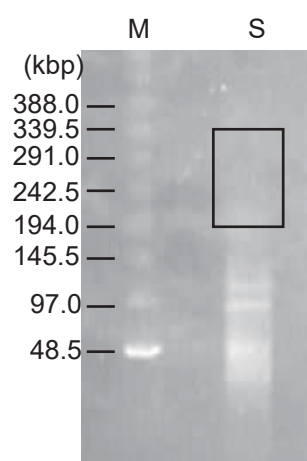
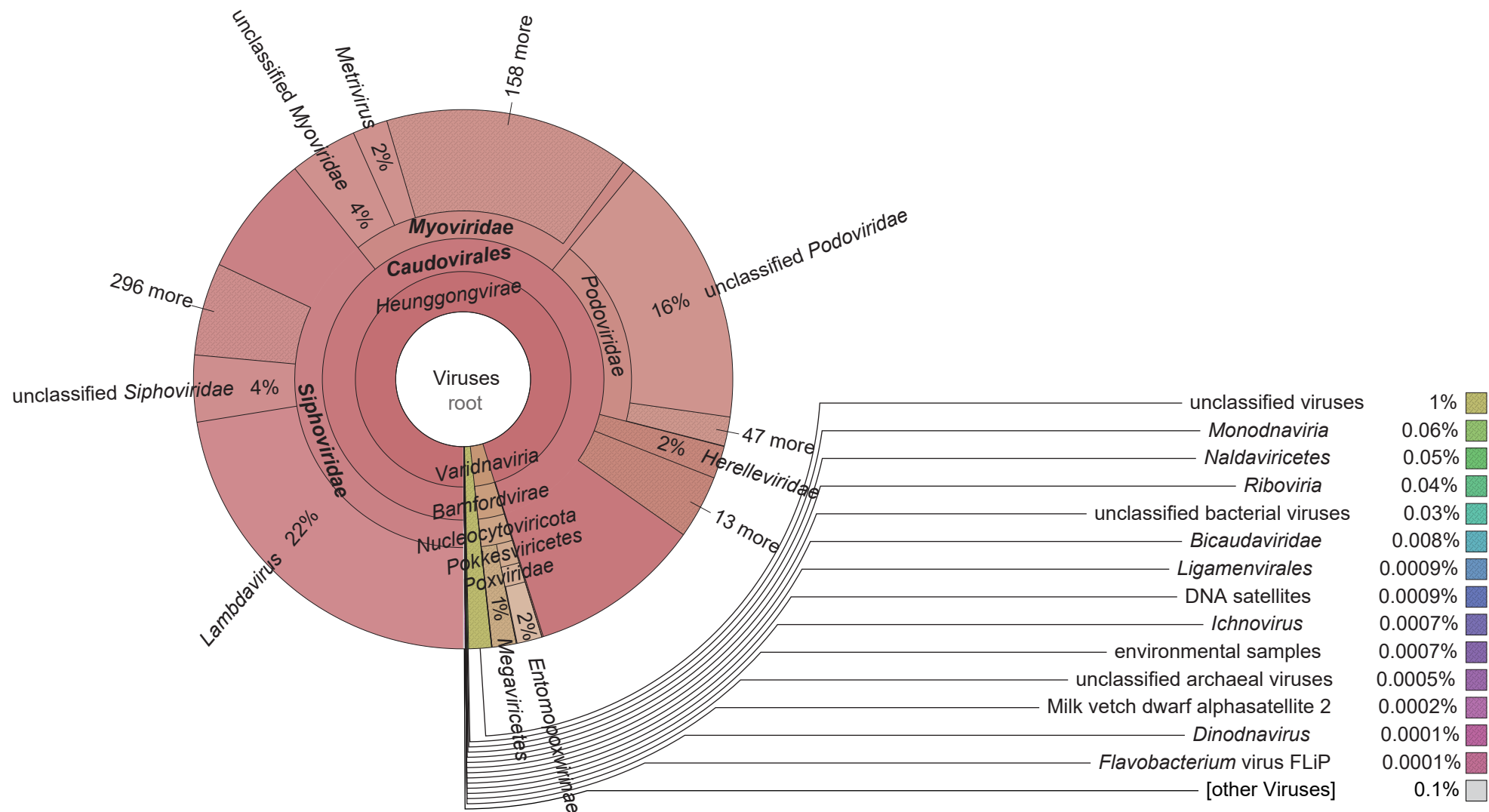
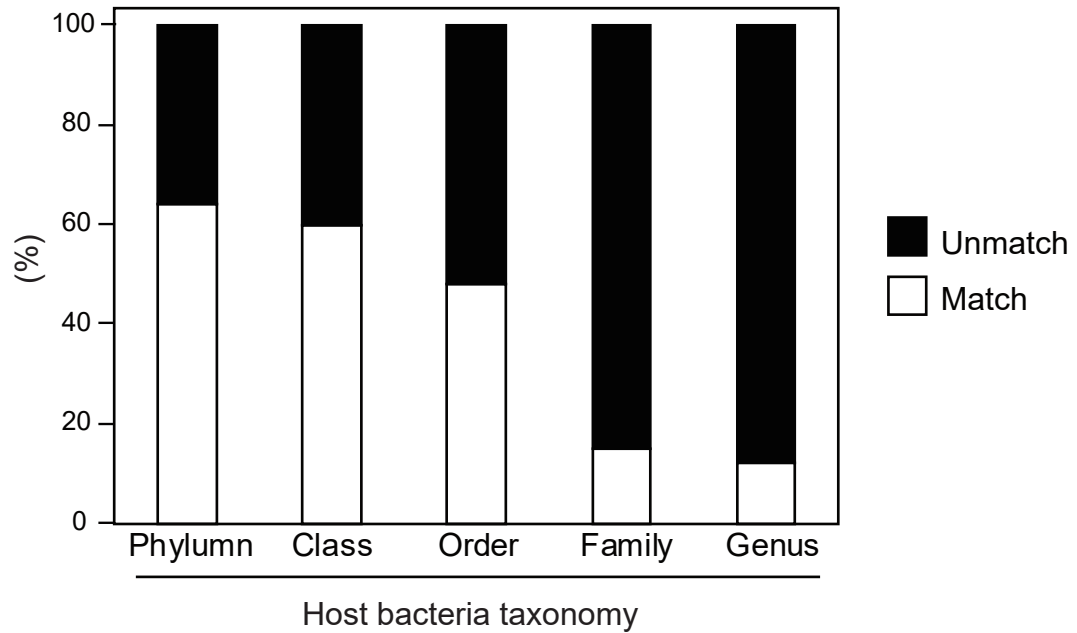




Supplementary Fig. 1. Pulsed-field gel electrophoregram of sewage sample. “M” and “S” represent the marker standard of the lambda ladder and the sewage sample, respectively. The molecular standard sizes are shown in the leftmost part of the figure. The black box in lane “S” is the excised area for DNA extraction.



Supplementary Fig. 2. Graphical representation of the relative abundance of viral diversity visualized using the Krona visualization tool implemented in Kaiju v1.8.2. The population of order *Caudovirales* contained the families of *Myoviridae* at 22%, *Podoviridae* at 18%, *Siphoviridae* at 39%, *Herelleviridae* at 2%, *Schitoviridae* at 1%, and other viral classification at 13%.



Supplementary Fig. 3. The match percentage of jumbo phage bacterial host taxonomy at phylum, class, order, family, and genus levels between actual and predicted host. The bacterial host taxonomy was predicted by VirHostMatcher-Net using 371 jumbo phage sequences, and host bacteria were successfully produced from 302 phage sequences. The host bacteria were compared with the predicted host bacteria, and the match percentage of bacterial taxonomy at phylum, class, order, family, and genus levels between actual and predicted host were calculated. The match rates at phylum, class, order, family, and genus levels are 63.9%, 59.9%, 48.0%, 14.9%, and 12.3%, respectively.

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
1	<i>Prevotella</i> phage Lak-B8	<i>Myoviridae</i>	GCA_004379655.1	Complete	0.55	26.0	MK250027.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/655/GCA_004379655.1_ASM437965v1
2	<i>Prevotella</i> phage Lak-B7	<i>Myoviridae</i>	GCA_004379635.1	Complete	0.55	26.0	MK250026.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/635/GCA_004379635.1_ASM437963v1
3	<i>Prevotella</i> phage Lak-B4	<i>Myoviridae</i>	GCA_004379575.1	Complete	0.55	26.0	MK250023.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/575/GCA_004379575.1_ASM437957v1
4	<i>Prevotella</i> phage Lak-B9	<i>Myoviridae</i>	GCA_004379675.1	Complete	0.55	26.0	MK250028.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/675/GCA_004379675.1_ASM437967v1
5	<i>Prevotella</i> phage Lak-B2	<i>Myoviridae</i>	GCA_004379535.1	Complete	0.55	26.0	MK250021.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/535/GCA_004379535.1_ASM437953v1
6	<i>Prevotella</i> phage Lak-B1	<i>Myoviridae</i>	GCA_004379515.1	Complete	0.55	26.0	MK250020.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/515/GCA_004379515.1_ASM437951v1
7	<i>Prevotella</i> phage Lak-B3	<i>Myoviridae</i>	GCA_004379555.1	Complete	0.55	26.0	MK250022.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/555/GCA_004379555.1_ASM437955v1
8	<i>Prevotella</i> phage Lak-B6	<i>Myoviridae</i>	GCA_004379615.1	Complete	0.55	26.0	MK250025.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/615/GCA_004379615.1_ASM437961v1
9	<i>Prevotella</i> phage Lak-B5	<i>Myoviridae</i>	GCA_004379595.1	Complete	0.54	26.1	MK250024.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/595/GCA_004379595.1_ASM437959v1
10	<i>Prevotella</i> phage Lak-A1	<i>Myoviridae</i>	GCA_004379455.1	Complete	0.54	25.9	MK250017.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/455/GCA_004379455.1_ASM437945v1
11	<i>Prevotella</i> phage Lak-A1	<i>Myoviridae</i>	GCA_004379415.1	Complete	0.54	25.9	MK250015.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/415/GCA_004379415.1_ASM437941v1
12	<i>Prevotella</i> phage Lak-A1	<i>Myoviridae</i>	GCA_004379475.1	Complete	0.54	25.9	MK250018.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/475/GCA_004379475.1_ASM437947v1
13	<i>Prevotella</i> phage Lak-A1	<i>Myoviridae</i>	GCA_004379435.1	Complete	0.54	25.9	MK250016.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/435/GCA_004379435.1_ASM437943v1
14	<i>Prevotella</i> phage Lak-A2	<i>Myoviridae</i>	GCA_004379495.1	Complete	0.54	26.0	MK250019.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/495/GCA_004379495.1_ASM437949v1
15	<i>Prevotella</i> phage Lak-C1	<i>Myoviridae</i>	GCA_004379695.1	Complete	0.54	25.8	MK250029.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/379/695/GCA_004379695.1_ASM437969v1
16	<i>Bacillus</i> phage G	<i>Myoviridae</i>	GCA_000917535.1	Complete	0.50	29.9	JN638751.1	2011/9/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/917/535/GCA_000917535.1_ViralProj240716
17	<i>Agrobacterium</i> phage Atu_ph07	<i>Myoviridae</i>	GCA_002628245.1	Complete	0.49	37.1	MF403008.1	2017/8/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/628/245/GCA_002628245.1_ASM262824v1
18	uncultured <i>Caudovirales</i> phage	Other	GCA_902993965.1	Complete	0.45	32.9	LR797252.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/993/965/GCA_902993965.1_UFOv-RH-23may17-C34
19	<i>Salicola</i> phage SCTP-2	<i>Myoviridae</i>	GCA_002625545.1	Complete	0.44	30.0	MF360958.1	2017/8/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/625/545/GCA_002625545.1_ASM262554v1
20	<i>Myoviridae</i> sp. isolate ctbc_4	<i>Myoviridae</i>	GCA_003657725.1	Complete	0.42	27.4	MH622943.1	2018/8/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/657/725/GCA_003657725.1_ASM365772v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
21	<i>Xanthomonas</i> phage XacN1	<i>Myoviridae</i>	GCA_003173815.1	Complete	0.38	50.4	AP018399.1	2017/10/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/173/815/GCA_003173815.1_ASM317381v1
22	<i>Escherichia</i> phage BF17	<i>Myoviridae</i>	GCA_020474835.1	Complete	0.38	35.4	MW822008.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/474/835/GCA_020474835.1_ASM2047483v1
23	<i>Pectinobacterium</i> phage vB_PcaM_CBB	<i>Myoviridae</i>	GCA_002609265.1	Complete	0.38	35.9	KU574722.1	2016/12/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/609/265/GCA_002609265.1_ASM260926v1
24	uncultured <i>Caudovirales</i> phage	Other	GCA_902983245.1	Complete	0.37	48.0	LR796167.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/983/245/GCA_902983245.1_UFOv-Jr-11may16-C5
25	<i>Escherichia</i> phage vB_EcoM_G17	<i>Myoviridae</i>	GCA_004521135.1	Complete	0.37	34.3	MK327931.1	2019/3/25	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/521/135/GCA_004521135.1_ASM452113v1
26	uncultured <i>Caudovirales</i> phage	Other	GCA_902983795.1	Complete	0.37	39.4	LR796233.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/983/795/GCA_902983795.1_UFOv-Jr-28aug17-C25
27	uncultured <i>Caudovirales</i> phage	Other	GCA_902983425.1	Complete	0.37	39.3	LR796187.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/983/425/GCA_902983425.1_UFOv-Jr-25may17-C5
28	uncultured <i>Caudovirales</i> phage	Other	GCA_903231945.1	Complete	0.37	39.3	LR798231.1	2020/5/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/903/231/945/GCA_903231945.1_UFOv-Jr-28jun17-C15
29	uncultured <i>Caudovirales</i> phage	Other	GCA_902984185.1	Complete	0.37	36.0	LR796274.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/984/185/GCA_902984185.1_UFOv-Jr-7aug17-C16
30	uncultured <i>Caudovirales</i> phage	Other	GCA_903232095.1	Complete	0.36	40.5	LR798243.1	2020/5/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/903/232/095/GCA_903232095.1_UFOv-Jr-28jun17-C16
31	<i>Cronobacter</i> phage vB_CsaM_GAP32	<i>Myoviridae</i>	GCA_000898015.1	Complete	0.36	35.6	JN882285.1	2012/10/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/898/015/GCA_000898015.1_ViralProj179410
32	<i>Erwinia</i> phage pEa_SNUABM_12	<i>Myoviridae</i>	GCA_014892715.1	Complete	0.36	34.4	MT939486.1	2020/10/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/892/715/GCA_014892715.1_ASM1489271v1
33	<i>Erwinia</i> phage pEa_SNUABM_49	<i>Myoviridae</i>	GCA_020476755.1	Complete	0.36	34.4	MW879344.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/755/GCA_020476755.1_ASM2047675v1
34	<i>Serratia</i> phage BF	<i>Myoviridae</i>	GCA_002619745.1	Complete	0.36	34.4	KY630187.1	2017/3/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/745/GCA_002619745.1_ASM261974v1
35	<i>Erwinia</i> phage pEa_SNUABM_50	<i>Myoviridae</i>	GCA_014892735.1	Complete	0.36	34.4	MT939488.1	2020/10/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/892/735/GCA_014892735.1_ASM1489273v1
36	<i>Erwinia</i> phage pEa_SNUABM_44	<i>Myoviridae</i>	GCA_020476695.1	Complete	0.36	34.5	MW879343.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/695/GCA_020476695.1_ASM2047669v1
37	<i>Erwinia</i> phage pEa_SNUABM_47	<i>Myoviridae</i>	GCA_014892725.1	Complete	0.36	34.5	MT939487.1	2020/10/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/892/725/GCA_014892725.1_ASM1489272v1
38	<i>Erwinia</i> phage pEa_SNUABM_19	<i>Myoviridae</i>	GCA_020476665.1	Complete	0.36	34.5	MW879342.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/665/GCA_020476665.1_ASM2047666v1
39	<i>Escherichia</i> phage Ecwhy_1	<i>Myoviridae</i>	GCA_004146585.1	Complete	0.35	35.6	MH791411.1	2019/2/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/146/585/GCA_004146585.1_ASM414658v1
40	<i>Yersinia</i> phage fHe-Yen9-04	<i>Myoviridae</i>	GCA_002990485.1	Complete	0.35	31.6	LT960551.1	2017/10/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/990/485/GCA_002990485.1_ASM299048v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
41	<i>Escherichia</i> phage UB	<i>Myoviridae</i>	GCA_003341455.1	Complete	0.35	34.0	MH383160.1	2018/7/21	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/341/455/GCA_003341455.1_ASM334145v1
42	<i>Escherichia</i> phage vB_EcoM_phAPEC6	<i>Myoviridae</i>	GCA_006529615.1	Complete	0.35	34.1	MK817115.1	2019/6/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/529/615/GCA_006529615.1_ASM652961v1
43	<i>Yersinia</i> phage fHe-Yen9-03	<i>Myoviridae</i>	GCA_002990515.1	Complete	0.35	31.7	LT960552.1	2017/10/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/990/515/GCA_002990515.1_ASM299051v1
44	<i>Escherichia</i> virus TH47	<i>Myoviridae</i>	GCA_013348585.1	Complete	0.35	35.1	MT446416.1	2020/6/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/013/348/585/GCA_013348585.1_ASM1334858v1
45	<i>Salmonella</i> phage Munch	<i>Myoviridae</i>	GCA_004015485.1	Complete	0.35	35.5	MK268344.1	2019/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/015/485/GCA_004015485.1_ASM401548v1
46	<i>Vibrio</i> phage V07	<i>Myoviridae</i>	GCA_012361095.1	Complete	0.35	43.1	MT135025.1	2020/4/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/012/361/095/GCA_012361095.1_ASM1236109v1
47	<i>Salmonella</i> phage 7t3	<i>Myoviridae</i>	GCA_006083215.1	Complete	0.35	35.6	MK773491.1	2019/6/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/083/215/GCA_006083215.1_ASM608321v1
48	<i>Salmonella</i> phage SE_PL	<i>Myoviridae</i>	GCA_011067555.1	Complete	0.35	35.6	MT001829.1	2020/3/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/011/067/555/GCA_011067555.1_ASM1106755v1
49	uncultured <i>Caudovirales</i> phage	Other	GCA_902996485.1	Complete	0.35	39.2	LR797503.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/996/485/GCA_902996485.1_UFOv-RH-9nov16-C4
50	<i>Escherichia</i> phage 121Q	<i>Myoviridae</i>	GCA_000926855.1	Complete	0.35	34.1	KM507819.1	2014/10/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/926/855/GCA_000926855.1_ViralProj266768
51	<i>Escherichia</i> phage PBECO 4	<i>Myoviridae</i>	GCA_001041035.1	Complete	0.35	34.1	KC295538.1	2013/1/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/041/035/GCA_001041035.1_ViralProj287965
52	<i>Escherichia</i> phage vB_Eco_slurp01	<i>Myoviridae</i>	GCA_900094095.1	Complete	0.35	34.1	LT603033.1	2016/8/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/900/094/095/GCA_900094095.1_vB_Eco_slurp01_ass
53	<i>Escherichia</i> phage SP27	<i>Myoviridae</i>	GCA_008033345.1	Complete	0.35	34.2	LC494302.1	2019/8/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/008/033/345/GCA_008033345.1_ASM803334v1
54	<i>Klebsiella</i> phage Muenster	<i>Myoviridae</i>	GCA_014857015.1	Complete	0.35	31.9	MT708547.1	2020/10/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/857/015/GCA_014857015.1_ASM1485701v1
55	<i>Klebsiella</i> phage K64-1	<i>Myoviridae</i>	GCA_001041755.1	Complete	0.35	31.7	AB897757.1	2014/12/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/041/755/GCA_001041755.1_ViralProj287963
56	<i>Klebsiella</i> phage vB_KleM_RaK2	<i>Myoviridae</i>	GCA_000903335.1	Complete	0.35	31.7	JQ513383.1	2012/2/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/903/335/GCA_000903335.1_ViralProj181223
57	<i>Ralstonia</i> phage RsoM2USA	<i>Myoviridae</i>	GCA_018603535.1	Complete	0.34	41.4	MG752970.1	2021/5/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/603/535/GCA_018603535.1_ASM1860353v1
58	uncultured <i>Caudovirales</i> phage	Other	GCA_902989045.1	Complete	0.34	40.3	LR796758.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/989/045/GCA_902989045.1_UFOv-RE-4nov15-C9
59	uncultured <i>Caudovirales</i> phage	Other	GCA_902989195.1	Complete	0.34	40.3	LR796776.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/989/195/GCA_902989195.1_UFOv-RE-9nov16-C10
60	uncultured <i>Caudovirales</i> phage	Other	GCA_902992585.1	Complete	0.34	40.3	LR797099.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/992/585/GCA_902992585.1_UFOv-RH-20APR16-C10

