

Prevalence and diversity analysis of candidate prophages to provide an understanding on their roles in *Bacillus thuringiensis*

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Table 1. Strains used for prophage prediction.

Bt strains	GenBank accession number	Number of prophages			All prophages size(bp)	Ratio in genomes
		Complete	Incomplete	Total		
97-27	NC_005957.1	0	2	2	35201	0.66%
YBT-1518	NC_022873.1	4	10	14	464133	6.96%
Al Hakam	NC_008600.1	0	2	2	30370	0.57%
BMB171	NC_014171.1	1	2	3	83252	1.48%
YBT-020	NC_017200.1	1	3	4	150423	2.65%
CT-43	NC_017208.1	3	5	8	322044	5.24%
HD-771	NC_018500.1	5	5	10	454175	7.05%
HD-789	NC_018508.1	2	3	5	169183	2.67%
MC28	NC_018693.1	3	5	8	255837	3.82%
Bt407-1	NC_018877.1	2	2	4	177905	2.90%
HD73	NC_020238.1	7	1	8	415382	7.03%
IS5056	NC_020376.1	3	5	8	323548	4.78%
YBT-1520	NZ_CP004858.1	4	3	7	360407	5.48%
HD-29	NZ_CP010089.1	4	3	7	304056	4.49%
HD-1	NZ_CP004870.1	2	4	6	303665	4.49%
YBT1520-2	NZ_CP007607.1	3	3	6	341892	5.24%
HD-1011	NZ_CP009335.1	1	3	4	91812	1.51%
HD571	NZ_CP009600.1	0	2	2	23955	0.45%
HD682	NZ_CP009720.1	0	2	2	97612	1.84%
97-27-2	NZ_CP010088.1	0	1	1	14777	0.28%
HD1002	NZ_CP009351.1	2	5	7	283451	4.31%
BGSC 4AA1	NZ_CP010577.1	4	4	8	387450	6.27%
YC-10	NZ_CP011349.1	6	1	7	403515	5.95%
HS18-1	NZ_CP012099.1	1	3	4	127410	1.99%
HD521	NZ_CP010106.1	2	2	4	191673	3.09%
YWC2-8	NZ_CP013055.1	4	4	8	389430	6.25%
CTC	NZ_CP013274.1	0	2	2	22608	0.42%
Pasteur Institute Standard	NZ_AP014864.1	8	7	15	699376	10.18%
Bt185	NZ_CP014282.1	3	0	3	162720	2.55%

HD12	NZ_CP014847.1	5	6	11	485701	7.48%
Bt407-1	NZ_CM000747.1	1	4	5	208507	3.46%
HD1	NZ_CP010005.1	4	3	7	402407	5.87%
BGSC 4Y1	NZ_CM000746.1	3	3	6	202145	3.59%
T01001	NZ_CM000748.1	1	9	10	290537	4.59%
T03a001	NZ_CM000751.1	0	10	10	224034	4.05%
BGSC 4AJ1	NZ_CM000752.1	1	8	9	207065	3.19%
ATCC 10792-1	NZ_CP021061.1	1	6	7	322324	5.15%
BGSC 4AW1	NZ_CM000754.1	0	4	4	154262	2.81%
BGSC 4BA1	NZ_CM000755.1	1	4	5	127755	2.12%
BGSC 4BD1	NZ_CM000756.1	1	4	5	107046	1.72%
BGSC 4CC1	NZ_CM000757.1	1	5	6	125476	2.09%
IBL 200	NZ_CM000758.1	1	4	5	143406	2.13%
IBL 4222	NZ_CM000759.1	1	8	9	236759	3.58%
DAR 81934	NZ_CM001804.1	0	1	1	12836	0.22%
T04001	CM000749.1	1	18	19	452225	7.40%
Bc601	NZ_CP015150.1	5	1	6	346418	5.67%
BGSC 4C1	NZ_CP015176.1	3	4	7	315900	5.43%
MYBT18246	NZ_CP015350.1	5	10	15	678847	10.05%
KNU-07	NZ_CP016588.1	0	3	3	157672	2.56%
Bt18247	NZ_CP015250.1	4	5	9	408728	6.66%
L-7601	NZ_CP020002.1	2	8	10	426869	6.77%
YGd22-03	NZ_CP019230.1	2	3	5	207572	3.29%
SCG04-02	NZ_CP017577.1	1	1	2	34046	0.58%
BM-BT15426	NZ_CP020723.1	0	2	2	60782	1.16%
c25	NZ_CP022345.1	2	2	4	164205	2.90%
ATCC 10792-2	NZ_CM000753.1	1	9	10	278757	4.45%
ST7	CP016194.1	3	5	8	302253	4.81%
ATCC 10792-3	CP020754.1	2	5	7	331464	5.14%
XL6	CP013000.1	1	3	4	164549	2.89%
T13001	NZ_CM000750.1	1	9	10	301419	4.99%
LM1212	CP024771.1	6	2	8	349306	5.53%

Table 2. Candidate prophages regions identified in Bt genomes.

Prophages	Total length (bp)	Positions in bacteria chromosome		Type of prophage	Best match phages	Coverage (%)	Identity (%)
		Start	End				
97-27 prophage-1	14940	1009871	1024810	incomplete			
97-27 prophage-2	20261	1199512	1219772	incomplete			
YBT-1518 prophage-1	42889	257730	300618	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	42	93.32
YBT-1518 prophage-2	31054	415206	446259	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	100	99.79
YBT-1518 prophage-3	31039	772058	803096	incomplete	<i>Bacillus</i> phage BMBtp1	8	90.23
YBT-1518 prophage-4	18763	848635	867396	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	78	90.56
YBT-1518 prophage-5	33609	882892	916500	complete	<i>Bacillus</i> phage BtCS33	67	94.13
YBT-1518 prophage-6	20482	1443308	1463789	incomplete			
YBT-1518 prophage-7	57001	1788360	1845360	incomplete	<i>Bacillus</i> phage Carmel_SA	17	91.8
YBT-1518 prophage-8	31727	2572024	2603750	incomplete	<i>Bacillus</i> phage phiCM3	5	83.53
YBT-1518 prophage-9	6980	3044091	3051070	incomplete			
YBT-1518 prophage-10	52143	4260401	4312543	complete	<i>Bacillus</i> phage 11143	15	85.62
YBT-1518 prophage-11	23854	4623183	4647036	incomplete	<i>Bacillus</i> phage BMBtp1	13	83.58
YBT-1518 prophage-12	40309	5316310	5356618	complete	<i>Bacillus</i> phage phi411	44	88.08
YBT-1518 prophage-13	40120	5517648	5557767	complete	<i>Bacillus</i> phage phi411	42	85.93
YBT-1518 prophage-14	34163	5647562	5681724	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	52	92.79
Al Hakam prophage-1	20381	1215373	1235753	incomplete			

Al Hakam prophage-2	9989	2364594	2374582	incomplete			
BMB171 prophage-1	20479	1196392	1216870	incomplete			
BMB171 prophage-2	45513	2498467	2543969	complete	<i>Bacillus</i> phage phiCM3	15	90.09
BMB171 prophage-3	17260	3580569	3597828	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	4	77.57
YBT-020 prophage-1	53160	390634	443893	complete	<i>Bacillus</i> phage vB_BceS-MY192	16	85.46
YBT-020 prophage-2	42537	1115027	1157563	incomplete	<i>Bacillus</i> phage phi4B1	90	100
YBT-020 prophage-3	15145	1352176	1367320	incomplete			
YBT-020 prophage-4	39581	4721857	4761437	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	37	91.88
CT-43 prophage-1	39114	694975	734088	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
CT-43 prophage-2	13004	1021860	1034863	incomplete			
CT-43 prophage-3	14886	1224209	1239094	incomplete			
CT-43 prophage-4	84201	1826113	1910313	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1 <i>Bacillus</i> phage BtCS33/ <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtiUFT6.51-F	7	89.15
CT-43 prophage-5	19645	2350991	2370635	incomplete		9	83.3
CT-43 prophage-6	66379	2588715	2655093	complete	<i>Bacillus</i> phage BVE2	5	89.27
CT-43 prophage-7	43658	3773368	3817025	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	24	84.4
CT-43 prophage-8	41157	4904766	4945922	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16 <i>Bacillus</i> phage phiS58/ <i>Bacillus</i> phage phi4J1/ <i>Bacillus</i> phage Waukesha92/ <i>Bacillus</i> phage BceA1/ <i>Staphylococcus</i> phage SpaA1	39	92.73
HD-771 prophage-1	37673	1087752	1125424	incomplete		1	72.41
HD-771 prophage-2	66113	1359225	1425337	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	24	94.34
HD-771 prophage-3	64662	2015855	2080516	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	10	92.36
HD-771 prophage-4	20301	2852622	2872922	incomplete			
HD-771 prophage-5	60395	2920758	2981152	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	15	84.39
HD-771 prophage-6	39777	4500609	4540385	complete	<i>Bacillus</i> phage phi4J1	30	87.76
HD-771 prophage-7	34536	4676595	4711130	incomplete	<i>Bacillus</i> phage BMBtp1	73	94.14
HD-771 prophage-8	40354	5195637	5236990	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	45	94.81
HD-771 prophage-9	48453	5442197	5490649	complete	Uncultured <i>Caudovirales</i> phage clone 7S_1	21	85.51
HD-771 prophage-10	41911	5764272	5806182	complete	<i>Bacillus</i> phage BtCS33	30	93.21
HD-789 prophage-1	14805	762327	777131	incomplete			
HD-789 prophage-2	61836	2938754	3000589	complete	<i>Bacillus</i> phage phiS3501	71	99.98
HD-789 prophage-3	40530	3050147	3090676	incomplete	<i>Bacillus</i> phage phiS3501	9	94.41
HD-789 prophage-4	37849	3328682	3366530	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	29	84.34
HD-789 prophage-5	14163	5293480	5307642	incomplete			
MC28 prophage-1	15006	413630	428635	incomplete			
MC28 prophage-2	17175	1441237	1458411	incomplete	<i>Bacillus</i> phage vB_BceS-MY192	6	80.9
MC28 prophage-3	20809	2819914	2840722	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	5	81.81
MC28 prophage-4	52670	2934767	2987436	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	24	87.4
MC28 prophage-5	20408	2999188	3019595	incomplete			
MC28 prophage-6	17679	3038714	3056392	incomplete			
MC28 prophage-7	49920	3102093	3152012	complete	<i>Bacillus</i> phage PfEFR-5/ <i>Bacillus</i> phage PfEFR-4	31	87.37
MC28 prophage-8	62170	5095369	5157538	complete	<i>Bacillus</i> phage vB_BtS_BMBtp16	10	93.31
Bt407-1 prophage-1	23241	696825	720065	incomplete	<i>Bacillus</i> phage phiCM3	8	98.26
Bt407-1 prophage-2	81548	1830538	1912085	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	7	89.15
Bt407-1 prophage-3	26933	2348009	2374941	incomplete	<i>Bacillus</i> phage phiCM3	6	83.59
Bt407-1 prophage-4	46183	2605770	2651952	complete	<i>Bacillus</i> phage BVE2	8	89.27

