Integrative structural analysis of *Pseudomonas* phage *DEV* reveals a genome ejection motor

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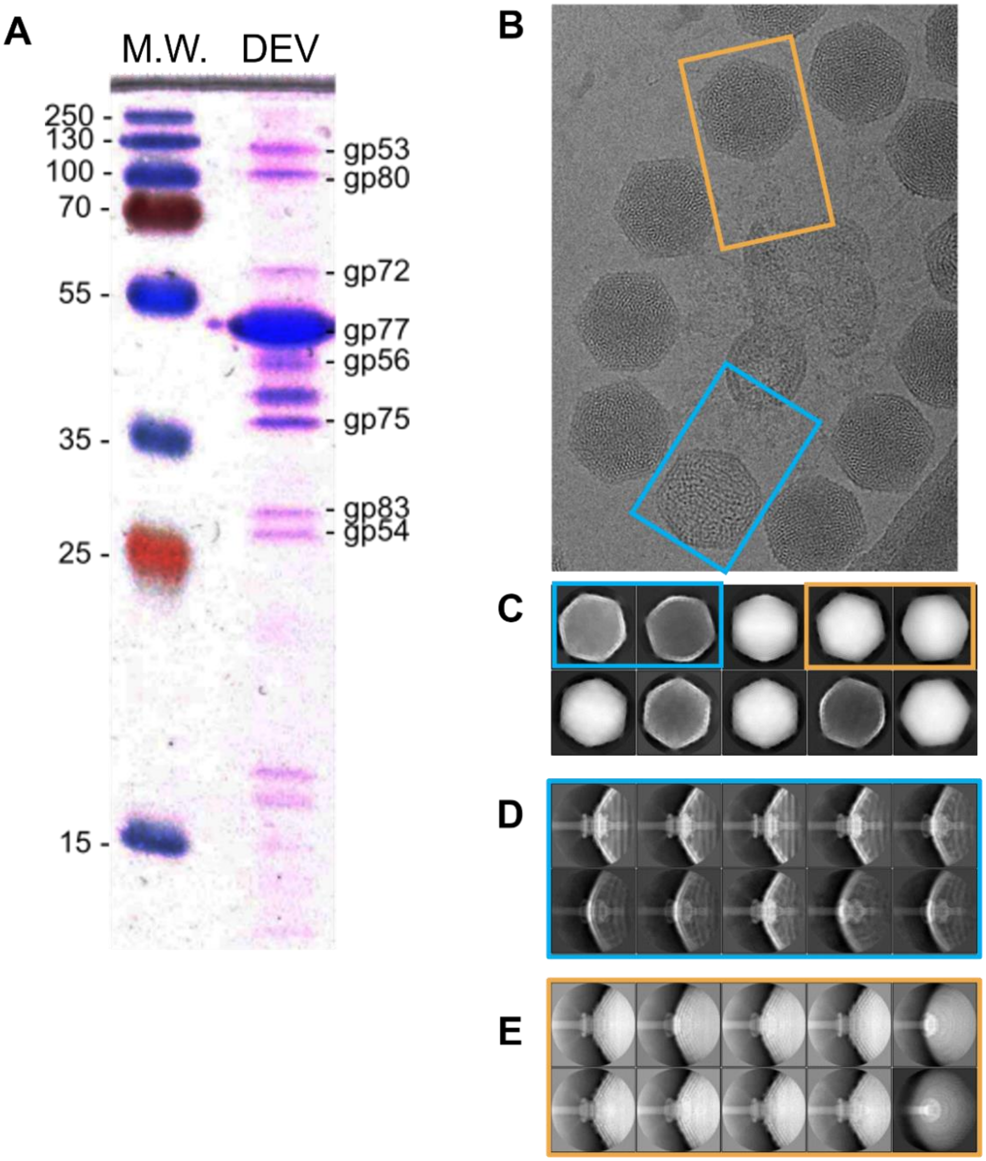
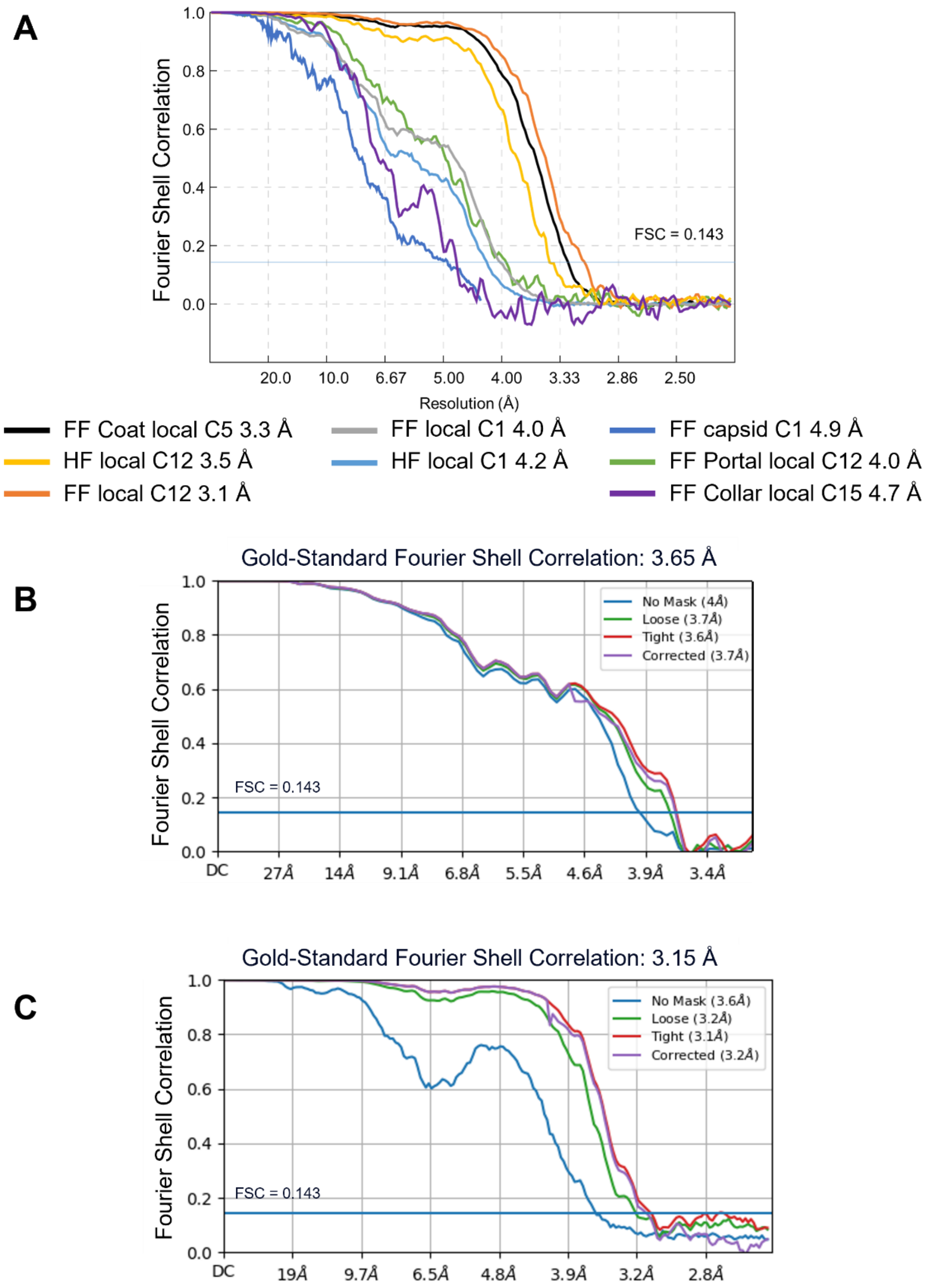
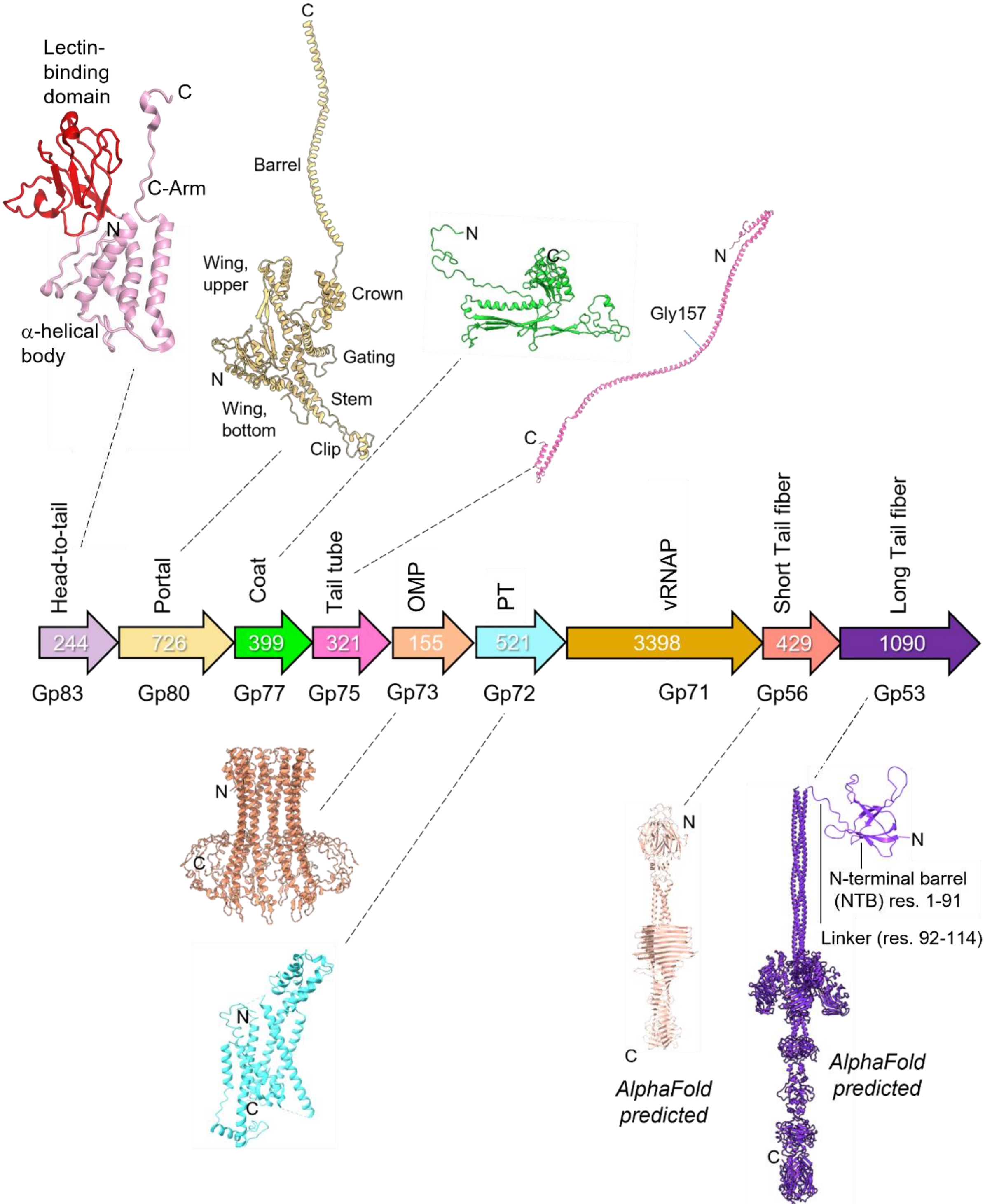
125-character teaser. Structural annotation of phage DEV structural components, host-absorption fibers, and ejection proteins.



