

Supplementary data

T4-like bacteriophages isolated from pig stools infect *Yersinia pseudotuberculosis* and *Yersinia pestis* using LPS and OmpF as receptors

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Supplementary Tables

Table S1. Bacterial strains used in this work.

Bacterial Strains	Serotype	Description	Reference or storage#
<i>Yersinia pseudotuberculosis</i>			
PB1	O:1a	Wild type, Guinea pig isolate	[1]
2812/79	O:1b	Human isolate, Turku, Finland	[2]
YPIII/PIB1	O:3	Wild type	[3]
PB1Δwb		Rough derivative of PB1, Km ^R	[4]
YpIIIΔwb		Rough derivative of YPIII, Km ^R	Constructed in parallel with strain PB1Δwb [4]
YPIII/pIB1::Δwb	O:3	Rough derivative of YPIII/pIB1, Km ^R	Constructed in parallel with strain PB1Δwb [4]
No.6	O:8	Cattle isolate, New Zealand. Spontaneous rough derivative of serotype O:1b	[5,6]
PB1-wbyM	O:1a	wbyM::pSW23T-wbyM, Clm ^R	[7]
15193/74-wbyM	O:1a	wbyM::pSW23T-wbyM, Clm ^R	[7]
BB1152	O:1a	Deer isolate, New Zealand	[8]
2884	O:2a	Wild type, rabbit isolate, Italy	[8]
Hatada A	O:2a	Wild type, human isolate, Japan	#3530
RD23	O:4b	Wild type, raccoon dog, Japan	[8]
1231	O:4b	Wild type, rodent isolate, Russia	[8]
6088	O:10	Racoon dog, Japan	[6]
MW387-1	O:10	Mountain water, Japan	#3896
OK5608	O:10	RD, Japan	[8]
R80	O:11	Wild rat, Japan	[6]
MW864-1	O:11	Mountain water, Japan	#3906
MW864-2	O:12	River water, Japan	[6]
MW896-2	O:12	Mountain water, Japan	#3915
N917	O:13	House rat, China	[8]
J51	O:13	Rabbit, China	[8]
CN3	O:14	Wild rat, China	[6]
93422	O:15	Human isolate	[6]
KHU9357	O:15	Human isolate, Korea	[8]
St.1	O:1a	Human isolate, Germany	[6]
Pa3606	O:1b	Human isolate, Japan	[6]
208	O:2a	Human isolate, Japan	[6]

1779	O:2b	Human isolate, Germany	[6]
366	O:2b	Human isolate, Japan	[8]
No.90	O:2b	Deer isolate, New Zealand	[8]
274	O:2c	Human isolate, Japan	[6]
C119	O:2c	Cat isolate, Japan	[8]
PC344	O:2c	Pig isolate, Japan	#3600
83	O:3	Human isolate	[6]
R1075-1	O:4a	Wild mice, Japan	#3672
546	O:4a	Human isolate, Russia	#3675
Pa3422	O:4b	Human isolate, Japan	[6]
PC594	O:4b	Pig isolate, Japan	#3721
PT593	O:4b	Pig isolate, Japan	#3722
204	O:5a	Human isolate	[6]
D54	O:5a	Dog isolate, Japan	[8]
D79	O:5a	Raccoon dog, Japan	#3759
197	O:5b	Human isolate, Japan	[6]
491	O:5b	Human isolate, Japan	#3795
OK5466	O:5b	Raccoon dog, Japan	[8]
DD110	O:6	Human isolate, Japan	[6]
DC226	O:6	Dog isolate, Japan	#3846
257	O:7	Dog isolate, Japan	[6]
MW99	O:7	Mountain water, Japan	#3865
R2093	O:7	Wild mice, Japan	#3866
151	O:8	Wild rat, Japan, spontaneous rough derivative of serotype O:4a	[5,6]
R670-1	O:9	Apodemus, Japan	#3887
R848	O:9	Mole, Japan	#3888
M1-fps2-wt	O:1a	Spontaneous phage fPS-2 resistant mutant	This work #6582
M2-fps2-wt	O:1a	Spontaneous phage fPS-2 resistant mutant	This work #6583
M3-fps2-wt	O:1a	Spontaneous phage fPS-2 resistant mutant	This work #6584
M1-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6585
M3-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6586
M4-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6587
M5-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6650
M6-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6651
M7-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6652
M8-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6653

M9-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6654
M10-fps90-wt	O:1a	Spontaneous phage fPS-90 resistant mutant	This work #6655
M1-fps65-wt	O:1a	Spontaneous phage fPS-65 resistant mutant	This work #6941
M2-fps65-wt	O:1a	Spontaneous phage fPS-65 resistant mutant	This work #6942
M3-fps65-wt	O:1a	Spontaneous phage fPS-65 resistant mutant	This work #6943
M4-fps90-wt/pTM100-ompF	O:1a	M4-fps90-wt complemented with wild type <i>ompF</i> gene, Clm ^R	This work #6887
M9-fps90-wt/pTM100-ompF	O:1a	M9-fps90-wt complemented with wild type <i>ompF</i> gene, Clm ^R	This work #6888
M1-fps90-wt/pTM100-galU	O:1a	M1-fps90-wt complemented with wild type <i>galU</i> gene, Tet ^R	This work #6889
M3-fps90-wt/pTM100-galU	O:1a	M3-fps90-wt complemented with wild type <i>galU</i> gene, Tet ^R	This work #6890
M5-fps90-wt/pTM100-galU	O:1a	M5-fps90-wt complemented with wild type <i>galU</i> gene, Tet ^R	This work #6891
M7-fps90-wt/pTM100-galU	O:1a	M7-fps90-wt complemented with wild type <i>galU</i> gene, Tet ^R	This work #6892
M10-fps90-wt/pTM100-galU	O:1a	M10-fps90-wt complemented with wild type <i>galU</i> gene, Tet ^R	This work #6893
M1-fps65-wt/pTM100-hldE	O:1a	M1-fps65-wt complemented with wild type <i>hldE</i> gene, Tet ^R	This work #7005
M3-fps65-wt/pTM100-hldE	O:1a	M3-fps65-wt complemented with wild type <i>hldE</i> gene, Tet ^R	This work #7006