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
61	uncultured <i>Caudovirales</i> phage	Other	GCA_902996605.1	Complete	0.34	40.3	LR797502.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/996/605/GCA_902996605.1_UFOv-RH-9nov16-C6
62	uncultured <i>Caudovirales</i> phage	Other	GCA_903064445.1	Complete	0.33	40.8	LR797824.1	2020/5/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/903/064/445/GCA_903064445.1_UFOv-Jr-25may17-C9
63	uncultured <i>Caudovirales</i> phage	Other	GCA_902984985.1	Complete	0.33	43.1	LR796341.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/984/985/GCA_902984985.1_UFOv-RE-15aug16-C2
64	<i>Caulobacter</i> phage CcrBL9	<i>Siphoviridae</i>	GCA_003443295.1	Complete	0.32	63.7	MH588546.1	2018/9/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/443/295/GCA_003443295.1_ASM344329v1
65	<i>Burkholderia</i> phage FLC9	<i>Myoviridae</i>	GCA_021355105.1	Complete	0.32	56.0	LC667451.1	2021/12/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/021/355/105/GCA_021355105.1_ASM2135510v1
66	<i>Caulobacter</i> phage CcrSC	<i>Siphoviridae</i>	GCA_003443315.2	Complete	0.32	64.2	MH588547.2	2018/9/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/443/315/GCA_003443315.2_ASM344331v2
67	<i>Pseudomonas</i> phage 201phi2-1	<i>Myoviridae</i>	GCA_000875305.1	Complete	0.32	45.3	EU197055.1	2008/6/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/875/305/GCA_000875305.1_ViralProj30097
68	<i>Pseudomonas</i> phage PhiPA3	<i>Myoviridae</i>	GCA_001502095.1	Complete	0.31	47.7	HQ630627.1	2011/6/8	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/502/095/GCA_001502095.1_ViralProj307764
69	<i>Pseudomonas</i> phage Phabio	<i>Myoviridae</i>	GCA_002624965.1	Complete	0.31	43.0	MF042360.1	2017/6/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/624/965/GCA_002624965.1_ASM262496v1
70	<i>Xanthomonas</i> phage Xoo-sp13	<i>Myoviridae</i>	GCA_013364725.1	Complete	0.31	40.9	MN047793.1	2020/6/21	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/013/364/725/GCA_013364725.1_ASM1336472v1
71	<i>Caulobacter</i> phage CcrPW	<i>Siphoviridae</i>	GCA_003443275.1	Complete	0.31	62.2	MH588545.1	2018/9/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/443/275/GCA_003443275.1_ASM344327v1
72	<i>Xanthomonas</i> phage vB_XciM_LucasX	<i>Myoviridae</i>	GCA_018388955.1	Complete	0.31	54.9	MW825358.1	2021/5/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/388/955/GCA_018388955.1_ASM1838895v1
73	uncultured <i>Caudovirales</i> phage	Other	GCA_902983945.1	Complete	0.31	41.0	LR796237.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/983/945/GCA_902983945.1_UFOv-Jr-28aug17-C38
74	<i>Pseudomonas</i> phage Psa21	<i>Myoviridae</i>	GCA_004340405.1	Complete	0.31	43.1	MK552327.1	2019/3/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/340/405/GCA_004340405.1_ASM434040v1
75	<i>Serratia</i> phage KpLz_1_41	<i>Myoviridae</i>	GCA_010702105.1	Complete	0.31	45.7	MN871447.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/105/GCA_010702105.1_ASM1070210v1
76	<i>Pseudomonas</i> phage PA1C	<i>Myoviridae</i>	GCA_004785505.1	Complete	0.30	43.6	MK599315.1	2019/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/785/505/GCA_004785505.1_ASM478550v1
77	<i>Serratia</i> phage KpXa_1	<i>Myoviridae</i>	GCA_010702215.1	Complete	0.30	45.7	MN871449.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/215/GCA_010702215.1_ASM1070221v1
78	<i>Serratia</i> phage KpYy_2_45	<i>Myoviridae</i>	GCA_010702325.1	Complete	0.30	45.7	MN871451.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/325/GCA_010702325.1_ASM1070232v1
79	<i>Pseudomonas</i> phage vB_PaeM_PS119XW	<i>Myoviridae</i>	GCA_008375575.1	Complete	0.30	43.6	MN103543.1	2019/9/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/008/375/575/GCA_008375575.1_ASM837557v1
80	<i>Serratia</i> phage KpZh_LPS_45	<i>Myoviridae</i>	GCA_010702445.1	Complete	0.30	45.7	MN871453.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/445/GCA_010702445.1_ASM1070244v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
81	<i>Serratia</i> phage KpSz_1	<i>Myoviridae</i>	GCA_010702175.1	Complete	0.30	45.7	MN871448.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/175/GCA_010702175.1_ASM1070217v1
82	<i>Serratia</i> phage KpZh_1	<i>Myoviridae</i>	GCA_010702375.1	Complete	0.30	45.7	MN871452.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/375/GCA_010702375.1_ASM1070237v1
83	<i>Klebsiella</i> phage KpLz-2_45	<i>Myoviridae</i>	GCA_010702075.1	Complete	0.30	45.7	MN871446.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/702/075/GCA_010702075.1_ASM1070207v1
84	uncultured <i>Caudovirales</i> phage	Other	GCA_902983925.1	Complete	0.29	31.6	LR796235.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/983/925/GCA_902983925.1_UFOv-Jr-28aug17-C39
85	<i>Erwinia</i> phage pEa_SNUABM_48	<i>Myoviridae</i>	GCA_020476725.1	Complete	0.29	49.5	MW879340.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/725/GCA_020476725.1_ASM2047672v1
86	<i>Erwinia</i> phage pEa_SNUABM_37	<i>Myoviridae</i>	GCA_020476585.1	Complete	0.29	49.5	MW845760.1	2021/7/27	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/585/GCA_020476585.1_ASM2047658v1
87	<i>Vibrio</i> phage vB_VmeM-Yong MS31	<i>Myoviridae</i>	GCA_009769835.1	Complete	0.29	45.9	MK308676.1	2019/12/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/769/835/GCA_009769835.1_ASM976983v1
88	<i>Vibrio</i> phage vB_VmeM-Yong XC32	<i>Myoviridae</i>	GCA_009769895.1	Complete	0.29	45.9	MK308675.1	2019/12/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/769/895/GCA_009769895.1_ASM976989v1
89	<i>Vibrio</i> phage vB_VmeM-Yong XC31	<i>Myoviridae</i>	GCA_009769875.1	Complete	0.29	45.9	MK308674.1	2019/12/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/769/875/GCA_009769875.1_ASM976987v1
90	<i>Vibrio</i> phage BONAISHI	<i>Myoviridae</i>	GCA_003441475.1	Complete	0.29	42.2	MH595538.1	2018/8/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/441/475/GCA_003441475.1_ASM344147v1
91	<i>Salmonella</i> phage vB_SalM_SA002	<i>Myoviridae</i>	GCA_014131285.1	Complete	0.29	48.8	MN445183.1	2020/8/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/131/285/GCA_014131285.1_ASM1413128v1
92	<i>Pseudomonas</i> phage vB_PaeM_PA5oct	<i>Myoviridae</i>	GCA_006516655.1	Complete	0.29	33.3	MK797984.1	2019/4/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/516/655/GCA_006516655.1_ASM651665v1
93	<i>Vibrio</i> phage vB_pir03	<i>Myoviridae</i>	GCA_014319855.1	Complete	0.29	43.6	MT811961.1	2020/8/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/319/855/GCA_014319855.1_ASM1431985v1
94	<i>Pseudomonas</i> phage OBP	<i>Myoviridae</i>	GCA_000896635.1	Complete	0.28	43.5	JN627160.1	2011/12/17	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/896/635/GCA_000896635.1_ViralProj81003
95	<i>Pseudomonas</i> phage U1B	<i>Myoviridae</i>	GCA_020484685.1	Complete	0.28	36.9	MT995927.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/484/685/GCA_020484685.1_ASM2048468v1
96	<i>Pseudomonas</i> phage U5	<i>Myoviridae</i>	GCA_020473375.1	Complete	0.28	36.9	MT995928.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/473/375/GCA_020473375.1_ASM2047337v1
97	<i>Pseudomonas</i> phage T2P	<i>Myoviridae</i>	GCA_020484695.1	Complete	0.28	36.9	MT995926.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/484/695/GCA_020484695.1_ASM2048469v1
98	<i>Pseudomonas</i> phage PA7	<i>Myoviridae</i>	GCA_019333575.1	Complete	0.28	36.8	MZ444140.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/019/333/575/GCA_019333575.1_ASM1933357v1
99	<i>Pseudomonas</i> phage Lu11	<i>Myoviridae</i>	GCA_000897175.1	Complete	0.28	50.9	JQ768459.1	2012/5/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/897/175/GCA_000897175.1_ViralProj167656
100	<i>Pseudomonas</i> phage phiKZ	<i>Myoviridae</i>	GCA_000842965.1	Complete	0.28	36.8	AF399011.1	2002/2/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/842/965/GCA_000842965.1_ViralProj14251

