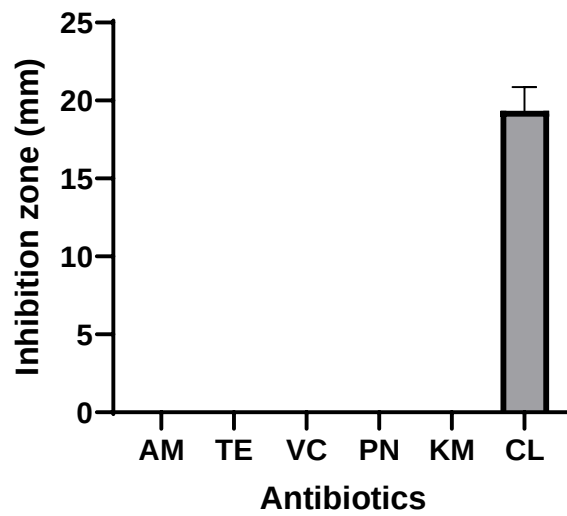
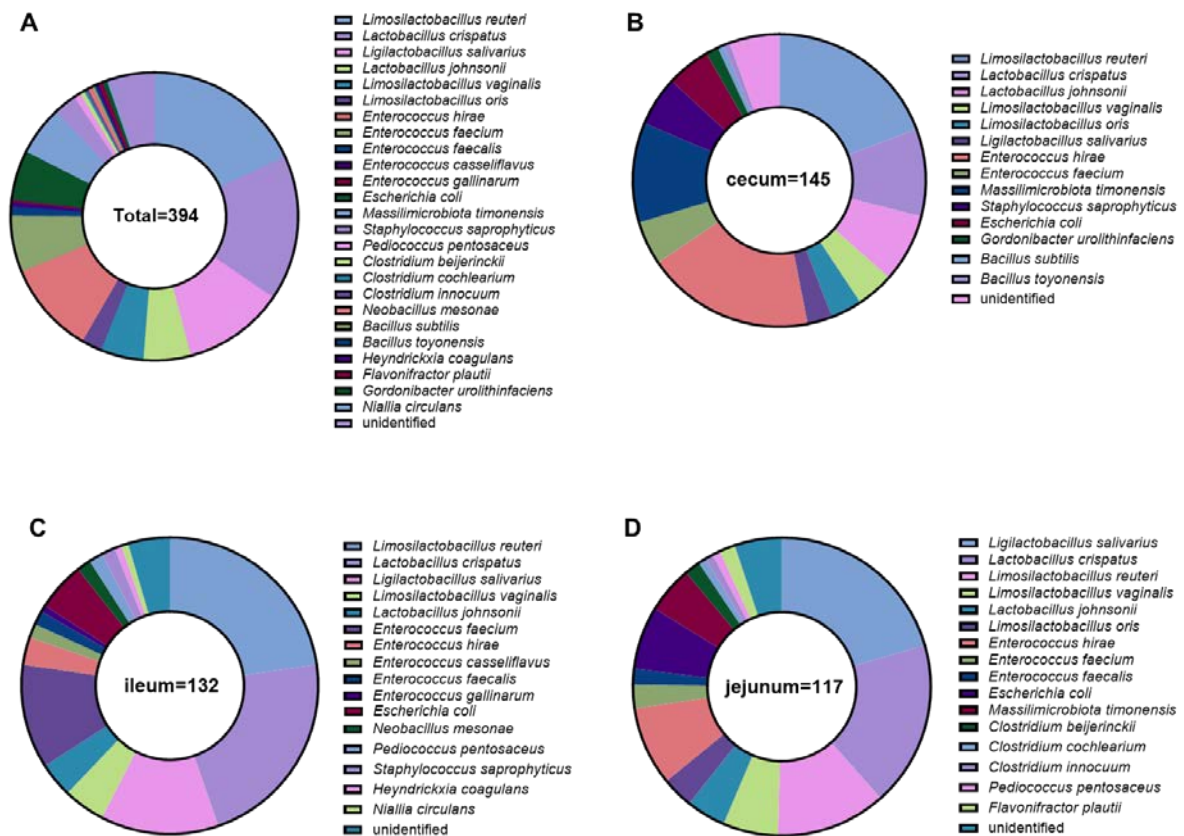
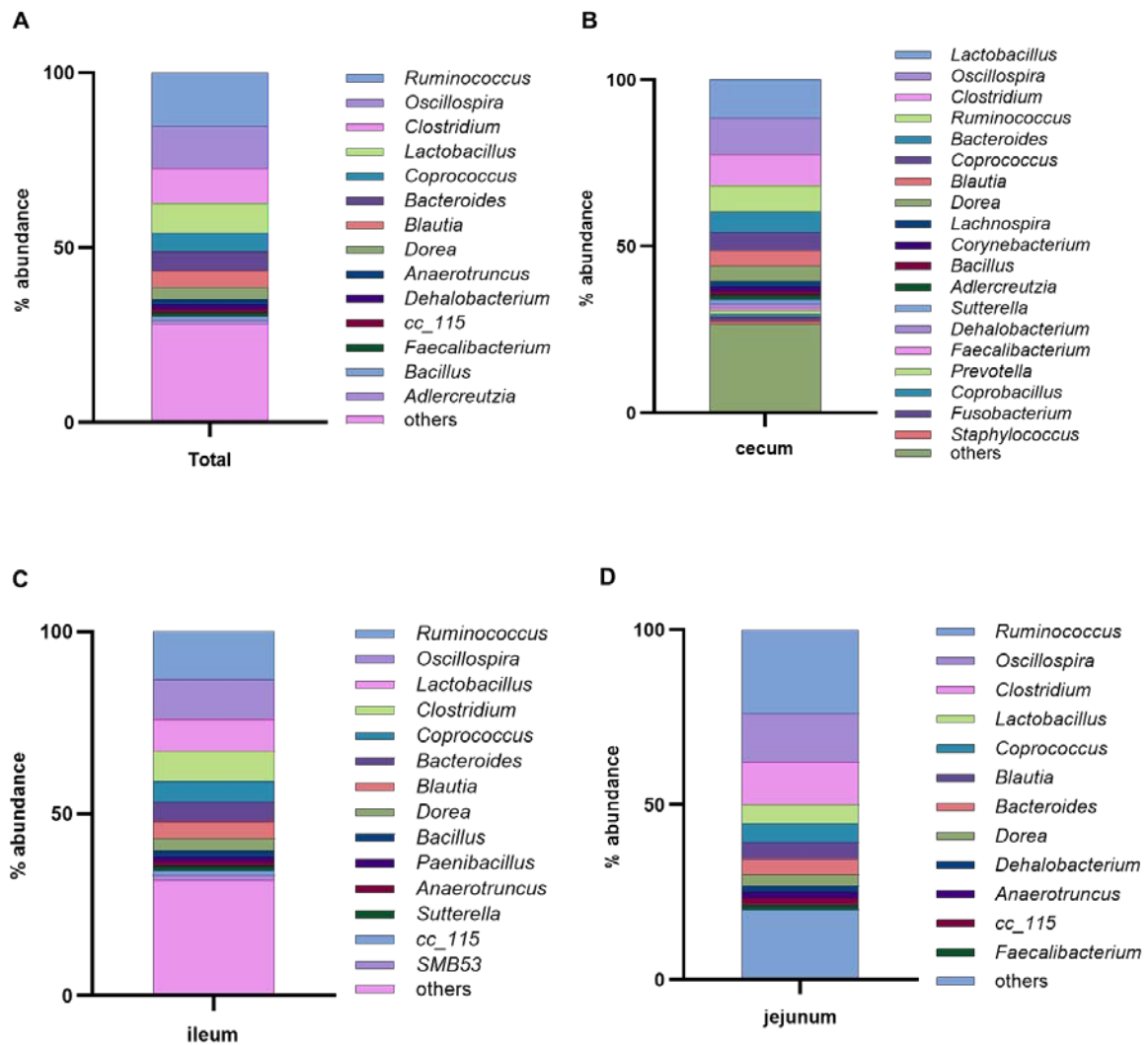




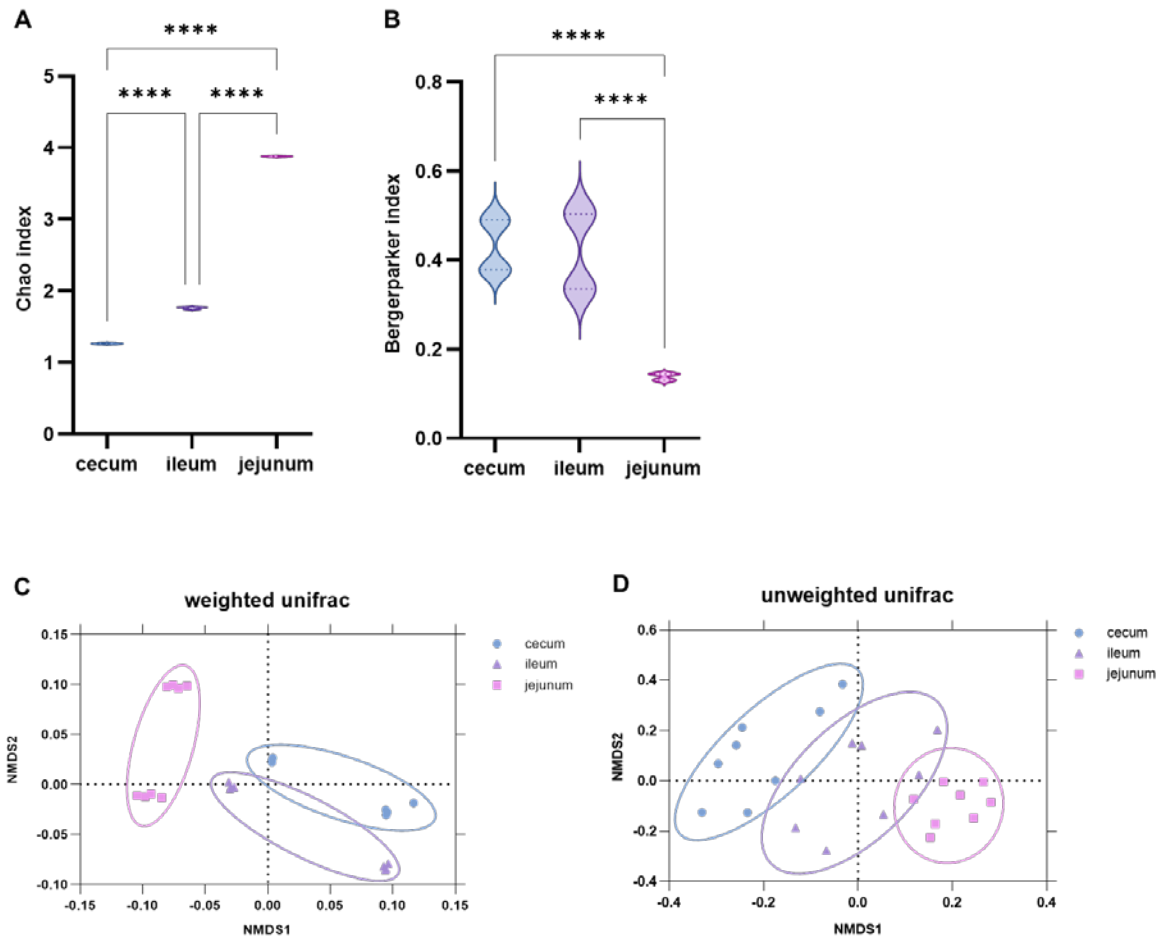
Supplementary Fig. S1. Antibiotic resistance using ST422. To test the antibiotic resistance of the host bacterium ST422 of SLAM_phiST45, six antibiotics were used, with details of the products listed in Supplementary Table S2. The results showed resistance to five of the six antibiotics, confirming that ST422 is a multi-drug resistant *Salmonella* strain.