Yersinia pestis

EV76 (#621)		Attenuated vaccine strain	[9,10]
EV76 (#1289)		Attenuated vaccine strain	[9,10]
EV76-c		Virulence plasmid-cured derivative of EV76	[10]
KIM M YP D1		Virulence plasmid-cured substrain of KIM10	[11]
KIM M YP D27		Nonpigmented substrain of KIM10	[11]
KIM M YP D34		Nonpigmented, pPla negative substrain of KIM10	[11]
KIM D27-ΔwaaQ		Deep rough, -2xHep, Km ^R	[4]
KIM D27-ΔwaaE		Deep rough, -Glc, Km ^R	[4]
KIM D27-ΔwaaL		Deep rough, -GlcNAc, Km ^R	[4]
KIM D27-ΔwabD		Deep rough, Km ^R	[4]

Yersinia similis

R2031	O:11	Apodemus, Japan	[8]
N916Ysi	O:12	House rat, China	[6]
Kuratani-2	O:1c	Mountain water, Japan	[6]
R220	O:6	Apodemus, Japan	[8]
R708	O:9	Wild rat, Japan	[6]

Yersinia wautersii

WP-931109	O:15	Water, Korea	[8]
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51	O:4a	France	[6]
<i>Enterobacter cloacae</i>			
tk5461		Human isolate, Turku, Finland	#804
123782		Human blood isolate, Finland	#5508
<i>Escherichia coli</i>			
IHE11002	O:1 K:1	Human urinary tract isolate, Finland	[12]
TKS 49		Human isolate, Turku, Finland	#802
tk5125		Human isolate, Turku, Finland	#803
tk533		Human isolate, Turku, Finland	#810
ATCC 35218		Canine, USA	#2102
DH10B		Cloning host	[13]
HB101		Cloning host	[14]
ω7249		Host strain for suicide plasmid delivery	[15]
<i>Klebsiella pneumoniae</i>			
tk5399		Human isolate, Turku, Finland	#808
123744		Human blood isolate, Helsinki, Finland	#5518
123695		Human blood isolate, Helsinki, Finland	#5529
123494		Human blood isolate, Helsinki, Finland	#5546
<i>Proteus mirabilis</i>			
O27 (50/57)	O:27		[16]
O28 (51/57)	O:28		[16]
S1959	O:3		Antoni Rozalski
<i>Providencia rettgeri</i>			
35415		Human isolate, Helsinki, Finland	#5030
31644		Human isolate, Helsinki, Finland	#5031
27815		Human isolate, Helsinki, Finland	#5032
<i>Salmonella enteritidis</i>			
SH94	Montevideo		[17]
ATCC 13311	Typhimurium		#1422
3851	Typhimurium	Human isolate, Oulu, Finland	#1423

<i>Shigella</i> 872	Quality control strain	#707
<i>Shigella flexneri</i> 784/83	Quality control strain	#519
<i>Shigella sonnei</i> 827/83	Quality control strain	#589
<i>Morganella</i> 61510	Human isolate, Helsinki, Finland	#5033

Table S2. Plasmids used in the study.

Plasmid	Description	Reference
pTM100-ompF	Complementation plasmid with wild-type <i>ompF</i> gene of <i>Y. pseudotuberculosis</i> PB1 cloned into the BamHI site of pTM100, Clm ^R	This work
pTM100-galU	Complementation plasmid with wild-type <i>galU</i> gene of <i>Y. enterocolitica</i> O:3 cloned into pTM100 at EcoRI and ScaI, Tet ^R	[18]
pRK2013	Triparental conjugation helper plasmid, Km ^R	[14]
pTM100-hldE	Complementation plasmid with wild-type <i>hldE</i> gene of <i>Y. enterocolitica</i> O:3 cloned into pTM100, Tet ^R , Diaminopimelic acid	[18]

Table S3. Host range and EOP analysis of the fPS-phages on different bacterial strains (Table S1).

Bacterial strains*	Spot assay			Relative EOP		
	fPS-2	fPS-65	fPS-90	fPS-2	fPS-65	fPS-90
<i>Y. pseudotuberculosis</i>						
PB1	+	+	+	1	1	1
2812/79	+	+	+	1.3×10^{-6}	1.6×10^{-4}	1.4×10^{-1}
YpIII/PIB1	-	+	-	-	1.6×10^{-7}	-
PB1 Δ wb	+	+	+	5.7×10^{-4}	1.3×10^{-4}	1.7×10^{-1}
YpIII Δ wb	-	+	-	-	1.7×10^{-5}	-
No.6	-	+	-	-	2.1×10^{-4}	-
PB1-wbyM	+	+	+	7×10^{-4}	2×10^{-4}	2.6×10^{-3}
15193/74-wbyM	+	+	+	5.7×10^{-7}	2.8×10^{-4}	6.2×10^{-3}
BB1152	+	+	+	1.8×10^{-1}	0.3	4.2×10^{-1}
2884	-	+	-	-	0.1	-
Hatada A	+	+	-	1.6×10^{-1}	1	-
RD23	-	+	-	-	0.4×10^{-1}	-
1231	+	+	+	1.6×10^{-6}	0.7×10^{-3}	2.1×10^{-2}
6088	-	-	-	-	-	-
MW387-1	-	-	-	-	-	-
OK5608	-	+	-	-	ND**	-
R80	-	-	-	-	--	-
MW864-1	-	-	-	-	-	-
MW864-2	+	-	+	ND	-	ND
MW896-2	-	-	-	-	-	-
N917	+	+	+	ND	ND	ND
J51	-	-	+	-	-	ND
CN3	-	+	-	-	ND	-
93422	-	-	-	-	-	-
KHU9357	-	+	-	-	ND	-
St.1	+	+	+	ND	ND	ND
Pa3606	-	-	-	-	-	-
208	+	+	-	ND	ND	-
1779	-	-	-	-	-	-