Supplemental Figure 1. Structural characterization of phage DEV. (**A**) SDS-PAGE analysis of DEV infectious virions. Proteins extracted from $CsCl_2$ gradient-purified DEV particles were analyzed using 15 % SDS-PAGE and Coomassie staining. M.W. = molecular weight marker (kDa). Tentative identification of DEV proteins based on their M.W., assuming possible ± 10% gel shifting, is reported on the right. Only proteins identified in the proteomic analyses of both DEV and LIT1 virions have been considered. The highly abundant gp77 (major coat protein; 44 kDa) migrates with an apparent size of ~50 kDa. The vRNApol gp71 (350 kDa) is not visible, most likely because it does not enter the gel. (**B**) Representative cryo-micrograph of double $CsCl_2$ gradient-purified DEV particles. The orange and blue boxes cover a fully-filled (FF) virion and a half-filled (HF) particle. (**C**) Representative 2D class averages reveal the existence of HF particles (blue frame) and FF virions (orange frame). Nonetheless, both HF and FF had a tail apparatus. Representative localized reconstruction of 2D classes of the neck region for (**D**) HF particles (blue frame) and (**E**) FF virions (orange frame).



Supplemental Figure 2. Fourier Shell Correlation (FSC) resolution curves. (**A**) FSC curves for all reconstructions of FF virions and HF particles. (**B**) FSC curves for the cryo-EM reconstruction of recombinant gp72 in the post-ejection conformation. (**C**) FSC curves for the cryo-EM reconstruction of the recombinant gp72:gp73 complex in the post-ejection conformation. For all curves, the resolution is indicated at 0.143 cut-off.



Supplemental Figure 3. Atlas of all protein structures built in this work. All DEV proteins were built *de novo* in cryo-EM maps, except for the long-tail fiber gp53 and short-tail fiber gp56, which were predicted by AlphaFold.

Supplemental

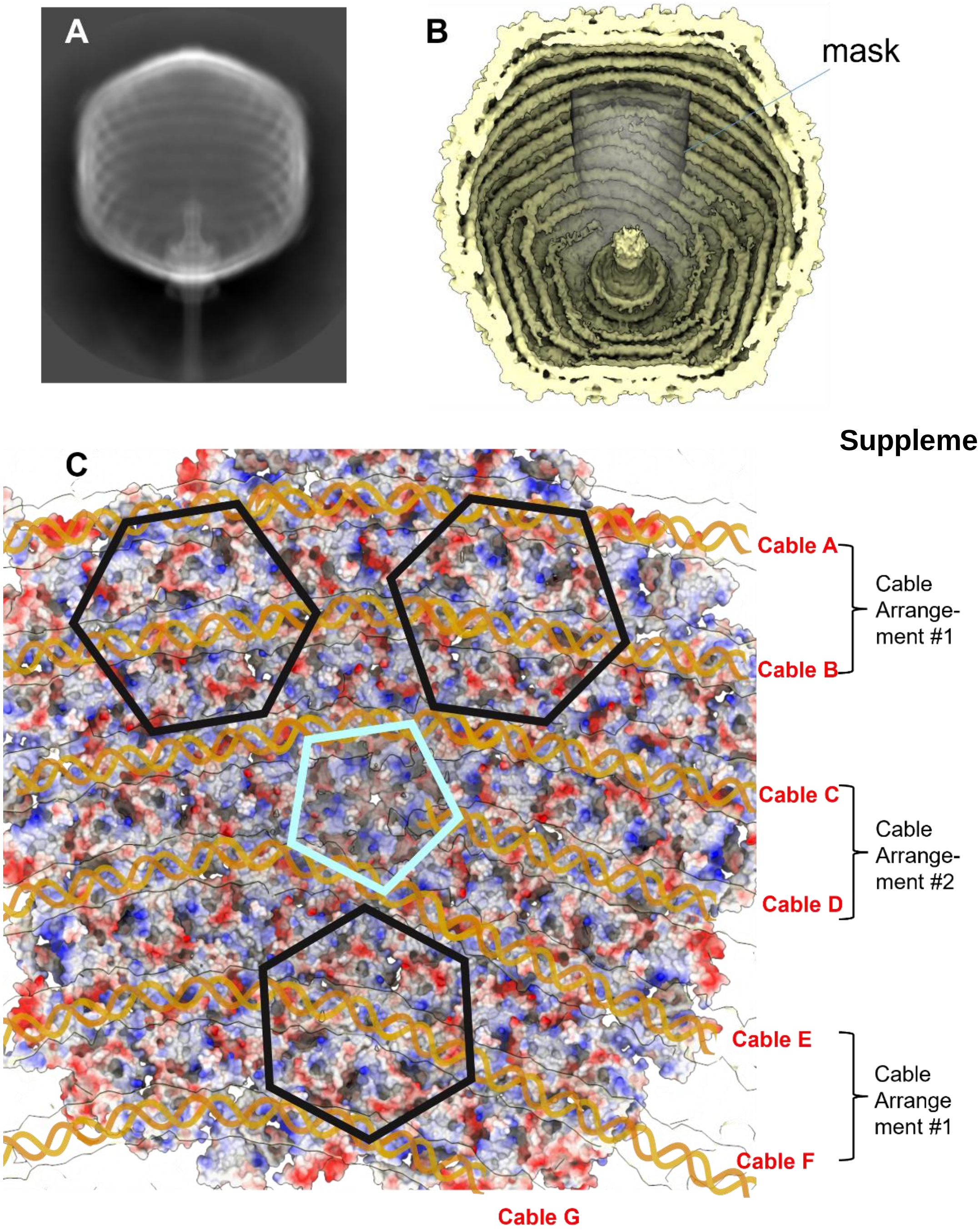
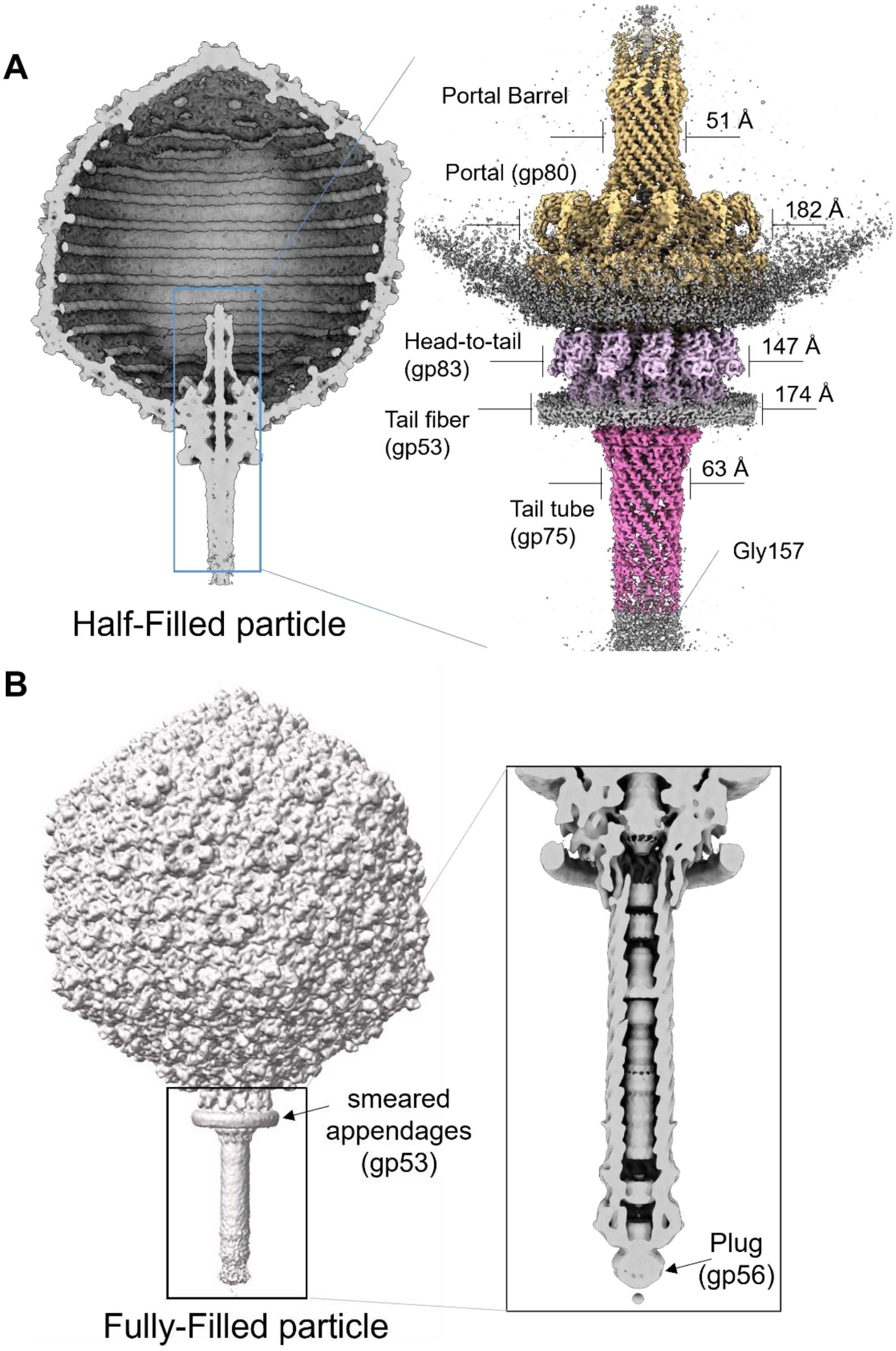
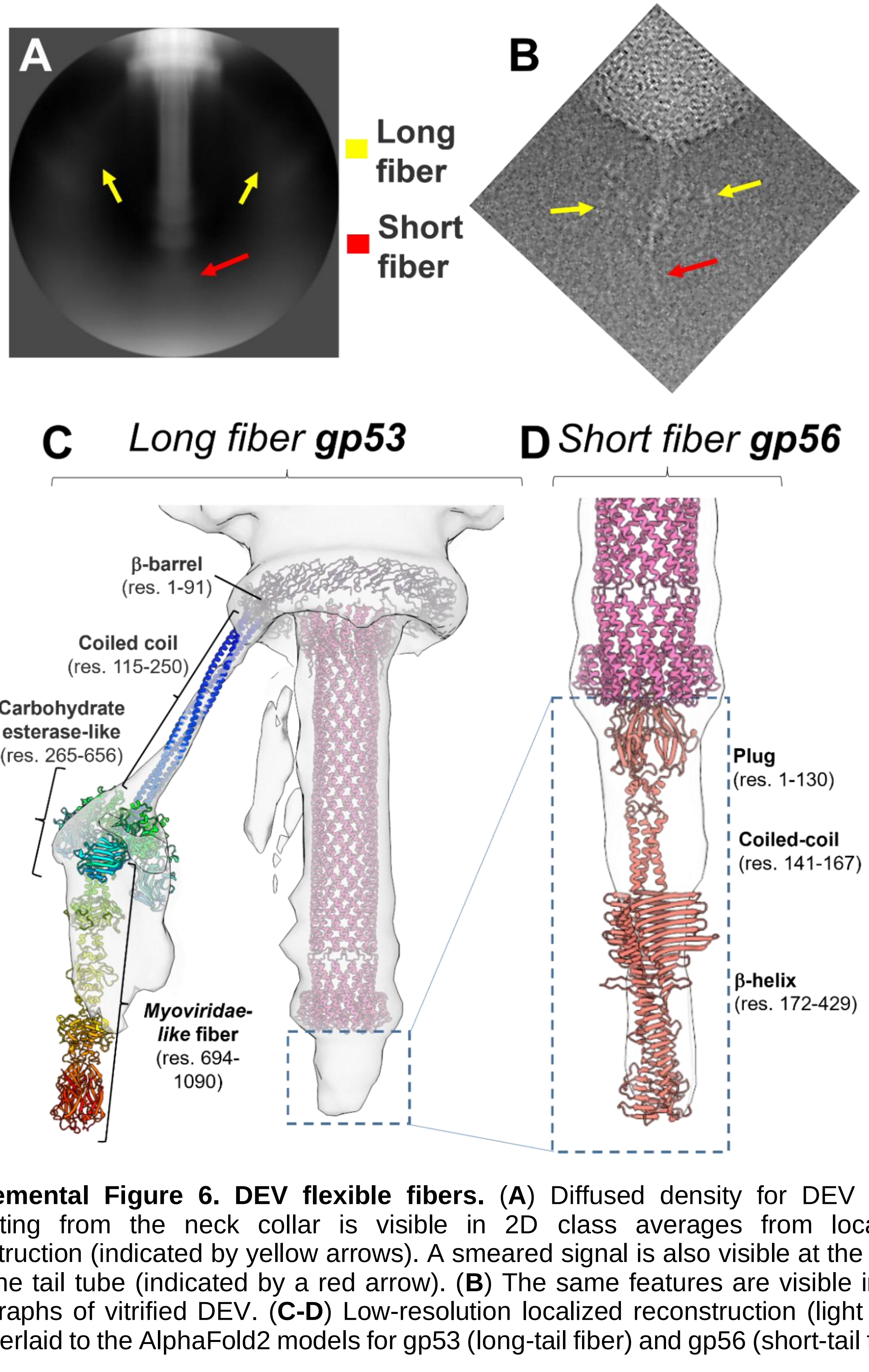