HD73 prophage-1	42253	231160	273413	complete	<i>Bacillus</i> phage phi4J1	20	94.71
HD73 prophage-2	61572	376296	437867	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	9	99.76
HD73 prophage-3	57693	760542	818234	complete	<i>Bacillus</i> phage BtCS33	72	99.97
HD73 prophage-4	55077	1282708	1337784	complete	<i>Bacillus</i> phage phi4J1	19	89.02
HD73 prophage-5	20416	1383091	1403506	incomplete			
HD73 prophage-6	54689	2138013	2192701	complete	<i>Bacillus</i> phage BtCS33	58	98.84
HD73 prophage-7	58499	5020287	5078785	complete	<i>Bacillus</i> phage phiS3501	63	95.02
HD73 prophage-8	44192	5232007	5276198	complete	<i>Bacillus</i> phage phi4J1	23	92.42
IS5056 prophage-1	39112	692092	731203	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
IS5056 prophage-2	13004	1018979	1031982	incomplete			
IS5056 prophage-3	20264	1216033	1236296	incomplete			
IS5056 prophage-4	79357	1841121	1920478	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1 <i>Bacillus</i> phage BtCS33/ <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtiUFT6.51-F	8	89.15
IS5056 prophage-5	20420	2356189	2376608	incomplete		9	83.3
IS5056 prophage-6	66381	2594876	2661256	complete	<i>Bacillus</i> phage BVE2	5	89.27
IS5056 prophage-7	43853	3776967	3820819	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	24	84.42
IS5056 prophage-8	41157	4909665	4950821	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	39	92.73
YBT-1520 prophage-1	90139	243519	333657	complete	<i>Bacillus</i> phage BMBtp1	9	87.57
YBT-1520 prophage-2	58551	756854	815404	complete	<i>Bacillus</i> phage phi4I1	59	99.99
YBT-1520 prophage-3	42947	1280945	1323891	complete	<i>Bacillus</i> phage phiS3501	4	82.53
YBT-1520 prophage-4	20460	1380714	1401173	incomplete			
YBT-1520 prophage-5	30424	2124300	2154723	incomplete	<i>Bacillus</i> phage phiS3501	40	89.22
YBT-1520 prophage-6	78741	4963649	5042389	complete	<i>Bacillus</i> phage phiS3501	46	94.97
YBT-1520 prophage-7	39145	5192924	5232068	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	46	96.3
HD-29 prophage-1	51911	156843	208753	complete	<i>Bacillus</i> phage phi4J1	26	99.59
HD-29 prophage-2	54586	843002	897587	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	75	100
HD-29 prophage-3	32765	2493852	2526617	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	14	82.98
HD-29 prophage-4	4296	2992879	2997175	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	27	74.93
HD-29 prophage-5	70288	4946878	5017166	complete	<i>Bacillus</i> phage BMBtp1	20	93.29
HD-29 prophage-6	46019	5030224	5076243	incomplete	Phage Wrath	31	92.42
HD-29 prophage-7	44191	5200050	5244240	complete	<i>Bacillus</i> phage phi4J1	23	92.42
HD-1 prophage-1	66552	258214	324765	complete	<i>Bacillus</i> phage phi4J1	15	94.69
HD-1 prophage-2	48464	400116	448579	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	5	99.7
HD-1 prophage-3	40506	781975	822480	incomplete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	43	96.78
HD-1 prophage-4	53101	1296841	1349941	incomplete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	20	87.3
HD-1 prophage-5	75871	4992087	5067957	incomplete	<i>Bacillus</i> phage phiCM3	39	97.33
HD-1 prophage-6	19171	5225976	5245146	incomplete	<i>Bacillus</i> phage phi4J1	22	91.41
YBT1520-2 prophage-1	73308	19909	93216	complete	<i>Bacillus</i> phage phi4J1	19	95.86
YBT1520-2 prophage-2	35925	707688	743612	incomplete	<i>Bacillus</i> phage BMBtp1	38	93.33
YBT1520-2 prophage-3	78739	894807	973545	complete	<i>Bacillus</i> phage phiS3501	46	94.97
YBT1520-2 prophage-4	53561	3791245	3844805	incomplete	<i>Bacillus</i> phage BtCS33	59	98.73
YBT1520-2 prophage-5	38379	4650515	4688893	incomplete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	19	85.81
YBT1520-2 prophage-6	61980	5153713	5215692	complete	<i>Bacillus</i> phage BtiUFT6.51-F	67	99.9
HD-1011 prophage-1	14779	2355738	2370516	incomplete			
HD-1011 prophage-2	51810	2910951	2962760	complete	<i>Bacillus</i> phage phi4I1	36	89.16

HD-1011 prophage-3	6681	3521183	3527863	incomplete			
HD-1011 prophage-4	18542	4542029	4560570	incomplete			
HD571 prophage-1	9989	103622	113610	incomplete			
HD571 prophage-2	13966	117579	131544	incomplete	<i>Bacillus</i> phage vB_BceS-MY192	14	82.64
HD682 prophage-1	67350	1214601	1281950	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	7	80.89
HD682 prophage-2	30262	2576180	2606441	incomplete			
97-27-2 prophage-1	14777	1213524	1228300	incomplete			
HD1002 prophage-1	52608	47815	100422	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	21	84.34
HD1002 prophage-2	37194	179210	216403	incomplete			
HD1002 prophage-3	56570	320439	377008	incomplete	<i>Bacillus</i> phage phiS3501	7	94.41
HD1002 prophage-4	66757	417583	484339	complete	<i>Bacillus</i> phage phiS3501	66	99.98
HD1002 prophage-5	12889	2639455	2652343	incomplete			
HD1002 prophage-6	33240	3597048	3630287	incomplete	Moraxella phage Mcat16	2	79.87
HD1002 prophage-7	24193	5047691	5071883	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	32	81.82
BGSC 4AA1 prophage-1	39416	642522	681937	incomplete	<i>Bacillus</i> phage BMBtp1	87	100
BGSC 4AA1 prophage-2	57403	1165897	1223299	complete	<i>Bacillus</i> phage vB_BtS_BMBtp3	13	99.98
BGSC 4AA1 prophage-3	12835	1269806	1282640	incomplete			
BGSC 4AA1 prophage-4	39650	1917165	1956814	imcomplete	<i>Bacillus</i> phage proCM3	94	99.97
BGSC 4AA1 prophage-5	64804	2610167	2674970	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	14	84.48
BGSC 4AA1 prophage-6	54220	3902354	3956573	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	16	82.98
BGSC 4AA1 prophage-7	46046	4593770	4639815	complete	<i>Bacillus</i> phage Carmel_SA	65	92.36
BGSC 4AA1 prophage-8	73076	5189813	5262888	complete	<i>Bacillus</i> phage phi4I1	48	95.78
YC-10 prophage-1	55152	579100	634251	complete	<i>Bacillus</i> phage BtCS33	58	98.81
YC-10 prophage-2	39965	1443466	1483430	imcomplete	<i>Bacillus</i> phage BMBtp1	22	88.51
YC-10 prophage-3	61975	1949726	2011700	complete	<i>Bacillus</i> phage phi4I1	67	100
YC-10 prophage-4	51804	2331105	2382908	complete	<i>Bacillus</i> phage vB_BtS_BMBtp16	12	85.99
YC-10 prophage-5	75947	2466727	2542673	complete	<i>Bacillus</i> phage phi4J1	16	94.71
YC-10 prophage-6	42540	3157229	3199768	complete	<i>Bacillus</i> phage phi4J1	23	92.42
YC-10 prophage-7	76132	3353688	3429819	complete	<i>Bacillus</i> phage phiCM3	40	96.57
HS18-1 prophage-1	12812	1194101	1206912	incomplete			
HS18-1 prophage-2	43215	1376234	1419448	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	22	87.31
HS18-1 prophage-3	20676	2489077	2509752	incomplete	<i>Bacillus</i> phage phiCM3	7	83.97
HS18-1 prophage-4	50707	2496265	2546971	complete	<i>Bacillus</i> phage phiCM3	38	87.88
HD521 prophage-1	39615	1988162	2027776	complete	<i>Bacillus</i> phage BtCS33	4	80.74
HD521 prophage-2	18844	2028783	2047626	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	4	75.35
HD521 prophage-3	88371	2287686	2376056	complete	<i>Bacillus</i> phage phiCM3	5	83.54
HD521 prophage-4	44843	3817538	3862380	incomplete	<i>Bacillus</i> phage PFeFR-5/ <i>Bacillus</i> phage PFeFR-4	9	82.83
YWC2-8 prophage-1	48053	1523	49575	imcomplete	<i>Bacillus</i> phage phi4J1	8	94.71
YWC2-8 prophage-2	42541	666907	709447	imcomplete	<i>Bacillus</i> phage phi4J1	23	92.42
YWC2-8 prophage-3	76135	863370	939504	complete	<i>Bacillus</i> phage phiCM3	40	96.58
YWC2-8 prophage-4	55155	3763087	3818241	complete	<i>Bacillus</i> phage BtCS33	58	98.81
YWC2-8 prophage-5	39965	4627496	4667460	imcomplete	<i>Bacillus</i> phage phi4J1	27	89.47

YWC2-8 prophage-6	61976	5133773	5195748	complete	<i>Bacillus</i> phage BtiUFT6.51-F	67	99.98
YWC2-8 prophage-7	51805	5515164	5566968	complete	<i>Bacillus</i> phage phiCM3	11	99.76
YWC2-8 prophage-8	13800	5656460	5670259	incomplete	<i>Bacillus</i> phage BceA1	55	87.97
CTC prophage-1	14730	1194064	1208793	incomplete	<i>Staphylococcus</i> phage SpaA1		
CTC prophage-2	7878	2512884	2520761	incomplete	<i>Bacillus</i> phage phi4J1	43	89.83
Pasteur Institute	51244	317809	369052	complete	Uncultured <i>Caudovirales</i> phage	20	87.15
Standard prophage-1	44877	573162	618038	complete	clone 3F_9	22	93.34
Pasteur Institute	38308	1061766	1100073	incomplete	<i>Bacillus</i> phage phiS3501	48	96.32
Standard prophage-2	98877	1295431	1394307	complete	<i>Bacillus</i> phage vB_BtS_BMBtp15	22	90.11
Pasteur Institute	68615	1913253	1981867	complete	<i>Bacillus</i> phage PfeFR-5	8	77.79
Standard prophage-3	51422	2086890	2138311	complete	<i>Bacillus</i> phage phiCM3	59	96.21
Pasteur Institute	7903	3247335	3255237	incomplete	<i>Bacillus</i> phage BtCS33		
Standard prophage-4	40112	3799140	3839251	imcomple	<i>Bacillus</i> phage phi4J1	89	95.71
Pasteur Institute	67089	4006836	4073924	imcomple	<i>Bacillus</i> phage proCM3	51	94.79
Standard prophage-5	34743	4608461	4643203	incomplete	<i>Bacillus</i> phage BtCS33	24	88.95
Pasteur Institute	42578	4661441	4704018	complete	<i>Bacillus</i> phage phi4I1	68	99.95
Standard prophage-6	61607	5100297	5161903	complete	<i>Bacillus</i> phage phi4J1		
Pasteur Institute	9769	5357908	5367676	incomplete	<i>Bacillus</i> phage phi4I1	22	94.72
Standard prophage-7	50429	5512767	5563195	complete	<i>Bacillus</i> phage BtCS33	11	76.35
Pasteur Institute	31803	5624567	5656369	imcomple	Dickeya phage phiDP10.3 clone	8	84.08
Standard prophage-8	65736	1760889	1826624	complete	pD10	30	91.68
Bt185 prophage-1	62376	2479645	2542020	complete	<i>Bacillus</i> phage phiCM3	60	88.61
Bt185 prophage-2	34608	4251904	4286511	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	16	86.23
Bt185 prophage-3	68685	328204	396888	complete	Uncultured <i>Caudovirales</i> phage	31	89.48
HD12 prophage-1	38777	1197527	1236303	incomplete	clone 3F_9	83	95.71
HD12 prophage-2	12835	1291598	1304432	incomplete	Uncultured <i>Caudovirales</i> phage	58	94.41
HD12 prophage-3	43771	1936887	1980657	imcomple	clone 7S_1	20	84.88
HD12 prophage-4	56821	2084122	2140942	complete	<i>Bacillus</i> phage phi4J1	1	82.71
HD12 prophage-5	30764	2713097	2743860	incomplete	<i>Bacillus</i> phage proCM3		
HD12 prophage-6	17322	2912967	2930288	incomplete	<i>Bacillus</i> phage phiS3501		
HD12 prophage-7	38935	3865425	3904359	incomplete	Uncultured <i>Caudovirales</i> phage		
HD12 prophage-8					clone 3F_8		
					Uncultured <i>Caudovirales</i> phage		
					clone 9AX_2		

