

Supplemental Table S1. Genomic Features of bacteriophages in this study

No.	phage	Isolation source of host bacteria	Genome size(kb)	Total CDSs	GC(%)	tRNA	Reference	GenBank Accession
1	<i>Yersinia</i> vB_YpeM_MHS112	<i>Yersinia pestis</i>	170.51	303	40.5	2	In this study	OP750247
2	<i>Yersinia</i> vB_YpeM_GMS130	<i>Yersinia pestis</i>	168.55	289	40.5	3	In this study	OP750248
3	<i>Aeromonas</i> phage 44RR2.8t	<i>Aeromonas salmonicida</i>	173.59	269	43.9	17	[1]	NC_005135
4	<i>Aeromonas</i> phage 65	<i>Aeromonas salmonicida</i>	235.23	454	37.2	16	[1]	NC_015251
5	<i>Aeromonas</i> phage Aeh1	<i>Aeromonas hydrophila</i>	233.23	375	42.8	23	[1]	NC_005260
6	<i>Enterobacteria</i> phage AR1	<i>Escherichia coli</i> O157:H7	167.44	291	35.3	10	[2]	NC_027983
7	<i>Enterobacteria</i> phage JS10	<i>Escherichia coli</i> K12	171.45	268	39.5	3	[3]	NC_012741
8	<i>Enterobacteria</i> phage JS98	<i>Escherichia coli</i>	170.52	269	39.5	3	[4]	NC_010105
9	<i>Enterobacteria</i> phage RB43	<i>Enterobacteriaceae</i>	180.500		43.2	1		NC_007023
10	<i>Enterobacteria</i> phage RB49	<i>Escherichia coli</i>	164.02	279	40.4	0	[1, 5]	NC_005066
11	<i>Enterobacteria</i> phage RB69	<i>Escherichia coli</i>	167.56	275	37.7	2	[1, 5]	NC_004928
12	<i>Enterobacteria</i> phage T4	<i>Escherichia coli</i>	168.9	288	35.3	8	[6]	NC_000866
13	<i>Vibrio</i> phage KVP40	<i>Vibrio parahaemolyticus</i>	244.83	415	42.6	29	[7]	NC_005083
14	<i>Vibrio</i> phage nt-1	<i>Vibrio natriegens</i> HER1138	247.51	405	41.3		[8, 9]	NC_021529
15	<i>Yersinia</i> phage JC221	<i>Yersinia pestis</i> EV76-CN	174.93	274	41.2		[10]	MN508817
16	<i>Yersinia</i> phage phiD1	<i>Yersinia pestis</i>	167.06	277	35.5		[11]	NC_027353
17	<i>Yersinia</i> phage PST		167.79	280	35.3	9	[12]	NC_027404
18	<i>Yersinia</i> phage PYPS2T	<i>Yersinia pseudotuberculosis</i>	169.604		35.4			NC_054944
19	<i>Yersinia</i> phage PYps5T	<i>Yersinia pseudotuberculosis</i>	169.38	267	35.4			MT828552
20	<i>Yersinia</i> phage PYps10T	<i>Yersinia pseudotuberculosis</i>	169.49	270	35.4			MT828553