Supplementary Fig. S2. Microbial composition using culturomics. (A) The relative distribution and diversity of the 394 bacterial species isolated using the culturomics approach are displayed in a circular map. (B)–(D). In addition, bacterial abundance in the cecum (B), ileum (C), and jejunum (D) is summarized for each section.

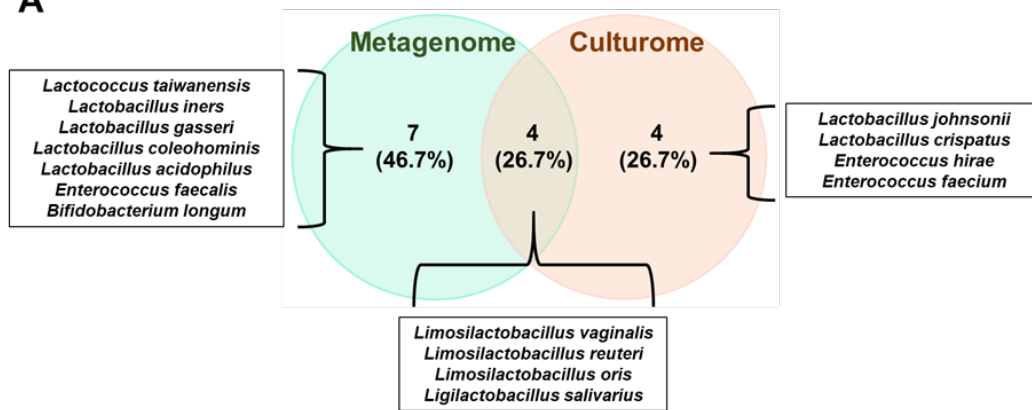


Supplementary Fig. S3. Microbial composition using metagenomics. The overall bacterial abundance analyzed using the metagenomics approach (A) is presented alongside the microbial composition of the cecum (B), ileum (C), and jejunum (D). Bacterial abundance was converted to percentages based on total read counts, and bacterial groups with <1% abundance were categorized as “others.”

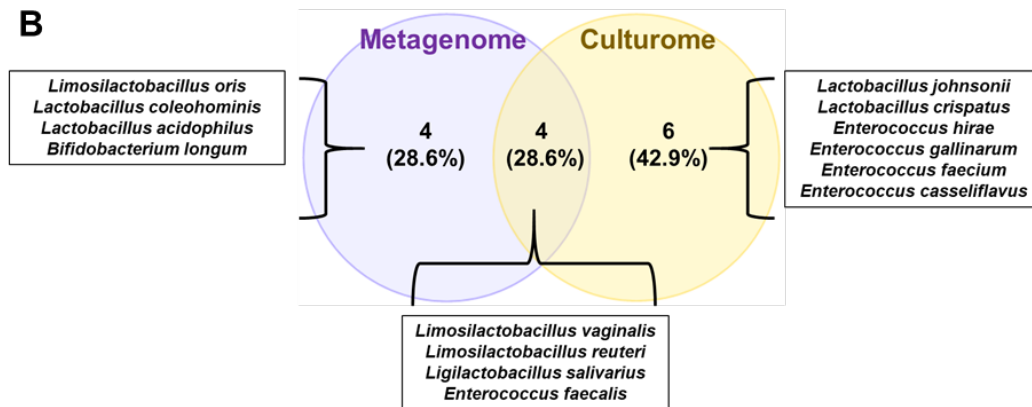


Supplementary Fig. S4. Diversity analysis of chicken gut microbiome using metagenomics. A, B. α -diversity of metagenomics. Chao (A) and bergerparker (B) diversity indices of each group in the cecum, ileum, and jejunum are shown. The experiments were conducted in triplicate. All values are expressed as the mean $\pm$ SD, and statistical significance was determined using the Student's t-test with $**p < 0.0001$. (C), (D). β -diversity of metagenomics. Beta-diversity results of the metagenomic analysis for each organ of the chicken were analyzed using both weighted and unweighted UniFrac methods. Each clustered plot represents the different groups (cecum, ileum, and jejunum), with the axes representing the two dimensions that account for the largest variance within the microbial communities.

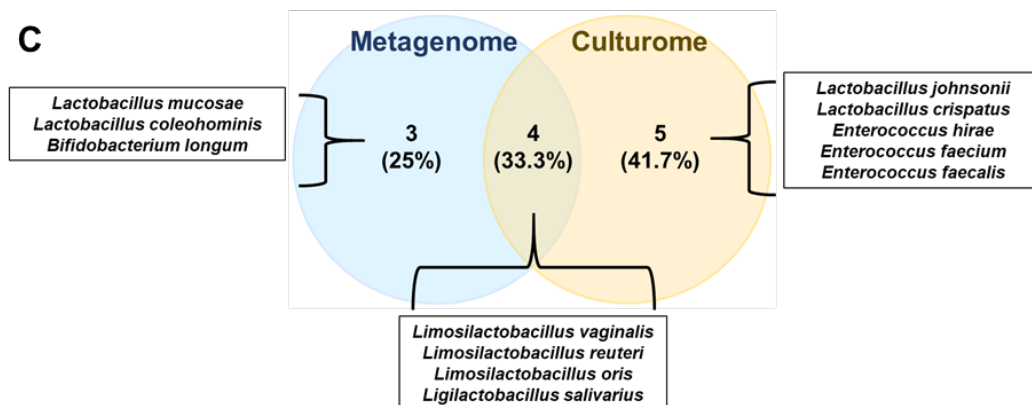
A



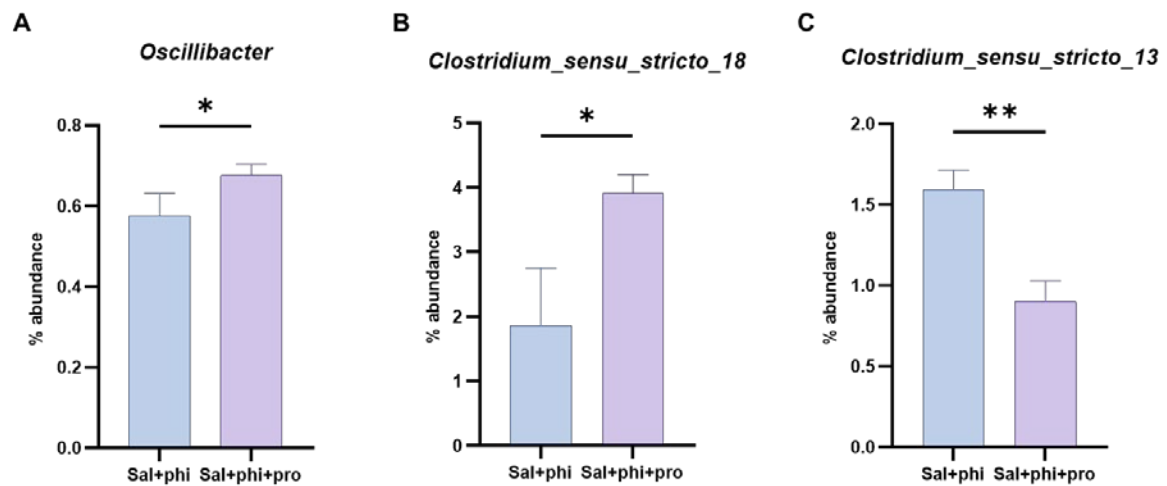
B



C



Supplementary Fig. S5. Comparison of metagenomic and culturomics approaches for characteristics of probiotics in chicken intestines. Species of probiotics identified using culturomics and metagenomics approaches were selected for multi-omics analysis and represented using a venn diagram. In addition to the results shown in Figure 1E, which includes all data, further analysis was conducted separately for the cecum (A), ileum (B), and jejunum (C), thus providing a comprehensive multi-omics analysis for each intestinal section.



Supplementary Fig. S6. Microbial changes between the phage-treated and the phage-probiotic treated groups. In the genus-level microbial composition analysis shown in Figure 8K, three bacterial genera, *Oscillibacter* (A), *Clostridium sensu stricto 18* (B), and *Clostridium sensu stricto 13* (C), were selected based on significant differences between the sal+phi and sal+phi+pro groups. The Y-axis represents the actual bacterial abundance in each group; the experiment was conducted in triplicate.

Supplementary Table S1. Bacteria list information for all the pathogenic strains used in this experiment is summarized

No.	Bacterial species	Strain no.	Name	Source	Growth condition	etc
1	<i>Salmonella</i> Typhimurium	KVCC-BA1900016	ST016	Swine	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
2		KVCC-BA2000161	ST161	Swine	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
3		KVCC-BA1600008	ST008 (=ST1)	Poultry	37°C, aerobic	Host bacteria of SLAM_phiST56 Antimicrobial activity test in figure 2D
4		KVCC-BA0000422	ST422 (=ST2)	Poultry	37°C, aerobic	Host bacteria of SLAM_phiST45 Antimicrobial activity test in figure 2D
5		KVCC-BA0000423	ST423	Poultry	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
6		KVCC-BA0000474	ST474	Poultry	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
7		KVCC-BA0000477	ST477	Poultry	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4 Antimicrobial activity test in figure 2D
8		KVCC-BA0000482	ST482 (=ST3)	Poultry	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
9		SL1344	SL1344	Human	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
10		ATCC14028	ATCC14028	Human	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
11		NCCP16207	NCCP16207	Human	37°C, aerobic	Liquid inhibition test in figure 7B EOP test in table 4
12	<i>Campylobacter jejuni</i>	KVCC-BA1800501	CJ1	Poultry	42°C, microaerophilic	Antimicrobial activity test in figure 2D
13		KVCC-BA1800502	CJ2	Poultry	42°C, microaerophilic	Antimicrobial activity test in figure 2D
14		KVCC-BA1800503	CJ3	Poultry	42°C, microaerophilic	Antimicrobial activity test in figure 2D

Additional details include references to the figures and tables in which the strains were used in this study.

Supplementary Table S2. Guidelines for antimicrobial discs used for susceptibility test

Antibiotics	Disc potency (µg)	≥ S (mm)	I (mm)	≤ R (mm)
Ampicillin	10	17	-	16
Tetracycline	30	19	15-18	14
Vancomycin	30	17	15-16	14
Penicillin	10 U	29	-	28
Kanamycin	30	18	14-17	13
Chloramphenicol	30	18	13-17	12

The list of antibiotics used in Table 1 and Supplementary Figure S1 to examine the antibiotic resistance of the host bacterium ST422 to SLAM_phiST45 and *Lactobacillus* spp. are provided. BD BBL™ Sensi-Disc™ antimicrobial susceptibility test discs were placed on a bacterial lawn plate and incubated for 24 h at 37 °C, repeated in triplicate.