HD12 prophage-9	43010	5097838	5140847	complete	<i>Bacillus</i> phage BMBtp1	38	90.41
HD12 prophage-10	77355	5284393	5361747	complete	<i>Bacillus</i> phage phiCM3	50	99.76
HD12 prophage-11	57426	5399779	5457204	complete	<i>Bacillus</i> phage vB_BtS_BMBtp15	46	95.39
Bt407-1 prophage-1	39111	623829	662940	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
Bt407-1 prophage-2	9016	941846	950862	incomplete			
Bt407-1 prophage-3	20444	1134828	1155272	incomplete			
Bt407-1 prophage-4	10702 9	3627284	3734313	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	10	84.4
Bt407-1 prophage-5	32907	4619642	4652549	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	49	92.73
HD1 prophage-1	42540	550875	593415	incomplete	<i>Bacillus</i> phage phi4J1	23	92.42
HD1 prophage-2	76133	747338	823471	complete	<i>Bacillus</i> phage phiS3501	48	95.02
HD1 prophage-3	55153	3647841	3702994	complete	<i>Bacillus</i> phage BtCS33	58	98.82
HD1 prophage-4	39964	4512247	4552211	incomplete	<i>Bacillus</i> phage phi4J1	27	89.47
HD1 prophage-5	52167	5028288	5080455	complete	<i>Bacillus</i> phage phi4I1	80	99.99
HD1 prophage-6	60502	5400392	5460894	incomplete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	10	99.76
HD1 prophage-7	75948	5535541	5611489	complete			
BGSC 4Y1 prophage-1	21536	1078124	1099660	incomplete			
BGSC 4Y1 prophage-2	25458	3365884	3391342	incomplete	Phage Wrath	3	91.19
BGSC 4Y1 prophage-3	52658	3400388	3453046	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	9	83.93
BGSC 4Y1 prophage-4	35726	3720053	3755779	complete	<i>Bacillus</i> phage BtiUFT6.51-F	42	88.55
BGSC 4Y1 prophage-5	18952	3885353	3904305	incomplete	<i>Bacillus</i> phage BVE2	32	90.24
BGSC 4Y1 prophage-6	47815	4052653	4100468	complete	<i>Bacillus</i> phage PfeFR-5	44	99.31
T01001 prophage-1	39112	619339	658450	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
T01001 prophage-2	15104	1099256	1114359	incomplete			
T01001 prophage-3	70184	3621373	3691545	incomplete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	9	89.15
T01001 prophage-4	11644	5382584	5394227	incomplete	<i>Bacillus</i> phage BMBtp1	3	81.35
T01001 prophage-5	35750	5397285	5433020	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp13	5	89.35
T01001 prophage-6	9114	5745011	5754124	incomplete			
T01001 prophage-7	9017	5840688	5849704	incomplete			
T01001 prophage-8	35640	6025724	6061363	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	47	92.73
T01001 prophage-9	38182	6161127	6199297	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	28	84.4
T01001 prophage-10	26790	6241373	6268151	incomplete	<i>Bacillus</i> phage phiNIT1	0	90.1
T03a001 prophage-1	22524	205376	227900	incomplete	<i>Bacillus</i> phage phi4J1	16	94.71
T03a001 prophage-2	6625	647481	654106	incomplete	<i>Bacillus</i> phage BtCS33	100	100
T03a001 prophage-3	20414	1082478	1102892	incomplete			
T03a001 prophage-4	16518	5002022	5018540	incomplete	Uncultured <i>Caudovirales</i> phage clone 7S_1	51	84.41
T03a001 prophage-5	4468	5021281	5025749	incomplete	<i>Bacillus</i> phage phiS3501	39	95.23
T03a001 prophage-6	14829	5065591	5080420	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	34	82.35
T03a001 prophage-7	11221	5087153	5098374	incomplete	<i>Bacillus</i> phage phiS3501	78	92.87
T03a001 prophage-8	17786	5219845	5237631	incomplete	<i>Bacillus</i> phage phiS3501	32	96.47
T03a001 prophage-9	36889	5362759	5399648	incomplete	<i>Bacillus</i> phage phiS3501	15	94.99
T03a001 prophage-10	72760	5441613	5514373	incomplete	<i>Bacillus</i> phage phiCM3	18	95.13
BGSC 4AJ1 prophage-1	16285	1096472	1112757	incomplete			
BGSC 4AJ1 prophage-2	25952	3379639	3405591	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	43	94.46
BGSC 4AJ1 prophage-3	15313	4303255	4318568	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	1	91.33
BGSC 4AJ1 prophage-4	24966	5370638	5395604	incomplete	<i>Bacillus</i> phage 250	1	82.45
BGSC 4AJ1 prophage-5	12048	5677945	5689993	incomplete	<i>Bacillus</i> phage PfiS075/ <i>Bacillus</i> phage PfiNC7401	35	92.34
BGSC 4AJ1 prophage-6	16864	6197528	6214392	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	100	100
BGSC 4AJ1 prophage-7	29105	6228308	6257413	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	39	100
BGSC 4AJ1 prophage-8	47868	6380454	6428322	complete	<i>Bacillus</i> phage phiS3501	37	89.53

BGSC 4AJ1 prophage-9	18664	6447146	6465810	incomplete	<i>Bacillus</i> phage PfIS075/ <i>Bacillus</i> phage PfNC7401	9	90.04
ATCC 10792-1 prophage-1	45060	529088	574148	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
ATCC 10792-1 prophage-2	12840	1070068	1082908	incomplete			
ATCC 10792-1 prophage-3	76649	1672195	1748844	incomplete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	8	89.15
ATCC 10792-1 prophage-4	29367	2189829	2219196	incomplete	<i>Bacillus</i> phage BtiUFT6.51-F/ <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtCS33	6	83.3
ATCC 10792-1 prophage-5	66379	2436315	2502694	complete	<i>Bacillus</i> phage BVE2	5	89.27
ATCC 10792-1 prophage-6	50430	3626948	3677378	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	21	84.42
ATCC 10792-1 prophage-7	41599	4760216	4801815	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	39	92.73
BGSC 4AW1 prophage-1	12408	1072703	1085111	incomplete			
BGSC 4AW1 prophage-2	29179	1744495	1773674	incomplete	<i>Bacillus</i> phage phiS3501	32	86.59
BGSC 4AW1 prophage-3	58109	5191126	5249235	incomplete	<i>Bacillus</i> phage phiS3501	12	92.13
BGSC 4AW1 prophage-4	54566	5297892	5352458	incomplete	<i>Bacillus</i> phage PfNC7401	11	87.92
BGSC 4BA1 prophage-1	16475	1080794	1097269	incomplete			
BGSC 4BA1 prophage-2	46913	1603487	1650400	complete	<i>Bacillus</i> phage phiS3501	44	89.41
BGSC 4BA1 prophage-3	6629	2204935	2211564	incomplete			
BGSC 4BA1 prophage-4	11085	3180277	3191362	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	8	81.93
BGSC 4BA1 prophage-5	46653	5143458	5190111	incomplete	<i>Bacillus</i> phage BVE2	3	88
BGSC 4BD1 prophage-1	14795	1080344	1095139	incomplete			
BGSC 4BD1 prophage-2	31750	1897694	1929444	incomplete	<i>Bacillus</i> phage phiCM3	6	83.2
BGSC 4BD1 prophage-3	31210	3543477	3574687	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	37	84.84
BGSC 4BD1 prophage-4	11304	5709665	5720969	incomplete			
BGSC 4BD1 prophage-5	17987	5760274	5778261	incomplete	<i>Bacillus</i> phage phiS58	5	84.93
BGSC 4CC1 prophage-1	20210	1120594	1140804	incomplete			
BGSC 4CC1 prophage-2	50410	2381307	2431717	complete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	38	88.85
BGSC 4CC1 prophage-3	18987	3401242	3420229	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	5	82.05
BGSC 4CC1 prophage-4	12735	5444130	5456865	incomplete	<i>Bacillus</i> phage PfEFR-5/ <i>Bacillus</i> phage PfEFR-4	3	75.82
BGSC 4CC1 prophage-5	12159	5604687	5616846	incomplete			
BGSC 4CC1 prophage-6	10975	5840515	5851490	incomplete			
IBL 200 prophage-1	14882	1108155	1123037	incomplete			

IBL 200 prophage-2	16981	4461372	4478353	incomplete			
IBL 200 prophage-3	22624	5560789	5583413	incomplete	<i>Bacillus</i> phage phiCM3	4	86.81
IBL 200 prophage-4	50472	6106610	6157082	complete	<i>Bacillus</i> phage BMBtp1	23	92.14
IBL 200 prophage-5	38447	6169806	6208253	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	37	97.07
IBL 4222 prophage-1	30230	366046	396276	incomplete	<i>Bacillus</i> phage phiS3501	52	99.99
IBL 4222 prophage-2	36557	3222822	3259379	incomplete	<i>Bacillus</i> phage phiCM3	3	89.42
IBL 4222 prophage-3	28706	5441836	5470542	incomplete			
IBL 4222 prophage-4	20470	5467483	5487953	incomplete	<i>Bacillus</i> phage phiS3501	83	99.99
IBL 4222 prophage-5	12794	5516015	5528809	incomplete	<i>Bacillus</i> phage phiS3501	58	100
IBL 4222 prophage-6	14227	5617122	5631349	incomplete	<i>Bacillus</i> phage TsarBomba	5	79.02
IBL 4222 prophage-7	33486	5648777	5682263	incomplete			
IBL 4222 prophage-8	45827	5981134	6026961	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	24	84.34
IBL 4222 prophage-9	14462	6552047	6566509	incomplete			
DAR 81934 prophage-1	12836	1394932	1407768	incomplete			
T04001 prophage-1	26878	275340	302218	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	7	92.97
					<i>Bacillus</i> phage BtiUFT6.51-F		
					/ <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtCS33/ <i>Bacillus</i> phage BceA1/ <i>Staphylococcus</i> phage SpaA1	7	76.81
T04001 prophage-2	36835	389552	426387	incomplete			
T04001 prophage-3	12902	1069979	1082881	incomplete			
T04001 prophage-4	25493	3156199	3181692	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	27	84.86
T04001 prophage-5	32770	3422790	3455560	complete	<i>Bacillus</i> phage BtCS33	31	94.4
T04001 prophage-6	12934	3459224	3472158	incomplete	<i>Bacillus</i> phage PteFR-5/ <i>Bacillus</i> phage PteFR-4	4	85.11
T04001 prophage-7	23158	3810649	3833807	incomplete	<i>Bacillus</i> phage PteFR-5	10	88.28
T04001 prophage-8	18233	3976107	3994340	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_9	18	82.57
T04001 prophage-9	25537	4550999	4576536	incomplete	<i>Streptococcus</i> phage 20617	5	74.83
T04001 prophage-10	27308	4622014	4649322	incomplete	Uncultured <i>Caudovirales</i> phage clone 7S_4	18	83.54
T04001 prophage-11	25439	4999236	5024675	incomplete	<i>Bacillus</i> phage BMBtp1	2	85.74
T04001 prophage-12	40589	5045354	5085943	incomplete	<i>Bacillus</i> phage BMBtp1	3	92.01
T04001 prophage-13	36097	5219160	5255257	incomplete	<i>Bacillus</i> phage BMBtp1	22	97.67
T04001 prophage-14	7499	5264088	5271587	incomplete			
T04001 prophage-15	15902	5305648	5321550	incomplete	<i>Bacillus</i> phage IEBH	29	86.93
T04001 prophage-16	15796	5369312	5385108	incomplete	Uncultured <i>Caudovirales</i> phage clone 7S_1	17	82.7
T04001 prophage-17	17326	5549515	5566841	incomplete	<i>Bacillus</i> phage Waukesha92	6	81.42
T04001 prophage-18	34982	5718999	5753981	incomplete	Uncultured <i>Caudovirales</i> phage clone 7S_1	31	85.5
T04001 prophage-19	16547	6061501	6078048	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	7	93
Bc601 prophage-1	75948	248980	324928	complete	<i>Bacillus</i> phage phi4J1	16	94.71
Bc601 prophage-2	54134	730098	784232	complete	<i>Bacillus</i> phage phi4I1	77	100
Bc601 prophage-3	39964	1255558	1295522	incomplete	<i>Bacillus</i> phage phi4J1	27	89.47
Bc601 prophage-4	56178	2107525	2163703	complete	<i>Bacillus</i> phage BtCS33	59	98.89
Bc601 prophage-5	74433	4985834	5060267	complete	<i>Bacillus</i> phage phiS3501	47	95.03
Bc601 prophage-6	45761	5210826	5256587	complete	<i>Bacillus</i> phage phi4J1	21	92.42
BGSC 4C1 prophage-1	46652	649148	695800	complete	<i>Bacillus</i> phage phi4J1	29	90.14
BGSC 4C1 prophage-2	45810	1020073	1065883	complete	<i>Bacillus</i> phage BMBtp1	26	90.8
BGSC 4C1 prophage-3	12824	1236282	1249106	incomplete			
BGSC 4C1 prophage-4	64576	2304587	2369163	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	7	85.89
BGSC 4C1 prophage-5	36565	3567743	3604308	incomplete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	1	82.71
BGSC 4C1 prophage-6	60880	4918921	4979801	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	30	96.3

BGSC 4C1 prophage-7	48593	5015923	5064516	complete	Uncultured <i>Caudovirales</i> phage clone 3F_9	18	86.75
MYBT18246 prophage-1	108818	333660	442478	complete	<i>Bacillus</i> phage vB_BtS_BMBtp16	20	86.29
MYBT18246 prophage-2	40601	631339	671940	incomplete	<i>Bacillus</i> phage BMBtp1	44	87.99
MYBT18246 prophage-3	31128	1251048	1282176	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	45	82.19
MYBT18246 prophage-4	14607	1343100	1357707	incomplete			
MYBT18246 prophage-5	15817	2455294	2471111	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	8	79.59
MYBT18246 prophage-6	28205	2902864	2931069	incomplete			
MYBT18246 prophage-7	63137	3560474	3623611	complete	<i>Bacillus</i> phage phiS3501	53	86.06
MYBT18246 prophage-8	74614	3633583	3708197	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp3	2	73.35
MYBT18246 prophage-9	54884	3744292	3799176	complete	<i>Bacillus</i> phage phiS3501	40	84.62
MYBT18246 prophage-10	42522	4484401	4526923	complete	Phage Wrath	7	80.38
MYBT18246 prophage-11	45663	5167291	5212954	complete	<i>Bacillus</i> phage BMBtp1	6	85.72
MYBT18246 prophage-12	59081	5235229	5294310	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	15	85.44
MYBT18246 prophage-13	57012	5384072	5441084	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	28	90.16
MYBT18246 prophage-14	35344	5509224	5544568	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	53	92.36
MYBT18246 prophage-15	7414	5813321	5820735	incomplete			
KNU-07 prophage-1	54045	1891772	1945817	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	20	84.42
KNU-07 prophage-2	38028	2019945	2057973	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	1	85
KNU-07 prophage-3	65599	3122355	3187954	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	16	84.6
Bt18247 prophage-1	106811	355506	462317	complete	<i>Bacillus</i> phage vB_BtS_BMBtp16	21	91.85
Bt18247 prophage-2	61612	784775	846387	complete	<i>Bacillus</i> phage BtCS33	50	91.28
Bt18247 prophage-3	46692	1162202	1208894	incomplete	<i>Bacillus</i> phage BMBtp1	15	88.43
Bt18247 prophage-4	12819	1411920	1424739	incomplete			
Bt18247 prophage-5	38658	1458087	1496745	incomplete			
Bt18247 prophage-6	13591	2092474	2106065	incomplete	<i>Bacillus</i> phage proCM3	35	97.79
Bt18247 prophage-7	51557	2664475	2716032	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	12	85.02
Bt18247 prophage-8	9308	2822205	2831513	incomplete			
Bt18247 prophage-9	67680	5195693	5263373	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	17	82.97
L-7601 prophage-1	34370	1141815	1176185	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_9	47	87.8
L-7601 prophage-2	12845	1231511	1244356	incomplete			
L-7601 prophage-3	55922	1396925	1452847	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	30	94.13
L-7601 prophage-4	65230	1746035	1811265	incomplete			
L-7601 prophage-5	14486	1944173	1958659	incomplete			
L-7601 prophage-6	74011	2017660	2091671	incomplete	<i>Bacillus</i> phage BtiUFT6.51-F / <i>Bacillus</i> phage phi411/ <i>Bacillus</i> phage BtCS33	7	84.17
L-7601 prophage-7	46734	3069777	3116511	complete	<i>Bacillus</i> phage Carmel_SA	52	91.98