366	+	+	-	ND	ND	-
No.90	-	-	-	-	-	-
274	-	+	-	-	ND	-
C119	+	+	-	ND	ND	-
PC344	-	+	-	-	ND	-
83	-	-	-	-	-	-
YPIII/pIB1::Δwb	-	+	-	-	ND	-
R1075-1	+	+	+	ND	ND	ND
546	-	+	-	-	ND	-
Pa3422	-	+	-	-	ND	-
PC594	+	+	+	ND	ND	ND
PT593	+	+	+	ND	ND	ND
204	+	+	+	ND	ND	ND
D54	-	-	-	-	-	-
D79	-	-	-	-	-	-
197	+	+	+	ND	ND	ND
491	-	-	-	-	-	-
OK5466	+	+	+	ND	ND	ND
DD110	-	-	-	-	-	-
DC226	-	-	-	-	-	-
257	+	+	+	ND	ND	ND
MW99	-	-	-	-	-	-
R2093	-	-	-	-	-	-
151	-	-	-	-	-	-
R670-1	-	-	-	-	-	-
R848	-	-	-	-	-	-

Y. pestis

EV76	-	+	-	-	1.3 × 10 ⁻⁴	-
EV76-c	-	+	-	-	ND	-
D1	-	+	-	-	ND	-
D34	-	+	-	-	ND	-
D27	-	+	-	-	2.6 × 10 ⁻⁵	-
D27-ΔwaaQ	-	+	-	-	2.6 × 10 ⁻⁵	-
D27-ΔwaaE	-	+	-	-	0.3 × 10 ⁻⁵	-
D27-ΔwaaL	-	+	-	-	2.2 × 10 ⁻⁵	-
D27-ΔwabD	-	+	-	-	2.3 × 10 ⁻⁵	-

Y. similis

R2031	-	-	-	-	-	-
N916Ysi	+	-	+	ND	-	ND
Kuratani-2	-	-	-	-	-	-
R220	-	-	-	-	-	-
R708	-	-	-	-	-	-

Y. wautersii

WP-931109	-	-	-	-	-	-
51	-	-	-	-	-	-

E. cloacae

tk461	-	-	-	-	-	-
123782	-	-	-	-	-	-

E. coli

IHE 11002	+	+	+	0.2×10^{-3}	1.5×10^{-4}	4×10^{-1}
TKS 49	-	-	-	-	-	-
tk125	-	-	-	-	-	-
tk33	-	-	-	-	-	-
ATCC 35218	-	-	-	-	-	-

K. pneumoniae

tk399	-	-	-	-	-	-
123744	-	-	-	-	-	-
123695	-	-	-	-	-	-
123494	-	-	-	-	-	-

P. mirabilis

O27 (50/57)	-	-	-	-	-	-
O28 (51/57)	-	-	-	-	-	-
S1959	-	-	-	-	-	-

P. rettgeri

35415	-	-	-	-	-	-
31644	-	-	-	-	-	-
27815	-	-	-	-	-	-

S. enteritidis

SH94	-	-	-	-	-	-
ATCC 13311	-	-	-	-	-	-
3851	-	-	-	-	-	-

Shigella

872	-	-	-	-	-	-
784/83	-	-	-	-	-	-

Morganella

61510	-	-	-	-	-	-
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* The bacterial species and serotypes are mentioned in details in Table S1.

** ND (Not done).

Table S4. Comparison of the gene products of the fPS-phages with the corresponding T4 gene products. Identity % compared to gene product of FPS-2 is given in parenthesis for the other phages.