Supplementary Table S3. Bacteriophage list information for the 61 *Salmonella* Typhimurium phages isolated in this experiment is provided

No.	Name	Host bacteria species	Host bacteria strain	Source	No.	Name	Host bacteria species	Host bacteria strain	Source
1	SLAM_phiST1	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	32	SLAM_phiST32	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
2	SLAM_phiST2	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	33	SLAM_phiST33	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
3	SLAM_phiST3	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	34	SLAM_phiST34	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
4	SLAM_phiST4	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	35	SLAM_phiST35	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
5	SLAM_phiST5	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	36	SLAM_phiST36	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
6	SLAM_phiST6	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	37	SLAM_phiST37	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
7	SLAM_phiST7	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	38	SLAM_phiST38	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge
8	SLAM_phiST8	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	39	SLAM_phiST39	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
9	SLAM_phiST9	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	40	SLAM_phiST40	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
10	SLAM_phiST10	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	41	SLAM_phiST41	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
11	SLAM_phiST11	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	42	SLAM_phiST42	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
12	SLAM_phiST12	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	43	SLAM_phiST43	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
13	SLAM_phiST13	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	44	SLAM_phiST44	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
14	SLAM_phiST14	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	45	SLAM_phiST45	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
15	SLAM_phiST15	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	46	SLAM_phiST46	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
16	SLAM_phiST16	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	47	SLAM_phiST47	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
17	SLAM_phiST17	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	48	SLAM_phiST48	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
18	SLAM_phiST18	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	49	SLAM_phiST49	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
19	SLAM_phiST19	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	50	SLAM_phiST50	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
20	SLAM_phiST20	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	51	SLAM_phiST51	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
21	SLAM_phiST21	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	52	SLAM_phiST52	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
22	SLAM_phiST22	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	53	SLAM_phiST53	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
23	SLAM_phiST23	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	54	SLAM_phiST54	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
24	SLAM_phiST24	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	55	SLAM_phiST55	<i>Salmonella</i> Typhimurium	KVCC-BA0000422	Sludge
25	SLAM_phiST25	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	56	SLAM_phiST56	<i>Salmonella</i> Typhimurium	KVCC-BA1600008	Sludge
26	SLAM_phiST26	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	57	SLAM_phiST57	<i>Salmonella</i> Typhimurium	ATCC14028	Sludge
27	SLAM_phiST27	<i>Salmonella</i> Typhimurium	KVCC-BA2000161	Sludge	58	SLAM_phiST58	<i>Salmonella</i> Typhimurium	ATCC14028	Sludge
28	SLAM_phiST28	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge	59	SLAM_phiST59	<i>Salmonella</i> Typhimurium	ATCC14028	Sludge
29	SLAM_phiST29	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge	60	SLAM_phiST60	<i>Salmonella</i> Typhimurium	ATCC14028	Sludge
30	SLAM_phiST30	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge	61	SLAM_phiST61	<i>Salmonella</i> Typhimurium	NCCP16207	Sludge
31	SLAM_phiST31	<i>Salmonella</i> Typhimurium	KVCC-BA0000482	Sludge					

All phages were sourced from sludge samples collected from the Tanchon, Jungnang, Seonam, and Nanji wastewater treatment plants in Seoul, South Korea. Host bacteria for SLAM_phiST45 and SLAM_phiST56 are highlighted in bold.

Supplementary Table S4. Primer lists for RT-qPCR.

Target		Primer sequences (5'→3')	Product size, bp	Reference
Total bacteria	F	CGGCAACGAGCGCAACCC	130	(58)
	R	CCATTGTAGCACGTGTGTAGCC		
invA gene	F	GCTGCTTTCTCTACTTAAC	95	(59)
	R	GTAATGGAATGACGAACAT		

The primers used in this study (shown in Figure 8G) were designed to measure the abundance of *Salmonella* and the total bacterial quantity, with a focus on the *invA* gene of *Salmonella* Typhimurium, which is commonly used to detect *Salmonella*

Supplementary Table S5. Host range analysis of *Salmonella* Typhimurium-infecting phages

Phage no.	Host bacteria	Host bacteria source	Salmonella Typhimurium strains											
			Pig		Chicken						Human			
			ST016	ST161	ST008	ST422	ST423	ST474	ST477	ST482	SL1344	ATCC14028	NCCP16207	
1	ST161	Pig	+/-	+	+/-	-	-	-	-	-	-	-	-	-
2			+/-	+	-	-	-	-	-	-	-	-	-	-
3			+/-	++	+/-	-	-	+/-	-	-	+/-	++	+/-	-
4			+/-	+	+/-	+	+/-	-	-	-	-	-	+/-	-
5			+/-	+	-	-	-	-	-	-	-	-	-	-
6			+	++	-	-	-	+/-	-	-	+/-	+/-	+/-	-
7			+/-	++	-	-	-	+	-	-	+/-	++	+	-
8			+/-	++	+/-	-	-	+	-	-	++	++	++	-
9			+/-	+	-	-	-	+/-	-	-	+/-	+/-	+/-	-
10			+/-	++	-	-	-	+/-	-	-	+/-	+/-	+/-	-
11			+	++	-	-	-	+/-	-	-	+/-	++	++	-
12			+/-	++	-	-	-	+	-	-	+/-	++	++	-
13			+/-	+	+/-	-	-	+/-	-	-	+/-	+/-	+/-	-
14			+/-	++	-	-	-	+/-	-	-	+/-	+/-	+	-
15			+/-	++	-	-	-	+	-	-	+	+	+	-
16			-	+	-	+	+/-	-	-	-	-	-	+	-
17			-	+	-	-	-	-	-	-	-	-	+/-	-
18			-	+	-	-	-	-	-	-	-	-	+/-	-
19			+/-	++	-	-	-	+/-	-	-	+/-	+	+/-	-
20			+/-	++	-	-	-	+/-	-	-	+/-	++	+/-	-
21			+	+	-	-	-	-	-	-	+/-	-	-	-
22			+/-	+	-	-	-	++	-	-	-	++	-	-
23			+	+	-	-	-	++	-	-	++	++	+/-	-
24			-	+	-	-	-	++	-	-	-	++	-	-
25			-	+	-	-	-	++	-	-	+/-	++	-	-
26			+/-	++	-	-	-	+/-	-	-	+	++	+/-	-
27			+/-	+/-	-	-	-	-	-	-	+/-	+/-	-	-
28	ST482	Chicken	-	-	-	-	-	-	-	+/-	-	-	-	
29			-	-	-	-	-	-	-	+/-	-	-	-	
30			-	-	-	-	-	-	-	+	-	-	-	
31			-	-	-	-	-	-	-	+/-	-	-	-	
32			-	-	-	-	-	-	-	+	-	-	-	
33			-	-	-	-	-	-	-	+	-	-	-	
34			-	-	-	-	-	-	-	+/-	-	-	-	
35			+/-	-	+/-	-	-	-	-	+/-	-	-	-	
36			+/-	-	-	-	-	-	-	+/-	-	-	-	
37			-	-	-	-	-	-	-	+	-	-	-	
38			-	-	-	-	-	-	-	+	-	-	-	
39	ST422	Chicken	+/-	-	+/-	+	+/-	+/-	-	+/-	+	+/-	-	
40			+/-	-	+/-	++	+	+/-	+/-	+	++	+/-	-	
41			+/-	+/-	+/-	++	++	+	-	+	++	-	-	
42			+/-	-	+/-	++	+/-	+/-	-	+/-	+/-	-	-	
43			-	-	-	++	+/-	-	-	-	-	-	-	
44			+/-	-	+/-	++	+/-	+/-	-	+/-	+	+/-	-	
45			+	+/-	+/-	++	++	++	-	++	++	+	+	
46			+/-	-	+/-	+/-	+/-	+/-	+/-	+	+/-	+/-	-	
47			-	-	-	+/-	+/-	-	-	-	-	-	-	
48			-	-	-	+/-	+	-	-	-	+/-	-	-	
49			-	-	-	+/-	+	-	-	-	-	-	-	
50			-	-	-	+/-	+/-	-	-	-	-	-	-	

51			-	-	-	+/-	+/-	-	-	-	-	-	-	-
52			-	-	-	+/-	+/-	-	-	-	-	-	-	-
53			-	-	-	+/-	+	-	-	-	-	-	-	-
54			+	-	+/-	+/-	+/-	+/-	-	++	+/-	+/-	-	-
55			+	-	+/-	+/-	+	+/-	-	++	+	+/-	-	-
56	ST008		+	+	++	+	+	+	+	+	-	-	++	+
57			+	+/-	-	-	-	+/-	-	-	+/-	+/-	+/-	+/-
58	ATCC14028		+/-	+/-	-	-	-	+/-	-	-	+/-	+	+/-	+/-
59		Human	+/-	++	-	-	-	+	-	-	+/-	++	-	-
60			+	+/-	-	-	-	+/-	-	-	++	+/-	+/-	+/-
61	NCCP16207		+	-	-	-	-	++	-	-	++	++	+	+

List of bacterial strains used to confirm the host range of 61 *Salmonella*-infecting phages. Phage lysate stock, diluted to 1×10^6 PFU/mL, was dotted onto plates containing bacterial lawn (10 uL per dot), and the plates were cultured for 24 h at 37 °C under both aerobic and anaerobic conditions.