L-7601 prophage-8	42078	4635391	4677469	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	56	95.4
L-7601 prophage-9	42341	5187539	5229880	incomplete	<i>Bacillus</i> phage phi4J1	24	90.76
L-7601 prophage-10	38852	5383654	5422506	incomplete	<i>Bacillus</i> phage phi4J1	34	90.78
YGd22-03 prophage-1	49309	1524341	1573650	complete	<i>Bacillus</i> phage vB_BtS_BMBtp15	1	75.35
YGd22-03 prophage-2	22838	3059922	3082760	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	2	84.1
YGd22-03 prophage-3	42711	3621642	3664353	complete	<i>Bacillus</i> phage phiS3501	89	92.98
YGd22-03 prophage-4	38151	4263649	4301800	incomplete	<i>Bacillus</i> phage BMBtp1	42	90.45
YGd22-03 prophage-5	54563	5324359	5378922	incomplete	<i>Bacillus</i> phage PteFR-5/ <i>Bacillus</i> phage PteFR-4	33	90.66
SCG04-02 prophage-1	22264	1343873	1366137	complete	<i>Bacillus</i> phage phiCM3	86	89.17
SCG04-02 prophage-2	11782	2434847	2446629	incomplete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	7	78.92
BM-BT15426 prophage-1	15410	3327264	3342674	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	6	80.89
BM-BT15426 prophage-2	45372	3630946	3676318	incomplete	<i>Bacillus</i> phage PteFR-5/ <i>Bacillus</i> phage PteFR-4	1	91.32
c25 prophage-1	30780	1268968	1299748	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp15	2	84.1
c25 prophage-2	55392	2317959	2373351	complete	<i>Bacillus</i> phage phiCM3	38	89.14
c25 prophage-3	16785	2547478	2564263	incomplete	<i>Bacillus</i> phage phiCM3	8	83.19
c25 prophage-4	61248	2801418	2862666	complete	<i>Bacillus</i> phage vB_BtS_BMBtp16	3	81.88
ATCC 10792-2 prophage-1	39110	611529	650639	incomplete	<i>Bacillus</i> phage phiCM3	14	98.09
ATCC 10792-2 prophage-2	20363	1097406	1117769	incomplete			
ATCC 10792-2 prophage-3	13504	3343977	3357481	incomplete			
ATCC 10792-2 prophage-4	64444	3611717	3676161	incomplete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	10	89.15
ATCC 10792-2 prophage-5	19843	5142697	5162540	incomplete	<i>Bacillus</i> phage BMBtp1	2	81.35
ATCC 10792-2 prophage-6	9099	5396438	5405537	incomplete			
ATCC 10792-2 prophage-7	28637	5443822	5472459	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	37	84.42
ATCC 10792-2 prophage-8	19466	5715856	5735322	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp13	8	89.35
ATCC 10792-2 prophage-9	32907	6083676	6116583	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	49	92.37
ATCC 10792-2 prophage-10	31384	6197746	6229130	incomplete			
ST7 prophage-1	52194	607713	659907	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	20	91.13
ST7 prophage-2	55030	767883	822913	complete	<i>Bacillus</i> phage BtiUFT6.51-F	47	88.6
ST7 prophage-3	23096	2662247	2685343	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	10	81.81
ST7 prophage-4	44641	2680316	2724957	complete	<i>Bacillus</i> phage phi4I1	44	93.17
ST7 prophage-5	23804	2951980	2975784	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	5	81.83
ST7 prophage-6	14989	3816675	3831664	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp14	17	81.83
ST7 prophage-7	30962	3926660	3957622	incomplete	<i>Bacillus</i> phage BtiUFT6.51-F / <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtCS33	6	83.92
ST7 prophage-8	57537	5199517	5257054	complete	Uncultured <i>Caudovirales</i> phage clone 3F_8	12	83.34
ATCC 10792-3 prophage-1	66307	1020833	1087140	complete	<i>Bacillus</i> phage BVE2	5	89.13
ATCC 10792-3 prophage-2	29304	1304069	1333373	incomplete	<i>Bacillus</i> phage BtiUFT6.51-F / <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtCS33	6	83.3

ATCC 10792-3 prophage-3	76597	1773960	1850557	complete	<i>Bacillus</i> phage BceA1 / <i>Staphylococcus</i> phage SpaA1	8	89.15
ATCC 10792-3 prophage-4	12829	2441513	2454342	incomplete			
ATCC 10792-3 prophage-5	58263	2948472	3006735	incomplete	<i>Bacillus</i> phage phiCM3	10	98.05
ATCC 10792-3 prophage-6	40127	4224890	4265017	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	40	92.68
ATCC 10792-3 prophage-7	48037	5361468	5409505	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	22	84.42
XL6 prophage-1	43843	702074	745917	incomplete	<i>Bacillus</i> phage PfeFR-5	58	96.77
XL6 prophage-2	29292	2081722	2111014	incomplete			
XL6 prophage-3	42016	3917982	3959998	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	12	83.93
XL6 prophage-4	49398	4413904	4463302	complete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	39	89.19
T13001 prophage-1	29394	288563	317957	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp16	20	96.98
T13001 prophage-2	22882	3301486	3324368	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	29	87.3
T13001 prophage-3	45313	3565109	3610422	complete	<i>Bacillus</i> phage PfeFR-4	35	92.33
T13001 prophage-4	45831	5188854	5234685	incomplete	Uncultured <i>Caudovirales</i> phage clone 3F_8	4	83.96
T13001 prophage-5	25365	5404806	5430171	incomplete	<i>Bacillus</i> phage phi4I1	28	93.55
T13001 prophage-6	19194	5459809	5479003	incomplete	<i>Bacillus</i> phage BtiUFT6.51-F / <i>Bacillus</i> phage phi4I1/ <i>Bacillus</i> phage BtCS33	7	85.41
T13001 prophage-7	26666	5701718	5728384	incomplete	<i>Bacillus</i> phage phiCM3	3	95.93
T13001 prophage-8	21611	5815466	5837077	incomplete	<i>Bacillus</i> phage BMBtp1	5	74.16
T13001 prophage-9	43735	5957707	6001442	incomplete	<i>Bacillus</i> phage BMBtp1	35	86.82
T13001 prophage-10	21428	6014165	6035593	incomplete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	29	79.81
LM1212 prophage-1	34180	60464	94644	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	35	88.11
LM1212 prophage-2	16087	91453	107540	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp13	7	79.26
LM1212 prophage-3	50130	1041746	1091876	complete	Uncultured <i>Caudovirales</i> phage clone 9AX_2	13	82.42
LM1212 prophage-4	44935	2002292	2047227	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	12	82.42
LM1212 prophage-5	47428	3143058	3190486	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	22	90.24
LM1212 prophage-6	67401	4642974	4710375	complete	<i>Bacillus</i> phage BVE2	1	79.69
LM1212 prophage-7	20777	4954700	4975477	incomplete	<i>Bacillus</i> phage vB_BtS_BMBtp13	3	78.09
LM1212 prophage-8	68368	5318512	5386880	complete	<i>Bacillus</i> phage vB_BtS_BMBtp13	18	90.24

Table 3. Putative complete prophages identified in Bt genomes.

Prophages	attR	attL	Integrase	Capsid	Teriminase
Positions in bacteria chromosomes					
YBT-1518 prophage-5	913910..913922	882892..882903	899646..900188	909162..910328	903699..905402
YBT-1518 prophage-10	4284285..4284298	4260401..4260412	4264755..4265477	4280831..4281994	4285529..4287187
	4312543..4312554				

YBT-1518	5355469..5355482	5320770..5320783	5355557..5356618	4280831..4281994	5337824..533
prophage-12					9518
YBT-1518	5554165..5554176	5518306..5518317	5554361..5555419	5531995..5533167	5536926..553
prophage-13					8620
BMB171	2541195..2541206	2498467..2498479	2499329..2500438	2521643..2522797	2518121..251
prophage-2	2543969..2543981	2500548..2500559			9701
YBT-020	443743..443754	391947..391958	395075..395536	414150..415304	410582..4122
prophage-1	443793..443804	394951..394962			49
CT-43	1890451..1890464	1826113..1826124	1886954..1887922	1870430..1871554	
prophage-4	1896349..1896362	1837189..1837202			
	1910313..1910324				
CT-43	2639579..2639590	2588715..2588726	2598154..2599263	2624360..2625484	2620760..262
prophage-6	2655093..2655104	2600165..2600176			2436
CT-43	3817025..3817038	3773368..3773381	3801235..3801777	3791939..3793102	3795054..379
prophage-7					6712
HD-771	1409459..1409470	1359225..1359236	1378283..1379242	1391295..1392458	1394384..139
prophage-2	1409729..1409740	1359274..1359285	1398889..1399431		6057
	1425337..1425348	1379258..1379269	1411339..1412445		
HD-771	2981152..2981164	2920758..2920770	2960590..2961993	2939486..2940649	2942601..294
prophage-5					4256
HD-771	4540385..4540405	4501661..4501681	4501816..4502952	4521807..4522970	4518200..451
prophage-6					9855
HD-771	5463643..5463654	5442197..5442208	5449306..5450475	5468624..5469778	5465019..546
prophage-9	5487465..5487476	5452949..5452960	5462482..5463024		6677
	5490649..5490660	5461773..5461784			
HD-771	5790522..5790533	5764272..5764285	5764325..5765455	5787041..5788225	5783322..578
prophage-10	5806181..5806192	5768464..5768475			5049
	5806182..5806195	5773215..5773226			
HD-789	2989118..2989129	2938754..2938768	2989579..2990640	2966133..2967299	2969476..297
prophage-2	3000589..3000603	2939099..2939110			1170
HD-789	3356039..3356050	3328682..3328693	3351848..3352390	3343219..3344382	3346331..334
prophage-4					7986
MC28	2969225..2969237	2934767..2934778	2961468..2962010	2950761..2951912	2953855..295
prophage-4	2987436..2987447	2934871..2934883			5522
MC28	3141461..3141474	3102093..3102105	3144929..3146059	3123444..3124625	3126585..312
prophage-7	3152012..3152024	3103507..3103520			8006
MC28	5152570..5152581	5095369..5095381	5100279..5101403	3123444..3124625	5124030..512
prophage-8	5157538..5157550	5103101..5103112			5697
Bt407-1	1845876..1845889	1830538..1830550	1894213..1895172	1877680..1878804	
prophage-2	1903600..1903613	1844439..1844452			
	1912085..1912097	1845876..1845889			
Bt407-1	2651952..2651964	2605770..2605782	2623390..2623932	2632838..2633962	2629238..263
prophage-4					0914

