRIVPYVITET	80
00037199.1	81	EKNSDNRSITTYASGAWVQIAKSGVIKQRIESKTVNEFIDMALIGMKWQERGQTDYAGFHTMTIDEFLDPLTFLKKIASL	160
00037255.1	81	EKNSDTRSITTYASGAWIQIAKSGIIPQRIESKTVNEFIDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
ARW58514.1	81	EKNSDTRSITTYASGAWIQIAKSGIIPQRIESKTVNEFIDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
ARW58396.1	81	EKNSDKRFITTYASGAWIQIAKSGVIKQRIESKTVNEFIDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
AZF88360.1	81	EKNSDTRSITTYASGAWIQIAKSGIIPQRIESKTVNEFIDLALLGMKWQRGVTEYAGFHTMTIDEYIDPLTFLKKIASL	160
YP 459979.1	81	EKNSDTRSITTYASGAWIQIAKSGIIPQRIESKTVNEFMDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
00037148.1	81	EKNSDKRSITTYASGAWIQIAKSGVIKQRIESKTVNEFIDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
ARW58457.1	81	EKNSDKRSITTYASGAWIQIAKSGVIKQRIESKTVNEFMDLALLGMKWQRGITEYAGFHTMTIDEYIDPLTFLKKIASL	160
ABA46383.1	81	EKNSDKRSITTYASGAWIQIAKSGVIKQRIESKTVNEFMDLALLGMKWQRGVTEYAGFHTMTIDEYMDSLTFLKKIASL	160
YP 338198.1	81	EKNSDKRSITTYASGAWIQIAKSGVIKQRIESKTVNEFMDLALLGMKWQRGVTEYAGFHTMTIDEYMDSLTFLKKIASL	160
YP 512324.1	81	EKNSDKRSITTYASGAWIQIAKSGVIKQRIESKTVNEFMDLALLGMKWQRGVTEYAGFHTMTIDEYMDSLTFLKKIASL	160
00037199.1	161	FKLEIQYRVEVKGSKIIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRDICTALVGFVKGEGDKVITIESINKGLPY	240
00037255.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
ARW58514.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
ARW58396.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
AZF88360.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
YP 459979.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
00037148.1	161	FKLEIRYRVEIKGSKIIGWYVMDIQKRGRDGTKEIELGKDXGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
ARW58457.1	161	FKLEIRYRVEIKGSRIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
ABA46383.1	161	FKLEIRYRVEIKGSKIIGWYVMDIQKRGRDGTKEIELGKDXGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
YP 338198.1	161	FKLEIRYRVEIKGSKIIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
YP 512324.1	161	FKLEIRYRVEIKGSKIIGWYVMDIQKRGRDGTKEIELGKDLGVTRIEHTRNICALVGFVKGEGDKVITIESINKGLPY	240
00037199.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
00037255.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
ARW58514.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
ARW58396.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
AZF88360.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
YP 459979.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
00037148.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
ARW58457.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
ABA46383.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
YP 338198.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
YP 512324.1	241	IVDADAFQRWNEHGQHKFGFYTPETEELDMPKRLTLMEIELKKRVNSSISYEVAQSIGRIFGLEHELINEGDTIKIK	320
00037199.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVQNEANETASNAK	400
00037255.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
ARW58514.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
ARW58396.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVQNEANETASNAK	400
AZF88360.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVQNEANETASNAK	400
YP 459979.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVQNEANETASNAK	400
00037148.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVQNEANETASNAK	400