Supplementary Table S6. Functional annotation of SLAM_phiST45

ORF	Start	Stop	Length (nt)	Strand	Function	Homology				
						Homology	Query coverage	E value	Per-identity	Accession No.
SLAM_phiST45_001	303	407	105	-	Hypothetical protein	hypothetical protein B09773_gg081 [Salmonella phage 180208_saf2]	100%	1.00E-36	100.00%	YP_009120727.1
SLAM_phiST45_002	407	601	195	-	Hypothetical protein	hypothetical protein AGC_8178 [Escherichia phage Epc7]	100%	4.00E-13	100.00%	YP_001837082.1
SLAM_phiST45_003	674	988	315	-	Hypothetical protein	hypothetical protein Ace_0401 [Escherichia coli phage vB_Eco5_Ace]	100%	2.00E-46	99.84%	QNR52287.1
SLAM_phiST45_004	1063	1329	267	-	Cas superinfection exclusion protein	Cas superinfection exclusion protein [Salmonella phage Stitch]	100%	1.00E-58	100.00%	YP_009160182.1
SLAM_phiST45_005	1413	3194	1782	+	Receptor-binding protein	receptor-binding protein [Escherichia coli phage vB_Eco5_Ace]	100%	0	99.83%	QNR52295.1
SLAM_phiST45_006	3205	3087	483	+	Terminase small subunit	terminase small subunit [Escherichia phage Epc7]	100%	1.00E-112	99.38%	YP_001837089.1
SLAM_phiST45_007	3087	5063	1317	+	Terminase large subunit	terminase large subunit [Salmonella phage SBB]	100%	0	100.00%	YP_000804133.1
SLAM_phiST45_008	5118	5555	438	+	Nicking endonuclease	nicking endonuclease [Escherichia phage SuperGat]	100%	1.00E-102	98.62%	QXV84038.1
SLAM_phiST45_009	5555	6772	1218	+	Portal protein	phage portal protein [Pseudomonas]	100%	0	100.00%	WP_015080425.1
SLAM_phiST45_010	7255	7087	633	+	Prohead protein	HK07 family phage prohead protein [Brevetia mollisima]	100%	1.00E-154	100.00%	WP_015080423.1
SLAM_phiST45_011	7085	9281	1377	+	Major capsid protein	phage major capsid protein [Salmonella enterica subsp. enterica serovar Hadar]	100%	0	100.00%	EDV130052.1
SLAM_phiST45_012	9342	9054	513	+	Head tail adaptor	head tail adaptor [Escherichia phage Epc7]	100%	2.00E-123	100.00%	YP_001837082.1
SLAM_phiST45_013	9054	10621	740	+	Tail completion protein	tail completion or Neck1 protein [Salmonella phage Stitch]	100%	0	99.61%	YP_001640082.1
SLAM_phiST45_014	10625	11310	486	+	Hypothetical protein	hypothetical protein HD13_31 [Salmonella phage HD13]	100%	2.00E-116	100.00%	LQV53107.1
SLAM_phiST45_015	11317	12546	1410	+	Major tail protein	major tail protein [Escherichia phage Epc7]	100%	0	100.00%	YP_001837079.1
SLAM_phiST45_016	12551	13458	908	+	Minor tail protein	minor tail protein [Salmonella phage BSP22A]	100%	0	100.00%	ABM09028.1
SLAM_phiST45_017	13013	14281	300	+	Tail assembly chaperone	tail assembly chaperone [Salmonella phage Sae2]	100%	3.00E-84	100.00%	YP_00081293.1
SLAM_phiST45_018	14362	10072	371	+	Tail length tape measure protein	tail length tape measure protein [Salmonella phage 3-29]	100%	0	100.00%	YP_00081290.1
SLAM_phiST45_019	10782	21641	2059	+	Tail fiber protein	tail fiber [Salmonella phage JN-S20201]	100%	0	100.00%	USC59064.1
SLAM_phiST45_020	21642	23609	2058	+	Straight fibre tail protein	straight fibre tail protein [Salmonella phage 1-09]	100%	0	99.85%	YP_000813006.1
SLAM_phiST45_021	23705	24127	423	+	Hypothetical protein	hypothetical protein HWC37_gg022 [Salmonella phage vB_Sac5_SB13]	100%	1.00E-20	100.00%	YP_000804029.1
SLAM_phiST45_022	24127	27078	2952	+	Tail fiber protein	tail fiber protein [Salmonella phage 3-29]	100%	0	100.00%	YP_000813002.1
SLAM_phiST45_023	20836	20911	876	+	Flag endonuclease	flag endonuclease [Escherichia phage Epc7]	100%	0	100.00%	YP_001837066.1
SLAM_phiST45_024	20911	20933	483	-	Hypothetical protein	hypothetical protein [Salmonella enterica subsp. enterica serovar Derby]	100%	3.00E-115	100.00%	EDA127036.1
SLAM_phiST45_025	20937	31235	10359	-	AAA family ATPase	AAA family ATPase [Salmonella enterica]	100%	0	100.00%	ECC1451702.1
SLAM_phiST45_026	32233	33006	774	-	Single strand DNA binding protein	single strand DNA binding protein [Salmonella phage SBB]	100%	0	100.00%	YP_000804036.1
SLAM_phiST45_027	33582	34054	1333	-	Helicase	helicase [Salmonella phage Stitch]	100%	0	100.00%	YP_001640073.1
SLAM_phiST45_028	33541	37008	2568	-	DNA polymerase	DNA polymerase [Salmonella phage LVR16A]	100%	0	99.88%	YP_000804418.1
SLAM_phiST45_029	40413	41189	768	-	Hypothetical protein	hypothetical protein [Salmonella enterica subsp. enterica serovar Typhimurium]	100%	1.00E-109	99.61%	EDV206340.1
SLAM_phiST45_030	42355	43126	972	-	NAD-dependent DNA ligase	NAD-dependent DNA ligase [Salmonella phage SI13]	100%	0	100.00%	YP_000804038.1
SLAM_phiST45_031	42317	45022	306	-	Transcriptional regulator	transcriptional regulator [Salmonella phage SBB]	100%	2.00E-48	99.81%	YP_000804039.1
SLAM_phiST45_032	45073	43809	297	-	Hypothetical protein	hypothetical protein [Circulatrix percutaneum]	100%	2.00E-45	100.00%	WP_110804412.1
SLAM_phiST45_033	43006	44416	411	-	DNA binding protein	DNA binding protein [Salmonella phage 180208_saf2]	100%	1.00E-93	99.26%	YP_009120808.1
SLAM_phiST45_034	40534	43358	765	-	Hypothetical protein	hypothetical protein [Circulatrix percutaneum]	100%	1.00E-170	100.00%	WP_110803786.1
SLAM_phiST45_035	40544	40833	290	-	Replication origin binding protein	replication origin binding protein [Salmonella phage Bionet1]	100%	0	99.87%	QNR52296.1
SLAM_phiST45_036	40539	40465	776	-	Hypothetical protein	hypothetical protein B09773_gg128 [Salmonella phage 180208_saf2]	100%	2.00E-86	98.47%	YP_001837065.1
SLAM_phiST45_037	40535	40487	393	-	Hypothetical protein	hypothetical protein B09773_gg129 [Salmonella phage 180208_saf2]	100%	206	100%	Q92379
SLAM_phiST45_038	40505	40002	507	-	NAD-dependent deacetylase	50k [NAD-dependent deacetylase] [Salmonella phage LVR16A]	100%	4.00E-121	100.00%	YP_000804043.1
SLAM_phiST45_039	40505	41558	852	-	NAD-dependent deacetylase	NAD-dependent deacetylase of SDE family [Salmonella phage Pseud]	100%	0	99.63%	QTY33072.1
SLAM_phiST45_040	31062	33736	1075	-	Aerobic ribonucleotide diphosphate reductase	aerobic ribonucleotide diphosphate reductase [Escherichia coli phage vB_Eco5_Ace]	100%	0	99.88%	QNR52293.1
SLAM_phiST45_041	40409	34461	733	+	Phosphate starvation inducible protein	Phd1 like phosphate starvation inducible [Salmonella phage Stitch]	100%	0	99.98%	YP_000804045.1
SLAM_phiST45_042	34463	33985	243	+	Tail length tape measure protein	tail length tape measure protein [Salmonella phage 180208_saf2]	100%	3.00E-51	100.00%	YP_000804044.1
SLAM_phiST45_043	33209	37539	2313	+	Aerobic ribonucleotide diphosphate reductase, large subunit	aerobic ribonucleotide diphosphate reductase, large subunit [Circulatrix phage YZU-L3]	100%	0	100.00%	W120077.1
SLAM_phiST45_044	37639	38137	138	+	Hypothetical protein	hypothetical protein HD133_gg080 [Salmonella phage SBB]	100%	4.00E-124	100.00%	YP_000804037.1
SLAM_phiST45_045	35043	39396	1146	+	Ribonucleotide diphosphate reductase beta subunit	ribonucleotide diphosphate reductase beta subunit [Escherichia phage IrmuTchad]	100%	0	99.74%	QV30405.1
SLAM_phiST45_046	35096	39812	128	+	Shadedplate enzyme	diffractase reductase [Escherichia phage Sae212]	100%	1.00E-124	100.00%	YP_000794063.1
SLAM_phiST45_047	39812	40467	655	+	Thymidylate synthase	thymidylate synthase [Brevetia mollisima]	100%	0	100.00%	WP_134060362.1
SLAM_phiST45_048	40706	40934	225	+	Hypothetical protein	hypothetical protein CPT_Stitch60 [Salmonella phage Stitch]	100%	1.00E-52	100.00%	YP_000160039.1
SLAM_phiST45_049	41034	43403	270	+	Hypothetical protein	hypothetical protein [Pseudomonas]	100%	3.00E-56	100.00%	WP_015080763.1
SLAM_phiST45_050	43303	43779	477	+	Rnaase II	Rnaase II [Escherichia phage Epc7]	100%	1.00E-114	100.00%	YP_001837044.1
SLAM_phiST45_051	40536	42534	279	+	Hypothetical protein	hypothetical protein P5a2_00320 [Escherichia phage P5a2]	100%	9.00E-59	100.00%	U1006672.1
SLAM_phiST45_052	42218	42733	516	+	Hypothetical protein	hypothetical protein [Escherichia phage SUT_E1320]	100%	2.00E-128	100.00%	WKN24066.1
SLAM_phiST45_053	42795	43018	216	+	Hypothetical protein	hypothetical protein [Circulatrix percutaneum]	100%	1.00E-40	100.00%	WP_015080761.1
SLAM_phiST45_054	43032	43264	233	+	Hypothetical protein	hypothetical protein [Pseudomonas]	100%	6.00E-43	100.00%	WP_015080762.1
SLAM_phiST45_055	43295	43096	702	+	Exoribonuclease	5'-3' exoribonuclease [Circulatrix percutaneum]	100%	3.00E-175	100.00%	WP_13366302.1
SLAM_phiST45_056	44067	44449	181	+	Hypothetical protein	hypothetical protein [Circulatrix percutaneum]	100%	3.00E-33	100.00%	WP_13366301.1
SLAM_phiST45_057	44304	44842	439	+	Hypothetical protein	hypothetical protein [Escherichia phage SUT_E1320]	100%	3.00E-158	100.00%	WKN24071.1
SLAM_phiST45_058	43306	45703	118	+	Hypothetical protein	hypothetical protein B09773_gg148 [Escherichia phage vB_Eco5_mae0813]	100%	5.00E-71	99.85%	YP_000160073.1
SLAM_phiST45_059	45709	46158	430	+	Endolysin	endolysin [Salmonella phage Stitch]	100%	2.00E-106	100.00%	YP_00160207.1
SLAM_phiST45_060	46227	46397	171	+	Hypothetical protein	hypothetical protein [Brevetia mollisima]	100%	4.00E-38	100.00%	WP_015080753.1
SLAM_phiST45_061	46397	46840	444	+	dsRNA amidotransferase	dsRNA amidotransferase [Salmonella phage 180208_saf2]	100%	1.00E-102	100.00%	YP_009120813.1
SLAM_phiST45_062	47005	47009	75	+	Hypothetical protein					
SLAM_phiST45_063	47006	48196	201	+	Hypothetical protein	hypothetical protein AGC_0088 [Escherichia phage Epc7]	100%	6.00E-38	100.00%	YP_001837011.1
SLAM_phiST45_064	48208	49152	945	+	Ligoprotein	ligoprotein [Salmonella phage Stitch]	100%	0	100.00%	YP_001602023.1
SLAM_phiST45_065	49415	70479	1056	+	Nicotinamide nucleotide adenylyltransferase	nicotinamide nucleotide adenylyltransferase [Salmonella phage S114]	100%	0	100.00%	YP_000804033.1
SLAM_phiST45_066	70472	71149	678	+	Nicotinamide ribotide transporter	nicotinamide ribotide transporter PncC [Brevetia mollisima]	100%	3.00E-157	100.00%	WP_134060343.1
SLAM_phiST45_067	71256	71552	297	+	Hypothetical protein	hypothetical protein CPT_Stitch77 [Salmonella phage Stitch]	100%	6.00E-45	99.98%	YP_000160018.1
SLAM_phiST45_068	71604	71607	94	+	(dNA-Sec)(g)					
SLAM_phiST45_069	71783	71789	78	+	(dNA-Mec)(g)					
SLAM_phiST45_070	71798	71983	186	+	Anti-termination protein	anti-termination protein Q18a [Salmonella phage Stitch]	100%	7.00E-35	95.88%	YP_000160017.1
SLAM_phiST45_071	71985	72523	538	+	Hypothetical protein	hypothetical protein HD133_gg154 [Salmonella phage SBB]	100%	3.00E-75	100.00%	YP_000804211.1
SLAM_phiST45_072	72532	72408	77	+	(dNA-Lec)(g)					
SLAM_phiST45_073	72424	72546	123	+	Hypothetical protein	hypothetical protein CPT_Stitch74 [Salmonella phage Stitch]	100%	1.00E-20	100.00%	YP_000160015.1
SLAM_phiST45_074	72568	72766	207	+	Hypothetical protein	hypothetical protein HWC37_gg200 [Salmonella phage vB_Sac5_SB13]	100%	2.00E-39	100.00%	YP_000804037.1
SLAM_phiST45_075	72837	73132	276	+	Hypothetical protein	hypothetical protein HD133_gg159 [Salmonella phage SI16]	100%	5.00E-59	100.00%	YP_000804283.1
SLAM_phiST45_076	73272	73339	88	+	(dNA-Ty)(g)					
SLAM_phiST45_077	73039	73035	77	+	(dNA-Gac)(g)					
SLAM_phiST45_078	73044	74020	77	+	(dNA-Trip)(g)					
SLAM_phiST45_079	74119	74391	273	+	Hypothetical protein	hypothetical protein HWC37_gg148 [Salmonella phage 1-20]	100%	5.00E-40	100.00%	YP_00082259.1
SLAM_phiST45_080	74442	74666	225	+	Hypothetical protein	hypothetical protein B09773_gg172 [Salmonella phage 180208_saf2]	100%	3.00E-45	100.00%	YP_001230881.1
SLAM_phiST45_081	74841	74816	76	+	(dNA-Cy)(g)					
SLAM_phiST45_082	74824	75006	83	+	(dNA-Aac)(g)					
SLAM_phiST45_083	75118	75295	186	+	Hypothetical protein	hypothetical protein CPT_Stitch60 [Salmonella phage Stitch]	100%	8.00E-33	100.00%	YP_000160009.1
SLAM_phiST45_084	75305	75381	77	+	(dNA-Aap)(g)					
SLAM_phiST45_085	75388	75463	76	+	(dNA-Ly)(g)					
SLAM_phiST45_086	75661	75734	74	+	(dNA-Gly)(g)					
SLAM_phiST45_087	76212	76289	78	+	(dNA-Pro)(g)					
SLAM_phiST45_088	76296	76373	78	+	(dNA-Mec)(g)					
SLAM_phiST45_089	76395	76539	145	+	Hypothetical protein	hypothetical protein B09773_gg177 [Salmonella phage 180208_saf2]	100%	2.00E-29	98.15%	YP_000120786.1
SLAM_phiST45_090	76562	76649	79	+	(dNA-Ly)(g)					
SLAM_phiST45_091	76838	76875	318	+	Hypothetical protein	hypothetical protein CPT_Stitch66 [Salmonella phage Stitch]	100%	3.00E-71	98.18%	YP_000160087.1
SLAM_phiST45_092	77189	77182	74	+	(dNA-Val)(g)					
SLAM_phiST45_093	77208	77561	354	+	Hypothetical protein	hypothetical protein HD133_gg144 [Salmonella phage SBB]	100%	3.00E-79	100.00%	YP_000804221.1
SLAM_phiST45_094	78228	78361	74	+	(dNA-Mal)(g)					
SLAM_phiST45_095	78387	78382	76	+	(dNA-Mal)(g)					
SLAM_phiST45_096	78462	78620	219	+	Hypothetical protein	hypothetical protein HD133_gg140 [Salmonella phage SI16]	100%	1.00E-40	98.61%	YP_000804213.1
SLAM_phiST45_097	78628	78708	81	+	(dNA-Lec)(g)					
SLAM_phiST45_098	78833	78874	92	+	(dNA-Sec)(g)					
SLAM_phiST45_099	78862	79071	90	+	(dNA-Sec)(g)					