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
101	<i>Pseudomonas</i> phage vB_PA32_GUMS	<i>Myoviridae</i>	GCA_018310595.1	Complete	0.28	36.9	MN563784.1	2021/5/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/310/595/GCA_018310595.1_ASM1831059v1
102	<i>Caulobacter</i> phage CcrColossus	<i>Siphoviridae</i>	GCA_000899635.1	Complete	0.28	62.2	JX100810.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/899/635/GCA_000899635.1_ViralProj179419
103	<i>Ralstonia</i> phage RP12	<i>Myoviridae</i>	GCA_002617345.1	Complete	0.28	53.4	AP017924.1	2016/12/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/617/345/GCA_002617345.1_ASM261734v1
104	<i>Pseudomonas</i> phage SL2	<i>Myoviridae</i>	GCA_002956015.1	Complete	0.28	36.9	MF805716.1	2017/11/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/956/015/GCA_002956015.1_ASM295601v1
105	<i>Pseudomonas</i> phage KTN4	<i>Myoviridae</i>	GCA_002607225.1	Complete	0.28	36.9	KU521356.1	2016/6/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/607/225/GCA_002607225.1_ASM260722v1
106	<i>Pseudomonas</i> phage PaSz-1_45_270k	<i>Myoviridae</i>	GCA_010706105.1	Complete	0.28	36.9	MN871480.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/706/105/GCA_010706105.1_ASM1070610v1
107	<i>Pseudomonas</i> phage fnug	<i>Myoviridae</i>	GCA_012837215.1	Complete	0.28	36.9	MT133560.1	2020/4/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/012/837/215/GCA_012837215.1_ASM1283721v1
108	<i>Pseudomonas</i> phage PaZh_1	<i>Myoviridae</i>	GCA_010706115.1	Complete	0.28	36.9	MN871489.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/706/115/GCA_010706115.1_ASM1070611v1
109	<i>Pseudomonas</i> phage Noxifer	<i>Myoviridae</i>	GCA_002625005.1	Complete	0.28	53.5	MF063068.1	2017/6/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/625/005/GCA_002625005.1_ASM262500v1
110	<i>Vibrio</i> phage vB_VmeM-Yong MS32	<i>Myoviridae</i>	GCA_009769855.1	Complete	0.28	45.9	MK308677.1	2019/12/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/769/855/GCA_009769855.1_ASM976985v1
111	<i>Ralstonia</i> phage RP31	<i>Myoviridae</i>	GCA_002617365.1	Complete	0.28	53.3	AP017925.1	2016/12/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/617/365/GCA_002617365.1_ASM261736v1
112	<i>Edwardsiella</i> virus pEtSU	<i>Myoviridae</i>	GCA_004800915.1	Complete	0.28	43.2	MK689364.1	2019/4/17	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/800/915/GCA_004800915.1_ASM480091v1
113	<i>Serratia</i> phage vB_SmaM_2050HW	<i>Myoviridae</i>	GCA_002628125.1	Complete	0.28	46.8	MF285618.1	2017/9/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/628/125/GCA_002628125.1_ASM262812v1
114	<i>Serratia</i> phage vB_SmaM_Yaphecito	<i>Myoviridae</i>	GCA_016455735.1	Complete	0.28	46.8	MW021758.1	2020/12/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/455/735/GCA_016455735.1_ASM1645573v1
115	<i>Erwinia</i> phage AH06	<i>Myoviridae</i>	GCA_020495965.1	Complete	0.28	48.1	MZ501268.1	2021/8/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/495/965/GCA_020495965.1_ASM2049596v1
116	<i>Erwinia</i> phage vB_EamM_MadMel	<i>Myoviridae</i>	GCA_002957755.1	Complete	0.28	49.7	MG655269.1	2017/12/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/957/755/GCA_002957755.1_ASM295775v1
117	<i>Serratia</i> phage vB_SmaM_Haymo	<i>Myoviridae</i>	GCA_021356055.1	Complete	0.27	46.8	OL539468.1	2021/12/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/021/356/055/GCA_021356055.1_ASM2135605v1
118	<i>Staphylococcus</i> phage Machias	<i>Myoviridae</i>	GCA_016759145.1	Complete	0.27	24.8	MW349128.1	2021/1/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/759/145/GCA_016759145.1_ASM1675914v1
119	<i>Serratia</i> phage Moabite	<i>Myoviridae</i>	GCA_006384735.1	Complete	0.27	46.8	MK994515.1	2019/6/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/384/735/GCA_006384735.1_ASM638473v1
120	<i>Erwinia</i> phage vB_EamM_Mortimer	<i>Myoviridae</i>	GCA_002957765.1	Complete	0.27	49.8	MG655270.1	2017/12/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/957/765/GCA_002957765.1_ASM295776v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
121	<i>Microcystis</i> phage MaAM05	<i>Siphoviridae</i>	GCA_017121825.1	Complete	0.27	54.2	MW495066.1	2021/2/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/017/121/825/GCA_017121825.1_ASM1712182v1
122	<i>Erwinia</i> phage Rebecca	<i>Myoviridae</i>	GCA_004521635.1	Complete	0.27	49.8	MK514281.1	2019/3/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/521/635/GCA_004521635.1_ASM452163v1
123	<i>Erwinia</i> phage vB_EamM_Deimos-Minion	<i>Myoviridae</i>	GCA_002624325.1	Complete	0.27	49.9	KU886225.1	2016/6/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/624/325/GCA_002624325.1_ASM262432v1
124	<i>Erwinia</i> phage vB_EamM_Special G	<i>Myoviridae</i>	GCA_002624385.1	Complete	0.27	49.8	KU886222.1	2016/6/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/624/385/GCA_002624385.1_ASM262438v1
125	<i>Serratia</i> phage BUCT660	<i>Myoviridae</i>	GCA_020523075.1	Complete	0.27	46.8	OK040170.1	2021/10/17	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/523/075/GCA_020523075.1_ASM2052307v1
126	<i>Erwinia</i> phage pEa_SNUABM_54	<i>Myoviridae</i>	GCA_020476785.1	Complete	0.27	48.2	MW879341.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/785/GCA_020476785.1_ASM2047678v1
127	<i>Erwinia</i> phage vB_EamM_Desertfox	<i>Myoviridae</i>	GCA_002957745.1	Complete	0.27	49.9	MG655268.1	2017/12/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/957/745/GCA_002957745.1_ASM295774v1
128	<i>Erwinia</i> phage vB_EamM_Bosolaphorus	<i>Myoviridae</i>	GCA_002957735.1	Complete	0.27	49.8	MG655267.1	2017/12/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/957/735/GCA_002957735.1_ASM295773v1
129	<i>Erwinia</i> phage vB_EamM_RAY	<i>Myoviridae</i>	GCA_002624345.1	Complete	0.27	49.9	KU886224.1	2016/6/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/624/345/GCA_002624345.1_ASM262434v1
130	<i>Erwinia</i> phage vB_EamM_Simmy50	<i>Myoviridae</i>	GCA_002624365.1	Complete	0.27	49.9	KU886223.1	2016/6/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/624/365/GCA_002624365.1_ASM262436v1
131	<i>Erwinia</i> phage Ea35-70	<i>Myoviridae</i>	GCA_000914635.1	Complete	0.27	49.9	KF806589.1	2014/2/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/914/635/GCA_000914635.1_ViralProj240017
132	uncultured <i>Caudovirales</i> phage	Other	GCA_902996175.1	Complete	0.27	36.2	LR797474.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/996/175/GCA_902996175.1_UFOv-RH-9nov16-C16
133	<i>Serratia</i> phage KpHz_2	<i>Myoviridae</i>	GCA_010701985.1	Complete	0.27	45.1	MN871445.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/701/985/GCA_010701985.1_ASM1070198v1
134	<i>Serratia</i> phage KpGz_1	<i>Myoviridae</i>	GCA_010701915.1	Complete	0.27	45.9	MN871444.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/701/915/GCA_010701915.1_ASM1070191v1
135	<i>Staphylococcus</i> phage PALS_2	<i>Myoviridae</i>	GCA_017347775.1	Complete	0.27	25.1	MN091626.1	2021/3/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/017/347/775/GCA_017347775.1_ASM1734777v1
136	<i>Erwinia</i> phage pEa_SNUABM_5	<i>Myoviridae</i>	GCA_016759125.1	Complete	0.27	48.9	MW366843.1	2021/1/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/759/125/GCA_016759125.1_ASM1675912v1
137	<i>Erwinia</i> phage pEa_SNUABM_28	<i>Myoviridae</i>	GCA_020488435.1	Complete	0.27	49.5	MZ443783.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/435/GCA_020488435.1_ASM2048843v1
138	<i>Erwinia</i> phage pEa_SNUABM_40	<i>Myoviridae</i>	GCA_020488515.1	Complete	0.27	49.5	MZ443780.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/515/GCA_020488515.1_ASM2048851v1
139	<i>Erwinia</i> phage pEa_SNUABM_1	<i>Myoviridae</i>	GCA_020488355.1	Complete	0.27	49.4	MZ443776.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/355/GCA_020488355.1_ASM2048835v1
140	<i>Erwinia</i> phage pEa_SNUABM_16	<i>Myoviridae</i>	GCA_020488365.1	Complete	0.27	49.6	MZ443782.1	2021/9/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/365/GCA_020488365.1_ASM2048836v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
141	<i>Staphylococcus</i> phage MarsHill	<i>Myoviridae</i>	GCA_016653775.1	Complete	0.27	25.2	MW248466.1	2021/1/13	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/653/775/GCA_016653775.1_ASM1665377v1
142	<i>Pseudomonas</i> phage vB_PaeM_kmuB	<i>Myoviridae</i>	GCA_015245195.1	Complete	0.27	37.0	MW057919.1	2020/11/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/015/245/195/GCA_015245195.1_ASM1524519v1
143	<i>Erwinia</i> phage vB_EamM_Alexandra	<i>Myoviridae</i>	GCA_003308555.1	Complete	0.27	50.1	MH248138.1	2018/7/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/308/555/GCA_003308555.1_ASM330855v1
144	<i>Erwinia</i> phage pEa_SNUABM_3	<i>Myoviridae</i>	GCA_020488445.1	Complete	0.27	49.5	MZ443770.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/445/GCA_020488445.1_ASM2048844v1
145	<i>Erwinia</i> phage pEa_SNUABM_18	<i>Myoviridae</i>	GCA_020488385.1	Complete	0.27	49.6	MZ443784.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/385/GCA_020488385.1_ASM2048838v1
146	<i>Erwinia</i> phage pEa_SNUABM_32	<i>Myoviridae</i>	GCA_020488465.1	Complete	0.27	49.2	MZ443774.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/465/GCA_020488465.1_ASM2048846v1
147	<i>Erwinia</i> phage pEa_SNUABM_20	<i>Myoviridae</i>	GCA_020488405.1	Complete	0.27	49.5	MZ443771.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/405/GCA_020488405.1_ASM2048840v1
148	<i>Erwinia</i> phage pEa_SNUABM_23	<i>Myoviridae</i>	GCA_020488425.1	Complete	0.27	49.5	MZ443772.1	2021/9/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/425/GCA_020488425.1_ASM2048842v1
149	<i>Erwinia</i> phage pEa_SNUABM_7	<i>Myoviridae</i>	GCA_020488175.1	Complete	0.27	49.0	MZ475896.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/175/GCA_020488175.1_ASM2048817v1
150	<i>Pseudomonas</i> phage pPa_SNUABM_DT01	<i>Myoviridae</i>	GCA_017903995.1	Complete	0.27	56.1	MW735835.1	2021/4/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/017/903/995/GCA_017903995.1_ASM1790399v1
151	<i>Staphylococcus</i> phage Madawaska	<i>Myoviridae</i>	GCA_016759155.1	Complete	0.27	25.1	MW349129.1	2021/1/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/759/155/GCA_016759155.1_ASM1675915v1
152	<i>Erwinia</i> phage pEa_SNUABM_2	<i>Myoviridae</i>	GCA_020488395.1	Complete	0.27	49.4	MZ443786.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/395/GCA_020488395.1_ASM2048839v1
153	<i>Erwinia</i> phage pEa_SNUABM_39	<i>Myoviridae</i>	GCA_020488505.1	Complete	0.27	49.4	MZ443787.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/505/GCA_020488505.1_ASM2048850v1
154	<i>Erwinia</i> phage pEa_SNUABM_22	<i>Myoviridae</i>	GCA_020488415.1	Complete	0.27	49.6	MZ443785.1	2021/9/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/415/GCA_020488415.1_ASM2048841v1
155	<i>Erwinia</i> phage pEa_SNUABM_21	<i>Myoviridae</i>	GCA_020487905.1	Complete	0.27	49.0	MZ475897.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/487/905/GCA_020487905.1_ASM2048790v1
156	<i>Erwinia</i> phage pEa_SNUABM_13	<i>Myoviridae</i>	GCA_020487885.1	Complete	0.26	48.9	MZ475891.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/487/885/GCA_020487885.1_ASM2048788v1
157	<i>Erwinia</i> phage pEa_SNUABM_34	<i>Myoviridae</i>	GCA_020488045.1	Complete	0.26	49.0	MZ475892.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/045/GCA_020488045.1_ASM2048804v1
158	<i>Erwinia</i> phage pEa_SNUABM_14	<i>Myoviridae</i>	GCA_020487895.1	Complete	0.26	49.0	MZ475895.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/487/895/GCA_020487895.1_ASM2048789v1
159	<i>Erwinia</i> phage pEa_SNUABM_17	<i>Myoviridae</i>	GCA_020488375.1	Complete	0.26	49.0	MZ443777.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/375/GCA_020488375.1_ASM2048837v1
160	<i>Erwinia</i> phage pEa_SNUABM_45	<i>Myoviridae</i>	GCA_020488095.1	Complete	0.26	49.0	MZ475893.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/095/GCA_020488095.1_ASM2048809v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
161	<i>Erwinia</i> phage pEa_SNUABM_46	<i>Myoviridae</i>	GCA_020488145.1	Complete	0.26	49.0	MZ475894.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/145/GCA_020488145.1_ASM2048814v1
162	<i>Burkholderia</i> phage BcepSaruman	<i>Myoviridae</i>	GCA_004771375.1	Complete	0.26	58.1	MK552140.1	2019/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/771/375/GCA_004771375.1_ASM477137v1
163	<i>Erwinia</i> phage pEa_SNUABM_33	<i>Myoviridae</i>	GCA_020488475.1	Complete	0.26	49.3	MZ443779.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/475/GCA_020488475.1_ASM2048847v1
164	<i>Staphylococcus</i> phage vB_SauM-UFV_DC4	<i>Myoviridae</i>	GCA_020496005.1	Complete	0.26	25.0	MZ779063.1	2021/9/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/496/005/GCA_020496005.1_ASM2049600v1
165	<i>Erwinia</i> phage pEa_SNUABM_25	<i>Myoviridae</i>	GCA_020488015.1	Complete	0.26	49.0	MZ475898.1	2021/8/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/015/GCA_020488015.1_ASM2048801v1
166	<i>Burkholderia</i> phage BcepSauron	<i>Myoviridae</i>	GCA_005394215.1	Complete	0.26	58.1	MK552141.1	2019/4/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/005/394/215/GCA_005394215.1_ASM539421v1
167	<i>Erwinia</i> phage AH04	<i>Myoviridae</i>	GCA_020495955.1	Complete	0.26	43.3	MZ501267.1	2021/8/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/495/955/GCA_020495955.1_ASM2049595v1
168	<i>Yersinia</i> phage phiR1-37	<i>Myoviridae</i>	GCA_000895615.1	Complete	0.26	32.5	AJ972879.2	2005/6/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/895/615/GCA_000895615.1_ViralProj76739
169	<i>Erwinia</i> phage pEa_SNUABM_35	<i>Myoviridae</i>	GCA_020488485.1	Complete	0.26	49.2	MZ443788.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/485/GCA_020488485.1_ASM2048848v1
170	<i>Erwinia</i> phage pEa_SNUABM_36	<i>Myoviridae</i>	GCA_020488495.1	Complete	0.26	49.2	MZ443789.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/495/GCA_020488495.1_ASM2048849v1
171	<i>Dickeya</i> phage vB_DsoM_AD1	<i>Myoviridae</i>	GCA_003568515.1	Complete	0.26	49.4	MH460463.1	2018/9/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/568/515/GCA_003568515.1_ASM356851v1
172	<i>Erwinia</i> phage vB_EamM_Y3	<i>Myoviridae</i>	GCA_002955045.1	Complete	0.26	47.2	KY984068.1	2017/12/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/955/045/GCA_002955045.1_ASM295504v1
173	<i>Erwinia</i> phage pEp_SNUABM_52	<i>Myoviridae</i>	GCA_020488525.1	Complete	0.26	47.2	MZ443769.1	2021/8/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/525/GCA_020488525.1_ASM2048852v1
174	<i>Staphylococcus</i> phage vB_StaM_SA1	<i>Myoviridae</i>	GCA_016836355.1	Complete	0.26	26.8	MW218148.1	2021/2/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/836/355/GCA_016836355.1_ASM1683635v1
175	<i>Aeromonas</i> phage LAh10	<i>Myoviridae</i>	GCA_006863975.1	Complete	0.26	47.5	MK838116.1	2019/7/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/863/975/GCA_006863975.1_ASM686397v1
176	<i>Aeromonas</i> phage D6	<i>Myoviridae</i>	GCA_007051205.2	Complete	0.26	47.6	MN131137.2	2019/7/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/007/051/205/GCA_007051205.2_ASM705120v2
177	<i>Erwinia</i> phage pEa_SNUABM_30	<i>Myoviridae</i>	GCA_020488455.1	Complete	0.26	49.3	MZ443778.1	2021/9/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/488/455/GCA_020488455.1_ASM2048845v1
178	<i>Erwinia</i> phage vB_EamM_Yoloswag	<i>Myoviridae</i>	GCA_002619345.1	Complete	0.26	46.9	KY448244.1	2017/3/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/345/GCA_002619345.1_ASM261934v1
179	uncultured <i>Caudovirales</i> phage	Other	GCA_902988355.1	Complete	0.26	37.6	LR796670.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/988/355/GCA_902988355.1_UFOv-RE-26jul17-C21
180	<i>Pseudomonas</i> phage PaBG	<i>Myoviridae</i>	GCA_000912555.1	Complete	0.26	55.8	KF147891.1	2013/8/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/912/555/GCA_000912555.1_ViralProj215670

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
181	Phage NCTB	<i>Myoviridae</i>	GCA_900092385.1	Complete	0.26	42.0	LT598654.1	2016/7/8	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/900/092/385/GCA_900092385.1_ASM90009238v1
182	<i>Bacillus</i> phage vB_BpuM-BpSp	<i>Myoviridae</i>	GCA_002607645.1	Complete	0.26	25.9	KT895374.1	2016/4/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/607/645/GCA_002607645.1_ASM260764v1
183	<i>Dickeya</i> phage vB_DsoM_JA33	<i>Myoviridae</i>	GCA_003568495.1	Complete	0.26	44.5	MH460462.1	2018/9/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/568/495/GCA_003568495.1_ASM356849v1
184	<i>Dickeya</i> phage vB_DsoM_JA11	<i>Myoviridae</i>	GCA_003613635.1	Complete	0.26	44.5	MH389777.1	2018/10/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/613/635/GCA_003613635.1_ASM361363v1
185	<i>Aeromonas</i> phage AP1	<i>Myoviridae</i>	GCA_014183365.1	Complete	0.25	40.3	MT713136.1	2020/8/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/183/365/GCA_014183365.1_ASM1418336v1
186	<i>Dickeya</i> phage vB_DsoM_JA13	<i>Myoviridae</i>	GCA_003568455.1	Complete	0.25	44.5	MH460460.1	2018/9/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/568/455/GCA_003568455.1_ASM356845v1
187	<i>Vibrio</i> phage 6E35.1a	<i>Myoviridae</i>	GCA_020483665.1	Complete	0.25	43.8	MW824377.1	2021/8/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/483/665/GCA_020483665.1_ASM2048366v1
188	<i>Klebsiella</i> phage Miami	<i>Myoviridae</i>	GCA_015502055.1	Complete	0.25	43.9	MT701590.1	2020/11/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/015/502/055/GCA_015502055.1_ASM1550205v1
189	<i>Klebsiella</i> phage N1M2	<i>Myoviridae</i>	GCA_010092605.1	Complete	0.25	40.9	MN642089.1	2020/1/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/092/605/GCA_010092605.1_ASM1009260v1
190	<i>Dickeya</i> phage vB_DsoM_JA29	<i>Myoviridae</i>	GCA_003568475.1	Complete	0.25	43.8	MH460461.1	2018/9/12	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/568/475/GCA_003568475.1_ASM356847v1
191	<i>Prochlorococcus</i> phage P-SSM2	<i>Myoviridae</i>	GCA_002745975.1	Complete	0.25	35.5	GU071092.1	2009/11/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/745/975/GCA_002745975.1_ASM274597v1
192	<i>Prochlorococcus</i> phage P-SSM2	<i>Myoviridae</i>	GCA_000859585.1	Complete	0.25	35.5	AY939844.2	2005/3/21	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/859/585/GCA_000859585.1_ViralProj15135
193	<i>Bacillus</i> phage vB_BspM_Internexus	<i>Myoviridae</i>	GCA_020495465.1	Complete	0.25	27.7	MW749003.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/495/465/GCA_020495465.1_ASM2049546v1
194	<i>Erwinia</i> phage pEa_SNUABM_11	<i>Myoviridae</i>	GCA_020475535.1	Complete	0.25	50.7	MW845758.1	2021/7/27	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/475/535/GCA_020475535.1_ASM2047553v1
195	<i>Bacillus</i> phage AR9	<i>Myoviridae</i>	GCA_001743835.1	Complete	0.25	27.8	KU878088.1	2016/6/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/743/835/GCA_001743835.1_ViralProj344146
196	<i>Salmonella</i> phage SPAsTU	<i>Myoviridae</i>	GCA_003183805.1	Complete	0.25	49.5	MH221129.1	2018/5/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/183/805/GCA_003183805.1_ASM318380v1
197	<i>Vibrio</i> phage phi-ST2	<i>Myoviridae</i>	GCA_002757135.1	Complete	0.25	41.2	KT919973.1	2016/3/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/757/135/GCA_002757135.1_ASM275713v1
198	uncultured <i>Caudovirales</i> phage	Other	GCA_902990675.1	Complete	0.25	33.6	LR796916.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/990/675/GCA_902990675.1_UFOv-RH-14apr17-C69
199	uncultured <i>Caudovirales</i> phage	Other	GCA_902993455.1	Complete	0.25	33.6	LR797195.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/993/455/GCA_902993455.1_UFOv-RH-23may17-C188
200	uncultured <i>Caudovirales</i> phage	Other	GCA_902990735.1	Complete	0.25	36.5	LR796923.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/990/735/GCA_902990735.1_UFOv-RH-14apr17-C72