Predicted function	fPS-2	<i>n</i> aa	fPS-65	<i>n</i> aa	fPS-90	<i>n</i> aa	T4 phage	Gene product in T4
rIIA lysis inhibitor	Gp001	725	Gp001 (99%)	725	Gp001 (97.6%)	733	rIIA (98.2%)	rIIA protector from prophage-induced early lysis
rIIA lysis inhibitor	Gp002	67	Gp002 (100%)	67	Gp002 (100%)	67	rIIA.1 (98.5%) Gp60 Gp60.1	rIIA.1 hypothetical protein topoisomerase II, large subunit, C-terminal region hypothetical protein
DNA gyrase (Phage DNA topoisomerase large subunit in fPS-90)	Gp003	605	Gp003 (100%)	605	Gp004 (97%)	265	Gp39 (98.3%)	gp39 topoisomerase II, large subunit, N-terminal region
homing endonuclease					Gp003	605		
Phage protein	Gp004	86	Gp004 (97%)	87	Gp005 (97.6%)	86	Gp39.1 (100%) Gp39.2	hypothetical protein gp39.2 hypothetical protein
Phage protein	Gp005	141	Gp005	123	Gp007 (90%)	58	goF (92.2%)	goF mRNA metabolism modulator
Phage protein			Gp006	58	Gp006 (98.2%)	139		
Phage protein			Gp007 (75.9%) to Gp005	137				
cef modifier of suppressor tRNAs	Gp006	71	Gp008 (98.6%)	71	Gp008 (98.5%)	71	cef (98.5%)	cef modifier of suppressor tRNAs
hypothetical protein	Gp007	37			Gp009 (91.8%)	37		
Transcriptional regulator	Gp008	165	Gp009 (90.3%)	163	Gp010 (90.3%)	162	MotB (88.4%)	MotB modifier of transcription
Transcriptional regulator	Gp009	180	Gp010 (74.5%)	167	Gp011 (94.4%)	180	MotB.1 (52.1%)	MotB.1 hypothetical protein
Transcriptional regulator	Gp010	170	Gp011 (92.3%)	170	Gp012 (63.7%)	167	MotB.2 (59.7%)	MotB.2 hypothetical protein
DexA exonuclease A	Gp011	227	Gp012 (99%)	227	Gp013 (99.5%)	227	DexA (99.5%)	DexA exonuclease A
Phage exonuclease	Gp012	80	Gp013 (92.5%)	80	Gp014 (98.7%)	80	DexA.1 (91.2%)	DexA.1 hypothetical protein
Phage exonuclease	Gp013	81	Gp014 (96.3%)	81	Gp015 (90.1%)	81	DexA.2 (95%)	DexA.2 hypothetical protein
Phage protein	Gp014	86	Gp015 (98.8%)	86	Gp016 (97.6%)	86		
DNA helicase	Gp015	439	Gp016 (99.3%)	439	Gp017 (99.3%)	439	dda (97.7%)	DNA helicase
Phage protein	Gp016	103	Gp017 (97%)	103	Gp018 (91.2%)	103	Dda.1 (98%)	Dda.1 hypothetical protein
Phage anti-termination	Gp017	251	Gp018 (98.3%)	248	Gp019 (98.3%)	248	Srd (98.3%)	Srd anti-sigma factor
ADP-ribosyltransferase modA	Gp018	200	Gp019 (99%)	200	Gp020 (98.5%)	200	ModA (97.5%)	ModA RNA polymerase ADP-ribosylase

ADP-ribosyltransferase modA	Gp019	207	Gp020 (96.6%)	207	Gp021 (98.5%)	207	ModB (95.6%)	ModB ADP-ribosylase
periplasmic molybdenum-binding protein ModA	Gp020	60	Gp021 (98.3%)	60	Gp022 (98.3%)	60	ModA.2 (96.6%)	ModA.2 hypothetical protein
periplasmic molybdenum-binding protein ModA	Gp021	156	Gp022 (96%)	156	Gp023 (94.8%)	156	ModA.3 (95.5%)	ModA.3 hypothetical protein
periplasmic molybdenum-binding protein ModA	Gp022	50	Gp023 (98%)	54	Gp024 (98%)	54	ModA.4 (98%)	ModA.4 hypothetical protein
Srh transcription modulator	Gp023	67	Gp024 (100%)	67	Gp025 (97%)	67	Srh (97%)	Srh transcription modulator
Phage protein	Gp024	161	Gp025 (98%)	161	Gp026 (76.4%)	161	Mrh (97.5%)	Mrh transcription modulator under heat shock
Phage protein	Gp025	113	Gp026 (97%)	113	Gp027 (94.3%)	164	Mrh.1 (95.7%)	Mrh.1 hypothetical protein
Phage protein	Gp026	68	Gp027 (100%)	68	Gp028 (100%)	68	Mrh.2 (98.5%)	Mrh.2 hypothetical protein
Phage capsid and scaffold hypothetical protein	Gp027	78	Gp028 (47%)	81	Gp029 (45.9%)	80	Soc (47.3%)	Soc small outer capsid protein
phage protein	Gp028	278	Gp029 Gp030	69 64				
dCTP pyrophosphatase	Gp029	172	Gp031 (68.6%)	172	Gp030 (96.5%)	172	SegF Gp56 (75.5%)	SegF homing endonuclease gp56 dCTPase
Adenine-specific methyltransferase			Gp032	259			Dam (97.6%)	DNA adenine methyltransferase
Phage-associated homing endonuclease	Gp030	216			Gp031 (99%)	216		
Phage protein hypothetical protein	Gp031	66	Gp034 (92%) Gp033	186 66	Gp032 (93.9%)	66		
DNA primase, DNA helicase	Gp032	342	Gp035 (99%)	342	Gp033 (99.4%)	342	Gp61 (99.1%)	gp61 DNA primase subunit
Phage protein	Gp033	54	Gp036 (98%)	54	Gp034 (98.1%)	54	Gp61.1 (98.1%)	gp61.1 hypothetical protein
Phage protein	Gp034	208	Gp037 (99%)	157	Gp035 (100%)	208	Gp61.2 (99%)	gp61.2 hypothetical protein
spackle periplasmic protein	Gp035	97	Gp038 (96%)	97	Gp036 (96.9%)	97	Sp (98.9%)	spackle periplasmic protein
Phage protein	Gp036	85	Gp039 (98.8%)	85	Gp037 (95.2%)	85	Gp61.4 (96.4%)	gp61.4 hypothetical protein