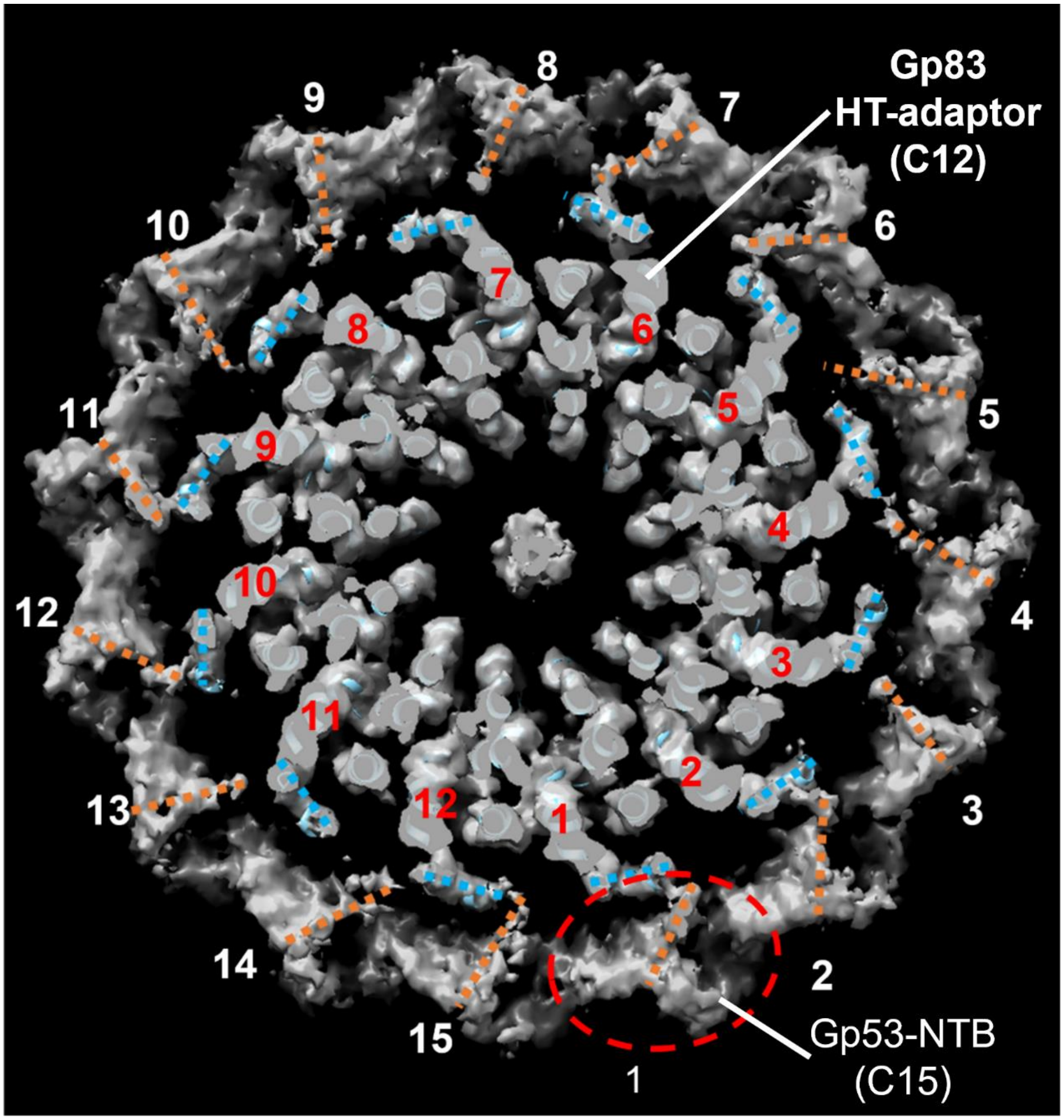
Figure 4. Localized reconstruction of DEV cables. (**A**) An averaged 2D projection from I3 expanded particles aligned locally with the tail (C5-C12 symmetry aligned). (**B**) A 3D reconstruction from C5-C12 aligned particles showing the interior of the capsid. (**C**) A focused reconstruction of one capsid five-fold vertex visualized from the inside of the capsid generated using the transparent cylindrical mask shown in panel (**B**). The density reveals an asymmetric pattern of seven cables (labeled A-G) relative to the capsid exons (black) and penton (gray). Double-stranded DNA helices were modeled inside the cable densities that are displayed onto an electrostatic surface representation of the DEV capsid interior.



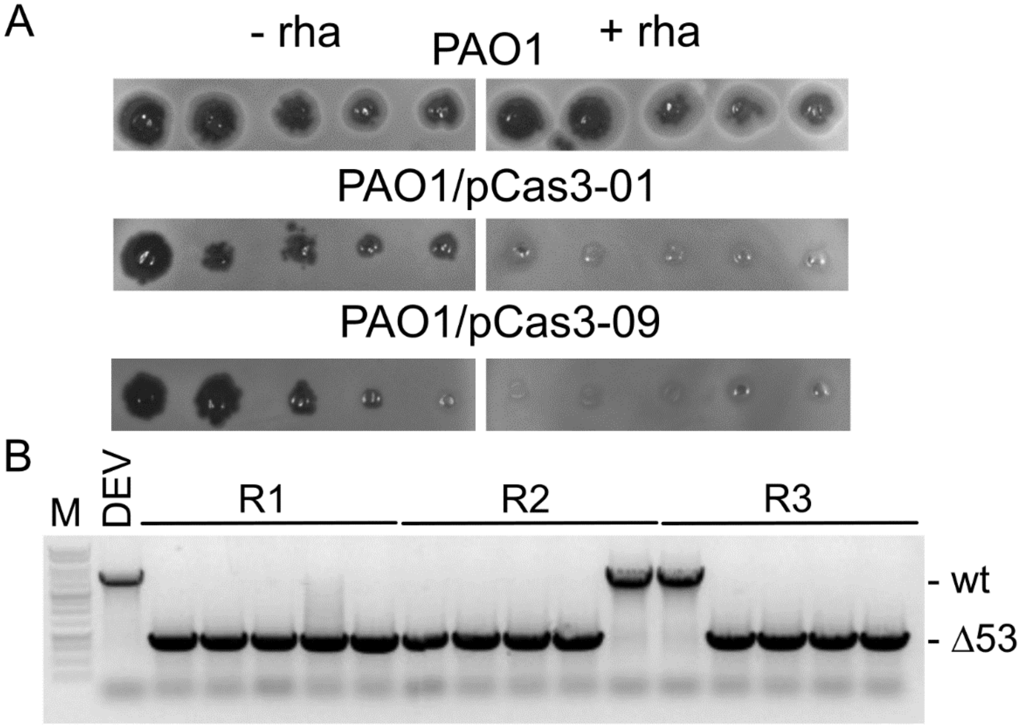
Supplemental Figure 5. Cryo-EM reconstructions. (**A**) **DEV tail apparatus from Half-Filled particles.** Section view of an HF particle, with a magnified view of the C12, symmetrized localized reconstruction of the unique vertex colored coded by component. The 3.5 Å map is contoured at 3.5σ. (**B**) C1 reconstruction of DEV mature virion calculated at 7 Å map and contoured at 2.0 σ reveals a plug-like density at the tail tube tip, distal from the capsid, that we assigned to gp56.