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
201	<i>Erwinia</i> phage pEa_SNUABM_8	<i>Myoviridae</i>	GCA_021354645.1	Complete	0.25	51.4	MW760841.1	2021/11/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/021/354/645/GCA_021354645.1_ASM2135464v1
202	<i>Erwinia</i> phage pEa_SNUABM_4	<i>Myoviridae</i>	GCA_018726365.1	Complete	0.25	51.4	MW812338.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/365/GCA_018726365.1_ASM1872636v1
203	<i>Erwinia</i> phage pEa_SNUABM_29	<i>Myoviridae</i>	GCA_018726355.1	Complete	0.25	50.3	MW812339.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/355/GCA_018726355.1_ASM1872635v1
204	<i>Vibrio</i> phage phi-Grn1	<i>Myoviridae</i>	GCA_002757115.1	Complete	0.25	41.3	KT919972.1	2016/3/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/757/115/GCA_002757115.1_ASM275711v1
205	<i>Vibrio</i> phage VS1	<i>Myoviridae</i>	GCA_020809685.1	Complete	0.25	42.5	OK905446.1	2021/11/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/809/685/GCA_020809685.1_ASM2080968v1
206	<i>Vibrio</i> phage ValKK3	<i>Myoviridae</i>	GCA_001501635.1	Complete	0.25	41.2	KP671755.1	2015/3/17	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/501/635/GCA_001501635.1_ViralProj307827
207	<i>Vibrio</i> phage Va3	<i>Myoviridae</i>	GCA_004771355.2	Complete	0.25	41.3	MK568540.2	2019/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/771/355/GCA_004771355.2_ASM477135v1
208	<i>Vibrio</i> phage nt-1	<i>Myoviridae</i>	GCA_000910195.2	Complete	0.25	41.3	HQ317393.2	2013/6/9	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/910/195/GCA_000910195.2_ViralProj209064
209	<i>Erwinia</i> phage pEa_SNUABM_9	<i>Myoviridae</i>	GCA_018726395.1	Complete	0.25	49.7	MW812341.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/395/GCA_018726395.1_ASM1872639v1
210	<i>Vibrio</i> phage vB_ValM_R10Z	<i>Myoviridae</i>	GCA_014337545.1	Complete	0.25	41.3	MT612988.1	2020/8/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/337/545/GCA_014337545.1_ASM1433754v1
211	<i>Vibrio</i> phage VH7D	<i>Myoviridae</i>	GCA_000914495.1	Complete	0.25	41.3	KC131129.1	2013/12/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/914/495/GCA_000914495.1_ViralProj239728
212	<i>Vibrio</i> phage vB_ValM_R11Z	<i>Myoviridae</i>	GCA_014337555.1	Complete	0.25	41.3	MT612989.1	2020/8/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/337/555/GCA_014337555.1_ASM1433755v1
213	Vibriophage phi-pp2	<i>Myoviridae</i>	GCA_002630725.1	Complete	0.25	42.6	JN849462.1	2012/7/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/630/725/GCA_002630725.1_ASM263072v1
214	<i>Erwinia</i> phage vB_EamM_Kwan	<i>Myoviridae</i>	GCA_001744315.1	Complete	0.25	52.1	KX397369.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/744/315/GCA_001744315.1_ViralProj344102
215	<i>Erwinia</i> phage vB_EamM_Asesino	<i>Myoviridae</i>	GCA_001744335.2	Complete	0.25	51.2	KX397364.2	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/744/335/GCA_001744335.2_ViralProj344106
216	<i>Vibrio</i> phage VH1_2019	<i>Myoviridae</i>	GCA_009931825.1	Complete	0.25	42.6	MN794232.1	2020/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/931/825/GCA_009931825.1_ASM993182v1
217	<i>Erwinia</i> phage Wellington	<i>Myoviridae</i>	GCA_003344985.1	Complete	0.24	52.1	MH426724.1	2018/7/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/344/985/GCA_003344985.1_ASM334498v1
218	<i>Synechococcus</i> phage B3	<i>Myoviridae</i>	GCA_009745215.1	Complete	0.24	35.4	MN695334.1	2019/12/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/745/215/GCA_009745215.1_ASM974521v1
219	<i>Erwinia</i> phage vB_EamM_ChrisDB	<i>Myoviridae</i>	GCA_001743655.1	Complete	0.24	49.4	KX397366.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/743/655/GCA_001743655.1_ViralProj344105
220	<i>Vibrio</i> phage KVP40	<i>Myoviridae</i>	GCA_000843785.1	Complete	0.24	42.6	AY283928.2	2003/8/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/843/785/GCA_000843785.1_ViralProj14416

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
221	<i>Erwinia</i> phage vB_EamM_Stratton	<i>Myoviridae</i>	GCA_002600675.1	Complete	0.24	51.3	KX397373.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/600/675/GCA_002600675.1_ASM260067v1
222	<i>Vibrio</i> phage V09	<i>Myoviridae</i>	GCA_012361135.1	Complete	0.24	42.6	MT135026.1	2020/4/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/012/361/135/GCA_012361135.1_ASM1236113v1
223	<i>Synechococcus</i> phage B23	<i>Myoviridae</i>	GCA_009745195.1	Complete	0.24	35.4	MN695335.1	2019/12/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/745/195/GCA_009745195.1_ASM974519v1
224	<i>Erwinia</i> phage phiEaH2	<i>Myoviridae</i>	GCA_000902915.1	Complete	0.24	51.3	JX316028.1	2012/9/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/902/915/GCA_000902915.1_ViralProj184155
225	<i>Vibrio</i> phage 2 TSL-2019	<i>Myoviridae</i>	GCA_006964105.1	Complete	0.24	43.6	MK368614.1	2019/7/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/964/105/GCA_006964105.1_ASM696410v1
226	<i>Proteus</i> phage 7	<i>Myoviridae</i>	GCA_014517885.1	Complete	0.24	48.5	MT679221.1	2020/9/8	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/517/885/GCA_014517885.1_ASM1451788v1
227	<i>Erwinia</i> phage pEa_SNUABM_43	<i>Myoviridae</i>	GCA_016759285.1	Complete	0.24	51.3	MW384823.1	2021/1/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/759/285/GCA_016759285.1_ASM1675928v1
228	<i>Erwinia</i> phage pEa_SNUABM_42	<i>Myoviridae</i>	GCA_018726375.1	Complete	0.24	51.3	MW812340.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/375/GCA_018726375.1_ASM1872637v1
229	<i>Erwinia</i> phage Machina	<i>Myoviridae</i>	GCA_002758035.1	Complete	0.24	51.0	KX397370.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/758/035/GCA_002758035.1_ASM275803v1
230	<i>Erwinia</i> phage vB_EamM_Caitlin	<i>Myoviridae</i>	GCA_001744955.1	Complete	0.24	52.2	KX397365.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/744/955/GCA_001744955.1_ViralProj344100
231	<i>Erwinia</i> phage vB_EamM_Parshik	<i>Myoviridae</i>	GCA_002758055.1	Complete	0.24	51.0	KX397371.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/758/055/GCA_002758055.1_ASM275805v1
232	<i>Salmonella</i> phage JN03	<i>Myoviridae</i>	GCA_014319805.1	Complete	0.24	48.4	MT799840.1	2020/8/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/319/805/GCA_014319805.1_ASM1431980v1
233	<i>Synechococcus</i> phage S-SRM01	<i>Myoviridae</i>	GCA_017654345.1	Complete	0.24	35.6	MW015081.1	2021/3/22	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/017/654/345/GCA_017654345.1_ASM1765434v1
234	<i>Erwinia</i> phage vB_EamM_Huxley	<i>Myoviridae</i>	GCA_001745635.1	Complete	0.24	51.1	KX397368.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/745/635/GCA_001745635.1_ViralProj344103
235	<i>Aeromonas</i> phage PS2	<i>Myoviridae</i>	GCA_009388305.2	Complete	0.24	38.8	MN453779.2	2019/10/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/388/305/GCA_009388305.2_ASM938830v2
236	<i>Salmonella</i> phage SPN3US	<i>Myoviridae</i>	GCA_001042275.1	Complete	0.24	48.5	JN641803.1	2011/10/9	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/042/275/GCA_001042275.1_ViralProj288000
237	<i>Escherichia</i> phage vB_EcoM_EC001	<i>Myoviridae</i>	GCA_014131305.1	Complete	0.24	48.5	MN445185.1	2020/8/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/131/305/GCA_014131305.1_ASM1413130v1
238	<i>Erwinia</i> phage pEa_SNUABM_6	<i>Myoviridae</i>	GCA_018726385.1	Complete	0.24	50.6	MW812343.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/385/GCA_018726385.1_ASM1872638v1
239	<i>Salmonella</i> phage pSal-SNUABM-04	<i>Myoviridae</i>	GCA_014824235.1	Complete	0.24	51.2	MT710307.1	2020/9/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/824/235/GCA_014824235.1_ASM1482423v1
240	<i>Enterobacteria</i> phage SEG1	<i>Myoviridae</i>	GCA_002601865.1	Complete	0.24	48.5	KU726251.1	2016/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/601/865/GCA_002601865.1_ASM260186v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
241	<i>Vibrio</i> phage pTD1	<i>Myoviridae</i>	GCA_002618825.1	Complete	0.24	44.5	AP017972.1	2017/2/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/618/825/GCA_002618825.1_ASM261882v1
242	<i>Erwinia</i> phage pEa_SNUABM_10	<i>Myoviridae</i>	GCA_018726345.1	Complete	0.24	51.4	MW812342.1	2021/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/018/726/345/GCA_018726345.1_ASM1872634v1
243	<i>Aeromonas</i> phage CF8	<i>Myoviridae</i>	GCA_006384595.2	Complete	0.24	42.2	MK774614.2	2019/6/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/384/595/GCA_006384595.2_ASM638459v2
244	<i>Vibrio</i> phage USC-1	<i>Myoviridae</i>	GCA_006864065.1	Complete	0.24	43.2	MK905543.1	2019/7/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/864/065/GCA_006864065.1_ASM686406v1
245	<i>Vibrio</i> phage 5 TSL-2019	<i>Myoviridae</i>	GCA_006964265.1	Complete	0.24	43.2	MK358448.1	2019/7/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/964/265/GCA_006964265.1_ASM696426v1
246	<i>Vibrio</i> phage Aphrodite1	<i>Myoviridae</i>	GCA_002958015.1	Complete	0.24	43.4	MG720308.1	2018/1/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/958/015/GCA_002958015.1_ASM295801v1
247	<i>Photobacterium</i> phage PDCC-1	<i>Myoviridae</i>	GCA_009800445.1	Complete	0.24	43.3	MN562221.1	2019/12/25	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/800/445/GCA_009800445.1_ASM980044v1
248	<i>Aeromonas</i> phage PS1	<i>Myoviridae</i>	GCA_007051165.2	Complete	0.24	38.8	MN032614.2	2019/7/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/007/051/165/GCA_007051165.2_ASM705116v2
249	<i>Escherichia</i> phage vB_EcoM_Goslar	<i>Myoviridae</i>	GCA_004521275.1	Complete	0.24	46.5	MK327938.1	2019/3/25	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/521/275/GCA_004521275.1_ASM452127v1
250	<i>Aeromonas</i> phage 65.2	<i>Myoviridae</i>	GCA_002618145.1	Complete	0.24	37.2	KY290955.1	2017/8/9	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/618/145/GCA_002618145.1_ASM261814v1
251	<i>Erwinia</i> phage vB_EamM_Joad	<i>Myoviridae</i>	GCA_002629065.1	Complete	0.24	48.3	MF459647.1	2017/8/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/629/065/GCA_002629065.1_ASM262906v1
252	<i>Aeromonas</i> virus 65	<i>Myoviridae</i>	GCA_000893255.1	Complete	0.24	37.2	GU459069.1	2010/11/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/893/255/GCA_000893255.1_ViralProj64543
253	<i>Erwinia</i> phage vB_EamM_RisingSun	<i>Myoviridae</i>	GCA_002629045.1	Complete	0.24	48.3	MF459646.1	2017/8/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/629/045/GCA_002629045.1_ASM262904v1
254	<i>Acinetobacter</i> phage vB_AbaM_ME3	<i>Myoviridae</i>	GCA_002609765.1	Complete	0.23	30.8	KU935715.1	2016/5/15	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/609/765/GCA_002609765.1_ASM260976v1
255	<i>Tenacibaculum</i> phage pT24	<i>Myoviridae</i>	GCA_002611925.1	Complete	0.23	28.7	LC168164.1	2016/7/23	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/611/925/GCA_002611925.1_ASM261192v1
256	<i>Aeromonas</i> phage Aeh1	<i>Myoviridae</i>	GCA_000843245.1	Complete	0.23	42.8	AY266303.2	2003/4/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/843/245/GCA_000843245.1_ViralProj14312
257	Cyanophage S-SSM6a	<i>Myoviridae</i>	GCA_002710385.1	Complete	0.23	39.1	HQ317391.1	2013/3/17	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/710/385/GCA_002710385.1_ASM271038v1
258	<i>Synechococcus</i> phage S-SSM7	<i>Myoviridae</i>	GCA_000890855.1	Complete	0.23	39.1	GU071098.1	2010/10/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/890/855/GCA_000890855.1_ViralProj64711
259	<i>Xanthomonas</i> phage Xoo-sp14	<i>Myoviridae</i>	GCA_014656665.1	Complete	0.23	58.0	MT939492.1	2020/9/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/656/665/GCA_014656665.1_ASM1465666v1
260	<i>Vibrio</i> phage pVa-21	<i>Myoviridae</i>	GCA_002619305.1	Complete	0.23	44.6	KY499642.1	2017/3/4	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/305/GCA_002619305.1_ASM261930v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
261	<i>Aeromonas</i> phage CC2	<i>Myoviridae</i>	GCA_000903495.1	Complete	0.23	38.8	JX123262.1	2012/7/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/903/495/GCA_000903495.1_ViralProj181987
262	<i>Ralstonia</i> phage phiRSL1	<i>Myoviridae</i>	GCA_000879455.1	Complete	0.23	58.0	AB366653.2	2008/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/879/455/GCA_000879455.1_ViralProj30059
263	<i>Aeromonas</i> phage ZPAH1	<i>Myoviridae</i>	GCA_016467545.1	Complete	0.23	38.2	MW272540.1	2021/1/2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/467/545/GCA_016467545.1_ASM1646754v1
264	<i>Aeromonas</i> phage AS-szw	<i>Myoviridae</i>	GCA_002743635.1	Complete	0.23	38.7	MF498773.1	2017/10/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/743/635/GCA_002743635.1_ASM274363v1
265	<i>Aeromonas</i> phage AS-zj	<i>Myoviridae</i>	GCA_002627665.1	Complete	0.23	38.7	MF448340.1	2017/8/19	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/627/665/GCA_002627665.1_ASM262766v1
266	<i>Bacillus</i> phage vB_BceM_WH1	<i>Myoviridae</i>	GCA_016456115.1	Complete	0.23	37.2	LC597490.1	2020/12/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/456/115/GCA_016456115.1_ASM1645611v1
267	<i>Aeromonas</i> phage Aswh_1	<i>Myoviridae</i>	GCA_004146945.1	Complete	0.23	38.4	MH791414.1	2019/2/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/146/945/GCA_004146945.1_ASM414694v1
268	<i>Erwinia</i> phage vB_EamM_Phobos	<i>Myoviridae</i>	GCA_001743635.1	Complete	0.23	49.1	KX397372.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/743/635/GCA_001743635.1_ViralProj344101
269	<i>Caulobacter</i> phage Ccr29	<i>Siphoviridae</i>	GCA_002619485.1	Complete	0.23	66.2	KY555145.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/485/GCA_002619485.1_ASM261948v1
270	<i>Aeromonas</i> phage Asswx_1	<i>Myoviridae</i>	GCA_004146865.1	Complete	0.23	38.8	MH791398.1	2019/2/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/146/865/GCA_004146865.1_ASM414686v1
271	<i>Synechococcus</i> phage S-SCSM1	<i>Myoviridae</i>	GCA_014190395.1	Complete	0.23	36.8	MK867354.1	2020/4/30	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/190/395/GCA_014190395.1_ASM1419039v1
272	<i>Aeromonas</i> phage AsSzw2	<i>Myoviridae</i>	GCA_010701755.1	Complete	0.23	37.8	MN871441.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/701/755/GCA_010701755.1_ASM1070175v1
273	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C90	<i>Myoviridae</i>	GCA_000982385.1	Complete	0.23	41.6	KJ019059.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/982/385/GCA_000982385.1_ViralProj282479
274	<i>Ochrobactrum</i> phage vB_OspM_OC	<i>Myoviridae</i>	GCA_011067635.1	Complete	0.23	37.7	MT028491.1	2020/3/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/011/067/635/GCA_011067635.1_ASM1106763v1
275	<i>Burkholderia</i> phage BCSR5	<i>Myoviridae</i>	GCA_016865805.1	Complete	0.23	54.7	MW460245.1	2021/2/8	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/865/805/GCA_016865805.1_ASM1686580v1
276	<i>Burkholderia</i> phage FLC6	<i>Myoviridae</i>	GCA_016811315.1	Complete	0.23	52.0	LC592711.1	2021/2/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/811/315/GCA_016811315.1_ASM1681131v1
277	<i>Tenacibaculum</i> phage PTm5	<i>Myoviridae</i>	GCA_009730715.1	Complete	0.23	29.7	AP019525.1	2019/12/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/730/715/GCA_009730715.1_ASM973071v1
278	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US17	<i>Myoviridae</i>	GCA_002593925.1	Complete	0.23	41.5	KJ019086.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/925/GCA_002593925.1_ASM259392v1
279	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C22	<i>Myoviridae</i>	GCA_002594485.1	Complete	0.23	41.6	KJ019150.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/485/GCA_002594485.1_ASM259448v1
280	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C6	<i>Myoviridae</i>	GCA_002593805.1	Complete	0.23	41.6	KJ019045.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/805/GCA_002593805.1_ASM259380v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
281	<i>Burkholderia</i> phage FLC8	<i>Myoviridae</i>	GCA_021355095.1	Complete	0.23	52.1	LC667450.1	2021/12/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/021/355/095/GCA_021355095.1_ASM2135509v1
282	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C34	<i>Myoviridae</i>	GCA_002594565.1	Complete	0.23	41.6	KJ019159.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/565/GCA_002594565.1_ASM259456v1
283	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C16	<i>Myoviridae</i>	GCA_002594405.1	Complete	0.23	41.6	KJ019146.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/405/GCA_002594405.1_ASM259440v1
284	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C80	<i>Myoviridae</i>	GCA_002593845.1	Complete	0.23	41.6	KJ019053.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/845/GCA_002593845.1_ASM259384v1
285	<i>Aeromonas</i> phage phiAS5	<i>Myoviridae</i>	GCA_000887715.1	Complete	0.23	43.0	HM452126.1	2010/9/8	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/887/715/GCA_000887715.1_ViralProj59729
286	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C15	<i>Myoviridae</i>	GCA_002594385.1	Complete	0.23	41.6	KJ019145.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/385/GCA_002594385.1_ASM259438v1
287	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C58	<i>Myoviridae</i>	GCA_002593785.1	Complete	0.23	41.6	KJ019037.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/785/GCA_002593785.1_ASM259378v1
288	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US24	<i>Myoviridae</i>	GCA_002593945.1	Complete	0.22	41.6	KJ019090.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/945/GCA_002593945.1_ASM259394v1
289	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US43	<i>Myoviridae</i>	GCA_002594165.1	Complete	0.22	41.6	KJ019102.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/165/GCA_002594165.1_ASM259416v1
290	<i>Tenacibaculum</i> phage PTm1	<i>Myoviridae</i>	GCA_009730695.1	Complete	0.22	29.7	AP019524.1	2019/12/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/730/695/GCA_009730695.1_ASM973069v1
291	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C12	<i>Myoviridae</i>	GCA_002594345.1	Complete	0.22	41.6	KJ019143.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/345/GCA_002594345.1_ASM259434v1
292	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US2	<i>Myoviridae</i>	GCA_002593985.1	Complete	0.22	41.6	KJ019092.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/985/GCA_002593985.1_ASM259398v1
293	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C24	<i>Myoviridae</i>	GCA_002594505.1	Complete	0.22	41.5	KJ019151.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/505/GCA_002594505.1_ASM259450v1
294	<i>Erwinia</i> phage pEa_SNUABM_38	<i>Myoviridae</i>	GCA_020476615.1	Complete	0.22	50.6	MW845759.1	2021/7/27	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/476/615/GCA_020476615.1_ASM2047661v1
295	<i>Cronobacter</i> phage CR5	<i>Myoviridae</i>	GCA_000910235.1	Complete	0.22	50.1	JX094500.1	2013/5/31	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/910/235/GCA_000910235.1_ViralProj209076
296	<i>Erwinia</i> phage Derbicus	<i>Myoviridae</i>	GCA_004521655.1	Complete	0.22	50.6	MK514282.1	2019/3/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/521/655/GCA_004521655.1_ASM452165v1
297	<i>Erwinia</i> phage vB_EamM_EarlPhillipIV	<i>Myoviridae</i>	GCA_001744975.1	Complete	0.22	50.6	KX397367.1	2016/8/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/744/975/GCA_001744975.1_ViralProj344104
298	<i>Ralstonia</i> phage RSL2	<i>Myoviridae</i>	GCA_001503055.1	Complete	0.22	52.1	AP014693.1	2014/12/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/503/055/GCA_001503055.1_ViralProj307833
299	<i>Caulobacter</i> phage CcrRogue	<i>Siphoviridae</i>	GCA_000900555.1	Complete	0.22	66.1	JX100814.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/900/555/GCA_000900555.1_ViralProj179422
300	<i>Listeria</i> phage LPJP1	<i>Myoviridae</i>	GCA_020475325.1	Complete	0.22	25.9	MZ422438.1	2021/9/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/475/325/GCA_020475325.1_ASM2047532v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
301	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US50	<i>Myoviridae</i>	GCA_002594225.1	Complete	0.22	41.6	KJ019106.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/225/GCA_002594225.1_ASM259422v1
302	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C8	<i>Myoviridae</i>	GCA_002593865.1	Complete	0.22	41.6	KJ019058.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/865/GCA_002593865.1_ASM259386v1
303	<i>Aeromonas</i> phage Aszh-1	<i>Myoviridae</i>	GCA_010701855.1	Complete	0.22	38.5	MN871442.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/701/855/GCA_010701855.1_ASM1070185v1
304	<i>Proteus</i> phage 10	<i>Myoviridae</i>	GCA_014071245.1	Complete	0.22	39.9	MT661596.1	2020/8/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/014/071/245/GCA_014071245.1_ASM1407124v1
305	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C21	<i>Myoviridae</i>	GCA_002594465.1	Complete	0.22	41.6	KJ019149.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/465/GCA_002594465.1_ASM259446v1
306	<i>Ralstonia</i> phage RSF1	<i>Myoviridae</i>	GCA_001500875.1	Complete	0.22	52.3	AP014927.1	2015/7/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/500/875/GCA_001500875.1_ViralProj307806
307	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US39	<i>Myoviridae</i>	GCA_002594085.1	Complete	0.22	41.6	KJ019098.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/085/GCA_002594085.1_ASM259408v1
308	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US34	<i>Myoviridae</i>	GCA_002594025.1	Complete	0.22	41.6	KJ019095.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/025/GCA_002594025.1_ASM259402v1
309	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C11	<i>Myoviridae</i>	GCA_002594325.1	Complete	0.22	41.6	KJ019142.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/325/GCA_002594325.1_ASM259432v1
310	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US13	<i>Myoviridae</i>	GCA_002593905.1	Complete	0.22	41.5	KJ019085.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/905/GCA_002593905.1_ASM259390v1
311	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C17	<i>Myoviridae</i>	GCA_002594425.1	Complete	0.22	41.6	KJ019147.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/425/GCA_002594425.1_ASM259442v1
312	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C10	<i>Myoviridae</i>	GCA_002594305.1	Complete	0.22	41.6	KJ019141.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/305/GCA_002594305.1_ASM259430v1
313	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US30	<i>Myoviridae</i>	GCA_002594005.1	Complete	0.22	41.6	KJ019093.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/005/GCA_002594005.1_ASM259400v1
314	<i>Aeromonas</i> phage PX29	<i>Myoviridae</i>	GCA_000920195.1	Complete	0.22	42.0	GU396103.1	2010/11/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/920/195/GCA_000920195.1_ViralProj240747
315	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C29	<i>Myoviridae</i>	GCA_002594545.1	Complete	0.22	41.6	KJ019155.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/545/GCA_002594545.1_ASM259454v1
316	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US57	<i>Myoviridae</i>	GCA_002594265.1	Complete	0.22	41.6	KJ019111.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/265/GCA_002594265.1_ASM259426v1
317	<i>Bacillus</i> phage SP-15	<i>Myoviridae</i>	GCA_001754685.1	Complete	0.22	38.6	KT624200.1	2016/3/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/754/685/GCA_001754685.1_ViralProj344602
318	<i>Caulobacter</i> virus CcrKarma	<i>Siphoviridae</i>	GCA_000901575.1	Complete	0.22	66.2	JX100811.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/901/575/GCA_000901575.1_ViralProj179420
319	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US37	<i>Myoviridae</i>	GCA_002594065.1	Complete	0.22	41.5	KJ019097.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/065/GCA_002594065.1_ASM259406v1
320	<i>Achromobacter</i> phage Motura	<i>Myoviridae</i>	GCA_006964305.1	Complete	0.22	53.7	MN094788.1	2019/7/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/964/305/GCA_006964305.1_ASM696430v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
321	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C25	<i>Myoviridae</i>	GCA_002594525.1	Complete	0.22	41.5	KJ019152.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/525/GCA_002594525.1_ASM259452v1
322	<i>Synechococcus</i> phage S-CAM7 isolate 0809CC03	<i>Myoviridae</i>	GCA_013426285.1	Complete	0.22	41.2	MT586120.1	2020/7/14	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/013/426/285/GCA_013426285.1_ASM1342628v1
323	<i>Aeromonas</i> phage AsFcp_1	<i>Myoviridae</i>	GCA_010701725.1	Complete	0.22	42.0	MN871440.1	2020/2/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/010/701/725/GCA_010701725.1_ASM1070172v1
324	<i>Aeromonas</i> phage Ah1	<i>Myoviridae</i>	GCA_002957415.1	Complete	0.22	42.0	MG250483.1	2017/12/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/957/415/GCA_002957415.1_ASM295741v1
325	<i>Caulobacter</i> phage CcrBL10	<i>Siphoviridae</i>	GCA_003443255.1	Complete	0.22	65.7	MH588544.1	2018/9/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/003/443/255/GCA_003443255.1_ASM344325v1
326	<i>Caulobacter</i> phage Ccr2	<i>Siphoviridae</i>	GCA_002619465.1	Complete	0.22	66.1	KY555143.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/465/GCA_002619465.1_ASM261946v1
327	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US7	<i>Myoviridae</i>	GCA_002594285.1	Complete	0.22	41.6	KJ019123.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/285/GCA_002594285.1_ASM259428v1
328	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US36	<i>Myoviridae</i>	GCA_002594045.1	Complete	0.22	41.5	KJ019096.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/045/GCA_002594045.1_ASM259404v1
329	<i>Sphingomonas</i> phage PAU	<i>Myoviridae</i>	GCA_000902455.1	Complete	0.22	31.3	JQ362498.1	2012/3/28	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/902/455/GCA_000902455.1_ViralProj181225
330	<i>Caulobacter</i> phage Ccr10	<i>Siphoviridae</i>	GCA_002619445.1	Complete	0.22	66.1	KY555142.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/445/GCA_002619445.1_ASM261944v1
331	<i>Caulobacter</i> phage CcrSwift	<i>Siphoviridae</i>	GCA_000899655.1	Complete	0.22	66.1	JX100809.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/899/655/GCA_000899655.1_ViralProj179423
332	<i>Aeromonas</i> phage AsFcp_2	<i>Myoviridae</i>	GCA_004146885.1	Complete	0.22	42.0	MH791401.1	2019/2/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/004/146/885/GCA_004146885.1_ASM414688v1
333	<i>Bacillus</i> phage 0305phi8-36	<i>Myoviridae</i>	GCA_000871045.1	Complete	0.22	41.8	EF583821.1	2007/8/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/871/045/GCA_000871045.1_ViralProj20653
334	<i>Caulobacter</i> phage CcrMagnet	<i>Siphoviridae</i>	GCA_000903095.1	Complete	0.22	66.1	JX100812.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/903/095/GCA_000903095.1_ViralProj179421
335	<i>Caulobacter</i> phage Ccr5	<i>Siphoviridae</i>	GCA_002619545.1	Complete	0.22	66.2	KY555144.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/545/GCA_002619545.1_ASM261954v1
336	uncultured <i>Caudovirales</i> phage	Other	GCA_903233215.1	Complete	0.22	36.6	LR798360.1	2020/5/18	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/903/233/215/GCA_903233215.1_UFOv-RE-27jun17-C9
337	<i>Erwinia</i> phage PhiEaH1	<i>Myoviridae</i>	GCA_000914555.1	Complete	0.22	52.3	KF623294.1	2014/2/25	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/914/555/GCA_000914555.1_ViralProj239740
338	<i>Aeromonas</i> phage Ahp1_CNU-2021	<i>Myoviridae</i>	GCA_016467505.1	Complete	0.22	47.9	MT161459.1	2021/1/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/467/505/GCA_016467505.1_ASM1646750v1
339	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US3	<i>Myoviridae</i>	GCA_002594105.1	Complete	0.22	41.6	KJ019099.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/105/GCA_002594105.1_ASM259410v1
340	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US44	<i>Myoviridae</i>	GCA_002594185.1	Complete	0.22	41.6	KJ019103.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/185/GCA_002594185.1_ASM259418v1