discriminator of mRNA degradation	Gp037	60	Gp040 (98%)	60	Gp038 (98.3%)	60	Dmd (100%)	Dmd discriminator of mRNA degradation
DNA primase/helicase	Gp038	475	Gp041 (99.7%)	475	Gp039 (99.7%)	475	Gp41 (99.7%)	gp41 DNA primase-helicase subunit
Phage capsid and scaffold	Gp039	114	Gp042 (100%)	114	Gp040 (100%)	114	Gp40 (100%)	gp40 head vertex assembly chaperone
Phage recombination protein	Gp040	393	Gp043 (99.7%)	393	Gp041 (99.7%)	393	UvsX (90.2%)	UvsX RecA-like recombination protein
Glucosyl transferase	Gp041	280	Gp044 (98.5%)	280	Gp042 (98.9%)	280	SegA B-gt	SegA homing endonuclease beta glucosyl transferase
hypothetical protein	Gp042	213						
Deoxycytidylate 5-hydroxymethyltransferase	Gp043	246	Gp045 (93%)	246	Gp043 (93%)	246	Gp42 (93%)	gp42 dCMP hydroxymethylase
Phage immunity	Gp044	49	Gp046 (100%)	83	Gp044 (100%)	83	Imm (97.9%)	Imm immunity to superinfection membrane protein
Phage immunity	Gp045	126	Gp047 (98.4%)	126	Gp045 (99.2%)	126	Imm.1 (100%)	Imm.1 hypothetical predicted membrane protein
hypothetical protein			Gp048	78	Gp046 (93.5%)	78		
DNA polymerase	Gp046	898	Gp049 (99.4%)	898	Gp047 (99.6%)	898	Gp43 (99.5%)	gp43 DNA polymerase
Phage protein			Gp050	73	Gp048 (95.8%)	73		
Phage endoribonulcease translational repressor of early genes, regA	Gp047	122	Gp051 (100%)	122	Gp049 (100%)	122	RegA (100%)	RegA translational repressor protein
Phage DNA polymerase clamp loader subunit Gp62	Gp048	187	Gp052 (92.4%)	187	Gp050 (98.4%)	187	Gp62 (98.4%)	gp62 clamp loader subunit, DNA polymerase accessory protein
Replication factor C small subunit / Phage DNA polymerase clamp loader subunit	Gp049	319	Gp053 (99.6%)	319	Gp051 (99.6%)	319	Gp44 (100%)	gp44 clamp loader subunit, DNA polymerase accessory protein
Sliding clamp DNA polymerase accessory protein	Gp050	228	Gp054 (99%)	228	Gp052 (99.1%)	228	Gp45 (98.6%)	gp45 sliding clamp, DNA polymerase accessory protein
RNA polymerase	Gp051	129	Gp055 (100%)	129	Gp053 (98.4%)	129	RpbA (100%)	RpbA RNA polymerase binding protein, function unknown
Phage protein	Gp052	62	Gp056 (98%)	62	Gp054 (98.3%)	62	Gp45.2 (100%)	gp45.2 conserved hypothetical protein

Phage recombination-related endonuclease Gp46	Gp053	560	Gp057 (95.7%)	560	Gp055 (95.2%)	546	Gp46 (99.8%)	gp46 recombination endonuclease subunit
Phage protein	Gp054	68	Gp058 (98.5%)	68	Gp056 (97%)	68	Gp46.1 (100%)	gp46.1 hypothetical protein
Phage protein	Gp055	87	Gp059 (99.6%)	87	Gp057 (97.7%)	87	Gp46.2 (97.7%)	gp46.2 hypothetical protein
Phage recombination-related endonuclease Gp47	Gp056	339	Gp060 (96.4%)	339	Gp058 (99.1%)	339	Gp47 (98.8%)	gp47 recombination endonuclease subunit
hypothetical protein					Gp059	207	Gp47.1	gp47.1 hypothetical predicted membrane protein
alpha glucosyl transferase	Gp057	400	Gp061 (98%)	400	Gp060 (90.5%)	400	a-gt (91%)	alpha glucosyl transferase
Phage-associated homing endonuclease	Gp058	227					MobB (98.6%)	MobB homing endonuclease
Phage protein	Gp059	57	Gp062 (93%)	57	Gp061 (91.2%)	57	a-gt.2 (90.5%)	a-gt.2 hypothetical protein
Phage protein	Gp060	67	Gp063 (98.5%)	67	Gp062 (100%)	67	a-gt.3 (98.5%)	a-gt.3 hypothetical protein
Phage protein	Gp061	105	Gp064 (100%)	105	Gp063 (100%)	105	a-gt.4 (100%)	a-gt.4 conserved hypothetical protein
Phage protein	Gp062	62	Gp065 (100%)	62	Gp064 (100%)	62	a-gt.5 (100%)	a-gt.5 hypothetical protein
T4-like phage RNA polymerase sigma factor for late transcription	Gp063	185	Gp066 (100%)	185	Gp065 (100%)	185	Gp55 (100%)	gp55 Sigma factor for T4 late transcription
Phage protein	Gp064	89	Gp067 (100%)	89	Gp066 (100%)	89		
Phage protein	Gp065	71	Gp068 (100%)	71	Gp067 (100%)	71	Gp55.1 (94.3%)	gp55.1 hypothetical protein
Phage protein	Gp066	108	Gp069 (98%)	108	Gp068 (98%)	108	Gp55.2 (99%)	gp55.2 hypothetical protein
Phage protein	Gp067	66	Gp070 (75.7%)	66	Gp069 (93.9%)	66	Gp55.3 (75.7%)	gp55.3 hypothetical protein
Phage protein	Gp068	43	Gp071 (95%)	43	Gp070 (95.3%)	43	Gp55.4 (97.6%)	gp55.4 conserved hypothetical protein
Phage protein	Gp069	97	Gp072 (97%)	97	Gp071 (100%)	97	Gp55.5 (100%)	gp55.5 conserved protein of unknown function
Phage protein	Gp070	60	Gp073 (100%)	60	Gp072 (98.3%)	60	Gp55.6 (85%)	gp55.6 conserved hypothetical protein
Glutaredoxin	Gp071	107	Gp074 (95%)	107	Gp073 (96%)	102	NrdH (96%)	NrdH glutaredoxin
Phage protein	Gp072	87	Gp075 (98.8%)	103				
Phage protein	Gp073	71	Gp076 (100%)	71	Gp074 (94.2%)	70	Gp55.8 (95.7%)	gp55.8 conserved hypothetical predicted membrane protein
Phage protein	Gp074	37	Gp077 (100%)	37	Gp075 (100%)	37		