ARW58457.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
ABA46383.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
YP 338198.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
YP 512324.1	321	DTGFTPELYLEARVIAGDESFTDPTQDKYFEGDYREIVNQNEELRKIYNRILSSLGNKQEMIDQLDKLVNEANETASNAK	400
00037199.1	401	KESEAAKALAEKVQENIKNNTVDIEAMNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
00037255.1	401	KESEAAKALAEKVQENIKNNTVEIIEAKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
ARW58514.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
ARW58396.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
AZF88360.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
YP 459979.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
00037148.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
ARW58457.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
ABA46383.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
YP 338198.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
YP 512324.1	401	KESEAAKALAEKVQENIKNNTVEIIESKNPPTGLKPKFTLWRDISNGKPGILKIWTGAWESVVPDVESVKKETLDQVN	480
00037199.1	481	KDIESTKTELNQKVQEAQNQATGQFNEVQEGLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIETLTKKDTEISSK	560
00037255.1	481	KDIETTTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITFDVQNEQGNINKVQTQIEQTSDFGFKTSIESLTKKDTEISSK	560
ARW58514.1	481	KDIETTTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDNKITKFEQDSSGFKTSIESLTKKDTEISSK	560
ARW58396.1	481	KDIETTTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
AZF88360.1	481	KDIETTTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSDVQNEQGNINKVQTQIEQTSDFGFKTSIETLTKKDTEISSK	560
YP 459979.1	481	KDIATTTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
00037148.1	481	KDIETITKTELNQKVQEAQNQATGQFNEVQEGLGQVSRITSSINENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
ARW58457.1	481	KDIETTTKTELNQKVQEAQNQATGQFNEVQEGLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
ABA46383.1	481	KDIESTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
YP 338198.1	481	KDIESTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
YP 512324.1	481	KDIESTKTELNQKVQEAQNQATGQFNEVKESLGQVSRITSNENKQGEIDKKVTKFEQDSSGFKTSIESLTKKDTEISSK	560
00037199.1	561	LNTVELTVEGKTKTISDVQQTNDLKKTTTIDKEEAGKISTKLEQVEART ---VGGENWLINTGP-----	622
00037255.1	561	LNTVESTVEGKTKTISDVQQTNDLKKTTTIDKEEAGKISTKLEQVEART ---VGGENWLINTGR-----	622
ARW58514.1	561	LNTVESTVEGKTKTISDIQSDTSLRKTTTNEIKTAEAGKTELTLQLETKVNDIKIGGPNLFINSGF-----	626
ARW58396.1	561	LNTVESTVEGKTKTISDIQSDTSLKQTTTIEKEQAGKISEKLTVEQKYDNMKIGGQNFYKQKSF-----gaagGT	632
AZF88360.1	561	LNTVESTVEGKTKTISDIQSDTSLKQTTTIEKEQAGKISEKLTVEQKYDNMKIGGQNFYKQKSF-----gaagGT	632
YP 459979.1	561	LNTVESTVEGKTKTISDVQQTNDLKKTTTIDKEEAGKISTKLEQVEART ---NYVINSDFSNVTNSWIGTAT	636
00037148.1	561	LNTVELTVEGKTKTISDVQQTASELTKTTTIEKEEAGRTKERMEQINSKVDGLEVGATNLIDGTEF-----inanGW	632

ARW58457.1	561	LNTVESTVEGKTKTISDIQSDTTSLKQTTEIKEEQAGKISEKLTSEQKYDNMKIGGQNFYKQKSF-----gaagGT	632
ABA46383.1	561	VNTIESTVEGKTKTISDVQQTSDLKKTTEIKEEAGKISEKLSMVETKVNNSDKAGGRNLLL-----GS	624
YP_338198.1	561	VNTIESTVEGKTKTISDVQQTSDLKKTTEIKEEAGKISEKLSMVETKVNNSDKAGGRNLLL-----GS	624
YP_512324.1	561	VNTIESTVEGKTKTISDVQQTSDLKKTTEIKEEAGKISEKLSMVETKVNNSDKAGGRNLLL-----GS	624
00037199.1	623	-----NEKPQTIG-----MVGGAQVNAKAF-----AVQ-----	645
00037255.1	623	-----NQRPQTIG-----MSGGAQVNAKAG-----SFN-----	645