HD73	296807..296818	242738..242807	266204..266746	272654..273817	269043..2707
prophage-1	305981..306050	256420..256431			01
HD73	414574..414585	376296..376307	436671..437768	414609..415781	409345..4110
prophage-2	423437..423448	390634..390645			60
	437867..437880	431465..431478			
HD73	796996..797007	760542..760553	781325..781867	789815..790981	785943..7876
prophage-3	816110..816121	765971..765982			37
	818234..818245	770770..770781			
HD73	1337784..1337797	1284495..1284508	1284517..1285920	1306566..1307750	1301488..130
prophage-4					3188
HD73	2190068..2190081	2138013..2138025	2139007..2140098	2160346..2161512	2156475..215
prophage-6	2190091..2190102	2142904..2142915			8169
	2192701..2192713	2153151..2153164			
HD73	5063056..5063067	5021812..5021823	5066377..5067438	5043964..5045130	5047307..504
prophage-7	5078785..5078796	5028484..5028495			9001
HD73	5274992..5275004	5232007..5232019	5275062..5276198	5255144..5256310	5258224..525
prophage-8					9909
IS5056	1897175..1897188	1843938..1843949	1893687..1894646	1877154..1878278	
prophage-4	1911537..1911550	1845350..1845363			
	1920478..1920489	1904710..1904723			
IS5056	2645742..2645753	2373786..2373802	2604315..2605424	2630522..2631646	2626922..262
prophage-6	2661256..2661267	2606326..2606337			8598
IS5056	3812229..3812240	3776967..3776980	3804979..3805521	3795683..3796846	3798798..380
prophage-7	3820819..3820832	3800822..3800833			0456
YBT-1520	314093..314105	243519..243530	252896..254074	319716..320879	
prophage-1	330925..330936	258484..258495			316105..3177
	333657..333668	273411..273423			63
YBT-1520	782681..782693	756854..756865	769460..770557	790540..791706	786669..7883
prophage-2	806943..806954	762282..762293	770554..772563		63
	813280..813291	765614..765626			
	815404..815415	782793..782804			
YBT-1520	1323891..1323902	1285256..1285267	1285311..1286714	1305777..1306961	1300711..130
prophage-3					2399
YBT-1520	5023953..5023964	4963649..4963661	5024616..5025677	5002202..5003368	5005545..500
prophage-6	5042389..5042401	4963922..4963933			7239
HD-29	204784..204795	156843..156855	177148..177690	183598..184761	179987..1816
prophage-1	208753..208765	167365..167376			45
HD-29	896651..896663	843002..843013	850346..851446	873103..873945	868492..8697
prophage-2	897587..897598	861002..861014			66
HD-29	5017166..5017178	4946878..4946890	4999387..5000448	4981848..4983218	4984988..498
prophage-5					6712
HD-29	5243034..5243046	5200050..5200062	5243089..5244240	5223185..5224351	5226265..
prophage-7					5227950

HD-1	279829..279840	258214..258264	267849..269027	275801..277063	278227..2798
prophage-1	315798..315809	266129..266140			19
	321656..321669	280529..280542			
	324765..324815	284807..284818			
HD-1	429557..429568	400116..400128	414683..415807	438746..439918	433482..4351
prophage-2	436463..436475	412937..412948			97
YBT1520-2	68940..68951	19909..19927	77614..78792	69578..70840	66822..68462
prophage-1	85269..85282	38803..38816			
	93216..93234	50310..50321			
YBT1520-2	973273..973284	894807..894819	911531..912592	933840..935006	929969..9316
prophage-3	973545..973557	913244..913255			63
YBT1520-2	5200300..5200311	5153713..5153726	5204432..5205532	5182436..5183602	5185780..518
prophage-6	5202525..5202536	5157824..5157835			7474
	5215692..5215705	5183607..5183618			
HD-1011	2941834..2941846	2910951..2910964	2913048..2914154	2938135..2939307	2934264..293
prophage-2	2960325..2960336	2914690..2914701			5958
	2962760..2962773	2924364..2924376			
HD1002	100422..100434	47815..47827	63811..64353	71819..72982	68215..69870
prophage-1					
HD1002	483298..483310	417583..417594	425248..426309	448589..449755	444718..4464
prophage-4	484339..484350	426879..426891			12
BGSC 4AA1	1223299..1223311	1165897..1165909	1198970..1199890	1189102..1190286	1183874..118
prophage-2					5574
BGSC 4AA1	3956573..3956584	3902354..3902365	3939345..3939887	3929306..3930457	3932358..393
prophage-6					4025
BGSC 4AA1	4639815..4639826	4597672..4597683	4598017..4599471	4618279..4619448	4621384..462
prophage-7					3081
BGSC 4AA1	5245207..5245219	5189813..5189826	5234168..5234710	5225606..5226772	5228949..523
prophage-8	5262888..5262901	5197140..5197152			0643
YC-10	617782..617793	579100..579111	629400..630491	607988..609154	611331..6130
prophage-1	626584..626595	579404..579415			25
	634251..634262	592304..592315			
YC-10	1996308..1996319	1949726..1949739	2000440..2001540	1978448..1979614	1981791..198
prophage-3	1998533..1998544	1953837..1953848			3485
	2011700..2011713	1979619..1979630			
YC-10	2374688..2374699	2331105..2331116	2331696..2332793	2353682..2354854	2358403..236
prophage-4	2376389..2376400	2335257..2335268	2332790..2334799		0118
	2382908..2382921	2376562..2376575	2377897..2379021		
YC-10	2511281..2511292	2466727..2466745	2527072..2528250	2493897..2495060	2516280..251
prophage-5	2540981..2540994	2470895..2470906			7920
	2542673..2542691	2515557..2515570			
YC-10	3199768..3199788	3157229..3157249	3157384..3158520	3177271..3178437	3173672..317
prophage-6					5357

YC-10	3429547..3429558	3353688..3353700	3370411..3371472	3392719..3393885	3388848..339
prophage-7	3429819..3429831	3372124..3372135			0542
HS18-1	2546971..2546984	2496265..2496278	2509207..2509749	2518570..2519742	2514699..251
prophage-4					6393
HD521	2010879..2010890	1988162..1988173	1996061..1997197	2024093..2025079	2019188..202
prophage-1	2022161..2022172	1994315..1994326			0594
HD521	2356518..2356530	2287686..2287698	2365944..2366486	2326820..2727944	
prophage-3	2363907..2363918	2287764..2287775			
	2376056..2376068	2288331..2288343			
YWC2-8	939232..939243	863370..863382	880094..881155	902403..903569	898532..9002
prophage-3	939504..939516	881807..881818			26
YWC2-8	3801771..3801782	3763087..3763098	3813390..3814481	3791977..3793143	3795320..379
prophage-4	3810573..3810584	3763391..3763402			7014
	3818241..3818252	3776293..3776304			
YWC2-8	5180356..5180367	5133773..5133786	5184488..5185588	5162495..5163661	5165838..516
prophage-6	5182581..5182592	5137884..5137895			7532
	5195748..5195761	5163666..5163677			
YWC2-8	5558748..5558759	5515164..5515175	5561957..5563081	5537741..5538913	5542462..554
prophage-7	5560449..5560460	5519316..5519327			4177
	5566968..5566981	5560622..5560635			
Pasteur	369052..369064	321101..321113	321260..322615	338289..339650	334706..3364
Institute					30
Standard					
Strain					
prophage-1					
Pasteur	609712..609725	573162..573175	575183..576244	596241..597377	592633..5943
Institute	618038..618051	588028..588041			03
Standard					
Strain					
prophage-2					
Pasteur	1380371..1380382	1295431..1295444	1300976..1302397	1364774..1365952	
Institute	1391180..1391191	1336823..1337014			
Standard	1394230..1394242	1343537..1343548			
Strain	1394307..1394320	1357163..1357174			
prophage-4					
Pasteur	1915522..1915533	1913253..1913264	1913277..1914242	1942335..1943498	1938724..
Institute	1969787..1969798	1918912..1918925			1940382
Standard	1981784..1981795	1922300..1922311			
Strain	1981867..1981880	1927102..1927113			
prophage-5					
Pasteur	2095009..2095020	2086890..2086901	2093643..2094734	2115089..2116255	2111218..211
Institute	2128352..2128365	2095228..2095239			2912
Standard	2138311..2138322	2105794..2105807			

Strain					
prophage-6					
Pasteur	4700897..4700908	4662921..4662932	4700934..4702367	4678924..4679862	4683198..4684418
Institute					
Standard					
Strain					
prophage-11					
Pasteur	5148153..5148164	5100297..5100310	5152285..5153385	5130280..5131446	5133623..5135317
Institute	5150378..5150389	5105708..5105719			
Standard	5161903..5161916	5131451..5131462			
Strain					
prophage-12					
Pasteur	5550502..5550514	5512767..5512780	5553846..5554903	5533860..5535023	5536943..5538598
Institute	5563195..5563208	5521081..5521093			
Standard					
Strain					
prophage-14					
Bt185	1824972..1824983	1760889..1760900	1825152..1826624	1799465..1800589	
prophage-1					
Bt185	2532463..2532476	2479645..2479656	2488358..2489467	2513207..2514370	2509661..2511280
prophage-2	2542020..2542031	2492171..2492184			
Bt185	4284811..4284822	4253115..4253126	4285120..4286511	4265978..4367288	4270719..4272443
prophage-3					
HD12	358392..358403	328204..328215	340463..341587	346700..347050	360996..
prophage-1	358601..358612	338708..338719			362651
	396888..396899	342317..342328			
HD12	2140940..2140951	2084122..2084133	2085115..2086206	2108285..2109451	2102738..2104432
prophage-5	2140942..2140953	2088271..2088282			
HD12	5139169..5139180	5097838..5097849	5139343..5140404	5129847..5130728	5123018..5124742
prophage-9					
HD12	5344066..5344078	5284393..5284406	5333027..5333569	5322789..5323955	5327808..5329502
prophage-10	5361747..5361760	5291720..5291732			
HD12	5452147..5452158	5399779..5399790	5452385..5453737	5430595..5431968	5435560..5437284
prophage-11					
Bt407-2	3627284..3627295	3724298..3724310	3636235..3637782	3658530..3659693	3654956..3656578
prophage-4	3646975..3646986	3729256..3729267			
	3650527..3650539	3734313..3734324			
HD1	747338..747350	802952..802963	778432..778974	786370..787536	782499..784193
prophage-2	763989..764004	808145..808160			
	777927..777938	823471..823483			
HD1	3647841..3647852	3684130..3684142	3698143..3699234	3676731..3677897	3680074..3681768
prophage-3	3648145..3648156	3695326..3695337			
	3649518..3649530	3702994..3703005			

HD1	5028288..5028299	5068911..5068923	5056359..5056901	5047246..5048412	5050589..505
prophage-5	5052884..5052895	5072587..5072598			2283
	5053663..5053674	5080312..5080323			
	5056259..5056271	5080455..5080466			
HD1	5535541..5535559	5580097..5580108	5569782..5570324	5587852..5589114	5585096..558
prophage-7	5535775..5535787	5595212..5595224			6736
	5539709..5539720	5611489..5611507			
BGSC 4Y1	3400388..3400399	3440042..3440053	3425526..3425972	3417239..3418390	3420291..342
prophage-3	3401398..3401409	3453046..3453057			1958
BGSC 4Y1	3722547..3722559	3753412..3753424	3734294..3734836	3744015..3745187	3740159..374
prophage-4					1838
BGSC 4Y1	4052653..4052664	4098214..4098225	4056990..4058186	4078734..4079915	4075080..407
prophage-6	4061278..4061289	4100468..4100479			6768
T01001	6162406..6162417	6199297..6199308	6162585..6163127	6171260..6172423	6167686..616
prophage-9					9308
BGSC 4AJ1	6380454..6380465	6426968..6426981	6396051..6396593	6404620..6405792	6400764..640
prophage-8	6385086..6385099	6428322..6428333			2443
ATCC 10792-	2436315..2436326	2487180..2487191	2462512..2463054	2471960..2473084	2468360..247
1 prophage-5	2447765..2447776	2502694..2502705			0036
BGSC 4BA1	1603487..1603498	1642131..1642142	1603769..1604875	1628856..1630028	1625000..162
prophage-2	1604897..1604908	1650352..1650363			6679
	1618862..1618873	1650400..1650411			
BGSC 4BD1	3543477..3543489	3574687..3574699	3543596..3544138	3553623..3554786	3550073..355
prophage-3					1674
BGSC 4CC1	2381307..2381319	2427969..2427980	2383162..2384271	2405987..2407159	2402131..240
prophage-2	2393259..2393270	2431717..2431729			3810
IBL 200	6106610..6106621	6155589..6155600	6155925..6157082	6135856..6137013	6132379..613
prophage-4					3956
IBL 4222	5981134..5981146	6024967..6024978	5981849..5983396	6003997..6005160	6000447..600
prophage-8	5985516..5985527	6026961..6026973			2048
T04001	3422790..3422802	3452701..3452713	280839..281966	3450358..3451521	3446813..344
prophage-5					8432
Bc601	248980..249030	270595..270606	250533..250976	266567..267829	268993..2705
prophage-1	256895..256906	315961..315972			85
	271295..271308	321819..321832			
	275573..275584	324928..324978			
Bc601	730098..730109	775771..775782	772671..773630	759369..760535	755498..7571
prophage-2	749525..749536	783765..783776			92
	751622..751633	784232..784243			
Bc601	2107525..2107537	2122907..2122919	2121919..2122458	2131352..2132518	2127481..212
prophage-4	2112416..2112427	2161070..2161083			9175
	2120490..2120502	2161093..2161104			
	2124158..2124171	2163703..2163715			