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No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
341	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US52	<i>Myoviridae</i>	GCA_002594245.1	Complete	0.22	41.5	KJ019107.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/245/GCA_002594245.1_ASM259424v1
342	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US42	<i>Myoviridae</i>	GCA_002594145.1	Complete	0.22	41.5	KJ019101.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/145/GCA_002594145.1_ASM259414v1
343	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C7	<i>Myoviridae</i>	GCA_002593825.1	Complete	0.22	41.6	KJ019052.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/825/GCA_002593825.1_ASM259382v1
344	uncultured <i>Caudovirales</i> phage	Other	GCA_902988965.1	Complete	0.22	38.3	LR796737.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/988/965/GCA_902988965.1_UFOv-RE-4nov15-C26
345	uncultured <i>Caudovirales</i> phage	Other	GCA_902985695.1	Complete	0.22	38.2	LR796418.1	2020/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/902/985/695/GCA_902985695.1_UFOv-RE-18aug17-C50
346	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US40	<i>Myoviridae</i>	GCA_002594125.1	Complete	0.22	41.5	KJ019100.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/125/GCA_002594125.1_ASM259412v1
347	<i>Caulobacter</i> phage Ccr34	<i>Siphoviridae</i>	GCA_002619525.1	Complete	0.22	66.2	KY555147.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/525/GCA_002619525.1_ASM261952v1
348	<i>Synechococcus</i> phage S-CAM7 isolate 0910CC49	<i>Myoviridae</i>	GCA_001882035.1	Complete	0.22	41.2	KU686212.1	2016/10/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/882/035/GCA_001882035.1_ViralProj353681
349	<i>Caulobacter</i> phage Ccr32	<i>Siphoviridae</i>	GCA_002619505.1	Complete	0.22	66.2	KY555146.1	2017/3/29	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/619/505/GCA_002619505.1_ASM261950v1
350	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C9	<i>Myoviridae</i>	GCA_002593885.1	Complete	0.22	41.6	KJ019066.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/593/885/GCA_002593885.1_ASM259388v1
351	<i>Caulobacter</i> phage phiCbK	<i>Siphoviridae</i>	GCA_000900535.1	Complete	0.22	66.2	JX100813.1	2012/10/16	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/900/535/GCA_000900535.1_ViralProj179418
352	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803US4	<i>Myoviridae</i>	GCA_002594205.1	Complete	0.22	41.6	KJ019105.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/205/GCA_002594205.1_ASM259420v1
353	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C19	<i>Myoviridae</i>	GCA_002594445.1	Complete	0.22	41.5	KJ019148.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/445/GCA_002594445.1_ASM259444v1
354	<i>Synechococcus</i> phage ACG-2014f isolate Syn7803C14	<i>Myoviridae</i>	GCA_002594365.1	Complete	0.21	41.5	KJ019144.1	2015/4/10	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/594/365/GCA_002594365.1_ASM259436v1
355	<i>Synechococcus</i> phage S-CAM7 isolate 0910SB42	<i>Myoviridae</i>	GCA_002612085.1	Complete	0.21	41.3	KU686213.1	2016/10/11	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/612/085/GCA_002612085.1_ASM261208v1
356	<i>Pseudomonas</i> phage PN05	<i>Myoviridae</i>	GCA_009931935.1	Complete	0.21	49.8	MN905546.1	2020/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/931/935/GCA_009931935.1_ASM993193v1
357	<i>Synechococcus</i> phage S-B43	<i>Myoviridae</i>	GCA_006869725.1	Complete	0.21	39.4	MN018232.1	2019/7/7	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/869/725/GCA_006869725.1_ASM686972v1
358	<i>Serratia</i> phage PCH45	<i>Myoviridae</i>	GCA_009187865.1	Complete	0.21	47.3	MN334766.1	2019/10/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/187/865/GCA_009187865.1_ASM918786v1
359	<i>Pseudomonas</i> phage phiEL	<i>Myoviridae</i>	GCA_000866825.1	Complete	0.21	49.3	AJ697969.1	2005/11/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/866/825/GCA_000866825.1_ViralProj16199
360	<i>Synechococcus</i> phage S-B05	<i>Myoviridae</i>	GCA_006083695.1	Complete	0.21	39.9	MK799832.1	2019/6/5	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/006/083/695/GCA_006083695.1_ASM608369v1

Supplementary Table S1. List of large phage genomes downloaded from the NCBI on January 29, 2022.