ARW58514.1	627	-----QNELFSWY-----FHNGKSAIIVSE-----ADE-----	649
ARW58396.1	633	-----TVKYDENNKWdditipvga-----s-gswkgILYNNKNAKLLVGRAYTISYEIYADE-----	683
AZF88360.1	633	-----TVKYDENNKWdditipvga-----s-gswkgILYNNKNAKLLVGRAYTISYEIYAE-----	683
YP_459979.1	637	-----LFKFVDVNISEasaikkgl-----qitsnkaFVYQKLPADVFKKKKGIASCIYNVSS-----	688
00037148.1	633	arwgsygTISVKESSLPSlptpgslvietkvngaeqavpn-gtqvqMRSSDRKFVKVKGQKYTVSFNVATSELgwllldy	711
ARW58457.1	633	-----TVKYDENNKWdditipvga-----s-gswkgILYNNKNAKLLVGRAYTISYEIYADE-----	683
ABA46383.1	625	-----NVKYEKTDYL-----INQYSLTENFFAGEEYTFVIKGSVPQ-----	660
YP_338198.1	625	-----NVKYEKTDYL-----INQYSLTENFFAGEEYTFVIKGSVPQ-----	660
YP_512324.1	625	-----NVKYEKTDYL-----INQYSLTENFFAGEEYTFVIKGSVPQ-----	660
00037199.1	646	PgEYIVLecSDH----TDSFYQ---FHLDN TKMGDFEKS KDMT LSLDLQNDvhvdFIlfqfinGVWSEN VQKGV PASN-V	717
00037255.1	646	E-DYMIvecTDH---TDSFYQ---FHLDN TKMGDY EKGD MTFSD LQNDvpidLIvfqfinGVWTE NLYSRFPVDN--	715
ARW58514.1	650	K-VIKFIpkDGE---SGGVYQRVGAKGNSTVVPFEKEQDYVVTVWLKSSndnqKL-----KISAEGLKSGFVNVGKV	718
ARW58396.1	684	V-IPTAI--DIN---NFGVATSTGTNDNDVVAKRIMRTPKTIAGQWVKVS---AT-----FIMPDNITQDFYDN SVI	746
AZF88360.1	684	V-IPTAI--DIN---NFGVATSTGTNDNDVVAKRIMRTPKTIAGQWVKVS---AT-----FIMPDNITQDFYDN SVI	746
YP_459979.1	689	F-TP-GT--DYP---RLYMRFTYDQNGTEKQYAILKQQEV TNG-WIRIS-----IPFDTTGYTGELKEV	745
00037148.1	712	I-YIMYT--DNA---NQRIPT-INTLDFPIIAKINDRENNN---YYRVK---FT-----F---TATKDD-DNAYL	764
ARW58457.1	684	V-IPTAI--DIN---NFGVATSTGTNDNDVVAKRIMRTPKTIAGQWVKVS---AT-----FIMPDNITQDFYDN SVI	746
ABA46383.1	661	G-QKFGI--WQNggssNVGYATSVYANGITYVT---FKAVATTSGNERKLS-----L-----YNYPSNTTKAIVE--	719
YP_338198.1	661	G-QKFGI--WQNggssNVGYATSVYANGITYVT---FKAVATTSGNERKLS-----L-----YNYPSNTTKAIVE--	719
YP_512324.1	661	G-QKFGI--WQNggssNVGYATSVYANGITYVT---FKAVATTSGNERKLS-----L-----YNYPSNTTKAIVE--	719
00037199.1	718	wkrevwtfnidTRATGWgLRRLRFARN-----TNSigkrfrFKKTKLEKGS IPT-----DFSKSTYLEQSV	778
00037255.1	716	wrrrsftfkidSRATGWgLRRLRFARN-----ENsgkkyrFKKAKLEKGSVPT-----DFSKSTYLEQSV	776
ARW58514.1	719	wkkhefkfkgTGVGNG---TITFYAD-----VSpigteyflKKPKVEMGN IATEYTTAL EEQVTTDEFTKKTTEIEKSV	789
ARW58396.1	747	-----GVGNGW---TPTKITN-----IK-----IRNMQLEEGNIPTSYRIPSEDQVTTDEFTKKTTEIEKSV	800
AZF88360.1	747	-----GVGNGW---TPTKITN-----IK-----IRNMQLEEGNIPTSYRIPSEDQVTTDEFTKKTTEIEKSV	800
YP_459979.1	746	-----RVNIAT---ADTTTID-----AT-----FTGI MVTFGDLIESWNLAPEDGVTQG VFQSKTTEIEKSV	799
00037148.1	765	-----LIG-GN---TKRALTGsngyawIR-----VNALKVEKGTIATDWDASNNDKVSLPVFEQKTTDIEKSV	823
ARW58457.1	747	-----GVGNGW---TPTKITN-----IK-----IRNMQLEEGNIPTSYRIPSEDQVTTDEFTKKTTEIEKSV	800
ABA46383.1	720	-----W-----W-----VALYKGNKPQDWTAPAEEQVTTDEFTKKTIEITKSV	756
YP_338198.1	720	-----W-----W-----VALYKGNKPQDWTAPAEEQVTTDEFTKKTIEITKSV	756
YP_512324.1	720	-----W-----W-----VALYKGNKPQDWTAPAEEQVTTDEFTKKTIEITKSV	756
00037199.1	779	DGVKTTVTNVQNSQAGFEKRMSTVEQTASGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAINAKVELKQVEDYVAGFK	858
00037255.1	777	DGVKTTVSKVQDSQVGFEKRVTTVEQTASGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAIGAKVELKQVEDYVAGFK	856
ARW58514.1	790	DGVKTTVTNVQNSQAGYEKRMSNVEQTASGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAIGAKVELKQVEDYVAGFK	869
ARW58396.1	801	DGVKTTVTNVQNSQAGFEKRMSTVEQTATGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAIGAKVELKQVEDYVAGFK	880
AZF88360.1	801	DGVKTTVTNVQNSQAGFEKRMSTVEQTATGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAIGAKVELKQVEDYVAGFK	880
YP_459979.1	800	DGVKTTVTNVQNSQAGFEKRMSTVEQTATGLSSTVSNLNNVSDQGGKLT EANTKLEQQATAIGAKVELKQVEDYVAGFK	879
00037148.1	824	EGIKTTVTKVQDSQAGFEKRMSTVEQTASGLSSTVSNLNNVSDQGGKLT EANTKIEQQATAIGAKVELKQVEDYVAGFK	903
ARW58457.1	801	DGIKETITKVENNQSGFENRVATVEKDATS IKQNVSLIQNTQT EQGKLQEA KAGWENTAKALEGKVELKQVEDYVAGFK	880
ABA46383.1	757	DGIKETITKVENNQSGFDRVATVEKDATAIKQNVSLIQNTQT EQGRQLQEA KAGWENTAKALEGKVELKQVEDYVAGFK	836
YP_338198.1	757	DGIKETITKVENNQSGFDRVATVEKDATAIKQNVSLIQNTQT EQGRQLQEA KAGWENTAKALEGKVELKQVEDYVAGFK	836
YP_512324.1	757	DGIKETITKVENNQSGFDRVATVEKDATAIKQNVSLIQNTQT EQGRQLQEA KAGWENTAKALEGKVELKQVEDYVAGFK	836
00037199.1	859	IPELKQTVNQNKQDLLNELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFAKDSYVRDMESRLQL	938
00037255.1	857	IPELKQTVNQNKQDLLNELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFAADS YVRDMESRLQI	936
ARW58514.1	870	IPELKQTVDNKNQDLLGELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATGS YVRDMESRLQL	949
ARW58396.1	881	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFAKDSYVRDMESRLQL	960
AZF88360.1	881	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTRIQADGQFAKDSYVRDMESRLQL	960
YP_459979.1	880	IPELKQTVDNKNQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATDS YVRDMESRLQL	959
00037148.1	904	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINELGINAAAKKTEVYTIEQANGQFAKDSYVRDMETRLQL	983
ARW58457.1	881	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATGS YVRDMETRLQL	960
ABA46383.1	837	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATGS YVRDMETRLQL	916
YP_338198.1	837	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATGS YVRDMETRLQL	916
YP_512324.1	837	IPELKQTVNQNKQDLLDELANKLATEQFNQKMTLIDNRFINEEGLNAAAKKTEVYTKTQADGQFATGS YVRDMETRLQL	916
00037199.1	939	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1018
00037255.1	937	TEKGVSVSVKENDVIAAFNMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYEKGVARSF	1016
ARW58514.1	950	TEKGVSVSVKENDVIAAINMSKENIKLHAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYEKGVARSF	1029
ARW58396.1	961	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1040
AZF88360.1	961	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1040
YP_459979.1	960	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1039
00037148.1	984	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1063
ARW58457.1	961	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	1040
ABA46383.1	917	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	996
YP_338198.1	917	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	996
YP_512324.1	917	TEKGVSVSVKENDVIAAINMSKENIKLNAARIDLVGKVAEWIKAGLLSGCQIRTSNTDNYVSLDDQFIRLYERGVARAF	996
00037199.1	1019	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISDGI VDGAVQKSVYWELQRNGISVLNANDYQA	1098
00037255.1	1017	LGHYRRTDGVSQPTFILGTDEKTSAPAGALFMSQAGAGWPGAYASIGISDGI VDGTVQKSVYWELQRNGLSVLNANDYHV	1096
ARW58514.1	1030	LGHYRRTDGVSQPTFILGTDEKTSAPAGALFMSQAGAGWPGAYASIGISDGI VDGTVQKSVYWELQRNGLSVLNANDYHV	1109
ARW58396.1	1041	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1120
AZF88360.1	1041	LGHYRRTDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1120
YP_459979.1	1040	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1119
00037148.1	1064	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1143
ARW58457.1	1041	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1120