	0005	0010	76			tRNA-Glu(tig)							
	0067	0021	75			tRNA-Gly(tcc)							
SLAM_phiST45_001	0028	0079	222	+		Hypothetical protein	hypothetical protein CPT_Switch3 [Salmonella phage Switch]	100%	3.00E-46	100.00%		VP_000143099.1	
	0067	0071	75			tRNA-Thr(tgg)							
SLAM_phiST45_002	0076	0100	294	+		Hypothetical protein	hypothetical protein CPT_Switch3 [Salmonella phage Switch]	100%	7.00E-43	98.97%		VP_000143097.1	
	0101	0116	76			tRNA-Ile(gat)							
	0117	0126	74			tRNA-Met(cac)							
SLAM_phiST45_003	0118	0106	360	+		Hypothetical protein	ribonucleotide reductase subunit [Salmonella phage Switch]	100%	4.00E-43	100.00%		VP_000143096.1	
SLAM_phiST45_004	0208	0207	300	+		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	6.00E-48	98.99%		WP_11584836.1	
SLAM_phiST45_005	0262	0267	186	+		Hypothetical protein	hypothetical protein H0733_gg133 [Salmonella phage S100]	100%	6.00E-36	100.00%		VP_000084230.1	
SLAM_phiST45_006	0276	0307	396	+		Hypothetical protein	hypothetical protein H0733_gg127 [Salmonella phage S126]	100%	2.00E-49	100.00%		VP_000085182.1	
SLAM_phiST45_007	0348	0348	273	+		Hypothetical protein	hypothetical protein B07673_gg053 [Salmonella phage 180308_s02]	100%	3.00E-58	100.00%		VP_000120779.1	
SLAM_phiST45_008	0349	0379	300	+		Hypothetical protein	hypothetical protein YZJ13_1_07 [Circobacter phage YZJ1-1.1]	100%	6.00E-45	100.00%		W120717.1	
SLAM_phiST45_009	0475	0469	285	+		Hypothetical protein	hypothetical protein [Brevibacterium melonis]	100%	2.00E-40	100.00%		WP_140404395.1	
SLAM_phiST45_009	0476	0523	348	+		Hypothetical protein	hypothetical protein H0017_gg049 [Salmonella phage S02]	100%	5.00E-77	99.13%		VP_000012185.1	
SLAM_phiST45_001	0529	0507	609	+		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	9.00E-172	100.00%		WP_015300712.1	
SLAM_phiST45_002	0637	0740	733	+		Deoxynucleoside monophosphate kinase	deoxynucleoside monophosphate kinase [Escherichia phage Epp7]	100%	0	100.00%		VP_000183069.1	
SLAM_phiST45_003	0722	0801	600	+		ATP-dependent protease	ATP-dependent protease [Escherichia phage saae132]	100%	5.00E-148	100.00%		VP_000194070.1	
SLAM_phiST45_004	0878	0834	637	+		Helix	helix [Escherichia phage saae132]	100%	2.00E-158	100.00%		VP_000194069.1	
SLAM_phiST45_005	0928	09736	417	+		Hypothetical protein	hypothetical protein CPT_Switch3 [Salmonella phage Switch]	100%	1.00E-94	100.00%		VP_000143079.1	
SLAM_phiST45_006	09812	09219	408	+		Hypothetical protein	hypothetical protein H09C03_gg010 [Salmonella phage 2-3]	100%	6.00E-93	100.00%		VP_000194068.1	
SLAM_phiST45_007	09736	10026	291	+		Thioredoxin	thioredoxin [Salmonella phage S116]	100%	4.00E-43	97.92%		VP_000194067.1	
SLAM_phiST45_008	01127	01007	861	+		Serine/threonine protein phosphatase	serine/threonine protein phosphatase [Salmonella enterica subsp. enterica serovar Derby]	99%	0	99.65%		EDL12308.1	
SLAM_phiST45_009	01007	02355	300	+		Hypothetical protein	hypothetical protein H0733_gg117 [Salmonella phage S100]	100%	1.00E-42	100.00%		VP_000084240.1	
SLAM_phiST45_100	02355	02361	207	+		Ra-like protein	Ra-like protein [Salmonella phage S100]	100%	4.00E-41	100.00%		VP_000084249.1	
SLAM_phiST45_101	02661	03151	591	+		Phosphotransferase	phosphotransferase [Salmonella phage L.V016A]	100%	4.00E-142	100.00%		VP_000084316.1	
SLAM_phiST45_102	03113	02744	432	+		Hypothetical protein	hypothetical protein [Salmonella enterica]	100%	1.00E-109	100.00%		E115700222.1	
SLAM_phiST45_103	02745	04275	531	+		Homing endonuclease	putative homing endonuclease [Salmonella phage S132]	100%	5.00E-128	100.00%		VP_000087081.1	
SLAM_phiST45_104	04342	04093	252	+		Hypothetical protein	hypothetical protein CPT_Switch3 [Salmonella phage Switch]	100%	1.00E-51	100.00%		VP_000143069.1	
SLAM_phiST45_105	04353	04091	399	+		Hypothetical protein	hypothetical protein H0733_gg111 [Salmonella phage S100]	100%	4.00E-90	99.24%		VP_000084241.1	
SLAM_phiST45_106	04088	02408	282	+		Hypothetical protein	hypothetical protein [Salmonella enterica]	100%	5.00E-55	100.00%		E13000000.1	
SLAM_phiST45_107	05561	05833	333	+		Hypothetical protein	hypothetical protein [Brevibacterium melonis]	100%	6.00E-74	100.00%		WP_140404375.1	
SLAM_phiST45_108	06211	06098	460	+		Hypothetical protein	hypothetical protein H05C02_gg003 [Escherichia phage saae132]	100%	5.00E-112	100.00%		VP_000194053.1	
SLAM_phiST45_109	06034	07552	219	+		Hypothetical protein	hypothetical protein H09W02_gg005 [Salmonella phage 3-20]	80%	1.00E-34	100.00%		VP_000194051.1	
SLAM_phiST45_110	07161	07558	198	+		Hypothetical protein	hypothetical protein H09W02_gg005 [Salmonella phage 3-20]	100%	2.00E-38	98.46%		VP_000083093.1	
SLAM_phiST45_111	07588	07922	543	+		Hypothetical protein	hypothetical protein H0733_gg011 [Salmonella phage S100]	100%	6.00E-133	99.44%		VP_000085062.1	
SLAM_phiST45_112	08032	08017	186	+		Hypothetical protein	hypothetical protein B0721A_120 [Salmonella phage B0721A]	100%	5.00E-31	100.00%		A00060007.1	
SLAM_phiST45_113	08017	08038	612	+		Hypothetical protein	hypothetical protein G0808_120 [Salmonella phage G0808]	100%	4.00E-149	98.52%		U0631786.1	
SLAM_phiST45_114	08038	09073	246	+		Hypothetical protein	hypothetical protein WC0333_Y1A_C100005 [Salmonella phage Yiga1PFP]	100%	3.00E-51	98.77%		X0019700.1	
SLAM_phiST45_115	09043	09019	808	+		Hypothetical protein	hypothetical protein B03091_G1_00042 [Escherichia phage vB_Eco-261750]	100%	0	98.31%		Q010990.1	
SLAM_phiST45_116	09179	04973	195	-		Hypothetical protein	hypothetical protein H0734_gg134 [Salmonella phage L.V016A]	100%	1.00E-38	100.00%		VP_000084301.1	
SLAM_phiST45_117	10297	10261	145	-		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	1.00E-77	100.00%		WP_115848376.1	
SLAM_phiST45_118	102751	102603	213	-		Hypothetical protein	hypothetical protein [Salmonella phage P10012]	100%	2.00E-42	100.00%		Q1VC0000.1	
SLAM_phiST45_119	102960	103115	158	-		Hypothetical protein	hypothetical protein AGC_0011 [Escherichia phage Epp7]	100%	1.00E-22	100.00%		VP_000083304.1	
SLAM_phiST45_120	103062	103392	231	-		Hypothetical protein	hypothetical protein H09C02_gg007 [Salmonella phage 1-20]	100%	4.00E-48	100.00%		VP_000082201.1	
SLAM_phiST45_121	103501	103992	492	-		Hypothetical protein	hypothetical protein H09C02_gg005 [Salmonella phage 1-20]	100%	2.00E-113	100.00%		VP_000082200.1	
SLAM_phiST45_122	104053	104070	1020	-		Hypothetical protein	hypothetical protein H09C02_gg005 [Salmonella phage 1-20]	100%	0	99.71%		VP_000082199.1	
SLAM_phiST45_123	104062	106380	219	+		Hypothetical protein	hypothetical protein B07673_gg013 [Salmonella phage 180308_s02]	100%	5.00E-44	100.00%		VP_000120737.1	
SLAM_phiST45_124	106043	106796	232	+		Hypothetical protein	hypothetical protein CPT_Switch3 [Salmonella phage Switch]	100%	3.00E-52	100.00%		VP_000143048.1	
SLAM_phiST45_125	106090	107312	417	+		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	4.00E-92	100.00%		WP_115848322.1	
SLAM_phiST45_126	107371	107598	228	+		Membrane protein	membrane protein [Salmonella phage Switch]	100%	1.00E-43	100.00%		VP_000143046.1	
SLAM_phiST45_127	107707	109371	1065	+		DNA transfer protein	DNA transfer protein [Salmonella phage MET_F1_137_112]	100%	0	98.92%		W1G14561.1	
SLAM_phiST45_128	109429	109702	279	+		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	1.00E-40	98.91%		WP_015300066.1	
SLAM_phiST45_129	109735	110127	393	+		Hypothetical protein	hypothetical protein [Circobacter parvocalensis]	100%	9.00E-91	100.00%		WP_015300065.1	
SLAM_phiST45_130	110211	110943	735	+		Deoxynucleoside 5'-monophosphate	deoxynucleoside 5'-monophosphate [Salmonella phage B011B]	100%	0	100.00%		EQ1K5101.1	