No.	Name	Organism group	Assembly	Level	Size (Mb)	G+C (%)	GenBank Accession	Release date (yyyy/mm/dd)	GenBank FTP
361	<i>Synechococcus</i> phage S-SKS1	<i>Myoviridae</i>	GCA_000904455.1	Complete	0.21	36.0	HQ633071.1	2013/3/24	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/904/455/GCA_000904455.1_ViralProj195489
362	<i>Vibrio</i> phage vB_VcorM_GR7B	<i>Myoviridae</i>	GCA_015767225.1	Complete	0.21	42.7	MT366760.1	2020/12/3	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/015/767/225/GCA_015767225.1_ASM1576722v1
363	<i>Rhizobium</i> phage RHph_TM30	<i>Myoviridae</i>	GCA_016835985.1	Complete	0.21	41.0	MN988521.1	2021/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/835/985/GCA_016835985.1_ASM1683598v1
364	<i>Rhizobium</i> phage RHph_TM40	<i>Myoviridae</i>	GCA_016835595.1	Complete	0.21	41.0	MN988522.1	2021/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/835/595/GCA_016835595.1_ASM1683559v1
365	<i>Rhizobium</i> phage RHph_Y65	<i>Myoviridae</i>	GCA_016836195.1	Complete	0.21	41.2	MN988525.1	2021/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/836/195/GCA_016836195.1_ASM1683619v1
366	<i>Rhizobium</i> phage RHph_TM3_3_6	<i>Myoviridae</i>	GCA_016835975.1	Complete	0.21	41.1	MN988524.1	2021/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/835/975/GCA_016835975.1_ASM1683597v1
367	<i>Sinorhizobium</i> phage phiN3	<i>Myoviridae</i>	GCA_001501175.1	Complete	0.21	49.1	KR052482.1	2015/5/6	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/501/175/GCA_001501175.1_ViralProj307735
368	<i>Rhizobium</i> phage RHph_TM2_3B	<i>Myoviridae</i>	GCA_016835905.1	Complete	0.21	41.1	MN988523.1	2021/1/26	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/016/835/905/GCA_016835905.1_ASM1683590v1
369	<i>Caulobacter</i> phage phiCbK	<i>Siphoviridae</i>	GCA_002602425.1	Complete	0.21	66.1	JX163858.1	2012/9/1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/602/425/GCA_002602425.1_ASM260242v1
370	<i>Synechococcus</i> phage Bellamy	<i>Myoviridae</i>	GCA_002627525.1	Complete	0.20	41.1	MF351863.1	2017/8/9	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/627/525/GCA_002627525.1_ASM262752v1
371	<i>Bacillus</i> phage vB_BspM_AgentSmith	<i>Myoviridae</i>	GCA_020495485.1	Complete	0.20	37.0	MW749006.1	2021/7/20	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/020/495/485/GCA_020495485.1_ASM2049548v1

Supplementary Table S2. BLASTn analysis of genome sequences of jumbophages S6 and PBS1 at the NCBI.

Query	Subject	Max score	Total score	Query coverage	E-value	Identity	Subject length (nt)	Accession No.
Phage S6	<i>Staphylococcus</i> phage PALS_2	91635	4.41E+05	96%	0	98.61%	268748	MN091626.1
	<i>Staphylococcus</i> phage vB_SauM-UFV_DC4	83357	4.47E+05	96%	0	98.60%	263185	MZ779063.1
	<i>Staphylococcus</i> phage Madawaska	72079	3.82E+05	92%	0	95.47%	265446	MW349129.1
	<i>Staphylococcus</i> phage MarsHill	70785	3.68E+05	90%	0	95.00%	266637	MW248466.1
	<i>Staphylococcus</i> phage vB_StaM_SA1	15232	1.73E+05	65%	0	86.61%	260727	MW218148.1
	<i>Staphylococcus</i> phage Machias	8636	1.54E+05	63%	0	84.97%	274478	MW349128.1
Phage PBS1	<i>Bacillus</i> phage AR9	74038	4.57E+05	98%	0	99.57%	251042	KU878088.1
	<i>Bacillus</i> phage vB_BspM_Internexus	43567	4.14E+05	93%	0	96.87%	252262	MW749003.1

Supplementary Table S3. Local tBLASTx analysis of jumbophages S6 and PBS1 against 371 large phage data.

Query	Subject			
	Name	Score ^a	E-value	GenBank accession
Phage S6	<i>Staphylococcus</i> phage vB_SauM-UFV_DC4	5492	0	MZ779063.1
	<i>Staphylococcus</i> phage PALS_2	3891	0	MN091626.1
	<i>Staphylococcus</i> phage Madawaska	2725	0	MW349129.1
	<i>Staphylococcus</i> phage MarshHill	2676	0	MW248466.1
	<i>Staphylococcus</i> phage Machias	2509	0	MW349128.1
	<i>Staphylococcus</i> phage vB_StaM_SA1	2461	0	MW218148.1
	<i>Listeria</i> phage LPJP1	566	0	MZ422438.1
	<i>Ochrobactrum</i> phage vB_OspM_OC	427	0	MT028491.1
	<i>Bacillus</i> phage vB_BpuM-BpSp	378	0	KT895374.1
	<i>Bacillus</i> phage vB_BspM_Internexus	371	0	MW749003.1
	<i>Bacillus</i> phage AR9	371	0	KU878088.1
	<i>Bacillus</i> phage G	319	0	JN638751.1
	<i>Yersinia</i> phage phiR1-37	216	0	AJ972879.2
	<i>Sphingomonas</i> phage PAU	280	3.00E-166	JQ362498.1
	<i>Bacillus</i> phage vB_BceM_WH1 DNA	278	5.00E-163	LC597490.1
	<i>Bacillus</i> phage SP-15	154	2.00E-65	KT624200.1

^a, The phage with > 100 are shown.

Supplementary Table S3. tBLASTx analysis of phage S6 and PBS1 against 371 jumbo phage data.

Query	Subject			
	Name	Score ^a	E-value	GenBank accession
PBS1	Bacillus phage AR9	3649	0	KU878088.1
	Bacillus phage vB_BspM_Internexus	3567	0	MW749003.1
	Bacillus phage vB_BpuM-BpSp	1118	0	KT895374.1
	Bacillus phage G	561	0	JN638751.1
	Listeria phage LPJP1	429	0	MZ422438.1
	Staphylococcus phage Machias	375	0	MW349128.1
	Staphylococcus phage vB_SauM-UFV_DC4	371	0	MZ779063.1
	Staphylococcus phage Madawaska	370	0	MW349129.1
	Staphylococcus phage Marshill	370	0	MW248466.1
	Staphylococcus phage PALS_2	369	0	MN091626.1
	Staphylococcus phage vB_StaM_SA1	350	0	MW218148.1
	Bacillus phage vB_BceM_WH1 DNA	339	0	LC597490.1
	Sphingomonas phage PAU	315	0	JQ362498.1
	Ochrobactrum phage vB_OspM_OC	281	0	MT028491.1
	Yersinia phage phiR1-37	280	0	AJ972879.2
	Rhizobium phage RHph_TM30	104	6.00E-97	MN988521.1
	Rhizobium phage RHph_TM40	104	6.00E-97	MN988522.1
	Rhizobium phage RHph_Y65	104	6.00E-97	MN988525.1
	Rhizobium phage RHph_TM3_3_6	104	6.00E-97	MN988524.1
	Rhizobium phage RHph_TM2_3B	104	6.00E-97	MN988523.1

^a, The phage with > 100 are shown.

Supplementary Table S4. Local tBLASTx analysis of jumbophages S6, PBS1, AR9, and phiR1-37 against 200 scaffold sequences.

Query: phage S6			Query: phage PBS1			Query : phage AR9			Query: phage phiR1-37		
Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value
scaffold_000	50.1	1.00E-10	scaffold_000	57.9	4.00E-15	scaffold_000	57.9	4.00E-15	scaffold_001	127	7.00E-32
scaffold_002	244	0	scaffold_001	40	3.00E-04	scaffold_001	40	3.00E-04	scaffold_002	780	0
scaffold_003	42.8	7.00E-07	scaffold_002	258	0	scaffold_002	257	0	scaffold_006	48.7	5.00E-16
scaffold_007	73.9	9.00E-28	scaffold_003	51.5	3.00E-06	scaffold_003	51.5	3.00E-06	scaffold_007	63.4	3.00E-08
scaffold_013	49.6	4.00E-09	scaffold_004	51.5	3.00E-06	scaffold_004	54.2	5.00E-07	scaffold_010	85.4	2.00E-28
scaffold_018	62	6.00E-14	scaffold_006	89.5	4.00E-20	scaffold_006	89.5	4.00E-20	scaffold_013	56.1	5.00E-06
scaffold_019	29	9.00E-04	scaffold_007	72.1	4.00E-21	scaffold_007	72.1	4.00E-21	scaffold_018	70.7	2.00E-15
scaffold_020	51.9	1.00E-07	scaffold_010	54.7	2.00E-16	scaffold_010	54.7	2.00E-16	scaffold_019	95.9	8.00E-33
scaffold_021	52.4	1.00E-07	scaffold_013	52.4	1.00E-14	scaffold_013	52.4	1.00E-14	scaffold_022	81.3	1.00E-13
scaffold_023	72.1	3.00E-15	scaffold_015	49.6	3.00E-06	scaffold_015	48.7	7.00E-06	scaffold_023	68.9	3.00E-20
scaffold_026	67.5	1.00E-28	scaffold_018	57.9	1.00E-08	scaffold_018	57.9	1.00E-06	scaffold_024	56.1	5.00E-06
scaffold_027	50.1	2.00E-12	scaffold_019	54.7	9.00E-22	scaffold_019	54.7	9.00E-22	scaffold_026	61.6	3.00E-22
scaffold_028	60.6	1.00E-22	scaffold_020	40	3.00E-05	scaffold_020	40	4.00E-04	scaffold_028	38.2	3.00E-10
scaffold_030	83.5	3.00E-35	scaffold_021	57.9	1.00E-06	scaffold_021	57.9	1.00E-06	scaffold_030	59.3	7.00E-24
scaffold_031	58.3	2.00E-15	scaffold_023	63.8	1.00E-43	scaffold_023	63.8	1.00E-43	scaffold_031	49.6	4.00E-04
scaffold_038	90	1.00E-16	scaffold_026	59.3	3.00E-24	scaffold_026	59.3	3.00E-24	scaffold_032	45.5	2.00E-06
scaffold_040	48.7	3.00E-05	scaffold_027	43.7	7.00E-05	scaffold_027	43.7	7.00E-05	scaffold_035	53.8	5.00E-06
scaffold_041	54.2	4.00E-20	scaffold_028	60.2	3.00E-10	scaffold_028	60.6	8.00E-09	scaffold_038	53.3	2.00E-14
scaffold_043	52.8	1.00E-08	scaffold_030	146	4.00E-52	scaffold_030	146	5.00E-50	scaffold_039	82.6	3.00E-35
scaffold_044	89	2.00E-26	scaffold_031	48.7	3.00E-13	scaffold_031	55.1	2.00E-12	scaffold_040	62.9	6.00E-26
scaffold_048	115	2.00E-100	scaffold_032	56.1	9.00E-11	scaffold_032	56.1	9.00E-11	scaffold_041	106	2.00E-21
scaffold_050	51	4.00E-08	scaffold_038	41.8	2.00E-10	scaffold_038	41.8	2.00E-10	scaffold_043	59.3	4.00E-11

Supplementary Table S4. Local tBLASTx analysis of jumbophages S6, PBS1, AR9, and phiR1-37 against 200 scaffold sequences.

Query: phage S6			Query: phage PBS1			Query : phage AR9			Query: phage phiR1-37		
Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value
scaffold_051	126	8.00E-32	scaffold_040	61.1	4.00E-20	scaffold_040	61.1	4.00E-20	scaffold_044	57	2.00E-06
scaffold_052	41.4	2.00E-04	scaffold_041	80.3	7.00E-27	scaffold_041	80.3	7.00E-27	scaffold_047	138	1.00E-71
scaffold_054	49.6	2.00E-16	scaffold_043	64.3	2.00E-08	scaffold_043	64.3	3.00E-10	scaffold_048	92.7	1.00E-44
scaffold_055	121	1.00E-31	scaffold_044	48.7	2.00E-05	scaffold_044	48.7	2.00E-05	scaffold_050	62	2.00E-27
scaffold_058	50.1	5.00E-12	scaffold_046	77.1	3.00E-26	scaffold_046	77.1	3.00E-26	scaffold_052	57	2.00E-11
scaffold_066	37.3	7.00E-04	scaffold_048	133	0	scaffold_048	133	0	scaffold_054	62.5	2.00E-08
scaffold_068	64.8	3.00E-24	scaffold_050	148	5.00E-74	scaffold_050	148	5.00E-74	scaffold_055	64.3	1.00E-35
scaffold_069	51	9.00E-05	scaffold_051	92.7	4.00E-17	scaffold_051	92.7	4.00E-17	scaffold_057	60.2	2.00E-08
scaffold_077	46	2.00E-06	scaffold_052	54.7	1.00E-08	scaffold_052	54.7	1.00E-08	scaffold_058	44.6	7.00E-06
scaffold_080	79	6.00E-13	scaffold_054	52.8	5.00E-09	scaffold_054	52.8	1.00E-12	scaffold_059	53.3	7.00E-18
scaffold_083	65.7	1.00E-18	scaffold_055	126	2.00E-34	scaffold_055	126	2.00E-34	scaffold_065	43.7	6.00E-12
scaffold_087	113	5.00E-28	scaffold_058	55.1	2.00E-07	scaffold_058	55.1	4.00E-10	scaffold_068	82.6	2.00E-19
scaffold_089	81.7	2.00E-21	scaffold_059	89	2.00E-30	scaffold_059	49.2	7.00E-25	scaffold_070	66.1	5.00E-09
scaffold_093	66.1	5.00E-09	scaffold_064	92.7	7.00E-22	scaffold_064	92.7	4.00E-17	scaffold_071	68.4	1.00E-23
scaffold_095	64.8	1.00E-20	scaffold_068	68.9	5.00E-19	scaffold_068	68.9	2.00E-19	scaffold_077	169	7.00E-51
scaffold_096	40.5	3.00E-15	scaffold_069	51.5	3.00E-10	scaffold_069	51.5	2.00E-10	scaffold_079	46.4	4.00E-04
scaffold_104	55.6	7.00E-06	scaffold_070	98.7	7.00E-19	scaffold_070	98.7	7.00E-19	scaffold_080	80.3	1.00E-18
scaffold_112	124	1.00E-26	scaffold_071	66.1	4.00E-09	scaffold_071	66.1	4.00E-09	scaffold_083	49.6	8.00E-08
scaffold_119	91.3	3.00E-118	scaffold_077	49.2	3.00E-05	scaffold_077	49.2	3.00E-05	scaffold_084	41.8	1.00E-07
scaffold_156	45.1	4.00E-04	scaffold_079	51.9	8.00E-05	scaffold_079	51.9	8.00E-05	scaffold_087	75.3	3.00E-29
scaffold_167	81.3	3.00E-34	scaffold_080	73	2.00E-21	scaffold_080	73	2.00E-21	scaffold_089	100	8.00E-84
scaffold_186	54.7	2.00E-07	scaffold_081	61.1	1.00E-07	scaffold_081	60.2	3.00E-07	scaffold_094	55.6	1.00E-29

Supplementary Table S4. Local tBLASTx analysis of jumbophages S6, PBS1, AR9, and phiR1-37 against 200 scaffold sequences.

Query: phage S6			Query: phage PBS1			Query : phage AR9			Query: phage phiR1-37		
Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value
scaffold_190	128	2.00E-30	scaffold_083	46.9	4.00E-04	scaffold_087	76.7	2.00E-25	scaffold_095	58.8	2.00E-10
scaffold_200	70.3	3.00E-37	scaffold_087	76.7	2.00E-25	scaffold_089	90.4	2.00E-31	scaffold_096	54.2	4.00E-09
scaffold_209	55.1	9.00E-06	scaffold_089	90.4	2.00E-21	scaffold_091	61.6	5.00E-16	scaffold_098	72.1	7.00E-11
scaffold_222	40.9	2.00E-04	scaffold_091	61.6	5.00E-16	scaffold_093	55.1	9.00E-06	scaffold_104	62	2.00E-18
scaffold_229	50.6	1.00E-04	scaffold_093	46	7.00E-06	scaffold_094	98.7	5.00E-43	scaffold_112	78	1.00E-12
scaffold_230	59.3	1.00E-08	scaffold_094	98.7	5.00E-43	scaffold_095	67	8.00E-36	scaffold_113	55.1	9.00E-06
scaffold_233	67.5	9.00E-28	scaffold_095	67	8.00E-36	scaffold_096	36.3	9.00E-08	scaffold_118	75.8	2.00E-22
scaffold_234	59.3	6.00E-10	scaffold_096	36.3	9.00E-08	scaffold_104	70.3	7.00E-23	scaffold_119	322	0
scaffold_266	47.8	6.00E-04	scaffold_104	70.3	7.00E-23	scaffold_112	91.8	8.00E-17	scaffold_120	130	1.00E-67
scaffold_271	46.4	2.00E-10	scaffold_112	91.8	8.00E-17	scaffold_113	87.2	7.00E-22	scaffold_123	46.9	1.00E-08
scaffold_343	39.1	7.00E-07	scaffold_113	87.2	7.00E-22	scaffold_118	45.1	2.00E-14	scaffold_124	62.5	6.00E-08
scaffold_347	51.5	9.00E-07	scaffold_118	45.1	2.00E-14	scaffold_119	101	4.00E-103	scaffold_137	79	3.00E-27
scaffold_364	55.6	7.00E-06	scaffold_119	101	9.00E-104	scaffold_123	86.8	3.00E-15	scaffold_167	60.6	6.00E-08
scaffold_389	49.6	4.00E-04	scaffold_123	86.8	3.00E-15	scaffold_130	76.7	6.00E-15	scaffold_169	51.5	3.00E-08
scaffold_397	41.4	1.00E-04	scaffold_130	76.7	6.00E-15	scaffold_137	61.1	4.00E-50	scaffold_172	49.2	6.00E-04
scaffold_443	115	1.00E-45	scaffold_137	61.1	4.00E-50	scaffold_159	58.8	7.00E-07	scaffold_186	40.5	7.00E-06
scaffold_472	48.3	8.00E-04	scaffold_159	58.8	7.00E-07	scaffold_167	73	4.00E-11	scaffold_190	80.8	3.00E-49
scaffold_490	64.8	3.00E-09	scaffold_167	73	4.00E-11	scaffold_169	52.8	5.00E-08	scaffold_200	65.2	9.00E-09
scaffold_753	44.6	7.00E-05	scaffold_169	52.8	1.00E-07	scaffold_171	40.5	7.00E-04	scaffold_218	50.1	3.00E-04
			scaffold_171	40.5	7.00E-04	scaffold_186	81.7	3.00E-20	scaffold_230	73.9	8.00E-46
			scaffold_186	81.7	3.00E-19	scaffold_187	73.5	3.00E-11	scaffold_235	51.5	1.00E-09
			scaffold_187	73.5	3.00E-11	scaffold_190	69.8	3.00E-10	scaffold_252	43.7	8.00E-06

Supplementary Table S4. Local tBLASTx analysis of jumbophages S6, PBS1, AR9, and phiR1-37 against 200 scaffold sequences.