ABA46383.1	997	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1076
YP_338198.1	997	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGAVQKSVYWELQRNGLSVLNANDYHV	1076
YP_512324.1	997	LGHYRRSDGAVQPTFILGSDEKTNAPEGTLFMSQAGAGWPGAYASIGISNGI VDGTVQKSVYWELQRNGLSVLNANDYHV	1076
00037199.1	1099	FYTGNGNWYFRRGKPGLYQTSLVLEDNGSDADRLPNVTLRNSRVAGYTGVIQMKSSV TQNGWGAIGNFMSPSLREYKS	1178
00037255.1	1097	FYAGNGSWYFRRGKPGLYQTSLVVEDNSTDSLRLPNITLRNSRAAGYTGI IQVKSPVTQNGWGSVQGNFMSPSLREYKS	1176

ARW58514.1	1110	FYAGNGSWYFRRGKVGLYQTSLVVEDNGTSDSLRPNITLRNSRAAGYTGIIVKSPVTQNGWGSVQGNFMTPSLREYKS	1189
ARW58396.1	1121	FYAGNGSWYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1200
AZF88360.1	1121	FYAGSGSWYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1200
YP_459979.1	1120	FYAGNGNWFYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1199
Q0037148.1	1144	FYAGNGSWYFRRGKPGLYQTSLVLEDNGTSDSLRPNVTIRNSRAAGYTGVIQLKSSVTQNGWGAVQGNFMTPSLREYKS	1223
ARW58457.1	1121	FYAGNGSWYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1200
ABA46383.1	1077	FYAGNGNWFYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1156
YP_338198.1	1077	FYAGNGNWFYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1156
YP_512324.1	1077	FYAGNGNWFYFRRGKPGLYQTSLVVEDNSTDSDLRPNVTIRNSRAAGYTGVIQLKSPVTQNGWGAVQGNFMTPSLREYKS	1156
Q0037199.1	1179	NIRDVSFSALEKIRNLKIRQFNYKNAVNELYQMREEKDPNDPPLTTQDIKTYYGIVDEADEDFIDESGKGIHLYSYASI	1258
Q0037255.1	1177	NIRDVSFSALEKIRNVRVREFNYKNAVNELYKMREEKDPNDPPLTTQDIKTYYGIVDESDEAFIDESGKGIHLYSYASL	1256
ARW58514.1	1190	NIRDVSFSALEKIRNVRVREFNYKNAVNELYKMREEKDPNDPPLTTQDIKTYYGIVDESDEAFIDESGKGIHLYSYASL	1269
ARW58396.1	1201	NIRDIPFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1280
AZF88360.1	1201	NIRDIPFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1280
YP_459979.1	1200	NIRDISFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1279
Q0037148.1	1224	NIRDISFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1303
ARW58457.1	1201	NIRDIPFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1280
ABA46383.1	1157	NIRDISFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1236
YP_338198.1	1157	NIRDISFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1236
YP_512324.1	1157	NIRDISFSALEKIRSLKIRQFNYKNAVNELYRMREEKSPNDPPLTTEDIKTYYGIVDECDMFVDES GKG IHL YSYASI	1236
Q0037199.1	1259	GIKGLQEVDEEVEQKVEIANLKSQVASQENRIAQLEE-LLQQLIDKKPEQP	1309
Q0037255.1	1257	TVKALQEV DATVQE QEGE IANLKSQVASQEDRIARLEELLQQLIDKKPEQP	1308
ARW58514.1	1270	TVKALQEV DATVQE QEGE IANLKSQVASQEDRIARLEELLQQLIDKKPEQP	1321
ARW58396.1	1281	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLINEKPEQP	1332
AZF88360.1	1281	GIKGLQEV DATVQE QEGE IENLKSQVASQEDRIARLEELLQQLIN K KPEQP	1332
YP_459979.1	1280	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLIN K KPEQP	1331
Q0037148.1	1304	GIKGLQEV DATVQE QEGE IENLKSQVASQEDRIARLEELLQQLIDKKPEQP	1355
ARW58457.1	1281	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLIN K KPEQL	1332
ABA46383.1	1237	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLIN K KPEQP	1288
YP_338198.1	1237	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLIN K KPEQP	1288
YP_512324.1	1237	GIKGLQEV DATVQE QEGE IANLKSQIASQEDRIARLEELLQQLIN K KPEQP	1288

Figure S3. Alignment of amino acid sequences of Tal/RBP proteins (J5a_015 and its counterparts) of J5a, F16Ba, z1a, and other Wbeta-like bacteriophages.