The genome of SLAM_phiST45 was 111,044 bp long, with 130 ORFs and 29 tRNAs. Among these, 55 ORFs (41.9%) were functionally annotated using the BLASTP algorithm. No genes encoding integrases or antibiotic resistance were identified.

Supplementary Table S7. Functional annotation of SLAM_phiST56

ORF	Start	Stop	Length (nt)	Strand	Function	Homology				
						Homology	Query coverage	E value	Pre. Identity	Accession No.
SLAM_phiST56_001	301	414	114	-	Hypothetical protein	hypothetical protein RP51506_110 [Salmonella phage RP51506]	100%	5.00E-17	100.00%	AL361927.1
SLAM_phiST56_002	1357	1365	549	-	Hypothetical protein	hypothetical protein HB204_31 [Salmonella phage vB_SpM_Sp116]	100%	4.00E-132	96.96%	YP_005146276.1
SLAM_phiST56_003	1919	2383	465	-	Hypothetical protein	hypothetical protein AVV43_gp125 [Escherichia phage JH2]	100%	1.00E-100	96.70%	YP_005219508.1
SLAM_phiST56_004	2416	2488	273	-	Hypothetical protein	hypothetical protein [Phage NBEcd04]	100%	4.00E-40	100.00%	Q8N5211.1
SLAM_phiST56_005	2742	2964	225	-	Hypothetical protein	hypothetical protein [Escherichia phage vB_EcoM-LT102]	100%	6.00E-42	96.65%	WV049457.1
SLAM_phiST56_006	3043	3546	504	-	Hypothetical protein	hypothetical protein [Escherichia coli]	100%	1.00E-119	96.20%	EC0497144.1
SLAM_phiST56_007	3845	4426	582	-	Hypothetical protein	hypothetical protein [Escherichia phage vB_EcoM_DE7]	100%	8.00E-142	100.00%	U0349226.1
SLAM_phiST56_008	4763	5054	294	-	Hypothetical protein	hypothetical protein [Escherichia coli]	100%	6.00E-64	100.00%	WP_135115063.1
SLAM_phiST56_009	5459	5857	399	-	Hypothetical protein	hypothetical protein [Phage NBEcd05]	100%	3.00E-52	100.00%	Q8Q4344.1
SLAM_phiST56_010	5909	6373	465	-	Endolysin	endolysin [Escherichia phage HEP5]	100%	7.00E-109	96.70%	W0513334.1
SLAM_phiST56_011	7002	7373	372	-	Hypothetical protein	hypothetical protein [Salmonella phage D1-2]	100%	7.00E-47	100.00%	QCG20845.1
SLAM_phiST56_012	7421	8011	591	-	Hypothetical protein	hypothetical protein AVV43_gp112 [Escherichia phage JH2]	100%	2.00E-139	99.40%	YP_005219535.1
SLAM_phiST56_013	8220	8381	162	-	Hypothetical protein	hypothetical protein P0407_13 [Enterobacteria phage UAR_P0407]	100%	2.00E-30	100.00%	YP_005130864.1
SLAM_phiST56_014	8631	9002	372	+	Hypothetical protein	hypothetical protein P0101_00007 [Salmonella phage FSL_SP_0101]	100%	3.00E-42	99.10%	AGF00772.1
SLAM_phiST56_015	9084	10499	1416	+	RNA-binding protein	RNA-binding protein [Escherichia phage HV02]	100%	0	99.15%	YP_005260408.1
SLAM_phiST56_016	10653	10741	77	-	dRNA-Pro(agg)	HNH binding endonuclease [Salmonella phage GSPY01]	100%	3.00E-101	99.30%	U074073.1
	10749	10826	78	-	dRNA-Gln(xc)					
	10810	10994	77	-	dRNA-Met(xc)					
	11072	11146	75	-	dRNA-Asn(agg)					
	11158	11245	88	-	dRNA-Tyr(xc)					
	11268	11066	429	+						
	11792	11777	76	-	dRNA-Lys(xc)					
	12207	12282	76	-	dRNA-Lys(xc)					
	12207	12363	77	-	dRNA-Met(xc)					
	12366	12440	75	-	dRNA-Ile(agg)					
	12778	12854	77	-	dRNA-Arg(xc)					
	13093	13182	90	-	dRNA-Ser(agg)					
	13439	13514	78	-	dRNA-Leu(agg)					
	13524	13599	76	-	dRNA-Lys(xc)					
	13606	13681	76	-	dRNA-Ala(agg)					
	13608	13742	75	-	dRNA-Gly(xc)					
	13770	13846	77	-	dRNA-Thr(agg)					
	13942	14014	75	-	dRNA-Val(xc)					
	14018	14095	78	-	dRNA-Leu(xc)					
	14031	14176	76	-	dRNA-Arg(agg)					
SLAM_phiST56_017	14034	14991	558	+	Holins	holin [Salmonella phage vB_SJF10]	100%	8.00E-130	97.30%	Q7235249.1
	15000	15075	76	-	dRNA-Gln(agg)					
	15070	15156	79	-	dRNA-Leu(xc)					
	15162	15237	76	-	dRNA-Gln(agg)					
	15200	15344	76	-	dRNA-His(agg)					
	15355	15426	76	-	dRNA-Phe(agg)					
SLAM_phiST56_018	15443	16177	735	+	Hypothetical protein	hypothetical protein [Escherichia phage vB_EcoM-LT102]	100%	4.00E-173	99.50%	W0740475.1
	16170	16271	93	-	dRNA-Ser(agg)					
	16276	16351	76	-	dRNA-Cys(agg)					
SLAM_phiST56_019	16374	16774	201	+	Hypothetical protein	hypothetical protein [Bacteria]	100%	2.00E-37	100.00%	WP_135090963.1
SLAM_phiST56_020	16796	16997	1462	-	Phage terminase large subunit	phage terminase large subunit [Enterococcus myogenes]	100%	0	100.00%	MDN12083.1
SLAM_phiST56_021	16814	16980	1467	+	Perial protein	perial protein [Enterobacteria phage UAR_P0407]	100%	0	100.00%	YP_005150194.1
SLAM_phiST56_022	16900	20300	591	+	Hypothetical protein	hypothetical protein HB204_30 [Salmonella phage vB_SpM_Sp116]	100%	7.00E-117	100.00%	YP_005162209.1
SLAM_phiST56_023	20300	20712	533	+	Head protein	head protein [Escherichia phage vB_EcoM_VpaE1]	100%	2.00E-72	97.00%	YP_005173222.1
SLAM_phiST56_024	16734	22070	1347	+	Signal peptide peptidase	signal peptide peptidase 10p1 [Escherichia coli]	100%	0	99.55%	WP_131074043.1
SLAM_phiST56_025	22067	22450	378	+	Hypothetical protein	hypothetical protein [Salmonella phage N132]	100%	3.00E-46	99.20%	W0730905.1
SLAM_phiST56_026	22450	23590	1107	-	Major head protein	major head protein [Salmonella phage D1-2]	100%	0	99.46%	QCG20828.1
SLAM_phiST56_027	23620	24600	450	+	Adaptase protein	adaptase protein [Escherichia phage vB_EcoM_ESSC06]	100%	5.00E-183	96.66%	UFW67341.1
SLAM_phiST56_028	24600	24533	483	+	Hypothetical protein	hypothetical protein PQ0101_gp116 [Salmonella phage vB_SAg_RP2N13]	100%	1.00E-112	100.00%	YP_010675613.1
SLAM_phiST56_029	25324	26670	1353	-	Tail sheath	tail sheath [Salmonella phage RP5171.1]	100%	0	96.67%	YP_000623577.1
SLAM_phiST56_030	26082	27330	447	+	Vicins structural protein	vicins structural protein [Salmonella phage RP51502]	100%	2.00E-184	99.32%	YP_005124615.1
SLAM_phiST56_031	27161	27000	309	-	Tail assembly chaperone	phage tail assembly chaperone [Escherichia coli]	100%	2.00E-90	100.00%	WP_131009153.1
SLAM_phiST56_032	27812	28053	240	+	Tail assembly chaperone	tail assembly chaperone [Salmonella phage vB_SpM_Sp116]	100%	2.00E-40	96.71%	YP_005163111.1
SLAM_phiST56_033	28051	30270	2229	+	Tail sheath protein	tail sheath protein [Salmonella phage GSPY01]	100%	0	96.65%	U0740731.1
SLAM_phiST56_034	30270	31070	798	+	Endolysin	endolysin [Salmonella phage vB_SAg_RP2N13]	100%	0	97.36%	YP_010675613.1
SLAM_phiST56_035	31070	31417	342	+	Hypothetical protein	hypothetical protein HB204_71 [Salmonella phage vB_SpM_Sp116]	100%	8.00E-70	99.12%	YP_005163103.1
SLAM_phiST56_036	31417	32394	978	+	Receptacle hub	receptacle hub [Salmonella phage Fels01]	100%	0	99.60%	NP_544910.1