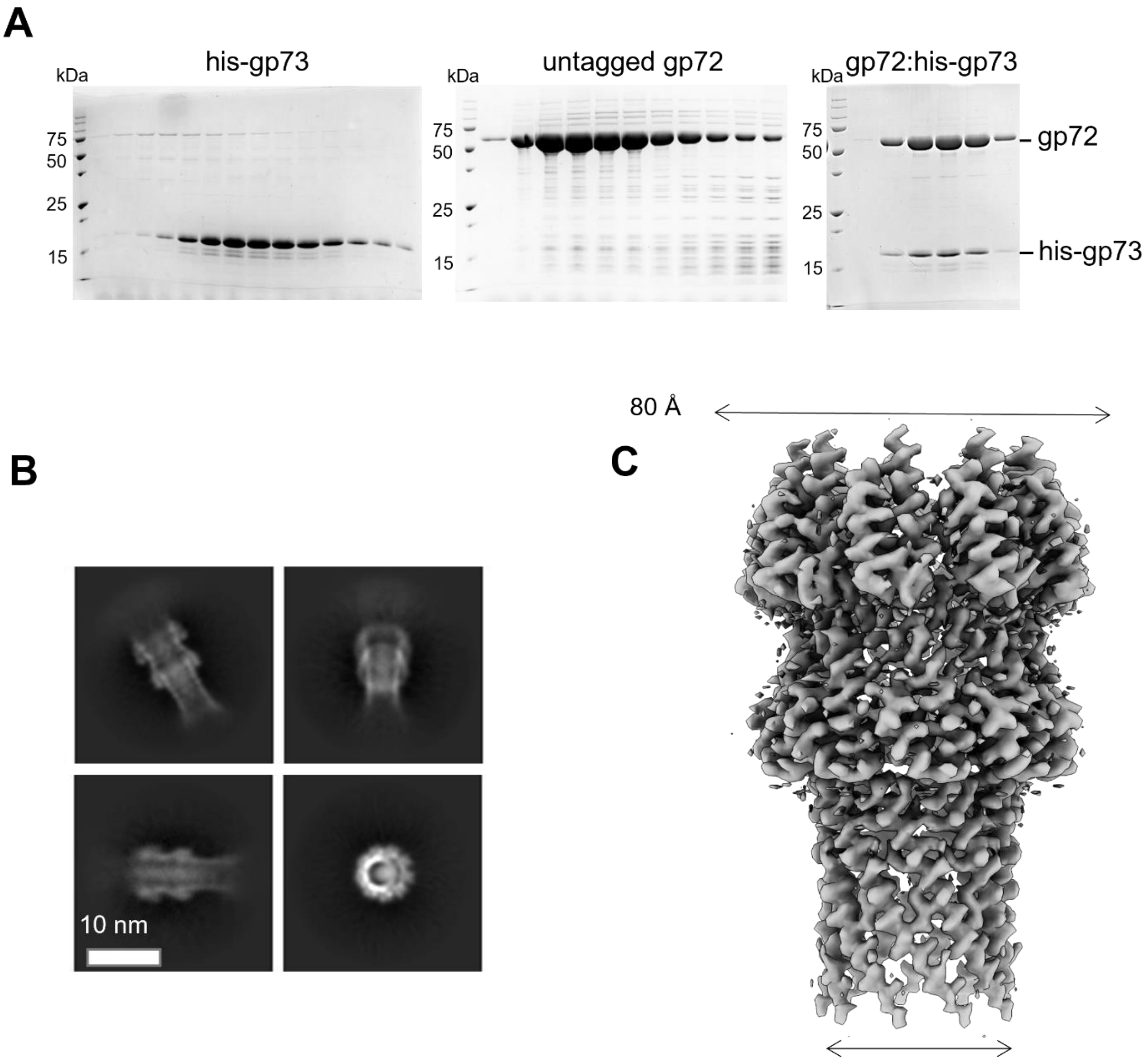
Supplemental Figure 6. DEV flexible fibers. (**A**) Diffused density for DEV fibers emanating from the neck collar is visible in 2D class averages from localized reconstruction (indicated by yellow arrows). A smeared signal is also visible at the distal tip of the tail tube (indicated by a red arrow). (**B**) The same features are visible in raw micrographs of vitrified DEV. (**C-D**) Low-resolution localized reconstruction (light gray) was overlaid to the AlphaFold2 models for gp53 (long-tail fiber) and gp56 (short-tail fiber).



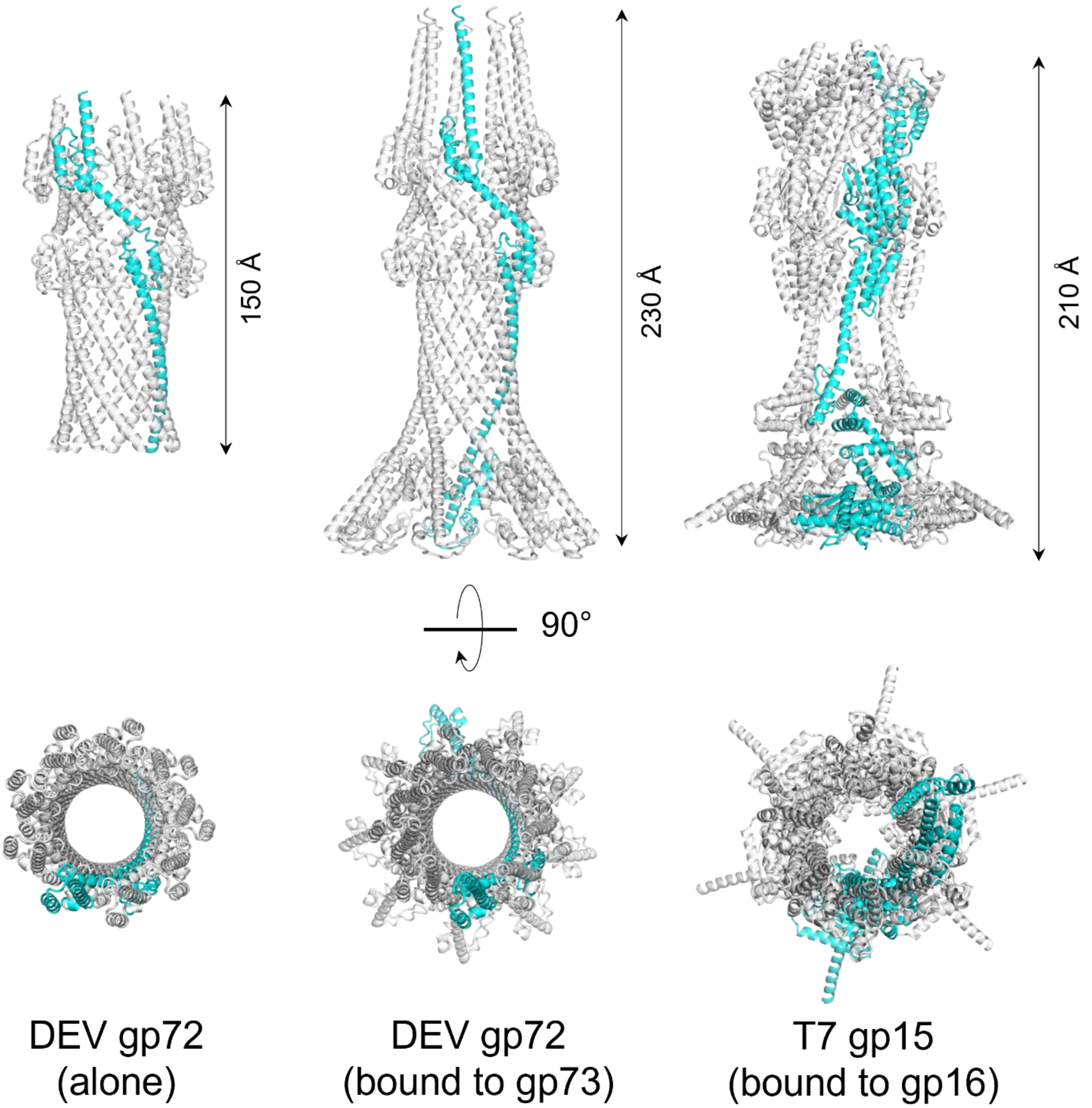
Supplemental Figure 7. Symmetry mismatch between DEV long tail fiber gp53 and the HT-adaptor gp83. A cut-out view from inside the capsid of the DEV tail shows a glimpse of the asymmetric C1 map. Gp53 exists in 15 copies (the protomer is circled in red), generating a symmetry mismatch with 12 copies of gp83 (numbered in red).