Ribonucleotide reductase of class III (anaerobic), activating protein	Gp075	130	Gp078 (96.9%)	156	Gp076 (98.4%)	156	NrdG (77.6%)	NrdG anaerobic NTP reductase, small subunit
Phage-associated homing endonuclease	Gp076	244						
Ribonucleotide reductase of class III (anaerobic), large subunit	Gp077	424	Gp079 (96.9%)	605	Gp077 (96.6%)	605	MobC NrdD (97.1%)	MobC homing endonuclease NrdD anaerobic NTP reductase, large subunit
Phage-associated homing endonuclease	Gp078	258					I-TevII (99.2%)	I-TevII homing endonuclease
Ribonucleotide reductase of class III (anaerobic), large subunit	Gp079	181					NrdD (83.8%)	NrdD anaerobic NTP reductase, large subunit
Phage-associated homing endonuclease	Gp080	273			Gp078 (100%)	273		
Phage endonuclease	Gp081	157	Gp080 (98.7%)	157	Gp079 (99.3%)	157	Gp49 (100%)	gp49 EndoVII packaging and recombination endonuclease VII
Pin protease inhibitor	Gp082	161	Gp081 (96.8%)	161	Gp080 (98.1%)	161	Pin (96.2%)	Pin protease inhibitor
Phage protein	Gp083	55	Gp082 (88%)	51	Gp081 (96.3%)	55	Gp49.1 (88.2%) Gp49.2 Gp49.3	gp49.1 conserved protein of unknown function gp49.2 hypothetical protein gp49.3 hypothetical protein
Nucleotide reductase subunit C			Gp083	106				
Phage protein	Gp084	64	Gp084 (89%)	56	Gp082 (90.6%)	64		
Phage protein	Gp085	71	Gp085 (98%)	71	Gp083 (100%)	71		
Thioredoxin, phage-associated	Gp086	87	Gp086 (100%)	87	Gp084 (100%)	87	NrdC (100%)	NrdC thioredoxin
Thioredoxin, phage-associated	Gp087	80	Gp087 (98.7%)	80	Gp085 (100%)	80	NrdC.1 (98.7%)	NrdC.1 conserved hypothetical protein
Thioredoxin, phage-associated	Gp088	108	Gp088 (78.6%)	98	Gp086 (98.1%)	129	NrdC.2 (74.6%)	NrdC.2 conserved hypothetical protein
Thioredoxin, phage-associated	Gp089	309	Gp089 (61.9%)	308	Gp087 (97%)	309	NrdC.3 (60.6%)	NrdC.3 conserved hypothetical protein
Thioredoxin, phage-associated					Gp088	333	NrdC.4 (90%)	NrdC.4 conserved hypothetical protein

Thioredoxin, phage-associated					Gp089	279	NrdC.5 (94.2%)	NrdC.5 conserved hypothetical protein
Thioredoxin, phage-associated					Gp090	60		
Thioredoxin, phage-associated	Gp090	295	Gp092 (97.9%)	295	Gp091 (97.2%)	295	NrdC.6 (97.3%)	NrdC.6 conserved hypothetical protein
Thioredoxin, phage-associated	Gp091	135	Gp093 (96.2%)	134	Gp092 (95.4%)	134	NrdC.7 (90.2%)	NrdC.7 conserved hypothetical, predicted membrane protein
Thioredoxin, phage-associated	Gp092	175	Gp094 (100%)	175	Gp093 (100%)	175	NrdC.8 (98.8%)	NrdC.8 conserved hypothetical protein
Thioredoxin, phage-associated	Gp093	100	Gp095 (97%)	100	Gp094 (96%)	100	NrdC.9 (98%)	NrdC.9 conserved hypothetical protein
Thioredoxin, phage-associated	Gp094	344	Gp096 (99.6%)	322	Gp095 (99.3%)	322	NrdC.10 (99%)	NrdC.10 conserved hypothetical protein
hypothetical protein			Gp097	87	Gp096 (97.7%)	87		
hypothetical protein			Gp098	49	Gp097 (100%)	49		
Thioredoxin, phage-associated			Gp099	81				
Thioredoxin, phage-associated	Gp095	336	Gp100 (99.6%)	253	Gp098 (98.8%)	336	NrdC.11 (97.9%)	NrdC.11 conserved hypothetical protein
hypothetical protein	Gp096	73	Gp101 (93.4%)	73	Gp099 (94.5%)	73		
							MobD	MobD homing endonuclease
Phage protein	Gp097	173	Gp102 (96.5%)	173	Gp100 (95.3%)	173	MobD.1 (25.1%)	MobD.1 conserved hypothetical protein
Phage protein	Gp098	181	Gp103 (93.8%)	185	Gp101 (83.3%)	102	MobD.1 (82.3%)	MobD.1 conserved hypothetical protein
					Gp102	43		
							MobD.2	MobD.2 conserved hypothetical protein
Phage protein	Gp099	57	Gp104 (96.4%)	57	Gp103 (98.2%)	57	MobD.2a (89.4%)	MobD.2a hypothetical protein
Phage protein	Gp100	64	Gp105 (96.8%)	64	Gp104 (95.3%)	64	MobD.3 (93.7%)	MobD.3 hypothetical protein
Phage protein	Gp101	67	Gp106 (85%)	67	Gp105 (98.5%)	67	MobD.4 (74.6%)	MobD.4 hypothetical protein
Phage protein	Gp102	62	Gp107 (96.7%)	62	Gp106 (100%)	62	MobD.5 (100%)	MobD.5 hypothetical protein
Phage protein	Gp103	128	Gp108 (100%)	128	Gp107 (100%)	106	MobD.6 (100%)	MobD.6 hypothetical protein
Phage rI lysis inhibition regulator	Gp104	97	Gp109 (96.9%)	97	Gp108 (96.9%)	97	rI (100%)	rI lysis inhibition regulator, membrane protein
Phage protein	Gp105	70	Gp110 (100%)	70	Gp109 (98.5%)	70	rI.1 (100%)	rI.1 conserved hypothetical protein