Query: phage S6			Query: phage PBS1			Query : phage AR9			Query: phage phiR1-37		
Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value	Subject	Score (bits)	E-value
			scaffold_190	69.8	3.00E-10	scaffold_200	73.5	2.00E-20	scaffold_271	55.1	2.00E-09
			scaffold_200	73.5	2.00E-20	scaffold_209	68.9	3.00E-10	scaffold_283	75.3	1.00E-34
			scaffold_209	68.9	3.00E-10	scaffold_233	79.4	7.00E-27	scaffold_284	54.7	4.00E-18
			scaffold_233	79.4	7.00E-27	scaffold_234	67	6.00E-13	scaffold_315	138	1.00E-82
			scaffold_234	67	6.00E-13	scaffold_252	82.6	5.00E-14	scaffold_343	53.3	3.00E-05
			scaffold_252	82.6	5.00E-14	scaffold_266	69.8	3.00E-10	scaffold_347	43.7	2.00E-09
			scaffold_266	69.8	3.00E-10	scaffold_271	51.9	3.00E-14	scaffold_397	108	1.00E-52
			scaffold_271	51.9	3.00E-14	scaffold_284	57.4	1.00E-08	scaffold_443	77.6	2.00E-12
			scaffold_284	57.4	1.00E-08	scaffold_343	45.1	1.00E-04	scaffold_490	43.2	8.00E-04
			scaffold_298	62	8.00E-08	scaffold_347	47.8	6.00E-10	scaffold_536	57.9	2.00E-19
			scaffold_343	45.1	1.00E-04	scaffold_397	45.5	1.00E-17	scaffold_562	90	9.00E-18
			scaffold_347	47.8	6.00E-10	scaffold_443	104	6.00E-57	scaffold_753	140	7.00E-70
			scaffold_364	50.6	4.00E-06	scaffold_486	53.8	4.00E-11	scaffold_989	38.2	1.00E-04
			scaffold_397	45.5	1.00E-17	scaffold_490	56.1	6.00E-08			
			scaffold_443	104	6.00E-57	scaffold_659	55.1	9.00E-06			
			scaffold_486	53.8	4.00E-11	scaffold_753	131	1.00E-46			
			scaffold_490	56.1	7.00E-08						
			scaffold_659	52.4	6.00E-05						
			scaffold_753	131	1.00E-46						

Supplementary Table S5. Information of 40 selected scaffolds.

No.	Common contigs	Length (nt)	GC (%)	CheckV analysis		Local tBLASTx analysis of scaffold sequence against the genomes of jumbophages S6, PBS1, AR9 and phiR1-37		
				Estimated genome completeness (%)	Expected genome length (bp)	Subject	Score (bits)	E-value
1	scaffold_002	200,670	25.9	76.5	262,391	phiR1-37	797	0
2	scaffold_007	111,289	41.7	40.8	272,963	PBS1	72.1	3.00E-22
3	scaffold_018	43,095	38.2	16.2	265,853	phiR1-37	70.7	7.00E-17
4	scaffold_019	33,391	30.3	15.9	210,234	phiR1-37	95.9	3.00E-31
5	scaffold_023	48,596	24.0	27.5	176,605	AR9	63.8	2.00E-46
6	scaffold_026	30,606	33.4	11.4	269,733	PBS1	74.4	3.00E-35
7	scaffold_028	30,161	31.8	11.4	263,600	S6	60.6	3.00E-24
8	scaffold_030	29,328	27.2	12.0	245,307	PBS1	146	3.00E-54
9	scaffold_031	29,247	32.7	10.4	280,046	S6	58.3	3.00E-17
10	scaffold_038	27,877	37.2	8.6	323,714	S6	90	2.00E-18
11	scaffold_040	42,260	28.6	10.8	391,797	phiR1-37	62.9	6.00E-27
12	scaffold_041	35,827	32.3	13.3	269,906	PBS1	101	9.00E-35
13	scaffold_043	31,057	44.0	10.1	268,177	phiR1-37	59.3	6.00E-13
14	scaffold_044	41,038	30.7	24.3	168,813	S6	89	5.00E-28
15	scaffold_048	48,446	30.3	19.7	246,225	PBS1	127	0
16	scaffold_050	54,450	29.4	35.1	154,949	AR9	155	3.00E-77
17	scaffold_052	33,552	44.2	12.3	272,939	phiR1-37	57	3.00E-13
18	scaffold_054	42,512	37.4	15.9	267,342	AR9	54.7	6.00E-22
19	scaffold_055	25,146	25.0	10.1	248,635	PBS1	134	1.00E-38
20	scaffold_058	38,886	36.4	14.5	268,857	S6	51	4.00E-16

Supplementary Table S5. Information of 40 selected scaffolds.

No.	Common contigs	Length (nt)	GC (%)	CheckV analysis		Local tBLASTx analysis of scaffold sequence against the genomes of jumbophages S6, PBS1, AR9 and phiR1-37		
				Estimated genome completeness (%)	Expected genome length (bp)	Subject	Score (bits)	E-value
21	scaffold_068	22,829	37.1	8.5	268,040	S6	64.8	1.00E-26
22	scaffold_077	22,788	28.2	6.5	350,962	phiR1-37	169	1.00E-52
23	scaffold_080	22,387	33.3	8.3	270,041	PBS1	73	2.00E-23
24	scaffold_087	22,729	28.5	9.5	240,573	phiR1-37	72.1	2.00E-30
25	scaffold_089	28,560	27.6	12.3	221,655	phiR1-37	100	8.00E-91
26	scaffold_096	21,244	28.4	9.3	229,532	S6	40.5	4.00E-17
27	scaffold_104	24,853	27.9	19.3	129,109	PBS1	70.3	1.00E-24
28	scaffold_112	53,343	33.5	46.0	115,897	S6	124	5.00E-28
29	scaffold_119	23,926	30.3	9.4	256,012	phiR1-37	346	0
30	scaffold_167	22,891	44.4	8.4	272,548	S6	67.5	9.00E-33
31	scaffold_186	24,684	36.2	8.5	235,725	AR9	81.7	5.00E-22
32	scaffold_190	45,654	25.0	15.3	299,119	phiR1-37	80.8	9.00E-51
33	scaffold_200	23,583	39.3	8.7	269,925	S6	70.3	4.00E-39
34	scaffold_271	22,652	30.8	7.8	258,571	PBS1	51.9	2.00E-16
35	scaffold_343	23,641	35.1	12.5	189,923	phiR1-37	53.3	5.00E-07
36	scaffold_347	22,219	32.1	8.2	269,844	PBS1	47.8	7.00E-12
37	scaffold_397	36,351	27.2	21.9	180,090	phiR1-37	108	2.00E-54
38	scaffold_443	21,605	25.5	11.3	213,512	AR9	104	8.00E-59
39	scaffold_490	20,368	32.4	8.7	234,069	S6	64.8	1.00E-10
40	scaffold_753	22,941	24.7	6.8	244,130	phiR1-37	140	7.00E-77

Supplementary Table S6. Local tBLASTx analysis of scaffold_002 and scaffold_007 sequences against 371 large phage genome sequences.

Query	Subject	Score (Bits)	E-value	GenBank accession
scaffold_002	<i>Yersinia</i> phage phiR1-37	797	0	AJ972879.2
scaffold_002	<i>Listeria</i> phage LPJP1	259	0	MZ422438.1
scaffold_002	<i>Bacillus</i> phage vB_BspM_Internexus	258	0	MW749003.1
scaffold_002	<i>Bacillus</i> phage AR9	257	0	KU878088.1
scaffold_002	<i>Bacillus</i> phage vB_BpuM-BpSp	253	0	KT895374.1
scaffold_002	<i>Staphylococcus</i> phage vB_SauM-UFV_DC4	244	0	MZ779063.1
scaffold_002	<i>Staphylococcus</i> phage Machias	244	0	MW349128.1
scaffold_002	<i>Staphylococcus</i> phage Madawaska	243	0	MW349129.1
scaffold_002	<i>Staphylococcus</i> phage MarsHill	243	0	MW248466.1
scaffold_002	<i>Staphylococcus</i> phage PALS_2	243	0	MN091626.1
scaffold_007	<i>Ralstonia</i> phage RP31	232	0	AP017925.1
scaffold_007	<i>Ralstonia</i> phage RP12	232	0	AP017924.1
scaffold_007	<i>Xanthomonas</i> phage Xoo-sp14	273	0	MT939492.1
scaffold_007	<i>Serratia</i> phage KpHz_2	248	0	MN871445.1
scaffold_007	<i>Serratia</i> phage KpGz_1	248	0	MN871444.1
scaffold_007	<i>Pseudomonas</i> phage Noxifer	242	0	MF063068.1
scaffold_007	<i>Erwinia</i> phage pEa_SNUABM_54	236	0	MW879341.1
scaffold_007	<i>Pseudomonas</i> phage vB_PaeM_kmuB	230	0	MW057919.1
scaffold_007	<i>Pseudomonas</i> phage Psa21	229	0	MK552327.1
scaffold_007	<i>Pseudomonas</i> phage T2P	228	0	MT995926.1

Top 10 hits are shown as a result for each scaffold.

Supplementary Table S7. Annotation of uncultured phage scaffold_002 and orthologous CDSs to *Yersinia* phage phiR1-37 proteins.

Uncultured phage scaffold_002						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	1333	1848	-	ORF001	hypothetical protein	g298	putative variable tail fibre protein
CDS	1898	2173	-	ORF002	hypothetical protein		
CDS	2180	2551	-	ORF003	hypothetical protein	g302	hypothetical protein
CDS	2725	3807	+	ORF004	putative ATPase	g304	ATPase
CDS	3875	6655	+	ORF005	hypothetical protein	g059	hypothetical protein
CDS	6652	8193	+	ORF006	hypothetical protein	g305	hypothetical protein
CDS	8260	8403	-	ORF007	hypothetical protein		
CDS	8633	8797	+	ORF008	hypothetical protein		
CDS	8841	9164	+	ORF009	hypothetical protein		
CDS	9181	9453	+	ORF010	hypothetical protein		
CDS	9526	10095	+	ORF011	putative guanylate kinase	g056	guanylate kinase
CDS	10183	11580	+	ORF012	putative ribonucleotide Reductase, subunit A		
CDS	11591	12013	+	ORF013	hypothetical protein		
CDS	12006	13766	+	ORF014	putative ribonucleoside- diphosphate reductase		
CDS	13899	14186	+	ORF015	hypothetical protein	g251	hypothetical protein
CDS	14237	14926	+	ORF016	hypothetical protein	g049	PhoH-like phosphate starvation- inducible protein
CDS	14965	15414	-	ORF017	hypothetical protein	g047	phage structural protein
CDS	15414	16025	-	ORF018	hypothetical protein	g046	hypothetical protein
CDS	16129	16731	-	ORF019	hypothetical protein		
CDS	16744	17367	-	ORF020	hypothetical protein		
CDS	17374	17922	-	ORF021	hypothetical protein		
CDS	18034	19203	+	ORF022	hypothetical protein	g191	hypothetical protein
CDS	19382	20698	-	ORF023	putative transposase		
CDS	20788	22446	-	ORF024	hypothetical protein	g193	hypothetical protein
CDS	22517	22966	-	ORF025	hypothetical protein		
CDS	23091	23636	-	ORF026	putative (p)ppGpp synthetase		
CDS	23692	24900	-	ORF027	hypothetical protein	g173	hypothetical protein
CDS	24929	25843	-	ORF028	hypothetical protein		
CDS	25921	26712	+	ORF029	hypothetical protein	g333	hypothetical protein
CDS	27198	27464	+	ORF030	hypothetical protein		
CDS	27524	27874	-	ORF031	hypothetical protein		
CDS	27996	28451	+	ORF032	hypothetical protein		
CDS	28776	30089	+	ORF033	putative DNA topoisomerase 4 subunit B	g311	DNA-topoisomerase II B-subunit
CDS	30303	31412	+	ORF034	putative type 2 topoisomerase subunit B	g314	DNA-gyrase B-subunit
CDS	31470	31724	+	ORF035	hypothetical protein		
CDS	31724	32065	+	ORF036	hypothetical protein		
CDS	32130	34613	+	ORF037	putative DNA gyrase subunit A	g327	DNA-gyrase IV A-subunit
CDS	34721	35389	+	ORF038	hypothetical protein		
CDS	35394	36104	+	ORF039	hypothetical protein		
CDS	36242	36880	+	ORF040	hypothetical protein		
CDS	37095	39872	+	ORF041	putative double-stranded DNA repair protein Rad50	g061	hypothetical protein
CDS	39932	40408	+	ORF042	hypothetical protein		
CDS	40860	41651	-	ORF043	hypothetical protein	g079	phage structural protein
CDS	41706	42530	-	ORF044	hypothetical protein	g080	hypothetical protein
CDS	42530	43870	-	ORF045	hypothetical protein	g081	phage structural protein
CDS	44009	49096	+	ORF046	hypothetical protein	g083	putative tape measure tail fibre protein
CDS	49183	52563	+	ORF047	putative transglycosylase		
CDS	52657	54012	+	ORF048	hypothetical protein	g085	hypothetical protein
CDS	54045	54596	+	ORF049	hypothetical protein	g086	Holliday junction resolvase endodeoxyribonuclease
CDS	54586	56043	+	ORF050	hypothetical protein	g087	hypothetical protein
CDS	56033	56293	+	ORF051	hypothetical protein	g088	phage structural protein

Supplementary Table S7. Annotation of uncultured phage scaffold_002 and orthologous CDSs to *Yersinia* phage phiR1-37 proteins.

Uncultured phage scaffold_002						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	56303	57640	+	ORF052	hypothetical protein	g089	phage structural protein
CDS	57710	58294	+	ORF053	hypothetical protein	g090	hypothetical protein
CDS	58387	58929	+	ORF054	hypothetical protein	g095	hypothetical protein
CDS	58977	60695	-	ORF055	hypothetical protein	g151	exonuclease ABC C subunit
CDS	60843	65018	-	ORF056	hypothetical protein	g099	putative RNA-polymerase beta-subunit
CDS	65105	65533	-	ORF057	putative peptidase M15	g084	phage K1E myramoyl peptidase
CDS	65923	66318	+	ORF058	hypothetical protein		
CDS	66333	66749	+	ORF059	hypothetical protein		
CDS	66742	67893	+	ORF060	hypothetical protein	g100	non-canonical purine NTP pyrophosphatase
CDS	68172	69008	+	ORF061	hypothetical protein	g101	phage structural protein
CDS	69318	69587	+	ORF062	hypothetical protein		
CDS	69714	71561	+	ORF063	hypothetical protein	g102	DNA-directed RNA polymerase, beta' subunit
CDS	71632	72318	+	ORF064	hypothetical protein		
CDS	72305	72940	+	ORF065	hypothetical protein	g103	CDP/dCDP deaminase zinc-binding
CDS	73059	74570	+	ORF066	hypothetical protein	g121	hypothetical protein
CDS	74622	75242	+	ORF067	hypothetical protein	g122	hypothetical protein
CDS	75244	75489	+	ORF068	hypothetical protein		
CDS	75499	75654	+	ORF069	hypothetical protein		
CDS	75647	75850	+	ORF070	hypothetical protein		
CDS	75911	76453	+	ORF071	hypothetical protein		
CDS	76570	77805	+	ORF072	hypothetical protein	g128	phage structural protein
CDS	77892	78302	+	ORF073	hypothetical protein		
CDS	78320	78889	+	ORF074	hypothetical protein	g130	hypothetical protein
CDS	79128	79520	+	ORF075	hypothetical protein	g131	histone family DNA-binding protein
CDS	79587	80099	+	ORF076	hypothetical protein		
CDS	80183	80803	+	ORF077	hypothetical protein	g134	phage structural protein
CDS	80921	82480	+	ORF078	hypothetical protein	g135	structural protein sp46 precursor
CDS	82580	82984	+	ORF079	hypothetical protein		
CDS	82984	83268	+	ORF080	putative membrane protein	g142	hypothetical protein
CDS	83261	85306	+	ORF081	hypothetical protein	g143	terminase large subunit, helicase
CDS	85317	86078	+	ORF082	hypothetical protein	g139	hypothetical protein
CDS	86130	86735	+	ORF083	hypothetical protein		
CDS	86806	87483	+	ORF084	hypothetical protein	g148	phage structural protein
CDS	87600	89369	+	ORF085	hypothetical protein	g149	putative contractile tail sheath structural protein
CDS	89384	90145	+	ORF086	hypothetical protein	g150	phage structural protein
CDS	90205	92844	-	ORF087	hypothetical protein	g160	phage structural protein
CDS	92854	93912	-	ORF088	hypothetical protein	g161	phage structural protein
CDS	93922	94965	-	ORF089	hypothetical protein	g048	phage structural protein
CDS	94969	95511	-	ORF090	hypothetical protein	g163	phage structural protein
CDS	95629	96267	+	ORF091	putative endonuclease		
CDS	96316	96726	-	ORF092	hypothetical protein		
CDS	96740	98743	-	ORF093	hypothetical protein	g164	hypothetical protein
CDS	98942	99361	+	ORF094	hypothetical protein	g168	phage structural protein
CDS	99415	100224	-	ORF095	hypothetical protein	g169	hypothetical protein
CDS	100402	102054	+	ORF096	hypothetical protein	g170	B-family DNA-polymerase
CDS	102215	102502	+	ORF097	hypothetical protein		
CDS	102509	103222	+	ORF098	hypothetical protein	g175	hypothetical protein
CDS	103249	104049	+	ORF099	hypothetical protein	g176	phage structural protein
CDS	104144	105004	+	ORF100	hypothetical protein	g177	hypothetical protein
CDS	105069	106514	+	ORF101	hypothetical protein	g178	RNA-polymerase beta'-subunit
CDS	106543	107556	+	ORF102	hypothetical protein		
CDS	108224	108754	+	ORF103	hypothetical protein		
CDS	108765	108899	+	ORF104	hypothetical protein		
CDS	109072	109443	+	ORF105	hypothetical protein		
CDS	109557	112148	+	ORF106	hypothetical protein	g196	phage structural protein

Supplementary Table S7. Annotation of uncultured phage scaffold_002 and orthologous CDSs to *Yersinia* phage phiR1-37 proteins.