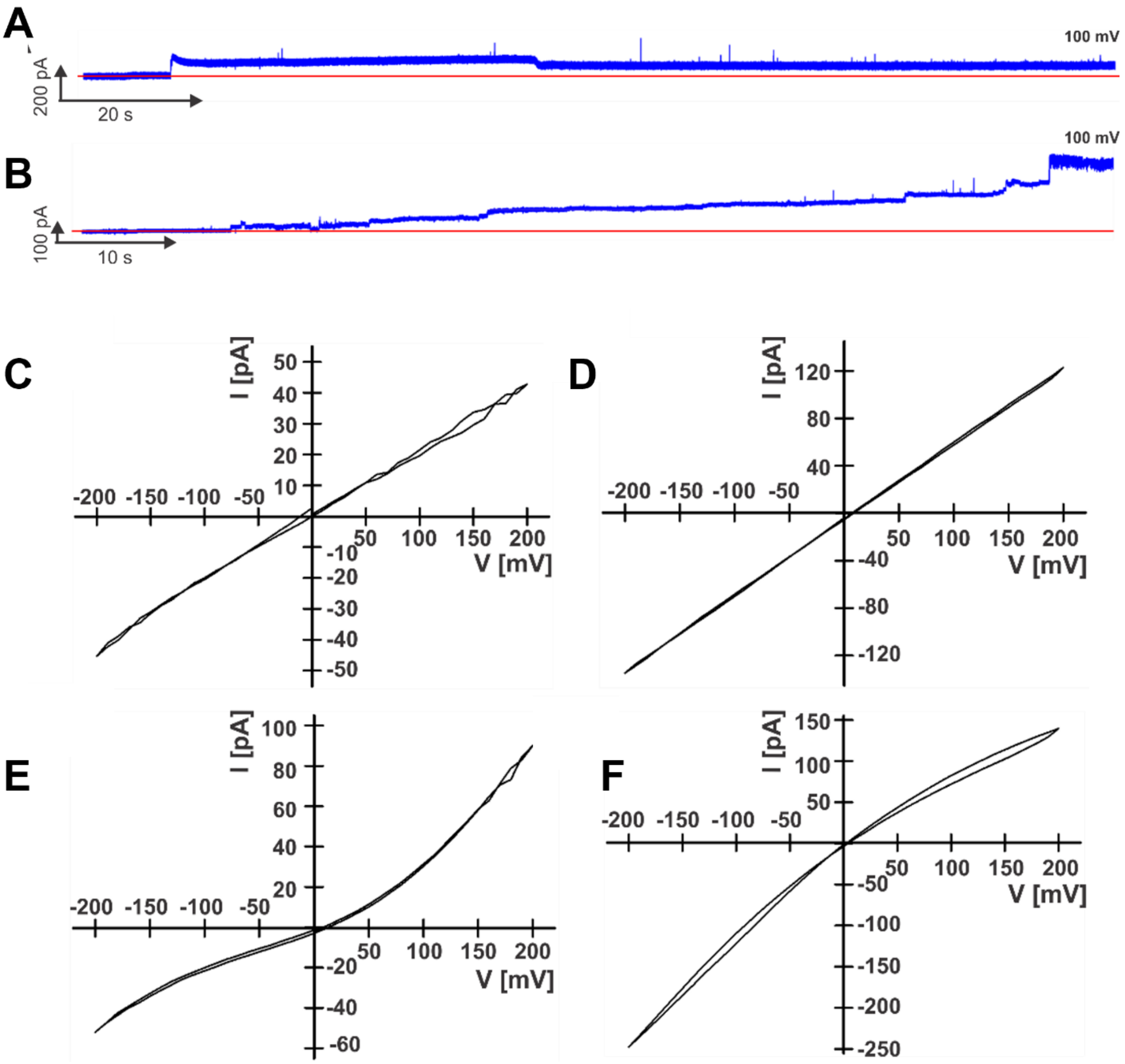
Supplemental Figure 8. DEV gp53 mutagenesis. (**A**) Induction with rhamnose (rha) of cr-RNA53 and cas genes cloned in pCas3-01 and pCas3-09 prevents DEV growth on PAO1. Serial dilutions (x10) of the indicated phages were replicated on the indicated strains with (+) or without (-) rhamnose in the medium. (**B**) PCR analysis of gp53 locus. Plaques formed by phages able to grow on PAO1 only in the presence of pD53 plasmid were analyzed by PCR with the oligonucleotides 3806-3809. Five plaques derived from each of three replicate mutagenesis experiments, indicated as R1, R2, and R3, were analyzed. DEV, PCR performed on purified DEV DNA.



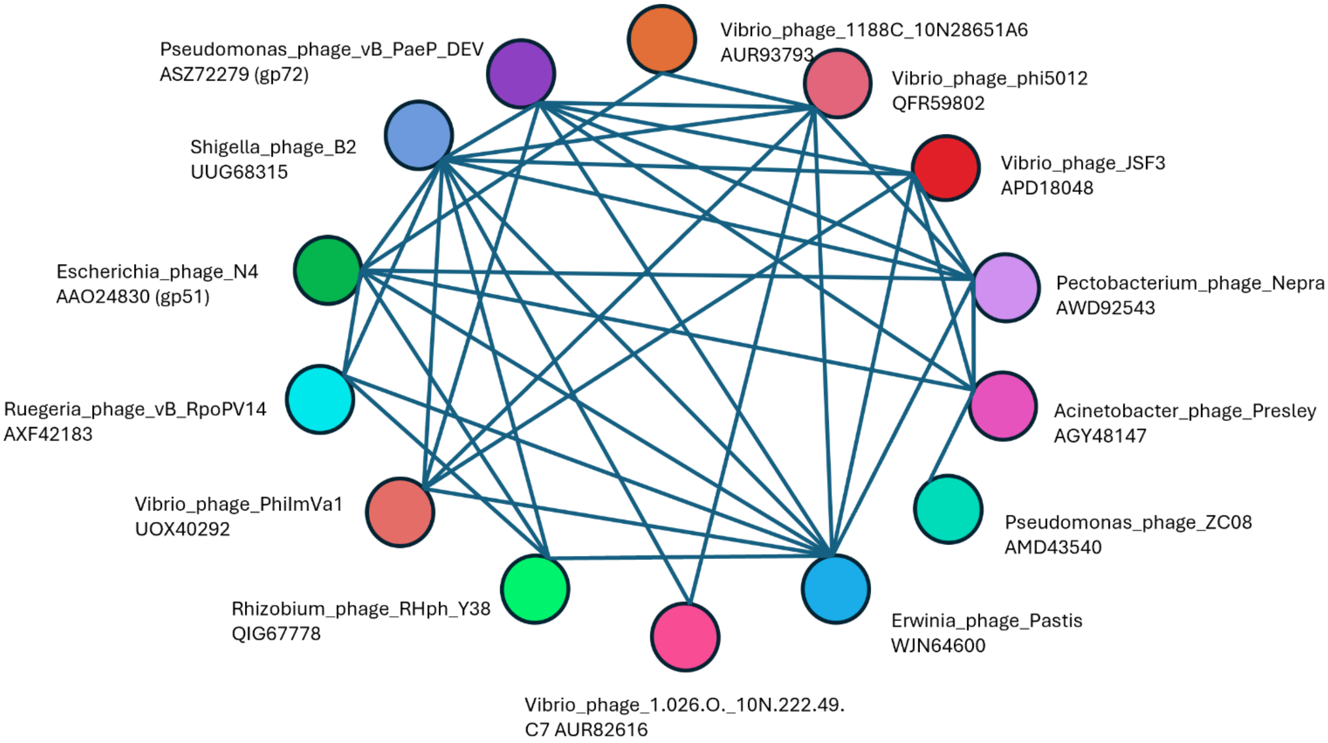
Supplemental Figure 9. DEV ejection protein gp72. (**A**) (left) SDS-PAGE analysis of purified his-gp73 solubilized from membranes; (middle) gp72 expressed under native conditions; (right) gel filtration fractions containing the gp72:gp73 complex. (**B**) Representative 2D classes of recombinant gp72. (**C**) 3D reconstruction of gp72 in the post-ejection conformation. The density is calculated at 3.65 Å resolution and is contoured at 3.5σ.



Supplemental Figure 10. Structural comparison of DEV gp72 (left and middle) and phage T7 gp17 periplasmic tunnel (PT). The central lumen of either tube-like structure measures 25-30 Å in diameter and is partially gated in T7. In all panels, only one protomer is colored in cyan, and all others are gray.



Supplemental Figure 11. Lipid bilayer experiments with purified gp73. Current traces with multiple insertions when 2.6 µg (**A**) or 1.9 µg (**B**) of protein is present in the cuvette. All experiments were performed at 100 mV applied potential in diphytanoyl phosphotidylcholine (DPhPC) membranes bathed in 1 M KCl, 10 mM HEPES, pH7.4 electrolyte. The protein samples were added to the grounded *cis* side of the cuvette which had 100 µm SU-8 aperture. (**C-F**) Current-voltage curves of purified gp72. Each panel shows current-voltage curves of one gp73 pore inserted in the membrane at the voltage range of -200 to 200 mV. All experiments were performed in diphytanoyl phosphotidylcholine (DPhPC) membranes bathed in 1 M KCl, 10 mM HEPES, pH 7.4 electrolyte. The protein samples were added to the grounded *cis* side of the cuvette which had 100 µm SU-8 aperture. At 100 mV pores had current amplitude of 21 pA (**C**), 60 pA (**D**), 31 pA (**E**), and 72 pA (**F**), respectively.



Supplemental Figure 12. Network diagram showing the significant predictions of gp72 homology based on comparisons of predicted tertiary structure. The disks are gp72-putative proteins for which Alphafold predicted the structure. The links show structures with >=90% probability of being homologs (according to Foldseek [1]).

Supplementary Table S1. DEV proteins identified by mass spectrometry.

Name[a]	Description	Length (AAs)[b]	MW [kDa][c]	Coverage [%]	Unique Peptides	SeqEst score	N4 homologous protein; virion presence[d]
gp27		184	21.7	24	5	12.04	NH
gp44		838	94.1	31	21	17.75	gp33; NI
gp50		170	18.7	29	6	34.07	NH
gp53	**Long Tail fiber**	**1090**	**117.9**	**23**	**19**	**42.70**	**NH**
gp54		**223**	**24.9**	**30**	**6**	**10.79**	**NH**
gp56	**Short Tail fiber**	**429**	**46.3**	**12**	**5**	**5.61**	**NH**
gp60	Putative DNA primase	724	82.4	21	15	8.65	gp43; NI
gp71	**vRNAP**	**3398**	**369.5**	**31**	**86**	**235.76**	**gp50**
gp72	**Ejection protein**	**521**	**57.1**	**35**	**14**	**7.95**	**NH**
gp75	**Tail tube**	**321**	**35.2**	**41**	**12**	**52.45**	**gp54**
gp76		221	25.0	47	5	9.77	gp55; NI
gp77	**Major coat protein**	**399**	**44.0**	**67**	**21**	**833.17**	**gp56; Y**
gp80	**Portal protein**	**726**	**81.6**	**50**	**32**	**164.74**	**gp59; Y**
gp83	**Head-tail adaptor**	**244**	**27.8**	**29**	**7**	**23.00**	**gp67; Y**

[a] Proteins identified by ≥ 5 unique peptides with a SeqEst score ≥ 5.
In bold, proteins identified also in the *Litunavirus* LIT1 virions [2].

DEV gp55, gp73, gp74, and gp78 orthologues of LIT1 virion proteins were identified by 1, 2, 8, and 7 unique peptides, respectively, and SeqEst score of 0. The orthologue of LIT1 gp52 was not detected.

[b] AAs, amino acids.
[c] MW, molecular weight.
[d] The gp names in this column refer to *E. coli* phage N4 nomenclature. NH, No Homologous protein in N4; NI, the homologous protein exists, but it was Not Identified in N4 virions [3]; Y, Yes, the homologous protein was identified in N4 virions [3].