Thymidine kinase	Gp106	193	Gp111 (99.4%)	193	Gp110 (98.4%)	193	Tk (98.4%) Tk.1	Tk thymidine kinase Tk.1 conserved hypothetical protein
Phage protein	Gp107	61	Gp112 (98.3%)	61	Gp111 (96.7%)	61	Tk.2 (98.4%)	Tk.2 conserved hypothetical protein
Phage protein	Gp108	57	Gp113 (100%)	57	Gp112 (96.4%)	57		
Phage protein	Gp109	68	Gp114 (98.5%)	68	Gp113 (89.7%)	68		
Phage protein	Gp110	70	Gp115 (95.7%)	70	Gp114 (100%)	70	Tk.3 (95.7%)	Tk.3 conserved hypothetical protein
Phage protein	Gp111	159	Gp116 (58%)	155	Gp115 (99.2%)	130	Tk.4 (58%)	Tk.4 conserved hypothetical protein
Valyl-tRNA synthetase	Gp112	115	Gp117 (97.3%)	113	Gp116 (97.3%)	113	Vs (99.1%)	Vs valyl-tRNA synthetase modifier
T4-like phage protein	Gp113	181	Gp118 (99.4%)	181	Gp117 (99.4%)	181	Vs.1 (99.4%)	Vs.1 conserved hypothetical protein
Endoribonuclease, RegB protein	Gp114	153	Gp119 (99.3%)	153	Gp118 (98.6%)	153	RegB (99.3%)	RegB site-specific RNA endonuclease
Phage protein	Gp115	92	Gp120 (96.7%)	92	Gp119 (98.9%)	92	Vs.3 (97.8%)	Vs.3 conserved hypothetical protein
Phage protein	Gp116	88	Gp121 (88.6%)	88	Gp120 (94.3%)	88	Vs.4 (94.3%)	Vs.4 conserved hypothetical protein
Phage protein	Gp117	73	Gp122 (98.6%)	73	Gp121 (97.2%)	73	Vs.5 (88.8%)	Vs.5 conserved hypothetical protein
Pyruvate formate-lyase	Gp118	120	Gp123 (99%)	120	Gp122 (98.3%)	120	Vs.6 (98.3%)	Vs.6 conserved hypothetical protein
Phage protein	Gp119	109	Gp124 (98%)	54	Gp123 (100%)	54	Vs.7 (98.1%)	Vs.7 conserved hypothetical protein
Phage protein	Gp120	179	Gp125 (90.5%)	179	Gp124 (88.8%)	179	Vs.8 (92.1%) DenV	Vs.8 conserved hypothetical protein DenV endonuclease V, N-glycosylase UV repair enzyme
Phage protein	Gp121	157	Gp126	138	Gp125 (98.7%)	157	IpII (31.1%)	IpII internal head protein
Phage endonuclease					Gp126	138	IpIII	IpIII internal head protein
T4-like phage baseplate hub + tail lysozyme	Gp122	164	Gp127 (99.3%)	164	Gp127 (100%)	164	e (96.9%)	Lysozyme murein hydrolase
Nudix hydrolase, phage-associated	Gp123	146	Gp128 (93%)	146	Gp128 (93.1%)	146	NudE (97.9%)	NudE nudix hydrolase
Phage protein	Gp124	102	Gp129 (100%)	162	Gp129 (87.6%)	162	e.2 (96%)	e.2 conserved hypothetical, predicted membrane protein
Phage protein	Gp125	120	Gp130 (90.8%)	120	Gp130 (85%)	120	e.3 (87.5%)	e.3 conserved hypothetical, predicted membrane protein
Phage protein	Gp126	130	Gp131 (96.3%)	82	Gp131 (95.1%)	82	e.4 (90.7%)	e.4 conserved hypothetical, predicted membrane protein
Phage protein	Gp127	200	Gp132 (97.5%)	200	Gp132 (97%)	202	e.5 (96%)	e.5 conserved hypothetical protein
Phage protein	Gp128	197	Gp133 (98.4%)	197	Gp133 (98.4%)	197	e.6 (100%)	e.6 conserved hypothetical protein