Bc601	4985834..4985846	5041831..5041842	5042494..5043555	5021781..5022947	5025124..502
prophage-5	4986107..4986118	5060267..5060279			6818
Bc601	5210826..5210838	5255381..5255393	44611..45762	5235534..5236700	5238614..524
prophage-6					0299
BGSC 4C1	653512..653525	692091..692104	653577..654737	673542..674705	669936..6715
prophage-1					91
BGSC 4C1	1025186..1025205	1065883..1065902	1025253..1026410	1046828..1047991	1024277..102
prophage-2					5233
BGSC 4C1	5015923..5015937	5059625..5059639	5059693..5061048	5055761..5056690	5043126..504
prophage-7					4781
MYBT18246	333660..333671	404585..404601	340653..341720	396888..397238	362656..3643
prophage-1	343902..343914	436267..436279			35
		442478..442489			
MYBT18246	3560474..3560485	3618338..3618349	3605111..3605653	3595314..3596486	3598663..360
prophage-7	3560706..3560717	3623611..3623622			0357
MYBT18246	3749224..3749235	3775523..3775534	3772645..3773187	3777999..3778805	3766831..376
prophage-9	3749477..3749488	3799176..3799187			8525
MYBT18246	4484401..4484413	4525846..4525858	4525862..4526923	4502334..4503455	4505366..450
prophage-10					7033
MYBT18246	5167291..5167303	5203231..5203242	5205034..5206095	5171646..5172752	5185209..518
prophage-11	5169443..5169454	5212954..5212966			5574
Bt18247	355506..355517	421815..421826	364102..365169	429065..430195	425475..4271
prophage-1	365762..365773	424764..424780			42
	367470..367481	432711..432722			
	378247..378263	449284..449295			
	397188..397199	462317..462328			
Bt18247	784775..784786	844743..844754	811500..812042	820040..821212	816169..8178
prophage-2	796219..796230	846387..846398			63
Bt18247	2664475..2664490	2715998..2716009	9603..10481	2701394..2702548	2701393..270
prophage-7	2683675..2683686	2716032..2716047			2547
Bt18247	5195693..5195704	5246362..5246373	5236280..5236822	5225519..5226676	5228595..523
prophage-9	5205339..5205350	5263373..5263384			0211
L-7601	1396925..1396937	1434071..1434082	1409067..1410176	1434095..1435258	1430484..143
prophage-3	1397146..1397158	1447531..1447543			2166
	1412615..1412626	1452847..1452859			
L-7601	3069777..3069788	3115319..3115330	3115450..3116511	3108757..3109638	3098908..310
prophage-7					0605
YGd22-03	1524341..1524365	1573650..1573674	1524617..1525753	1548240..1549265	1543767..154
prophage-1					5044
YGd22-03	3621642..3621656	3657270..3657282	3663235..3664296	3640560..3641732	3643908..364
prophage-3	621703..3621715	3664353..3664367			5602
SCG04-02	1343873..1343884	1365109..1365120	1344064..1344606	1352988..1354160	1349117..135
prophage-1					0811

c25	2317959..2317970	2358353..2358365	26483..27025	2335487..2336659	2338836..234
prophage-2	2333450..2333462	2373351..2373362			0530
c25	2801418..2801430	2838948..2838959	2857599..2858735	2830849..2831835	2835347..283
prophage-4	2802066..2802078	2851305..2851317			6624
	2807753..2807764	2862666..2862678			
ATCC 10792-	5448585..5448597	5472459..5472471	5448642..5449184	5457317..5458480	5453743..545
2 prophage-7					5365
ST7	767883..767894	815363..815374	788522..789064	796779..797951	792908..7946
prophage-2	773469..773480	820788..820799			02
	776594..776605	822913..822924			
ST7	2680316..2680327	2712368..2712380	2681643..2682185	2694190..2695362	2690320..269
prophage-4	2684120..2684132	2724957..2724968			2014
ST7	5199517..5199528	5235816..5235827	5242221..5243282	5222258..5223409	5225350..522
prophage-8	5202453..5202464	5236650..5236661			7005
	5205024..5205035	5257054..5257065			
ATCC 10792-	1020833..1020844	1075712..1075725	1060451..1060993	1050423..1051547	1053471..105
3 prophage-1	1020879..1020892	1087140..1087151			5147
ATCC 10792-	1773960..1773973	1814557..1814568	1775070..1775897	1805338..1806582	
3 prophage-3	1777469..1777482	1836595..1836608			
	1778449..1778460	1850557..1850570			
XL6	4413904..4413915	4463041..4463052	4417658..4418767	4442082..4443254	4438211..443
prophage-4	4428086..4428097	4463302..4463313			9905
T13001	3565109..3565123	3610422..3610436	3573860..3574591	3586499..3587680	3582959..358
prophage-3					4533
LM1212	60464..60476	91242..91254	91445..91987	83382..84533	86470..88086
prophage-1					
LM1212	1041746..1041757	1090286..1090297	1090374..1091435	1067728..1068900	1071077..107
prophage-3					2771
LM1212	2002292..2002303	2005841..2005852	2004038..2005162	2026772..2027914	2021635..202
prophage-4	2005844..2005856	2047227..2047239			3245
LM1212	3143058..3143069	3171400..3171419	3162748..3163290	3171432..3172595	3166248..316
prophage-5	3151845..3151864	3190486..3190497			7933
LM1212	4645921..4647384	4710375..4710388	4645921..4647384	4670083..4671207	
prophage-6					
LM1212	5318512..5318523	5360398..5360410	5370860..5371951	5349876..5351039	5352968..535
prophage-8	5336898..5336910	5370297..5370308			4650
	5370300..5370313	5386880..5386893			

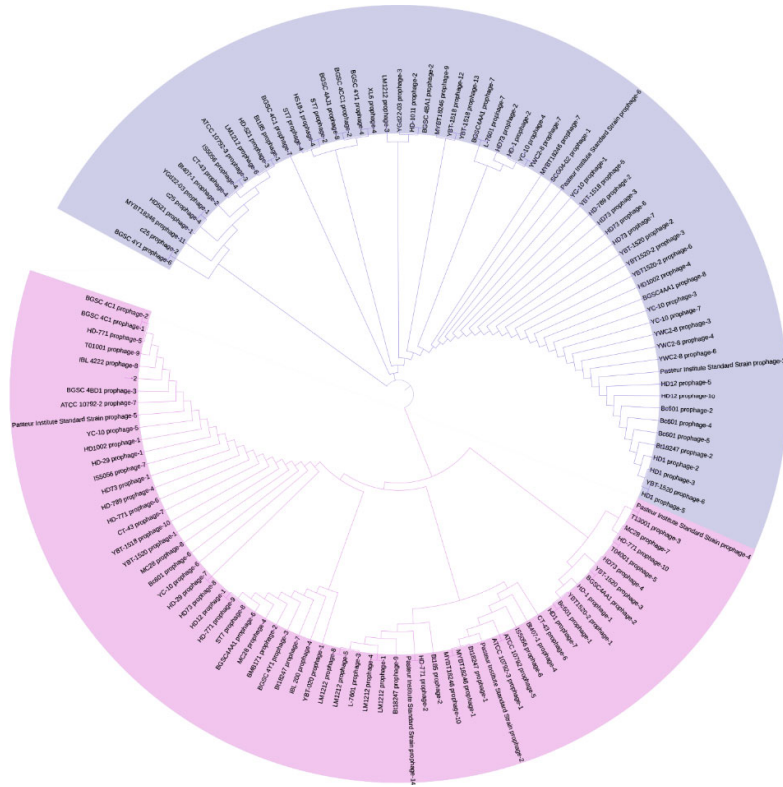


Figure 1. Phylogenetic analysis of Bt prophages by using the major capsid proteins. The amino acid sequences of major capsid proteins from 135 Bt prophages were collected and used for phylogenetic tree construction. The two clades of the phylogenetic tree are indicated in different colors.

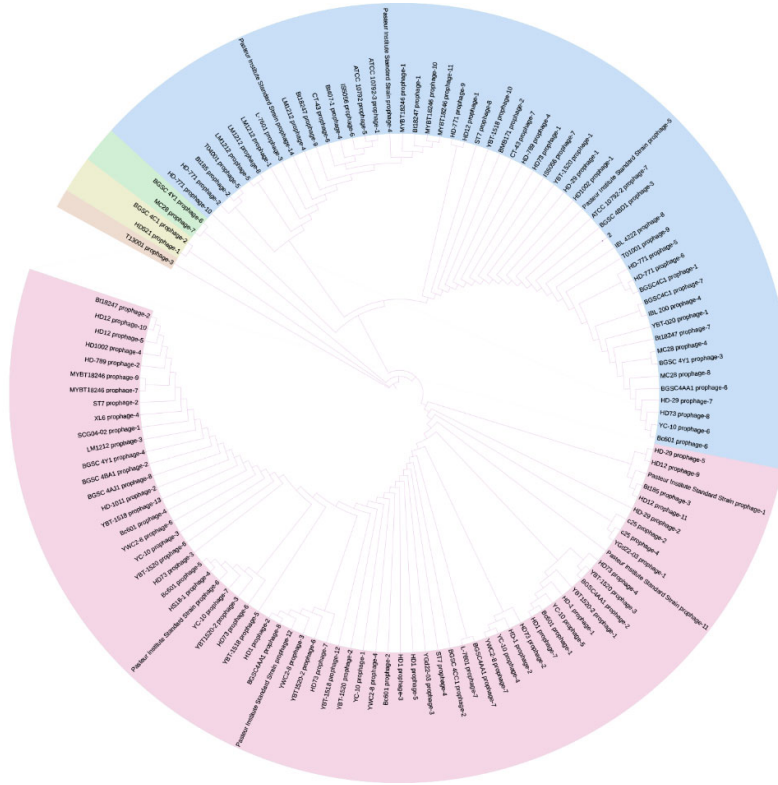


Figure 2. Phylogenetic analysis of Bt prophages by using the terminase large subunit proteins. The amino acid sequences of terminase large subunit from 127 Bt prophages were collected and used for phylogenetic tree construction. The two clades of the phylogenetic tree are indicated in different colors.

Table 4. *Bacillus* phages used for pairwise comparison. The order of phage genomes used for comparison were listed as the rule in this table.

Phage	Accession Number	Genome length	Gene Number
0305phi8-36	NC_009760.1	218948 nt	246
vB_BanS-Tsamsa	NC_023007.1	168876 nt	272
AvesoBmore	NC_028887.1	167431 nt	301
BigBertha	NC_022769.1	165238 nt	291
Phrodo	NC_031100.1	164443 nt	288
Spock	NC_022763.1	164297 nt	283
Zuko	NC_031116.1	163345 nt	294
Nigalana	NC_031037.1	163041 nt	302
Troll	NC_022088.2	163019 nt	289
Riley	NC_024788.1	162816 nt	290
B4	NC_018863.1	162596 nt	277
TsarBomba	NC_028890.1	162486 nt	247
DirtyBetty	NC_031054.1	162415 nt	302
Nemo	NC_031070.1	162375 nt	301
SageFayge	NC_031027.1	162359 nt	300

Belinda	NC_031024.1	162308 nt	295
Eyuki	NC_028944.1	162252 nt	300
Kida	NC_031012.1	162151 nt	304
NofTheCreek	NC_031049.1	161929 nt	296
DIGNKC	NC_031006.1	161552 nt	291
SalinJah	NC_031034.1	161140 nt	292
CAM003	NC_024216.1	160541 nt	287
Bobb	NC_024792.1	160281 nt	247
Hoody T	NC_024205.1	159837 nt	270
Evoli	NC_024207.1	159656 nt	294
BPS10C	NC_023501.1	159590 nt	271
JBP901	NC_027352.1	159492 nt	201
BCP8-2	NC_027355.1	159071 nt	220
Megatron	NC_024211.1	158750 nt	290
vB_BceM_Bc431v3	NC_020873.1	158621 nt	238
BPS13	NC_018857.1	158305 nt	268
Hakuna	NC_024213.1	158100 nt	294
Deep Blue	NC_031056.1	157501 nt	226
W.Ph.	NC_016563.1	156897 nt	274
BCP78	NC_018860.1	156176 nt	227
Bastille	NC_018856.1	153962 nt	273
Bcp1	NC_024137.1	152778 nt	229
Shanette	NC_028983.1	138877 nt	220
CP-51	NC_025423.1	138658 nt	221
JL	NC_028982.1	137918 nt	218
BCD7	NC_019515.1	93839 nt	140
250	NC_029024.1	56505 nt	54
IEBH	NC_011167.1	53104 nt	86
vB_BtS_BMBtp3	NC_028748.2	51366 nt	76
Waukesha92	NC_025424.1	45648 nt	72
phiS3501	NC_019502.1	44401 nt	51
PfEFR-5	NC_031055.1	43773 nt	68
BtCS33	NC_018085.1	41992 nt	57
phi4J1	NC_029008.1	41486 nt	67
PBC1	NC_017976.1	41164 nt	50
BCJA1c	NC_006557.1	41092 nt	58
WBeta	NC_007734.1	40867 nt	53
phiCM3	NC_023599.1	38772 nt	56

phi4B1	NC_028886.1	38663 nt	56
Fah	NC_007814.1	37974 nt	50
TP21-L	NC_011645.1	37456 nt	56
Gamma	NC_007458.1	37253 nt	53
vB_BtS_BMBtp2	NC_019912.1	36932 nt	53
MG-B1	NC_021336.1	27190 nt	42
Claudi	NC_031015.1	26504 nt	46
Aurora	NC_031121.1	25908 nt	40
GA-1	NC_002649.1	21129 nt	35
VMY22	NC_028789.1	18609 nt	25
Bam35c	NC_005258.1	14935 nt	32
GIL16c	NC_006945.1	14844 nt	31
AP50	NC_011523.1	14398 nt	31
Wip1	NC_022094.1	14319 nt	27