Supplementary Table S2. Bacteria, phages, and plasmids

Bacteria

Name	Relevant feature	Reference
PAO1	Standard lab strain	[4]
PADR6	Frame shift mutation in *wzy*	[5]
PAER5b	Nonsense mutation in *wapH*	[5]
PAER6b	Frame shift mutation in *galU*	[5]
PAER10b	Nonsense mutation in *algC*	[5]

Bacteriophages

Name	Relevant features[a]	Reference
DEV		[6]
DEV Δ53	Deletion 29656-32966; it eliminates gp53	This work

Plasmids

Name	Relevant features[a]	Reference
pCas3cRh	It expresses the components of Type I-C CRISPR-Cas system	[7]
pCas3-01	pCas3cRh derivative carrying DEV 31196-31229 region; it expresses cr-RNA53 targeting gp53	This work
pCas3-09	pCas3-01 derivative carrying the two gp53 flanking regions with coordinates 29171-29655 and 32967-33450	This work
pD53	pGM2148 derivative with 9 silent point mutations in the 31198-31230 region targeted by cr-RNA53	This work
pGM931	Shuttle vector carrying *araC-araBp* region	[8]
pGM2148	pGM931 derivative carrying the gp53-encoding 29656-32949 region	This work
gp72_pET 30b(+)	untagged gp72 cloned in pET30b(+) between NdeI and XhoI	This work
gp73_pET 22b(+)	gp73 cloned in pET22b(+) between NdeI and XhoI comprising C-terminal 6x his tag	This work

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[a] Coordinates refer to Genbank MF490238.1

Supplementary Table S3. Oligonucleotides used in this study

Name	Sequence[a]	Coordinates[b]
3697	GAAAC*GTGCCCTGCATGGAGTTGAACAGCACTACCTGAG*G	31195-31229
3698	GCGAC*CTCAGGTAGTGCTGTTCAACTCCATGCAGGGCAC*G	31229-31195
3804	CTCTCTACTGTTTCTCCATGGTAC*ACGGTACACTGCACGCTC*	32966-32949
3805	GACTCTAGAGGATCCCCGGGTAC*TTATTTCCACCGTCCTACTGCG*	29656-29677
3806	*CCCTCATGGTTTCATGGAC*	33450-33432
3807	*TTATTCGATGGCCAACAAAGG*	32967-32987
3808	***CCTTTGTTGGCCATCGAATAAT**GCAATTCATCCTCAAGCCTG*	**32987-32967**
		29654-29635
3809	*GTGAGGTCAGCTGTCTCC*	29171-29188
3840	CGGGGATTCCTTAAGGTA*CCCTCATGGTTTCATGGAC*	33450-33432
3841	GTTATGCAGCGGAAAGTA*GTGAGGTCAGCTGTCTCC*	29171-29188
3859	*GAAGAGGACAACTTGTGCACCGACAGCATGAAGC*	31230-31198
3955	*AATTCGATGCAAGGGACGAAGGCGTACAACGATG*	31212-31179
3969	*CGTCACCAGCAGCAGTCTG*	54401-54419
3970	*TTCGGAGTCGAGTTGGATACTTC*	56827-56805
Gp72-f	CGCTATGGCATATGAACGAAGAACACGCTATTC	
Gp72-r	CGCTATCTCGAGTTACTCTTCATCCTCCTCTTC	
Gp73-f	CGCTATGGCATATGGCCTATCCGTACAGTGATATG	
Gp73-r	CGCTATCTCGAGGCGAATCCGGTTCCGTTCC	

[a]DEV sequences are in italics. Silent mutations in 3859 and 3955 are in yellow.
[b]Coordinates refer to GenBank MF490238.1

Supplementary Table S4. Residues involved in the intermolecular interactions between gp72-gp73.

Gp72	Residue position (Chain)	Gp73	Residue position (Chain)	Type of interaction	Non-bonded contacts (<4Å)
Gln44	J	Phe64	A	H bond	56
Gly25	J	Ala94	B	H bond	27
Gly25	J	Gln98	B	H bond	
Gly25	K	Ala94	C	H bond	32
Asn50	K	Gln73	C	H bond	
Gln44	K	Phe64	I	H bond	56
Gln44	L	Phe64	B	H bond	38
Gly25	L	Ala94	D	H bond	31
Gly25	M	Ala94	E	H bond	29
Gly25	M	Gln98	E	H bond	
Gln44	M	Phe64	F	H bond	55
Asn50	N	Gln73	F	H bond	25
Gly25	N	Gln98	F	H bond	
	N		G		40
Gly25	O	Ala94	G	H bond	28
Gln44	O	Phe64	H	H bond	56
Gly25	P	Ala94	H	H bond	26
Asn50	P	Gln73	H	H bond	
	P		C		62
Gly25	Q	Ala94	I	H bond	29
Gly25	Q	Gln98	I	H bond	
Asn50	Q	Gln73	I	H bond	
Gln44	Q	Phe64	D	H bond	47
Gly25	R	Gln98	A	H bond	29
Asn50	R	Gln73	A	H bond	
Gln44	R	Phe64	E	H bond	57

Intermolecular interactions between gp72 (chains J-R) and gp73 (chains A-I). The total number of non-bonded contacts (<4Å) between the chains of the gp72 and gp73 are shown in the last column.

Supplementary Table S5. Summary of lipid bilayer experiments with purified DEV ejection proteins at 100 mV in DPhPC membranes.

Sample	Total membranes	Membranes with insertions	Comments
Buffer	6	0	The buffer does not produce any insertion-like events.
gp73	88	17 (a total of 33 insertions)	Insertions observed in the range of 0.3 – 2.6 µg protein; observed pores were heterogeneous.
gp72	7	0	24 µg of protein was tested, which was 10 times greater than gp73.
gp72:gp73	19	1	No insertions, one membrane had 10-20 pA fluctuations of the baseline when 10 µg of protein sample was in the cuvette.

Supplementary Table S6. Names and accession numbers for all *Schitoviridae* genome sequences considered in this study. Accession numbers for gp71/gp50, gp72/gp51 and gp73/gp52 homologs are provided for each genome.

Phage	Genome sequence Accession	GP71 candidate	GP72 candidate	GP73 candidate	Clade*	Exemplar **
Escherichia_phage_vB_EcoM_PD205	GCA_024830925.1	UVK80525.1	UVK80524.1	UVK80523.1	1	
Escherichia_phage_KKP_3715	GCA_030875165.1	WLW40941.1	WLW40940.1	WLW40939.1	1	
Escherichia_phage_vB_EcoP_SP5M	GCA_013426605.1	QLF80667.1	QLF80676.1	QLF80705.1	1	
Escherichia_phage_vB_EcoP-ZQ2	GCA_019095225.1	QWY13177.1	QWY13176.1	QWY13175.1	1	
Escherichia_phage_PD38	GCA_003575305.1	AXY81341.1	AXY81342.1	AXY81343.1	1	
Shigella_virus_Moo19	GCA_020882845.1	UEN68863.1	UEN68864.1	UEN68865.1	1	
Escherichia_phage_PGN829.1	GCA_003575565.1	AXY82599.1	AXY82598.1	AXY82596.1	1	
Escherichia_phage_HK2	GCA_038023635.1	WYA83849.1	WYA83848.1	WYA83847.1	1	
Escherichia_phage_EC1-UPM	GCA_002617245.1	AGC31565.1	AGC31566.1	AGC31567.1	1	
Escherichia_phage_vB_EcoS_Uz-1	GCA_025085925.1	UWJ04322.1	UWJ04319.1	UWJ04318.1	1	
Escherichia_phage_UE-S5a	GCA_036584225.1	WVP99857.1	WVP99856.1	WVP99855.1	1	
Escherichia_phage_ECBP1	GCA_000900235.1	AFR52009.1	AFR52010.1	AFR52011.1	1	
Escherichia_phage_IME11	GCA_000903115.1	AFV29065.1	AFV29064.1	AFV29063.1	1	
Escherichia_phage_N4	GCA_000867865.1	AAO24831.2	AAO24830.1	AAO24829.1	1	Yes
Escherichia_phage_phi_G17	GCA_003307555.1	AWY03381.1	AWY03380.1	AWY03379.1	1	
Escherichia_phage_AlfredRasser	GCA_020892825.1	QXV75793.1	QXV75792.1	QXV75791.1	1	
Escherichia_phage_Bp4	GCA_000922735.2	AJB43741.1	AJB43738.1	AHN83378.1	1	
Escherichia_phage_OLB145	GCA_003723055.1	AYR04234.1	AYR04235.1	AYR04236.1	1	
Escherichia_phage_E20	GCA_027183915.1	WAQ79258.1	WAQ79267.1	WAQ79292.1	1	
Escherichia_phage_vB_Eco_SPSP	GCA_920105895.1	CAH0462296.1	CAH0462297.1	CAH0462298.1	1	
Escherichia_phage_St11Ph5	GCA_002956185.1	ATS92525.1	ATS92526.1	ATS92527.1	1	
Escherichia_phage_U1G	GCA_020475385.1	QXV71896.1	QXV71897.1	QXV71899.1	1	
Escherichia_phage_VEc25	GCA_016103715.1	QPN96319.1	QPN96320.1	QPN96322.1	1	

Escherichia_phage_vB_Eco_F22	GCA_027617965.1	WBF79664.1	WBF79673.1	WBF79699.1	1	
Escherichia_phage_vB_EcoP_3HA13	GCA_013112055.1	QDF14948.1	QDF14949.1	QDF14950.1	1	
Escherichia_phage_vB_EcoP_PhAPEC7	GCA_000924215.1	AHV82680.1	AHV82681.1	AHV82682.1	1	
Escherichia_phage_PMBT57	GCA_002958365.1	AUV59054.1	AUV59055.1	AUV59056.1	1	
Escherichia_phage_vB_EcoP_PhAPEC5	GCA_000922515.1	AGV99338.1	AGV99339.1	AGV99340.1	1	
Escherichia_phage_vB_Eco_AL25	GCA_943323295.1	CAH6421870.1	CAH6421871.1	CAH6421872.1	1	
Escherichia_phage_vB_Eco_Jura	GCA_905219675.1	CAE6410147.1	CAE6410162.1	CAE6410178.1	1	
Klebsiella_phage_VLCpiP4b	GCA_025085455.1	UVX31104.1	UVX31105.1	UVX31106.1	1	
Klebsiella_phage_KP8	GCA_002997455.1	AVJ48977.2	AVJ48978.1	AVJ48979.2	1	
Klebsiella_phage_VLCpiP4a	GCA_025085425.1	UVX30959.1	UVX30958.1	UVX30957.1	1	
Achromobacter_phage_JWAlpha	GCA_000914775.1	AHC94021.1	AHC94022.1	AHC94023.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy04	GCA_006964325.1	QDH83729.1	QDH83737.1	QDH83760.1	1	
Achromobacter_phage_JWDelta	GCA_002604185.1	AHC56581.1	AHC56582.1	AHC56583.1	1	
Achromobacter_phage_phiAxp-3	GCA_002211055.1	ALA45523.1	ALA45524.1	ALA45525.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy10	GCA_006964385.1	QDH83913.1	QDH83920.1	QDH83946.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy13	GCA_006964445.1	QDH84159.1	QDH84166.1	QDH84191.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy24	GCA_006964625.1	QDH84720.1	QDH84728.1	QDH84752.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy11	GCA_006964405.1	QDH83996.1	QDH84004.1	QDH84030.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy12	GCA_006964425.1	QDH84077.1	QDH84084.1	QDH84109.1	1	
Achromobacter_phage_vB_AxyP_19-32_Axy22	GCA_006964585.1	QDH84592.1	QDH84599.1	QDH84626.1	1	
Pseudomonas_phage_inbricus	GCA_002957155.1	ATW58114.1	ATW58115.1	ATW58116.1	1	
Pseudomonas_phage_Zuri	GCA_008375435.2	QEM41168.1	QEM41169.1	QEM41170.1	1	
Erwinia_phage_vB_EamP_Rexella	GCA_002757695.1	ANJ65299.1	ANJ65300.1	ANJ65301.1	1	
Erwinia_phage_vB_EamP_Frozen	GCA_002211075.1	ANJ65200.1	ANJ65201.1	ANJ65202.1	1	
Erwinia_phage_vB_EamP_Gutmeister	GCA_002757715.1	ANJ65375.1	ANJ65376.1	ANJ65377.2	1	
Erwinia_phage_Ea9-2	GCA_000917295.1	AHI60130.1	AHI60131.1	AHI60132.1	1	
Erwinia_phage_Kuerle	GCA_027886455.1	WBQ32526.1	WBQ32527.1	WBQ32528.1	1	