21	<i>Yersinia</i> phage PYps11T	<i>Yersinia pseudotuberculosis</i>	169.49	268	35.4			MT515751
22	<i>Yersinia</i> phage PYps14T	<i>Yersinia pseudotuberculosis</i>	166.94	267	35.4			MT526905
23	<i>Yersinia</i> phage PYps15T	<i>Yersinia pseudotuberculosis</i>	166.93	267	35.4			MT515752
24	<i>Yersinia</i> phage PYps32T	<i>Yersinia pseudotuberculosis</i>	165.73	263	35.5			MT515753
25	<i>Yersinia</i> phage PYps35T	<i>Yersinia pseudotuberculosis</i>	166.97	264	35.4			MT515754
26	<i>Yersinia</i> phage PYps47T	<i>Yersinia pseudotuberculosis</i>	165.78	262	35.5			MT515755
27	<i>Yersinia</i> phage PYps55T	<i>Yersinia pseudotuberculosis</i>	167.71	267	35.4			MT515756
28	<i>Yersinia</i> phage v_YepM_ZN18	<i>Yersinia pseudotuberculosis</i>	167.95	275	35.4	11		NC_054945
29	<i>Yersinia</i> phage fPS-2	<i>Yersinia pseudotuberculosis</i>	169.06		35.3		[13]	NC_054943
30	<i>Yersinia</i> phage fPS-65	<i>Yersinia pseudotuberculosis</i>	167.06		35.3		[13]	NC_055724
31	<i>Yersinia</i> phage fPS-90	<i>Yersinia pseudotuberculosis</i>	167.13		35.3		[13]	NC_055723
32	<i>Shigella</i> phage SP18	<i>Shigella sonnei</i>	170.61	289	40.4	3	[14]	NC_014595
33	<i>Enterobacteria</i> phage vB_EcoM_VR20	<i>Escherichia coli</i>	170.34	288	40.4	2	[15]	NC_028894
34	<i>Enterobacteria</i> phage vB_EcoM_VR25	<i>Escherichia coli</i>	170.82	295	40.4	2	[16]	NC_028925
35	<i>Enterobacteria</i> phage vB_EcoM_VR26	<i>Escherichia coli</i>	171.54	292	40.2	1	[16]	NC_028957
36	<i>Enterobacteria</i> phage vB_EcoM_VR7	<i>Escherichia coli</i>	169.29	294	40.3	1	[15]	NC_014792
37	<i>Escherichia</i> phage CJ20	<i>Escherichia coli</i>	169.88	307	40.4			MT533174
38	<i>Escherichia</i> phage DK-13	<i>Escherichia coli</i>	172.28	292	40.2			MT611523
39	<i>Escherichia</i> phage MN01	enterotoxigenic <i>Escherichia Coli</i>	172.58	290	40.4	2		MT129652
40	<i>Escherichia</i> phage P479	<i>Escherichia coli</i> 187	172.03	288	40.3		[17]	MW269952
41	<i>Escherichia</i> phage P896	<i>Escherichia coli</i>	170.66	293	40.4	2		OL451225
42	<i>Escherichia</i> phage PSD2001	<i>Escherichia coli</i>	172.18	285	40.3			OK254198
43	<i>Escherichia</i> phage UPEC01	<i>Escherichia coli</i>	169.80	307	40.4		[18]	MW233709

		<i>S3Lug</i>						
44	<i>Escherichia</i> phage UPEC07	<i>Escherichia coli</i>	170.00	308	40.3		[18]	MW250787
45	<i>Escherichia</i> phage vB_EcoM_RZ	<i>Escherichia coli</i> str. K-12 substr. MG1655	170.32	291	40.1			MW598459
46	<i>Escherichia</i> virus TH15	<i>Escherichia coli</i>	171.59		40.3			MT446392
47	<i>Escherichia</i> virus TH22	<i>Escherichia coli</i>	170.09		40.3			MT446396
48	<i>Escherichia</i> virus TH40	<i>Escherichia coli</i>	171.73		40.3			MT446411
49	<i>Escherichia</i> virus TH41	<i>Escherichia coli</i>	170.56		40.5			MT446412
50	<i>Escherichia</i> virus TH44	<i>Escherichia coli</i>	171.08		40.6			MT446415
51	<i>Escherichia</i> virus TH54	<i>Escherichia coli</i>	170.99		40.4			MT446420
52	<i>Escherichia</i> virus TH55	<i>Escherichia coli</i>	170.39		40.3			MT446421
53	<i>Escherichia</i> virus TH57	<i>Escherichia coli</i>	171.23		40.4			MT446422
54	<i>Vibrio</i> phage KVP20 major capsid protein	<i>Vibrio</i>					[19]	D83517
55	<i>Enterobacteria</i> phage Tula major capsid protein (g23)	<i>Escherichia coli</i>					[1]	AF221994
56	<i>Enterobacteria</i> phage KC69 major capsid protein (g23)	<i>Escherichia coli</i>						AF221999

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Microbiol Resour Announc. 2022;11(3):e0081121. Epub 2022/03/10. doi: 10.1128/mra.00811-21. PubMed PMID: 35262399; PubMed Central PMCID: PMC8928767.

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