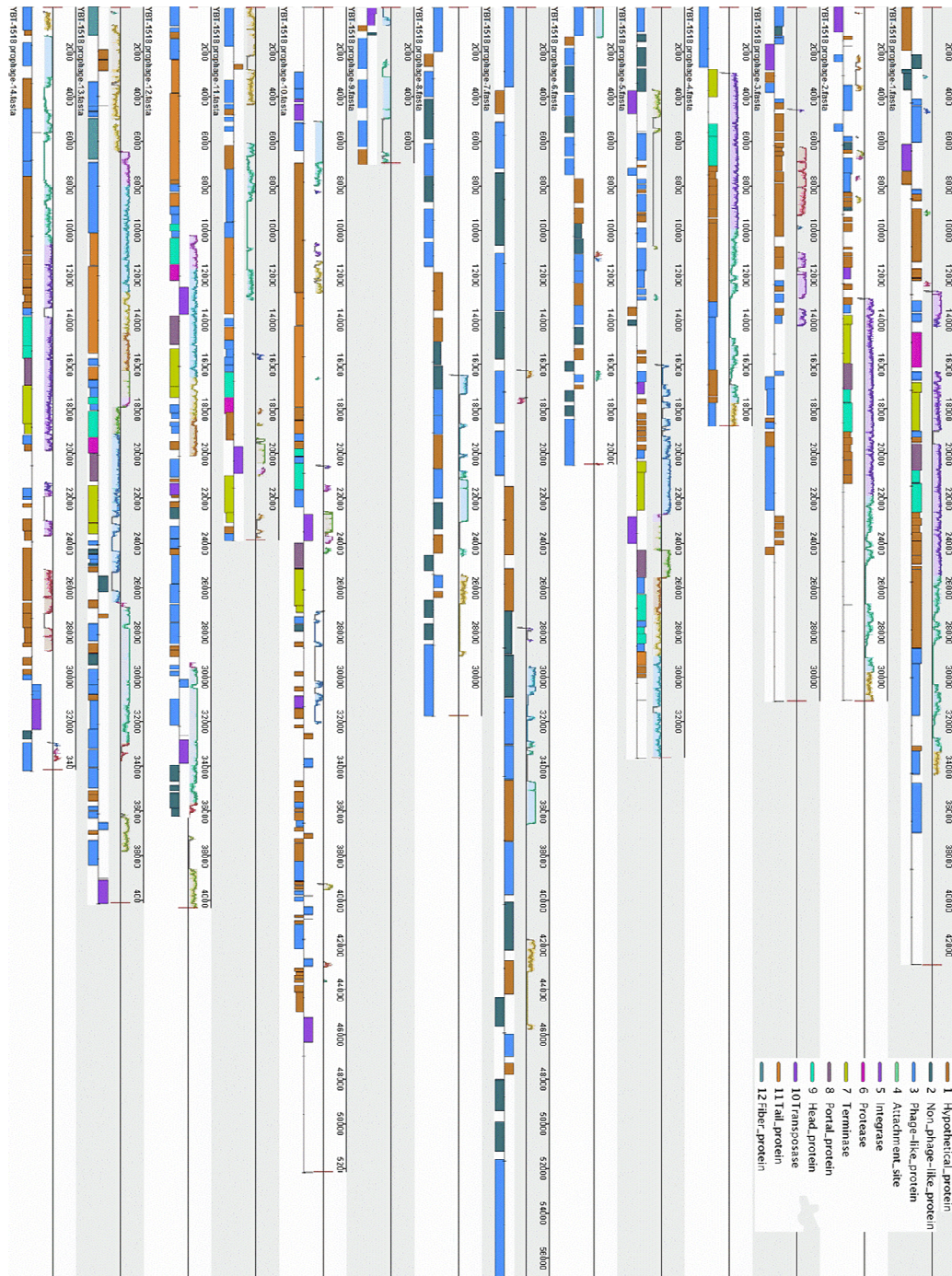


Figure 3. Comparative genomic analysis of prophages from Bt strain YBT-1518. The functions of prophage genes are indicated as different colors and the similarities of the prophage sequences are analyzed by using Mauve.

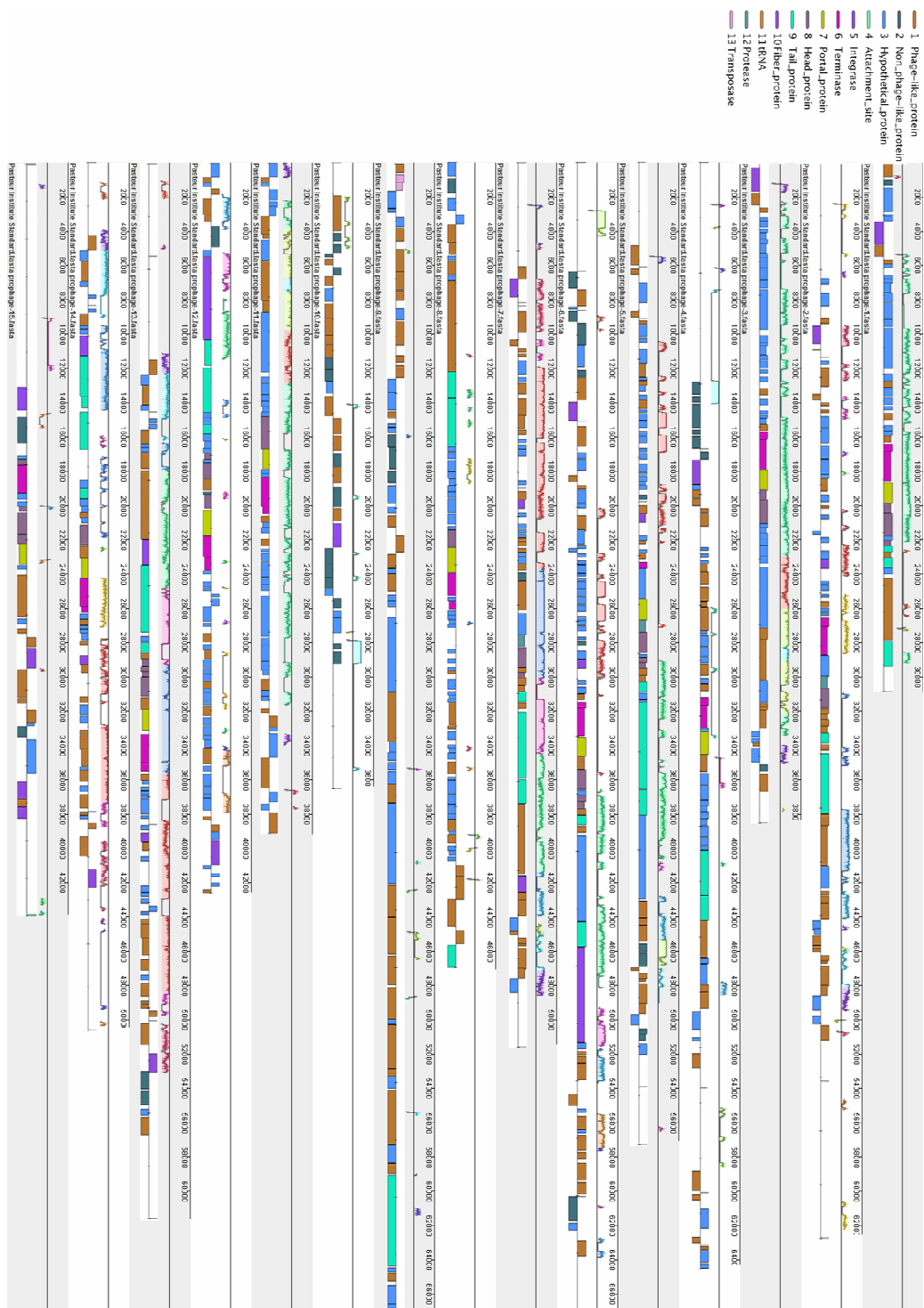


Figure 4. Comparative genomic analysis of prophages from Bt Pasteur Institute Standard strain. The functions of prophage genes are indicated as different colors and the similarities of the prophage sequences are analyzed by using Mauve.

Table 5. Host range of phage induced from Bt strains.

Strain	4	4	H	H	4BD1	CT-43	HD-1011	HD-521	HD-73	BMB171
	C	A	D	D						

	C	J	2	-						
	1	1	9	1						
H43	+	+	-	-	-	-	-	+	-	+
a										
4AJ1	+	+	-	-	-	-	-	+	-	-
HD-11	+	+	-	-	-	++	-	+	-	-
HD-201	-	+	-	+	+	-	-	+	-	-
HZ39-04	+	+	-	+	+	-	-	+	-	-
HD-1	+	+	-	-	+	-	-	+	-	-
HD-73	-	+	-	+	-	-	-	+	-	+
HD-541	+	+	-	-	-	-	-	-		-
4BD1	-	+	-	+	-	-	-	+	-	+
YK30-04	+	+	-	+	+	-	-	+	-	-
YGd22-03	-	+	+	-	-	-	-	-	-	-
			+							
Scg04-02	-	+	-	-	-	-	-	++	-	-
H33	+	+	-	+	+	-	-	+	-	-
H44	-	+	-	+	+	-	-	+	-	-
HD-868	-	+	-	-	-	-	-	+	-	-
NXP15-04	+	+		+	++	-	-	+		-
H54	+	+	-	+	+	-	-	+	-	-
KK31-01	+	+	-	-	-	-	-	+	-	+
HD-137	+	+	-	+	+	-	-	-	-	-
HD-867	+	+		+	+	-	-	-	-	-
H55	+	+	-	+	+	-	-	+	-	-
HD-521	-	+	-	-	-	-	-	-	-	+
H38	+	+	-	-	+	-	-	+	-	-
HD-866	+	+	-	+	+	-	-	+	-	+
HD-1012	+	+		-	-	-	-	-	-	-
H58	+	+	-	-	+	-	-	+	-	-
HD-7	+	+	-	+	+	-	-	+	-	-
HD-554	-	+	-	-	-	-	-	+	-	+
140	+	+		+	-	-	-	+	+	+
HD-974	+	+	-	+	-	-	-	+	-	+
HD-29	+	+	-	+	-	-	-	+	++	-
		+	+							
H31	+	+	-	+	+	-	-	+	-	-
CT-43	+	+		-	-	-	-	-	-	-
4CC1	-	-	-	-	-	-	-	+	-	-
HD-1011	+	+	-	-	-	-	-	+	-	-
H57	+	+	-	+	-	-	-	-	+	-
H49	+	+	-	-	-	-	-	+	-	+
H39	+	+		-	-	-	-	-	-	-
H16	-	+	-	-	-	-	-	+	-	-
HD-4	+	+	-	+	+	-	-	-	-	-
H23	+	+	-	+	+	-	-	+	-	-
H66	+	+	-	-	-	-	-	+	-	-
BMB171	-	-	-	-	-	+	-	+	-	-

^a Strains could be infected by induced supernatants and caused lysis zones are indicated as “+”, otherwise indicated as “-”. The strains used for the purification of the induced phages are indicated as “++”.

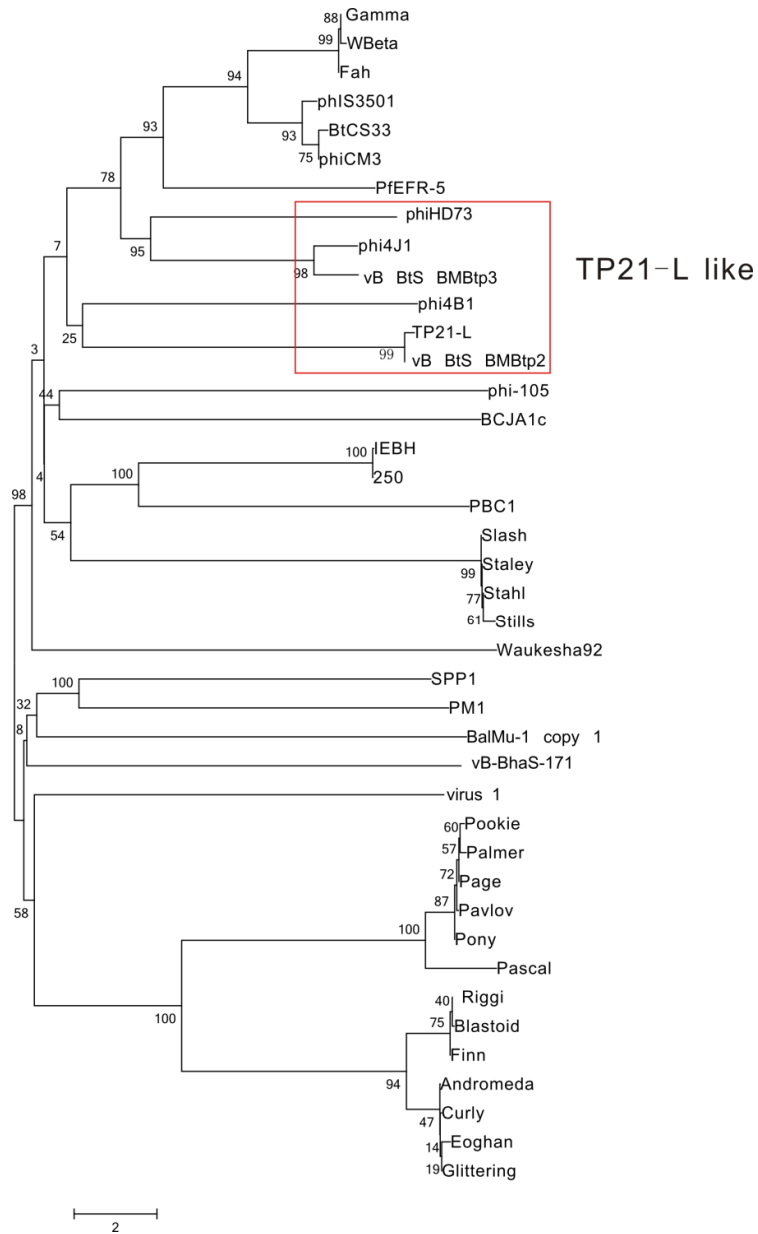


Figure 5. Phylogenetic analysis of 41 *Siphoviridae* family phages. The genome sequences of 40 *Siphoviridae* family phages were collected from GenBank and used for phylogenetic tree construction together with the genome of phage phiHD73.