Erwinia_phage_Fifi067	GCA_026898295.1	WAK44948.1	WAK44947.1	WAK44946.1	1	
Stenotrophomonas_phage_Piffle	GCA_020484305.1	QYW01922.1	QYW01923.1	QYW01924.1	1	
Stenotrophomonas_phage_Paxi	GCA_020484155.1	QYW01833.1	QYW01834.1	QYW01835.1	1	
Xanthomonas_virus_PB119	GCA_032918195.1	UZV39846.1	UZV39847.1	UZV39848.1	1	
Xanthomonas_phage_RiverRider	GCA_003014195.2	AVO23151.1	AVO23152.1	AVO23153.1	1	
Stenotrophomonas_phage_Pokken	GCA_008215305.1	QEG09290.1	QEG09291.1	QEG09292.1	1	
Podoviridae_sp._ctda_1	GCA_003657585.1	AXH72064.1	AXH72079.1	AXH72022.1	1	
Stenotrophomonas_phage_Philippe	GCA_020484275.1	QYW02270.1	QYW02271.1	QYW02272.1	1	
Stenotrophomonas_phage_C121	GCA_022213615.1	UKL14807.1	UKL14808.1	UKL14809.1	1	
Alcaligenes_phage_vB_Af_QDWS595	GCA_020523195.2	UCR75508.1	UCR75507.1	UCR75506.1	1	
Delftia_phage_RG-2014	GCA_002037815.1	AIU44322.1	AIU44323.1	AIU44324.1	1	
Burkholderia_phage_vB_BpP_HN02	GCA_036429425.1	WVK89986.1	WVK89988.1	WVK89989.1	1	
Burkholderia_phage_vB_BpP_HN01	GCA_023239875.1	UNI71499.1	UNI71500.1	UNI71501.1	1	
Sinorhizobium_phage_ort11	GCA_008605685.1	QEP29865.1	QEP29866.1	QEP29867.1	2	
Rhizobium_phage_RHph_I1_6	GCA_016835625.1	QIG76594.1	QIG76595.1	QIG76596.1	2	
Rhizobium_phage_RHph_Y2_6	GCA_016835375.1	QIG68811.1	QIG68812.1	QIG68813.1	2	
Rhizobium_phage_RHEph16	GCA_020492045.1	QXV74378.1	QXV74379.1	QXV74380.1	2	
Rhizobium_phage_RHph_X3_15	GCA_020492015.1	QWY83756.1	QWY83757.1	QWY83758.1	2	
Rhizobium_phage_RHEph24	GCA_020492085.1	QXV74841.1	QXV74842.1	QXV74843.1	2	
Rhizobium_phage_RHph_N38	GCA_016835845.1	QIG70535.1	QIG70536.1	QIG70537.1	2	
Rhizobium_phage_RHEph22	GCA_020492075.1	QXV74747.1	QXV74748.1	QXV74749.1	2	
Rhizobium_phage_RHph_X2_28B	GCA_020492005.1	QWY83520.1	QWY83521.1	QWY83522.1	2	
Rhizobium_phage_RHph_Y38	GCA_016836155.1	QIG67777.1	QIG67778.1	QIG67779.1	2	Yes
Agrobacterium_phage_OLIVR2	GCA_017903505.1	QIW87388.1	QIW87389.1	QIW87390.1	2	
Agrobacterium_phage_OLIVR3	GCA_017903515.1	QIW87495.1	QIW87496.1	QIW87497.1	2	
Agrobacterium_phage_OLIVR1	GCA_017903485.1	QIW87281.1	QIW87282.1	QIW87283.1	2	
Pseudomonas_phage_ZC08	GCA_002605525.1	AMD43541.1	AMD43540.1	AMD43539.1	3	Yes

Pseudomonas_phage_ZC03	GCA_002605505.1	AMD43402.1	AMD43403.1	AMD43404.1	3	
Roseovarius_Plymouth_podovirus_1	GCA_008725535.1	CBX87992.1	CBX87993.1	CBX87994.1	4	
Dinoroseobacter_phage_DS-1410Ws-06	GCA_003329145.1	ANJ20714.1	ANJ20715.1	ANJ20716.1	4	
Roseobacter_phage_RD-1410Ws-07	GCA_003329165.1	ANJ20865.1	ANJ20866.1	ANJ20867.1	4	
Dinoroseobacter_phage_DFL12phi1	GCA_000923015.1	AHX00983.1	AHX00982.1	AHX00981.1	4	
Ruegeria_phage_vB_RpoP-V21	GCA_003308675.1	AWY09017.1	AWY09018.1	AWY09019.1	4	
Ruegeria_phage_vB_RpoP-V13	GCA_003308735.1	AWY09411.1	AWY09412.1	AWY09413.1	4	
Ruegeria_phage_vB_RpoP-V14	GCA_003369325.1	AXF42182.1	AXF42183.1	AXF42184.1	4	Yes
Roseovarius_sp._217_phage_1	GCA_003329185.1	CBW47056.1	CBW47057.1	CBW47058.1	4	
Dinoroseobacter_phage_vB_DshP-R7L	GCA_020489665.1	UAT28905.1	UAT28906.1	UAT28907.1	4	
Ruegeria_phage_vB_RpoP-V17	GCA_003308775.1	AWY09578.1	AWY09579.1	AWY09580.1	4	
Silicibacter_phage_DSS3phi2	GCA_000882935.1	ACL81328.1	ACL81329.1	ACL81330.1	4	
Ruegeria_phage_vB_RpoP-V12	GCA_003308615.1	AWY08849.1	AWY08850.1	AWY08851.1	4	
Dinoroseobacter_phage_vBDshPR2C	GCA_002604525.1	AID16877.1	AID16878.1	AID16879.1	4	
Roseobacter_phage_RD-1410W1-01	GCA_003329205.1	ANJ20798.1	ANJ20799.1	ANJ20800.1	4	
Sulfitobacter_phage_phiCB2047-B	GCA_000905995.1	AGH07392.1	AGH07390.1	AGH07389.1	4	
Erwinia_phage_Pastis	GCA_033311155.1	WJN64599.1	WJN64600.1	WJN64601.1	5	Yes
Erwinia_phage_vB_EamP-S6	GCA_000901855.1	AEJ81598.1	AEJ81599.1	AEJ81600.1	5	
Salmonella_phage_vB_SenP_UTK0002	GCA_028897615.1	WDR22564.1	WDR22565.1	WDR22566.1	6	
Escherichia_phage_Pollock	GCA_001042195.1	AIX12418.1	AIX12419.1	AIX12420.1	6	
Pseudomonas_phage_MY01	GCA_035135045.1	WQY99713.1	WQY99714.1	WQY99715.1	6	
Salmonella_phage_FSL_SP-076	GCA_000909555.1	AGF88373.1	AGF88374.1	AGF88375.1	6	
Klebsiella_phage_KpCHEMY26	GCA_007998555.1	QEA03295.1	QEA03303.1	QEA03328.1	6	
Enterobacter_phage_EcP1	GCA_000900655.1	ADU79201.1	ADU79202.1	ADU79203.1	6	
Salmonella_phage_FSL_SP-058	GCA_000908895.1	AGF88174.1	AGF88175.1	AGF88176.1	6	
Shigella_phage_B2	GCA_024606155.1	UUG68314.1	UUG68315.1	UUG68316.1	6	Yes
Salmonella_phage_vB_SenP_UTK0001	GCA_028897605.1	WDR22471.1	WDR22472.1	WDR22473.1	6	