SLAM_phiST56_037	32394	33017	624	+	Receptacle spike	receptacle spike [Escherichia phage vB_EcoM_VpaE1]	100%	1.00E-153	100.00%	YP_005147370.1
SLAM_phiST56_038	33017	33430	420	+	Receptacle wedge subunit	receptacle wedge subunit [Escherichia phage vB_EcoM_A0E]	100%	5.00E-97	99.20%	YP_005208253.1
SLAM_phiST56_039	33430	34095	1470	+	Receptacle assembly protein	receptacle assembly protein [Escherichia phage shaden]	100%	0	99.39%	Q8H017277.1
SLAM_phiST56_040	34000	33745	858	+	Receptacle protein	receptacle protein [Salmonella phage RP517W1]	100%	0	100.00%	YP_000621605.1
SLAM_phiST56_041	33745	34067	303	+	Hypothetical protein	hypothetical protein [Escherichia coli]	100%	7.00E-47	100.00%	WP_135115063.1
SLAM_phiST56_042	34070	37236	1167	+	Tail fiber protein	tail fiber protein [Salmonella phage RP517W1]	100%	0	100.00%	YP_000621605.1
SLAM_phiST56_043	37200	30726	2459	+	Tail fiber protein	tail fiber protein [Salmonella phage RP517W1]	100%	0	99.08%	YP_000621605.1
SLAM_phiST56_044	39006	40000	195	+	Phage conserved protein	Phage conserved protein [Salmonella phage Fels01]	100%	6.00E-36	96.44%	NP_544925.1
SLAM_phiST56_045	40001	40372	372	+	Holins	holin [Escherichia phage elex]	100%	1.00E-81	99.19%	Q8H075275.1
SLAM_phiST56_046	40412	41331	900	-	Thymidylate synthase	thymidylate synthase [Salmonella phage RP517W1]	100%	0	100.00%	YP_000621605.1
SLAM_phiST56_047	41333	41058	546	-	Dihydrodolate reductase	dihydrodolate reductase [Escherichia phage P10B11]	100%	6.00E-120	99.45%	Q8J00654.1
SLAM_phiST56_048	42116	42631	516	-	Hypothetical protein	hypothetical protein TD1022_gp074 [Salmonella phage RP517W1]	100%	1.00E-120	100.00%	YP_000621605.1
SLAM_phiST56_049	42645	43004	360	-	Hypothetical protein	hypothetical protein PQ0101_gp092 [Salmonella phage vB_SAg_RP2N13]	100%	2.00E-82	100.00%	YP_010675613.1
SLAM_phiST56_050	42920	43510	213	-	Hypothetical protein	hypothetical protein AVY81_gp091 [Escherichia phage vB_EcoM_AY0145A]	100%	3.00E-42	100.00%	YP_000621605.1
SLAM_phiST56_051	43512	43095	384	-	Hypothetical protein	hypothetical protein TD1022_gp070 [Salmonella phage RP517W1]	100%	4.00E-89	100.00%	YP_000621605.1
SLAM_phiST56_052	44073	45273	1101	-	DNA ligase	DNA ligase [Salmonella phage vB_SpM_Sp116]	100%	0	99.73%	YP_005146333.1
SLAM_phiST56_053	45463	45660	207	-	Hypothetical protein	hypothetical protein OPTSAL01_00013 [Salmonella phage OPT_SAL01]	100%	2.00E-41	96.53%	UFW67306.1
SLAM_phiST56_054	45670	45097	219	-	Hypothetical protein	hypothetical protein SP4_001 [Salmonella phage SP4_MH-2010]	100%	8.00E-45	100.00%	Q8N00050.1
SLAM_phiST56_055	45949	46462	534	-	HNH endonuclease	HNH endonuclease motif containing protein [Salmonella phage vB_SacM_p5521]	100%	3.00E-127	99.44%	U0740425.1
SLAM_phiST56_056	46406	47040	555	-	DNA polymerase	receptacle hub [Salmonella phage RP517W1]	100%	2.00E-132	100.00%	YP_000621672.1
SLAM_phiST56_057	47270	49453	2184	-	DNA polymerase	DNA polymerase [Salmonella phage MBP0406116]	100%	0	99.86%	WJ354231.1
SLAM_phiST56_058	49710	50132	423	+	Hypothetical protein	hypothetical protein HKAMN_ZQ_CDS_0104 [Salmonella phage F G10]	100%	9.00E-97	96.57%	W0707112.1
SLAM_phiST56_059	50134	50934	801	+	Minor tail protein	minor tail protein [Escherichia phage vB_EcoM_AY0145A]	100%	0	96.87%	YP_005208039.1
SLAM_phiST56_060	50996	51730	744	+	Dinucleoside monophosphate kinase	putative dinucleoside monophosphate kinase [Salmonella phage SupYZ001]	100%	5.00E-100	99.19%	Q8N00025.1
SLAM_phiST56_061	51941	53926	1986	+	DNA primase/helicase	DNA primase/helicase [Escherichia phage HK3]	100%	0	99.70%	WY17825.1
SLAM_phiST56_062	54170	54420	150	+	Hypothetical protein	ribonucleoside triphosphate reductase alpha chain [Stigeella phage Z31]	100%	8.00E-25	97.36%	WP_131073300.1
SLAM_phiST56_063	54400	55257	858	+	Hypothetical protein	hypothetical protein [Stigeella phage Z31]	100%	0	100.00%	WP_135360823.1
SLAM_phiST56_064	55320	56366	1047	+	Exonuclease	exonuclease [Salmonella phage SWM-02]	100%	0	96.56%	W5510006.1
SLAM_phiST56_065	56841	57441	591	+	NAD synthetase	NAD synthetase [Salmonella phage Modavirus]	100%	4.00E-110	98.00%	YP_000000393.1
SLAM_phiST56_066	57587	58342	756	+	Phosphoribosyl-ATP pyrophosphohydrolase	putative phosphoribosyl-ATP pyrophosphohydrolase-like protein [Salmonella phage SupYZ001]	100%	0	99.20%	Q8N00054.1
SLAM_phiST56_067	58630	58974	346	+	Hypothetical protein	hypothetical protein andrews_31 [Escherichia phage Andrews]	100%	1.00E-75	96.20%	Q8H07000.1
SLAM_phiST56_068	59021	61255	2235	+	Ribonucleoside triphosphate reductase alpha chain	ribonucleoside triphosphate reductase alpha chain [Stigeella phage Z31]	100%	0	100.00%	Q8H40821.1
SLAM_phiST56_069	61565	62630	1074	+	Ribonucleoside-diphosphate reductase subunit beta	ribonucleoside-diphosphate reductase subunit beta [Escherichia coli]	100%	0	99.72%	E58313092.1
SLAM_phiST56_070	62630	62800	243	+	Glucoamylase	glucoamylase [Salmonella phage vB_SpM_Sp116]	100%	2.00E-52	96.75%	YP_005146333.1
SLAM_phiST56_071	63238	64327	1200	+	Anaerobic ribonucleoside reductase large subunit	ribonucleoside reductase of class III [anaerobic], large subunit [Salmonella phage L27]	100%	0	99.50%	BB12008.1
SLAM_phiST56_072	64754	65508	855	+	Anaerobic ribonucleoside triphosphate reductase	anaerobic ribonucleoside triphosphate reductase [Bacteriophage sp.]	100%	0	99.70%	U0740833.1
SLAM_phiST56_073	65631	65986	356	+	Hypothetical protein	hypothetical protein AVV43_gp013 [Escherichia phage JH2]	100%	3.00E-74	99.10%	YP_005219543.1
SLAM_phiST56_074	66018	66109	132	+	Hypothetical protein	hypothetical protein AVY81_gp013 [Escherichia phage JH2]	100%	5.00E-23	100.00%	U0740836.1
SLAM_phiST56_075	66078	66077	300	-	Hypothetical protein	hypothetical protein ACQ401_gp027 [Escherichia phage vB_SaM_SF041]	100%	6.00E-47	98.99%	YP_005147300.1
SLAM_phiST56_076	66087	67372	408	+	Anaerobic ribonucleoside reductase activating protein	ribonucleoside reductase of class III [anaerobic] activating protein [Enterobacteria phage XTG1]	100%	1.00E-117	100.00%	AN232533.1
SLAM_phiST56_077	67439	67687	249	+	Hypothetical protein	hypothetical protein [Escherichia phage vB_EcoM_UJ100]	100%	2.00E-50	98.78%	W0740731.1
SLAM_phiST56_078	67609	68010	312	+	HNH endonuclease	putative HNH endonuclease [Enterobacteria phage vB_EcoM_JM130]	100%	8.00E-40	100.00%	A0701406.1