Uncultured phage scaffold_002						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	112211	113140	-	ORF107	hypothetical protein	g199	structural protein sp24 precursor
CDS	113222	114313	-	ORF108	hypothetical protein	g210	phage structural protein
CDS	114326	115480	-	ORF109	hypothetical protein	g209	phage structural protein
CDS	115613	116659	+	ORF110	hypothetical protein	g208	phage structural protein
CDS	116666	117418	+	ORF111			
CDS	117385	119184	+	ORF112	hypothetical protein	g207	hypothetical protein
CDS	119246	120259	+	ORF113	hypothetical protein	g206	phage structural protein
CDS	120345	121505	+	ORF114	hypothetical protein	g205	phage structural protein
CDS	121518	123254	+	ORF115	hypothetical protein	g204	phage structural protein
CDS	123267	124067	+	ORF116	hypothetical protein	g203	phage structural protein
CDS	124116	125129	-	ORF117	hypothetical protein	g195	hypothetical protein
CDS	125113	125694	-	ORF118	hypothetical protein		
CDS	125752	127206	-	ORF119	hypothetical protein	g194	hypothetical protein
CDS	127231	127827	-	ORF120	putative ribonuclease H	g213	ribonuclease H
CDS	127934	129781	-	ORF121	putative 60 kDa chaperonin	g243	chaperonin GroEL
CDS	129865	130035	-	ORF122	hypothetical protein	g242	hypothetical protein
CDS	130095	131561	-	ORF123	hypothetical protein	g241	hypothetical protein
CDS	131644	132108	-	ORF124	hypothetical protein	g240	phage structural protein
CDS	132119	132544	-	ORF125	hypothetical protein	g239	phage structural protein
CDS	132559	133143	-	ORF126	hypothetical protein		
CDS	133170	133823	-	ORF127	hypothetical protein	g237	phage structural protein
CDS	133967	135112	-	ORF128	putative transposase		
CDS	135844	136734	+	ORF129	hypothetical protein	g144	hypothetical protein
CDS	136745	137077	+	ORF130	hypothetical protein	g235	hypothetical protein
CDS	137092	139524	+	ORF131	hypothetical protein	g234	hypothetical protein
CDS	139571	140254	+	ORF132	hypothetical protein	g233	phage structural protein
CDS	140504	141793	+	ORF133	hypothetical protein	g231	DNA-directed RNA-polymerase beta-subunit
CDS	141861	143249	+	ORF134	hypothetical protein	g171	hypothetical protein
CDS	143533	143760	+	ORF135	hypothetical protein		
CDS	143753	144157	+	ORF136	hypothetical protein		
CDS	144254	144649	+	ORF137	hypothetical protein		
CDS	144710	145939	-	ORF138	hypothetical protein	g237	hypothetical protein
CDS	146157	146978	+	ORF139	hypothetical protein	g244	phage structural protein
CDS	147036	148541	+	ORF140	hypothetical protein	g245	hypothetical protein
CDS	148658	149716	+	ORF141	hypothetical protein	g247	hypothetical protein
CDS	149729	150223	+	ORF142	hypothetical protein		
CDS	150324	150980	+	ORF143	hypothetical protein		
CDS	150999	152246	+	ORF144	hypothetical protein	g250	hypothetical protein
CDS	152333	152647	+	ORF145	hypothetical protein		
CDS	152699	153871	+	ORF146	transposase		
CDS	154419	156326	+	ORF147	putative DNA-directed RNA polymerase subunit beta	g261	DNA-directed RNA polymerase beta subunit C-terminus
CDS	156329	156724	+	ORF148	hypothetical protein		
CDS	156865	157482	+	ORF149	hypothetical protein		
CDS	157454	158668	+	ORF150	putative transposase		
CDS	158788	159171	+	ORF151	hypothetical protein		
CDS	159248	159721	+	ORF152	hypothetical protein		
CDS	159821	161866	+	ORF153	putative DNA ligase	g267	NAD-dependent DNA-ligase
CDS	161933	162616	+	ORF154	hypothetical protein		
CDS	162613	163185	+	ORF155	hypothetical protein		
CDS	163253	163687	+	ORF156	hypothetical protein		
CDS	163701	164240	+	ORF157	hypothetical protein		
CDS	164307	165839	+	ORF158	hypothetical protein		
CDS	165926	166096	+	ORF159	hypothetical protein		
CDS	166144	167112	-	ORF160	hypothetical protein	g270	phage structural protein
CDS	167125	168846	-	ORF161	hypothetical protein	g271	phage structural protein
CDS	168887	170212	-	ORF162	hypothetical protein	g272	phage structural protein

Supplementary Table S7. Annotation of uncultured phage scaffold_002 and orthologous CDSs to *Yersinia* phage phiR1-37 proteins.

Uncultured phage scaffold_002						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	170242	170382	-	ORF163	hypothetical protein		
CDS	170845	171867	-	ORF164	hypothetical protein	g179	hypothetical protein
CDS	171941	173152	-	ORF165	putative DNA-directed RNA polymerase subunit beta	g274	RNA-polymerase beta-subunit RpoC N-terminus
CDS	173290	173538	+	ORF166	hypothetical protein		
CDS	173535	174302	+	ORF167	hypothetical protein	g276	hypothetical protein
CDS	174342	174725	-	ORF168	hypothetical protein	g277	hypothetical protein
CDS	174718	175515	-	ORF169	hypothetical protein	g278	hypothetical protein
CDS	175590	175796	+	ORF170	hypothetical protein		
CDS	175817	176221	+	ORF171	hypothetical protein		
CDS	176330	176464	+	ORF172	hypothetical protein		
CDS	176592	176792	+	ORF173	hypothetical protein		
CDS	176866	177147	+	ORF174	hypothetical protein		
CDS	177223	177735	+	ORF175	hypothetical protein		
CDS	177839	178045	+	ORF176	hypothetical protein		
CDS	178274	178489	+	ORF177	hypothetical protein		
CDS	178550	179173	+	ORF178	hypothetical protein		
CDS	179366	180025	+	ORF179	hypothetical protein		
CDS	180171	180704	+	ORF180	hypothetical protein		
CDS	180718	181269	+	ORF181	hypothetical protein		
CDS	181274	181483	+	ORF182	hypothetical protein		
CDS	181576	182046	+	ORF183	hypothetical protein		
CDS	182056	182775	+	ORF184	hypothetical protein		
CDS	182889	183551	+	ORF185	hypothetical protein		
CDS	183680	183820	+	ORF186	hypothetical protein		
CDS	184085	184354	+	ORF187	hypothetical protein		
CDS	184445	185203	-	ORF188	hypothetical protein	g282	hypothetical protein
CDS	185361	185552	+	ORF189	hypothetical protein		
CDS	185641	185979	+	ORF190	putative endolytic peptidoglycan transglycosylase RlpA		
CDS	186089	186451	+	ORF191	hypothetical protein		
CDS	186500	186817	+	ORF192	hypothetical protein		
CDS	186948	187472	+	ORF193	hypothetical protein		
CDS	187475	188266	+	ORF194	hypothetical protein		
CDS	188268	188642	+	ORF195	hypothetical protein		
tRNA	189003	189079	+		tRNA-Arg		
CDS	189208	189384	+	ORF196	hypothetical protein		
CDS	189451	189825	+	ORF197	hypothetical protein		
CDS	189894	190052	+	ORF198	hypothetical protein		
CDS	190119	191042	+	ORF199	hypothetical protein		
CDS	191047	191526	+	ORF200	hypothetical protein		
CDS	191537	191920	+	ORF201	hypothetical protein		
CDS	192016	192813	+	ORF202	hypothetical protein		
CDS	192907	193722	-	ORF203	hypothetical protein	g285	phage structural protein
CDS	193779	194156	+	ORF204	hypothetical protein		
CDS	194280	194819	+	ORF205	putative exodeoxyribonuclease V		
CDS	195177	197201	+	ORF206	putative exodeoxyribonuclease V	g286	exodeoxyribonuclease V alpha chain
CDS	197225	197677	+	ORF207	hypothetical protein		
CDS	197680	198285	+	ORF208	hypothetical protein		
CDS	198335	198595	-	ORF209	hypothetical protein		
CDS	198663	199292	-	ORF210	putative lysozyme		
CDS	199397	200017	-	ORF211	hypothetical protein		

Supplementary Table S8. Annotation of uncultured phage scaffold_007 and orthologous CDSs to *Ralstonia* phage RP31 proteins.

Uncultured phage scaffold_007						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	1494	2264	-	ORF001	hypothetical protein	ORF085	putative virion structural protein
CDS	2319	4961	+	ORF002	hypothetical protein	ORF084	putative virion structural protein
CDS	5046	5936	+	ORF003	hypothetical protein		
CDS	6047	6928	+	ORF004	hypothetical protein		
CDS	6940	10158	+	ORF005	hypothetical protein		
CDS	10172	10954	+	ORF006	hypothetical protein		
CDS	10840	13605	+	ORF007	hypothetical protein		
CDS	13660	16338	+	ORF008	hypothetical protein		
CDS	16354	17649	+	ORF009	hypothetical protein		
CDS	17704	18588	+	ORF010	hypothetical protein		
CDS	18604	21183	+	ORF011	hypothetical protein	ORF013	hypothetical protein
CDS	21260	22507	+	ORF012	hypothetical protein		
CDS	22580	25186	+	ORF013	hypothetical protein		
CDS	25212	25448	+	ORF014	hypothetical protein		
CDS	25452	26069	+	ORF015	hypothetical protein		
CDS	26152	26637	+	ORF016	hypothetical protein		
CDS	26654	27187	+	ORF017	hypothetical protein		
CDS	27273	28196	+	ORF018	hypothetical protein	ORF083	putative virion structural protein
CDS	28224	28772	+	ORF019	hypothetical protein	ORF082	putative crossover junction endodeoxyribonuclease RuvC
CDS	28766	29242	+	ORF020	hypothetical protein		
CDS	29348	32521	+	ORF021	hypothetical protein		
CDS	32737	33438	+	ORF022	hypothetical protein		
CDS	33491	34162	+	ORF023	hypothetical protein		
CDS	34286	35206	+	ORF024	hypothetical protein		
CDS	35199	35498	+	ORF025	hypothetical protein		
CDS	35498	36370	+	ORF026	hypothetical protein		
CDS	36357	36785	+	ORF027	hypothetical protein		
CDS	36785	37228	+	ORF028	hypothetical protein		
CDS	37238	37744	+	ORF029	hypothetical protein		
CDS	37762	39429	+	ORF030	hypothetical protein	ORF162	hypothetical protein
CDS	39506	40378	+	ORF031	hypothetical protein		
CDS	40473	40658	+	ORF032	hypothetical protein		
CDS	40662	41228	+	ORF033	hypothetical protein		
CDS	41436	41885	+	ORF034	hypothetical protein		
CDS	41986	42156	+	ORF035	hypothetical protein		
CDS	42207	42776	+	ORF036	hypothetical protein		
CDS	42841	43461	+	ORF037	hypothetical protein		
CDS	43526	44122	-	ORF038	hypothetical protein		
CDS	44133	44972	-	ORF039	hypothetical protein		
CDS	44985	46958	-	ORF040	hypothetical protein		
CDS	46981	48639	-	ORF041	hypothetical protein	ORF070	hypothetical protein
CDS	48641	48769	-	ORF042	hypothetical protein		
CDS	48768	50051	+	ORF043	hypothetical protein	ORF067	putative virion structural protein
CDS	50180	50311	+	ORF044	hypothetical protein		
CDS	50368	50961	+	ORF045	hypothetical protein		
CDS	50973	51389	+	ORF046	hypothetical protein		
CDS	51433	52317	-	ORF047	hypothetical protein	ORF028	putative major virion structural protein
CDS	52382	54700	-	ORF048	hypothetical protein	ORF027	putative tail sheath
CDS	54862	55341	+	ORF049	hypothetical protein		
CDS	55344	55589	+	ORF050	hypothetical protein		
CDS	55690	56646	+	ORF051	hypothetical protein	ORF026	hypothetical protein
CDS	56643	59384	+	ORF052	hypothetical protein	ORF025	putative virion structural protein
CDS	59387	61060	+	ORF053	hypothetical protein	ORF024	putative virion structural protein
CDS	61150	63306	+	ORF054	hypothetical protein	ORF023	putative terminase, large subunit
CDS	63366	63752	+	ORF055	hypothetical protein		
CDS	63736	64125	+	ORF056	hypothetical protein		
CDS	64170	65390	-	ORF057	hypothetical protein	ORF022	hypothetical protein

Supplementary Table S8. Annotation of uncultured phage scaffold_007 and orthologous CDSs to *Ralstonia* phage RP31 proteins.

Uncultured phage scaffold_007						Orthologous genes predicted by Coregenes software	
	Start	End	Direction	Gene	Predicted function	Gene	Predicted function
CDS	65479	65811	-	ORF058	hypothetical protein	ORF200	hypothetical protein
CDS	65892	66611	+	ORF059	hypothetical protein		
CDS	66694	66963	+	ORF060	hypothetical protein		
CDS	67008	67274	-	ORF061	hypothetical protein		
CDS	67560	68099	+	ORF062	hypothetical protein		
CDS	68159	68413	+	ORF063	hypothetical protein		
CDS	68495	68878	+	ORF064	hypothetical protein		
CDS	69084	70016	+	ORF065	hypothetical protein		
CDS	70006	70254	+	ORF066	hypothetical protein		
CDS	70416	70793	+	ORF067	hypothetical protein		
CDS	70828	71130	+	ORF068	hypothetical protein		
CDS	71189	71713	+	ORF069	hypothetical protein		
CDS	71714	72145	+	ORF070	hypothetical protein		
CDS	72149	72634	+	ORF071	putative dihydrofolate reductase	ORF182	hypothetical protein
CDS	72644	73612	+	ORF072	hypothetical protein	ORF063 ORF065 ORF078 ORF062 ORF061 ORF058 ORF055 ORF051 ORF049 ORF048 ORF043 ORF041 ORF040	hypothetical protein hypothetical protein hypothetical protein putative SbcC-ATPase hypothetical protein hypothetical protein putative virion structural protein putative ribonuclease H putative UvsX protein putative virion structural protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
CDS	73609	74196	+	ORF073	hypothetical protein		
CDS	74240	74524	+	ORF074	hypothetical protein		
CDS	74451	74663	+	ORF075	hypothetical protein		
CDS	75089	76408	-	ORF076	putative ribonucleoside- diphosphate reductase subunit beta		
CDS	76527	77435	+	ORF077	hypothetical protein		
CDS	77469	77783	+	ORF078	hypothetical protein		
CDS	77932	78435	+	ORF079	hypothetical protein		
CDS	78446	78676	+	ORF080	hypothetical protein		
CDS	78687	79133	+	ORF081	hypothetical protein		
CDS	79144	79782	+	ORF082	hypothetical protein		
CDS	79814	80119	+	ORF083	hypothetical protein		
CDS	80183	80575	-	ORF084	hypothetical protein		
CDS	80686	81297	+	ORF085	hypothetical protein		
CDS	81428	81904	+	ORF086	hypothetical protein		
CDS	81906	82400	+	ORF087	hypothetical protein		
CDS	82436	83359	-	ORF088	hypothetical protein		
CDS	83433	85952	+	ORF089	hypothetical protein		
CDS	86369	87526	+	ORF090	hypothetical protein		
CDS	87571	88182	-	ORF091	hypothetical protein		
CDS	88192	88842	-	ORF092	hypothetical protein		
CDS	88854	90197	-	ORF093	hypothetical protein		
CDS	90266	90670	+	ORF094	hypothetical protein		
CDS	90722	91048	+	ORF095	hypothetical protein		
CDS	91041	91415	+	ORF096	hypothetical protein		
CDS	91402	92616	+	ORF097	putative ribonuclease H		
CDS	92635	93102	+	ORF098	hypothetical protein		
CDS	93155	94027	-	ORF099	hypothetical protein		
CDS	94117	95514	+	ORF100	hypothetical protein		
CDS	95545	95826	+	ORF101	hypothetical protein		
CDS	95823	96500	+	ORF102	hypothetical protein		
CDS	96504	96998	+	ORF103	hypothetical protein		
CDS	96976	97746	+	ORF104	hypothetical protein		
CDS	97805	98428	+	ORF105	hypothetical protein		
CDS	98476	98970	-	ORF106	hypothetical protein		
CDS	99046	99594	+	ORF107	hypothetical protein		
CDS	99575	99988	+	ORF108	hypothetical protein		
CDS	99988	101142	+	ORF109	hypothetical protein		
CDS	101188	103524	-	ORF110	hypothetical protein		
CDS	103585	111177	-	ORF111	putative lytic transglycosylase		