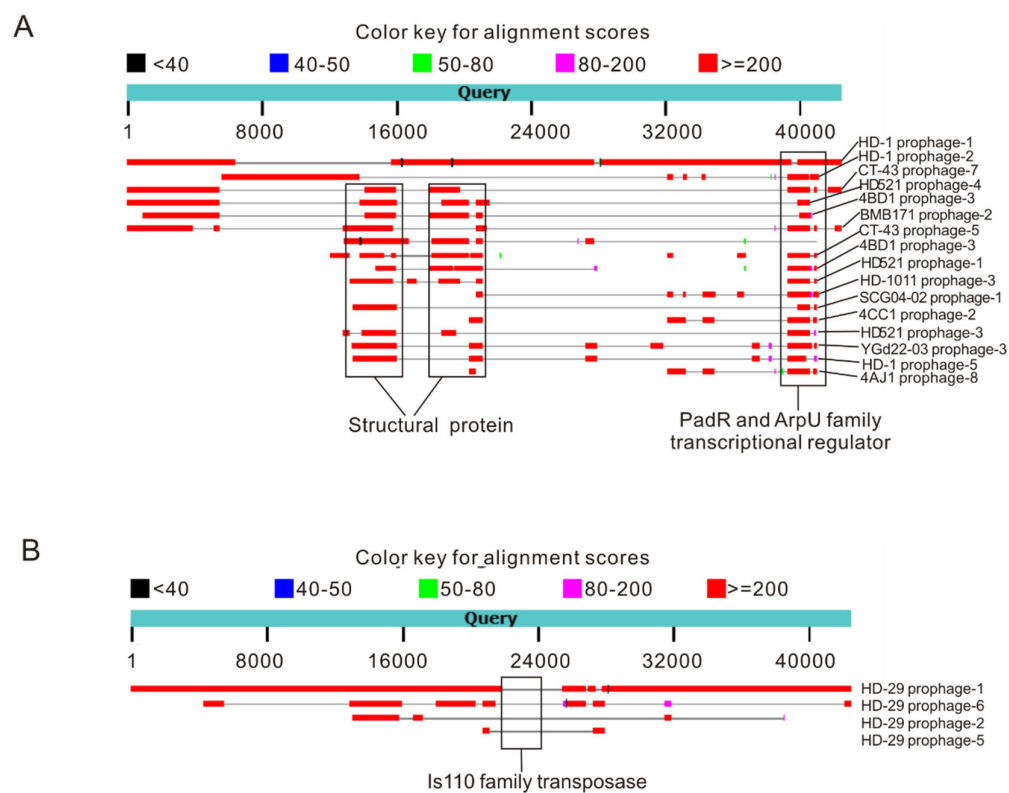


Figure 6. The genome sequences comparison between induced phage phiHD73 and candidate prophages in resistant and susceptible Bt strains by using Blastn. (A) The genome comparison of phiHD73 with prophages in resistant Bt strains. (B) The genome comparison of phiHD73 with prophages in susceptible Bt strain, HD-29, which could be infected by the induced phage phiHD73.

Beta-lactamase(HD-521 prophage-1)	MKIRGQITCASLALLIAGSSLYTTSTSIIVKPEETNVSS	40
D-alanyl-D-alanine carboxypeptidase	MVSGTVGRGTALGAVILLALIVPFCAGTA	29
Consensus	g a p q	
Beta-lactamase(HD-521 prophage-1)	SLQTNMQDRTSVKQAMRDTLQLGYPGILAKTSEGKRWG	80
D-alanyl-D-alanine carboxypeptidase	AAADLPADDTGLQAVLHTALSCGAPGAMVRVDDNGTIHQ	69
Consensus	d t l g pg g	Gly65
Beta-lactamase(HD-521 prophage-1)	YAGCIADLRKKPKMTLRRFRIGSVTKTFDAIVVLQLVGE	120
D-alanyl-D-alanine carboxypeptidase	LSEGVADRATGRAITTTIRFRVGSVTKSFSANVLLQLVDE	109
Consensus	g ad t t rfr gsvtk f a v lqlv e	
Beta-lactamase(HD-521 prophage-1)	NRKLLDDYIEDWLPGVICQNGYDGNKITIREILNHTSGIA	160
D-alanyl-D-alanine carboxypeptidase	GRILLDASVNTYLPGLLPDD.....RITVRQVMSHSGLY	144
Consensus	l ld lpg it r h sg	
Beta-lactamase(HD-521 prophage-1)	EYSRSKDVDFTD.....TKKSYTAEBIVKIGISLPDFEAP	195
D-alanyl-D-alanine carboxypeptidase	DYINDMFACTVPGFESVRNKVFSYQDITITLSLKHGVINAP	184
Consensus	y k l ap	
Beta-lactamase(HD-521 prophage-1)	GKGWSYSNTGYVLGLIEKVTGNSVPEEVENRIIEPLEL	235
D-alanyl-D-alanine carboxypeptidase	GAAYSYSNTNFWVAGMLIEKLTGHSVATEYONRIETPLNL	224
Consensus	g sysnt v g liek tg s a e nri pl l	
Beta-lactamase(HD-521 prophage-1)	SNTELPGNSSVIPGTNHARGYFQPDGAS.ELEKDVITYNFS	274
D-alanyl-D-alanine carboxypeptidase	TDTHYVHPDTVIPGT.HANGYLTPDEAGGATVDSIEQTWS	263
Consensus	tf vipgt ha gy pd a l d t s	
Beta-lactamase(HD-521 prophage-1)	PASAGDMISTADLNKFFSVTLGGKTLKECQLKQLTTV	314
D-alanyl-D-alanine carboxypeptidase	WACSAGAVISSTQDLDTEFSRLMSGQIMSAQLKQCCWT	303
Consensus	a sag is dl ffs l g l ql gm	Gln298
Beta-lactamase(HD-521 prophage-1)	PTGKEGIDGYGLGIYETKLPSCVSIHGHTGGILGFTTLVG	354
D-alanyl-D-alanine carboxypeptidase	TVN..STGGYGLGLRRRLISCGISVVGHTGTVCQGYTYAF	341
Consensus	gyglg l g s ghtg g t	
Beta-lactamase(HD-521 prophage-1)	GKLGGRHTLVVNWNSLGRIDSNNPFKKILLAEFNK.....	389
D-alanyl-D-alanine carboxypeptidase	ASKDGRSVTALANTSNNVNVINTMARTLESFECGKPTTA	381
Consensus	gk n n l f	

Figure 7. The amino acid sequences alignment of beta-lactamase in HD-521 prophage-1 with the beta-lactamase (PDB database accession number: 1yqs) from *Streptomyces* R61. The catalytic site residues are indicated in red boxes.

Beta-lactamase(HD-771 prophage-2)	TGQVKHKNCATHKEFSQLEKKFDARLGVAIDTGTNQTIS	80
Beta-lactamase	HPEILVKVKDADQLGARVGYIELDLSNGKILE	33
Consensus	t e a r g d	
Beta-lactamase(HD-771 prophage-2)	.YRENERFAFFSTYKKTAAAGVLIQ..QNSIDTINEVITFT	117
Beta-lactamase	SFRERERFEMSLERKVLGAVLSRIDAGQECLGRRIHYS	73
Consensus	rp erf s t k l g l l i	
	Ser45 Lys48	
Beta-lactamase(HD-771 prophage-2)	KEDLVQYSPVTEKHVDTGMLGEIAEAAVRSNDTANIL	157
Beta-lactamase	QNDLVEYSPVTEKHLITGMLVRELCSAAITSDNTAANLL	113
Consensus	dlv yspvtekh gm e aa s d n t a n l	
	Ser45	
Beta-lactamase(HD-771 prophage-2)	FNKIGGPKGYEKAIRRMGDRITMSDRFDLNEAIEGDIR	197
Beta-lactamase	LTTIGGPRELTALHNMGDHVTRLDWEELNEAIEIDER	153
Consensus	iggpk l mgd t dr e elneaip d r	
	Glu141	
Beta-lactamase(HD-771 prophage-2)	DTSTAKAATNKAFTVGNATPAEKRRKITEWPKGNATGD	237
Beta-lactamase	DTTFEVAATTLAKLLTGELLTLASRQQLIDWEADKVAG	193
Consensus	dt a at l g l r l w m	
Beta-lactamase(HD-771 prophage-2)	KLIRAGVETDWVVGKSGASYGDENDIIVWFEENRAPII	277
Beta-lactamase	KLIRSALEAGWFIAKSGAGERGSGIIPALGIDGKFSRI	233
Consensus	l r p w c k s g a g r i a p i	
	Lys209 Ala212	
Beta-lactamase(HD-771 prophage-2)	IAILSSKDEKEATYDNLIAEATEVIVKALR	308
Beta-lactamase	VVIYITGSQATMDERNQIAEIGASLIKHW.	263
Consensus	i n i a e k	

Figure 8. The amino acid sequences alignment of beta-lactamase in HD-771 prophage-2 with the beta-lactamase (PDB database accession number: 1btl) from *Escherichia coli*. The catalytic site residues are indicated in red boxes.

Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	LTAYLFVVKTAFTLFPFLAMFLIPFLIFNYRKYCYLNKW	40
D-alanine-D-alanine ligase	MTDKIAVILGGTSAEREVSLNSGAAVLAGIRE..	32
Consensus	1 g	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	RSFILYSLLLYLLNAYFLVILPLPQTFTDCSLQPANTQHM	80
D-alanine-D-alanine ligase	GGIDAYFVDFPKEVDVTCIKSMGFQKVF..IPAHGRGGEDG	70
Consensus	y 1 f 1	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	QLSPFYFIQEISSHTSAVLTKPATYFYLLKESAFLLQVAFN	120
D-alanine-D-alanine ligase	TLQGMLELMGLPYTGSGVMAS.ALSMDKIRSKLLWCGAG.	108
Consensus	1 s v a 1 q a	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	VLLTVFFGIYLYRYYRFRSFLCTICISFFLSIFFELTQVTG	160
D-alanine-D-alanine ligase	.LPVPEWVALTRAEEKGLSDKQLAEISALIGLFPVIVKPS	146
Consensus	1 p r f 1 1	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	LYGIYNCAIYRLFIDDLFLNLLGGVIGFIIAPIFTYFLPK	200
D-alanine-D-alanine ligase	REGSS.VGMSKVVAENALQDAIRLAFQHDEEVLLIEKWLSG	185
Consensus	g 1 1	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	TNELDSHIDLETFEVGFIRRLIAMCIDWIFLSIVVPVVKKN	240
D-alanine-D-alanine ligase	PEFTVAILGEEILLES.....IRNCPSGTFEYDYEAAYLSD	219
Consensus	e p 1 q f	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	KGNSEFVSNMQSYTNMYELIFITCSILLYFIILIPYFTNGK	280
D-alanine-D-alanine ligase	ETQYECFAGLEASQEAN.....IQALVFKAWTLGL.	249
Consensus	f 1 1 t g	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	TIIGKALLRIHFKGKSDRITLDELFIYRGIFYFALGGINYI	320
D-alanine-D-alanine ligase	CKGWRIDVMIIDSDG.QFYILLEANISEGMTSHSLIVPMAAR	288
Consensus	g 1 1 e g 1	
	Gly276	
Glycopeptide antibiotics resistance protein (Pasteur Institute Standard strain prophage-12)	LSSSSMLNHTPEPLVLVLLFLFIINGLFIIHVLLHVFSR	360
D-alanine-D-alanine ligase	QAGMSFSQLVVRILELAD.....	306
Consensus	s 1	

Figure 9. The amino acid sequences alignment of glycopeptide resistance protein in Pasteur Institute Standard strain prophage-12 with the glycopeptide resistance protein (PDB database accession number: 2dln) from *Escherichia coli*. The catalytic site residue is indicated in red box.