Salmonella_phage_SP154	GCA_030221985.1	WIC41624.1	WIC41625.1	WIC41626.1	6	
Salmonella_phage_vB_SalP_TR2	GCA_017347905.1	QSJ04060.1	QSJ04059.1	QSJ04058.1	6	
Pseudomonas_phage_phCDa	GCA_003341435.1	AXC36451.1	AXC36452.1	AXC36453.1	7	
Pseudomonas_phage_98PfluR60PP	GCA_003143395.1	AWH15475.1	AWH15476.1	AWH15477.1	7	
Pseudomonas_phage_Littlefix	GCA_002958475.1	AUV61826.1	AUV61827.1	AUV61828.1	7	
Pseudomonas_phage_vB_PaeS_TUMS_P6	GCA_021216575.1	UGL60893.1	UGL60892.1	UGL60891.1	7	
Pseudomonas_phage_vB_PaeP_YL2	GCA_038023055.1	WMI40382.1	WMI40381.1	WMI40380.1	7	
Pseudomonas_phage_phiPA1-3	GCA_030439585.1	WJY90848.1	WJY90849.1	WJY90850.1	7	
Pseudomonas_phage_vB_Pae575P-3	GCA_002611145.1	ANT44349.1	ANT44350.1	ANT44351.1	7	
Pseudomonas_phage_vB_Pae1396P-5	GCA_002611165.1	ANT44439.1	ANT44440.1	ANT44441.1	7	
Pseudomonas_phage_vB_PaeP_PYO2	GCA_002955935.1	ASZ72120.1	ASZ72121.1	ASZ72122.1	7	
Pseudomonas_phage_vB_PaeS_TUMS_P81	GCA_021216585.1	UGL60979.1	UGL60978.1	UGL60977.1	7	
Pseudomonas_phage_vB_PaeP_4029	GCA_025767325.1	UYE96391.1	UYE96483.1	UYE96482.1	7	
Pseudomonas_phage_YH30	GCA_001551385.1	AKC04779.1	AKC04777.1	AKC04776.1	7	
Pseudomonas_phage_LP14	GCA_003307395.1	AWY02724.1	AWY02723.1	AWY02722.1	7	
Pseudomonas_phage_PAP02	GCA_022516425.1	QKE55114.1	QKE55115.1	QKE55116.1	7	
Pseudomonas_phage_Pa2	GCA_001040995.1	AIZ94913.1	AIZ94914.1	AIZ94915.1	7	
Pseudomonas_phage_phi176	GCA_002756415.1	AIZ95005.1	AIZ95006.1	AIZ95007.1	7	
Pseudomonas_phage_PASB7	GCA_034857665.1	WNV46167.1	WNV46168.1	WNV46169.1	7	
Pseudomonas_phage_PEV2	GCA_001745375.1	ANJ63774.1	ANJ63775.1	ANJ63776.1	7	
Pseudomonas_phage_vB_Pae-PA14	GCA_030294685.1	QWT71827.1	QWT71828.1	QWT71829.1	7	
Pseudomonas_phage_KPP21	GCA_001501535.1	BAR94673.1	BAR94561.1	BAR94562.1	7	
Pseudomonas_phage_PaVOB	GCA_029948365.1	WGN90647.1	WGN90650.1	WGN90676.1	7	
Pseudomonas_phage_vB_PaeP_YL1	GCA_038023045.1	WMI40290.1	WMI40291.1	WMI40292.1	7	
Pseudomonas_phage_VB_PaeP_VL1	GCA_021354665.1	UGV19870.1	UGV19871.1	UGV19873.1	7	
Pseudomonas_phage_PWJ	GCA_031678305.1	WMX17950.1	WMX17951.1	WMX17952.1	7	
Pseudomonas_phage_Ka4	GCA_036494945.1	WVM05154.1	WVM05155.1	WVM05156.1	7	

Pseudomonas_phage_LIT1	GCA_000884615.1	CAZ66327.1	CAZ66328.1	CAZ66329.1	7	
Pseudomonas_phage_vB_PaeP_TUMS_P121	GCA_020906675.1	UEP18653.1	UEP18652.1	UEP18651.1	7	
Pseudomonas_phage_vB_PaeP_4034	GCA_025767365.1	UYE96669.1	UYE96670.1	UYE96671.1	7	
Pseudomonas_phage_vB_PaeP_FMD5	GCA_037198375.1	WWY65178.1	WWY65177.1	WWY65176.1	7	
Pseudomonas_phage_vB_Pae_AM.P2	GCA_016117675.1	QKE55967.1	QKE55968.1	QKE55969.1	7	
Pseudomonas_phage_LUZ7	GCA_000886235.1	CAZ66214.1	CAZ66215.1	CAZ66216.1	7	
Pseudomonas_phage_vB_PaeP_PS28	GCA_030378535.1	WBM84633.1	WBM84725.1	WBM84724.1	7	
Pseudomonas_phage_PA26	GCA_002617265.1	AFO70568.1	AFO70569.1	AFO70570.1	7	
Pseudomonas_phage_vB_PaeP_DEV	GCA_002955955.1	ASZ72278.1	ASZ72279.1	ASZ72280.1	7	Yes
Pseudomonas_phage_CMS1	GCA_022818375.1	UNY40777.1	UNY40778.1	UNY40779.1	7	
Pseudomonas_phage_vB_PaeP_MAG4	GCA_001744375.1	AKH49516.1	AKH49517.1	AKH49518.1	7	
Pseudomonas_phage_vB_PaeP_TUMS_P10	GCA_022694565.1	UNI71975.1	UNI71974.1	UNI71973.1	7	
Pseudomonas_phage_PJNP053	GCA_036852185.1	WVX91144.1	WVX91145.1	WVX91146.1	7	
Pseudomonas_phage_PA15	GCA_022213705.1	WJZ49002.1	WJZ49003.1	WJZ49004.1	7	
Pseudomonas_phage_vB_PaeP_4032	GCA_025767355.1	UYE96582.1	UYE96484.1	UYE96485.1	7	
Pseudomonas_phage_YH6	GCA_001041435.1	AIX13227.1	AIX13228.1	AIX13229.1	7	
Pseudomonas_phage_Ka3	GCA_035135025.1	WQZ52371.1	WQZ52372.1	WQZ52373.1	7	
Pseudomonas_phage_vB_PaeP_C2-10_Ab09	GCA_000918275.1	CDN96879.1	CDN96880.1	CDN96881.1	7	
Pseudomonas_phage_DL64	GCA_001502375.1	AKF13985.1	AKF13984.1	AKF13983.1	7	
Pseudomonas_phage_vB_Pae_HMKU_23	GCA_035680835.1	WRN92285.1	WRN92284.1	WRN92283.1	7	
Pseudomonas_phage_RWG	GCA_002756395.1	AIZ94822.1	AIZ94823.1	AIZ94824.1	7	
Pseudomonas_phage_vB_PaeP_FBPa1	GCA_024830825.1	UVN14444.1	UVN14445.1	UVN14446.1	7	
Pseudomonas_phage_L15	GCA_032460475.1	WNV49457.1	WNV49456.1	WNV49455.1	7	
Pseudomonas_phage_vB_Pae_TUMS_P11	GCA_034513485.1	WQA18395.1	WQA18394.1	WQA18393.1	7	
Pseudomonas_phage_vB_PaP_HN01	GCA_036418805.1	WVH07442.1	WVH07441.1	WVH07440.1	7	
Klebsiella_phage_VB_KpP_HS106	GCA_026898345.1	WAK45185.1	WAK45186.1	WAK45187.1	8	
Klebsiella_phage_vB_KpP_FBKp27	GCA_016811475.1	QQV91599.1	QQV91616.1	QQV91642.1	8	

Klebsiella_phage_vB_KpnP_P184	GCA_017347815.2	QSJ03719.1	QSJ03718.1	QSJ03717.1	8	
Klebsiella_phage_pKP-BM327-1.1	GCA_026273175.1	UZN24491.1	UZN24492.1	UZN24493.1	8	
Kosakonia_phage_Kc283	GCA_021029385.1	QYN79871.1	QYN79872.1	QYN79873.1	8	
Pectobacterium_phage_vB_PatP_CB3	GCA_002989935.1	ARB11906.1	ARB11907.1	ARB11908.1	8	
Pectobacterium_phage_Horatius	GCA_015767185.1	QPL11026.1	QPL11027.1	QPL11028.1	8	
Pectobacterium_phage_Possum	GCA_015767195.1	QPL10924.1	QPL10925.1	QPL10926.1	8	
Pectobacterium_phage_vB_PatP_CB1	GCA_002989895.1	ARB11804.1	ARB11805.1	ARB11806.1	8	
Pectobacterium_phage_Nepra	GCA_003094315.1	AWD92544.1	AWD92543.1	AWD92542.1	8	Yes
Pectobacterium_phage_vB_PatP_CB4	GCA_002989955.1	AQT27923.1	AQT27924.1	AQT27925.1	8	
Acinetobacter_phage_Presley	GCA_000917335.1	AGY48146.1	AGY48147.1	AGY48148.1	9	Yes
Acinetobacter_phage_nACB1	GCA_027574535.1	WAW11592.1	WAW11599.1	WAW11633.1	9	
Vibrio_phage_1.025.O._10N.222.46.B6	GCA_003926495.1	AUR82509.1	AUR82508.1	AUR82507.1	10	
Vibrio_phage_vB_VspP_pVa5	GCA_002615085.1	APC46019.1	APC46042.1	APC46051.1	10	
Vibrio_phage_1.152.O._10N.222.46.E1	GCA_003928575.1	AUR90932.1	AUR90931.1	AUR90930.1	10	
Vibrio_phage_2.130.O._10N.222.46.C2	GCA_003931375.1	AUS02400.1	AUS02399.1	AUS02398.1	10	
Vibrio_phage_1.026.O._10N.222.49.C7	GCA_003926515.1	AUR82617.1	AUR82616.1	AUR82615.1	10	Yes
Vibrio_phage_1.150.O._10N.222.46.A6	GCA_003928535.1	AUR90759.1	AUR90758.1	AUR90757.1	10	
Vibrio_phage_VBP47	GCA_000904475.1	AGH57069.1	AGH57070.1	AGH57071.1	10	
Vibrio_phage_VBP32	GCA_000906955.1	AGH57223.1	AGH57222.1	AGH57221.1	10	
Vibrio_phage_phi50-12	GCA_009388365.1	QFR59803.1	QFR59802.1	QFR59801.1	11	Yes
Vibrio_phage_BUCT194	GCA_020475525.1	UAW01149.1	UAW01150.1	UAW01151.1	12	
Vibrio_phage_PhiImVa-1	GCA_029269715.1	UOX40291.1	UOX40292.1	UOX40293.1	12	Yes
Vibrio_phage_pVco-5	GCA_002620725.1	ARM71100.1	ARM71101.1	ARM71102.1	13	
Vibrio_phage_12VC501	GCA_025787795.1	UYF10881.1	UYF10880.1	UYF10879.1	13	
Vibrio_phage_VCO139	GCA_002603165.1	AGI61882.1	AGK85679.1	AGI61883.1	13	
Vibrio_phage_JSF3	GCA_002615685.1	APD18049.1	APD18048.1	APD18047.1	13	Yes
Vibrio_phage_JA-1	GCA_000908755.1	AGI61805.1	AGI61806.1	AGI61807.1	13	

Vibrio_phage_1.188.C._10N.286.51.A6	GCA_003929215.1	AUR93794.1	AUR93793.1	AUR93792.1	14	Yes
Vibrio_phage_1.188.B._10N.286.51.A6	GCA_003929195.1	AUR93708.1	AUR93707.1	AUR93706.1	14	
Vibrio_phage_1.169.O._10N.261.52.B1	GCA_003928835.1	AUR92093.1	AUR92094.1	AUR92095.1	14	
Vibrio_phage_1.188.A._10N.286.51.A6	GCA_003929175.1	AUR93622.1	AUR93621.1	AUR93620.1	14	
Vibrio_phage_1.261.O._10N.286.51.A7	GCA_003930555.1	AUR99055.1	AUR99054.1	AUR99053.1	14	
Vibrio_phage_1.224.A._10N.261.48.B1	GCA_003929875.1	AUR96421.1	AUR96420.1	AUR96420.1	14	

***** Refers to the clade to which the gp71/gp50 homolog was assigned.
** Sequences used as “exemplars” are indicated.

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