SLAM_phiST56_879	68573	68853	279	+	Hypothetical protein	hypothetical protein SP187_08245 [Salmonella phage FSL SP-187]	100%	7.00E-62	100.00%	AGF09493.1
SLAM_phiST56_880	68863	69744	882	+	Ribose phosphate diphosphokinase	ribose phosphate diphosphokinase [Escherichia coli]	100%	0	99.66%	WP_193115396.1
SLAM_phiST56_881	69791	71572	1782	+	Nicotinamide phosphoribosyltransferase	nicotinamide phosphoribosyltransferase [Escherichia phage HK3]	100%	0	98.99%	WP_193117724.1
SLAM_phiST56_882	71626	71963	336	+	Hypothetical protein	hypothetical protein [Escherichia coli]	100%	2.00E-75	100.00%	WP_193115394.1
SLAM_phiST56_883	72148	74514	2367	+	RIIA lysis inhibitor	RIIA lysis inhibitor [Escherichia phage JN81]	100%	0	99.37%	QJ872545.1
SLAM_phiST56_884	74594	75783	1189	+	RIIB lysis inhibitor	putative rIIB lysis inhibitor [Escherichia phage vR_SonM p5321]	100%	0	98.18%	UGL68388.1
SLAM_phiST56_885	75884	76332	549	+	Lysin	putative lysin [Escherichia phage skodon]	100%	2.00E-129	99.45%	QJ8847394.1
SLAM_phiST56_886	77836	77580	465	+	Hypothetical protein	hypothetical protein Faf01p011 [Escherichia phage Faf01C1]	100%	4.00E-184	99.35%	NP_544787.1
SLAM_phiST56_887	77553	77990	348	+	Rz-like spanin	Rz-like spanin [Escherichia phage HY 82]	100%	5.00E-78	99.13%	VP_005284989.1
SLAM_phiST56_888	78868	78529	279	+	Hypothetical protein	hypothetical protein [Salmonella enterica subsp. enterica serovar Enteritidis]	100%	3.00E-49	100.00%	EEM3738965.1
SLAM_phiST56_889	78633	78860	228	+	Hypothetical protein	hypothetical protein [Salmonella phage D1-2]	100%	1.00E-45	100.00%	QJCF28748.1
SLAM_phiST56_890	79854	79839	786	+	O-acetyl-ADP-ribrose deacetylase	O-acetyl-ADP-ribrose deacetylase [Salmonella phage D1-2]	100%	0	99.62%	QJCF28748.1
SLAM_phiST56_891	79826	88878	153	+	Phage protein	phage protein [Escherichia phage L27]	100%	2.00E-25	98.00%	B8J27815.1
SLAM_phiST56_892	88858	88756	207	+	Hypothetical protein	hypothetical protein BPS1558_38 [Salmonella phage BPS1558]	100%	2.00E-41	100.00%	ALN519315.1
SLAM_phiST56_893	88845	81225	381	+	Hypothetical protein	hypothetical protein PQD19_g0829 [Salmonella phage vR_SAg-BP9213]	100%	3.00E-86	100.00%	VP_010676246.1
SLAM_phiST56_894	81314	81684	291	+	Hypothetical protein	hypothetical protein FD122_g010 [Salmonella phage BPS17W1]	100%	2.00E-61	100.00%	VP_009621622.1
SLAM_phiST56_895	81895	82287	513	+	Hypothetical protein	hypothetical protein FD122_g080 [Salmonella phage BPS17W1]	100%	2.00E-122	100.00%	VP_009621621.1
SLAM_phiST56_896	82289	82923	333	+	Hypothetical protein	hypothetical protein FD122_g0807 [Salmonella phage BPS17W1]	100%	3.00E-72	100.00%	VP_009621619.1
SLAM_phiST56_897	83812	83284	273	+	Hypothetical protein	hypothetical protein FD122_g0807 [Salmonella phage BPS17W1]	100%	3.00E-72	100.00%	VP_009621619.1
SLAM_phiST56_898	83378	83774	405	+	Hypothetical protein	hypothetical protein FD122_g080 [Salmonella phage BPS17W1]	100%	9.00E-49	100.00%	VP_009621618.1
SLAM_phiST56_899	83876	84079	204	+	Hypothetical protein	hypothetical protein FD122_g080 [Salmonella phage BPS17W1]	100%	5.00E-92	100.00%	VP_009621617.1
SLAM_phiST56_900	84172	84714	543	+	Hypothetical protein	hypothetical protein FD122_g080 [Salmonella phage BPS17W1]	100%	2.00E-129	100.00%	VP_009621615.1
SLAM_phiST56_901	84781	85814	234	+	Hypothetical protein	hypothetical protein BPS1552_126 [Salmonella phage BPS1552]	100%	2.00E-48	100.00%	VP_0095124787.1
SLAM_phiST56_902	85182	85443	342	+	Hypothetical protein	hypothetical protein FD122_g080 [Salmonella phage BPS17W1]	100%	1.00E-78	100.00%	VP_009621613.1
SLAM_phiST56_903	85869	85917	249	+	Hypothetical protein	hypothetical protein [Bacteriophage sp.]	100%	3.00E-54	100.00%	UVX17781.1
SLAM_phiST56_904	86665	86779	114	+	Hypothetical protein	hypothetical protein BPS1558_118 [Salmonella phage BPS1558]	100%	5.00E-17	100.00%	ALN519317.1

The genome of SLAM_phiST56 was 87,026 bp long, with 104 ORFs and 26 tRNAs. Among these, 52 ORFs (50.0%) were functionally annotated using the BLASTP algorithm. No genes encoding integrases or antibiotic resistance were identified.

Supplementary Table S8. Genome based BLASTN analysis using SLAM_phiST45

No.	Species	Subfamily	Max score	Total score	Query coverage	E value	Per. Identity	Acc. Length	Accession
1	Phage NBSal002, complete genome	<i>Markadamsvirinae</i>	89532	1.98E+05	95%	0	98.01%	120250	MN994501.1
2	<i>Salmonella</i> phage BSP22A, complete genome	<i>Markadamsvirinae</i>	89430	1.82E+05	95%	0	97.98%	110741	KY787212.1
3	<i>Salmonella</i> phage 9-29, complete genome	<i>Markadamsvirinae</i>	88575	1.79E+05	94%	0	97.97%	110776	MN218190.1
4	<i>Salmonella</i> phage SE18, complete genome	<i>Markadamsvirinae</i>	85794	1.82E+05	95%	0	98.53%	110795	MK972717.1
5	<i>Enterobacteria</i> phage EPS7, complete genome	<i>Markadamsvirinae</i>	84274	1.66E+05	92%	0	96.73%	111382	NC_010583.1
6	<i>Escherichia coli</i> phage NG_S8 DNA, complete sequence	<i>Markadamsvirinae</i>	76557	1.78E+05	92%	0	98.71%	108459	LC788711.1
7	<i>Salmonella</i> phage 3-29, complete genome	<i>Markadamsvirinae</i>	76258	1.78E+05	93%	0	97.95%	110377	NC_048145.1
8	<i>Salmonella</i> phage BD13, complete genome	<i>Markadamsvirinae</i>	75981	1.89E+05	92%	0	98.55%	121769	OL451946.1
9	<i>Salmonella</i> phage 1-29, complete genome	<i>Markadamsvirinae</i>	75024	1.83E+05	95%	0	98.07%	111636	NC_048811.1
10	<i>Escherichia</i> phage PSa2, complete genome	<i>Markadamsvirinae</i>	73819	1.66E+05	91%	0	96.68%	110539	OL770310.1
11	<i>Salmonella</i> phage Seafire, complete genome	<i>Markadamsvirinae</i>	73276	1.69E+05	91%	0	97.69%	111851	NC_048110.1
12	<i>Salmonella</i> phage faergetype, complete genome	<i>Markadamsvirinae</i>	72945	1.70E+05	91%	0	97.55%	110183	NC_048867.1
13	<i>Escherichia</i> phage SuperGirl strain Bas29, complete genome	<i>Markadamsvirinae</i>	70354	1.64E+05	92%	0	97.43%	110821	MZ501105.1
14	<i>Salmonella</i> phage JN-S202001, complete genome	<i>Markadamsvirinae</i>	68332	1.66E+05	91%	0	98.50%	111256	OL502173.1
15	<i>Salmonella</i> phage 1-19, complete genome	<i>Markadamsvirinae</i>	57651	1.79E+05	94%	0	98.43%	110775	NC_048819.1
16	<i>Salmonella</i> phage 8sent65, complete genome	<i>Markadamsvirinae</i>	57345	1.61E+05	91%	0	96.37%	112133	MT653145.1
17	<i>Salmonella</i> phage vB_SenS_SB6, complete genome	<i>Markadamsvirinae</i>	56142	1.63E+05	91%	0	96.80%	112311	MK809530.1
18	<i>Salmonella</i> phage 1Sgal2PP, complete genome	<i>Markadamsvirinae</i>	56041	1.59E+05	91%	0	96.74%	113352	PP779479.1
19	<i>Salmonella</i> phage S116, complete genome	<i>Markadamsvirinae</i>	45858	1.80E+05	96%	0	98.47%	110664	NC_048007.1
20	<i>Salmonella</i> phage SH9, partial genome	<i>Markadamsvirinae</i>	45783	1.78E+05	95%	0	98.42%	111607	NC_047999.1

A BLASTN search was conducted using the whole-genome sequence of SLAM_phiST45. Based on the maximum score, the top 20 closely related species were identified and organized. In addition, the subfamilies of these species, as specified in NCBI taxonomy, are summarized.

Supplementary Table S9. Genome based BLASTN analysis using SLAM_phiST56

No.	Species	Subfamily	Max score	Total score	Query coverage	E value	Per. Identity	Acc. Length	Accession
1	<i>Salmonella</i> phage D1-2, complete genome	<i>Ounavirinae</i>	85172	1.42E+05	97%	0	96.71%	86878	MN481367.1
2	<i>Salmonella</i> phage NJ12, complete genome	<i>Ounavirinae</i>	53511	1.41E+05	96%	0	98.46%	87366	OQ845959.1
3	<i>Salmonella</i> phage GSP193, complete genome	<i>Ounavirinae</i>	53262	1.37E+05	96%	0	97.75%	87084	ON855038.1
4	<i>Salmonella</i> phage BPS17S6, complete genome	<i>Ounavirinae</i>	51675	1.42E+05	95%	0	98.10%	87628	MG646671.1
5	<i>Salmonella</i> phage BPS15S6, complete genome	<i>Ounavirinae</i>	51675	1.42E+05	95%	0	98.10%	87609	MG646670.1
6	<i>Salmonella</i> phage BPS17W1, complete genome	<i>Ounavirinae</i>	51675	1.42E+05	95%	0	98.10%	87609	NC_042097.1
7	<i>Salmonella</i> phage vB_SAg-RPN213, complete genome	<i>Ounavirinae</i>	43659	1.37E+05	95%	0	96.43%	86124	NC_071010.1
8	<i>Salmonella</i> phage BPSELC-1, complete genome	<i>Ounavirinae</i>	43473	1.39E+05	96%	0	97.69%	86996	MN227145.1
9	<i>Salmonella</i> phage UAB_69, complete genome	<i>Ounavirinae</i>	42451	1.26E+05	93%	0	96.21%	87060	OL656108.1
10	<i>Salmonella</i> phage BPS17L1, complete genome	<i>Ounavirinae</i>	41901	1.31E+05	94%	0	96.83%	84916	NC_042096.1
11	<i>Salmonella</i> phage SUT_S720, complete genome	<i>Ounavirinae</i>	39685	1.29E+05	94%	0	96.55%	86621	OQ871555.1
12	<i>Enterobacteria</i> phage KhF1, complete genome	<i>Ounavirinae</i>	38932	1.25E+05	93%	0	95.86%	88356	KT184313.1
13	<i>Escherichia</i> phage ZX4221, complete genome	<i>Ounavirinae</i>	38799	1.27E+05	94%	0	94.59%	89258	OR498728.1
14	<i>Escherichia</i> phage vB_EcoM_ASO1B, complete genome	<i>Ounavirinae</i>	38749	1.25E+05	93%	0	95.72%	89496	MZ726792.1
15	<i>Escherichia</i> phage VpaE1_ev035 genome assembly, chromosome: 1	<i>Ounavirinae</i>	38485	1.18E+05	90%	0	95.52%	88002	LR699048.1
16	<i>Salmonella</i> phage GEC_vB_BS, complete genome	<i>Ounavirinae</i>	38463	1.25E+05	93%	0	96.05%	85840	MW006475.1
17	<i>Salmonella</i> phage GEC_vB_B1, complete genome	<i>Ounavirinae</i>	38463	1.25E+05	94%	0	96.05%	87369	MW006474.1
18	<i>Enterobacteria</i> phage KhF3, complete genome	<i>Ounavirinae</i>	38452	1.23E+05	93%	0	95.50%	88016	KT184315.1
19	<i>Escherichia</i> phage vB_EcoM_ASO1A, complete genome	<i>Ounavirinae</i>	38416	1.25E+05	93%	0	95.48%	87613	MZ726791.1
20	<i>Salmonella</i> phage GEC_vB_NS7, complete genome	<i>Ounavirinae</i>	38385	1.25E+05	94%	0	95.99%	86886	MW006482.1

A BLASTN search was conducted using the whole-genome sequence of SLAM_phiST56. Based on the maximum score, the top 20 closely related species were identified and organized. In addition, the subfamilies of these species, as specified in the NCBI for Biotechnology Information taxonomy, are summarized.