Phage protein	Gp129	110					e.7 (76.5%)	e.7 hypothetical protein
Phage protein	Gp130	87	Gp134 (100%)	87	Gp134 (100%)	87	e.8 (98.8%)	e.8 conserved hypothetical protein
Phage protein			Gp135	187	Gp135 (100%)	187		
Phage protein	Gp131	157	Gp136 (97.9%)	112	Gp136 (95.5%)	157		
Phage-associated homing endonuclease	Gp132	221			Gp137 (99.5%)	221	SegB (83.7%)	SegB homing endonuclease
Phage protein			Gp137	116				
Phage protein	Gp133	95	Gp138 (96.8%)	95	Gp138 (96.8%)	95	Trna.2 (94.7%)	Trna.2 conserved hypothetical protein
Phage protein	Gp134	126	Gp139 (60.4%)	132	Gp139 (61.2%)	132	Trna.3 (58%)	Trna.3 conserved hypothetical protein
Phage protein	Gp135	61	Gp140 (100%)	61	Gp140 (100%)	61	Trna.4 (100%)	Trna.4 conserved hypothetical predicted membrane protein
Phage protein	Gp136	95	Gp142 (53.8%)	85	Gp141 (53.8%)	77	IpI (100%)	IpI internal head protein
hypothetical protein			Gp141	77	Gp142	85		
Phage protein	Gp137	151	Gp143 (100%)	47	Gp143 (100%)	151	Gp57B (100%)	gp57B conserved hypothetical protein
Phage tail fiber assembly protein	Gp138	80	Gp144 (97.3%)	76	Gp144 (97.3%)	76	Gp57A (97.5%)	gp57A chaperone for tail fiber formation
Deoxynucleotide monophosphate kinase	Gp139	237	Gp145 (95.8%)	241	Gp145 (99.5%)	237	Gp1 (97.1%)	gp1 dNMP kinase
Phage tail completion protein	Gp140	176	Gp146 (100%)	176	Gp146 (99.4%)	176	Gp3 (100%)	gp3 tail completion and sheath stabilizer protein
Phage-associated homing endonuclease	Gp141	219						
Phage DNA end protector during packaging	Gp142	275	Gp147 (98%)	274	Gp147 (98.9%)	274	Gp2 (98.9%)	gp2 DNA end protector protein
Phage head completion protein	Gp143	150	Gp148 (99.3%)	150	Gp148 (99.3%)	150	Gp4 (98.6%)	gp4 head completion protein
Phage baseplate wedge subunit	Gp144	196	Gp149 (98.4%)	196	Gp149 (97.9%)	196	Gp53 (98.9%)	gp53 baseplate wedge subunit
T4-like phage baseplate hub + tail lysozyme	Gp145	576	Gp150 (99.4%)	575	Gp150 (99.1%)	575	Gp5 (99.1%)	gp5 baseplate hub subunit and tail lysozyme
							RepEB	RepEB oriE replication initiation protein
							RepEA	RepEA oriE replication initiation protein
Phage-associated homing endonuclease	Gp146	288						
Phage protein	Gp147	164	Gp151 (99.3 %)	164	Gp151 (95.1%)	164	Gp5.1 (97.5%)	gp5.1 conserved hypothetical protein

							SegC	SegC homing endonuclease
							Gp5.3	gp5.3 conserved hypothetical protein
Phospholipase	Gp148	97	Gp152 (100 %)	97	Gp152 (100%)	97	Gp5.4 (100%)	gp5.4 conserved hypothetical protein
Phage baseplate wedge subunit (T4-like gp6)	Gp149	660	Gp153 (99%)	660	Gp153 (99.2%)	660		
							Gp6	gp6 baseplate wedge subunit
Phage baseplate wedge subunit	Gp150	1032	Gp154 (98.5%)	1032	Gp154 (98.3%)	1032	Gp7 (98.2%)	gp7 baseplate wedge initiator
Phage baseplate wedge subunit (T4-like gp8)	Gp151	334	Gp155 (98.2%)	334	Gp155 (97.9%)	334	Gp8 (98.2%)	gp8 baseplate wedge subunit
Phage baseplate wedge tail fiber connector (T4-like gp9)	Gp152	288	Gp156 (99.3%)	288	Gp156 (97.5%)	288	Gp9 (99.6%)	gp9 baseplate wedge tail fiber connector
Phage baseplate wedge subunit and tail pin (T4-like gp10)	Gp153	601	Gp157 (97.6%)	601	Gp157 (98.3%)	601	Gp10 (85%)	gp10 baseplate wedge subunit and tail pin
Phage baseplate wedge subunit and tail pin (T4-like gp11)	Gp154	219	Gp158 (95.8%)	219	Gp158 (97.2%)	219	Gp11 (68%)	gp11 baseplate wedge subunit and tail pin
Phage short tail fiber protein #T4-like phage Gp12	Gp155	516	Gp159 (97.8%)	516	Gp159 (96.1%)	516	Gp12 (63.4%)	gp12 Short tail fibers
Phage neck whiskers (Phage fibrin (wac) protein in fPS-65&90)	Gp156	485	Gp160 (78.7%)	485	Gp160 (78.3%)	485	Wac (81.6%)	Wac fibrin neck whiskers
T4-like phage head completion, neck heterodimeric protein (T4-like gp13)	Gp157	309	Gp161 (99.3%)	309	Gp161 (98.3%)	309	Gp13 (98.7%)	gp13 neck protein
Phage-associated homing endonuclease	Gp158	270						
T4-like phage head completion, neck heterodimeric protein (T4-like gp14)	Gp159	256	Gp162 (99.6%)	256	Gp162 (99.2%)	256	Gp14 (99.2%)	gp14 neck protein

Proximal tail sheath stabilization protein	Gp160	272	Gp163 (99.6%)	272	Gp163 (99.6%)	272	Gp15 (100%)	gp15 tail sheath stabilizer and completion protein
Phage terminase, small subunit	Gp161	164	Gp164 (100%)	164	Gp164 (100%)	164	Gp16 (100%)	gp16 terminase DNA packaging enzyme, small subunit
Phage terminase, large subunit	Gp162	610	Gp165 (99.3%)	610	Gp165 (99%)	610	Gp17 (99%)	gp17 terminase DNA packaging enzyme, large subunit
							Gp17'A	gp17'A unknown function
							Gp17'B	gp17'B unknown function
							Gp17''	gp17'' unknown function
Phage tail sheath monomer	Gp163	659	Gp166 (99%)	659	Gp166 (98.9%)	659	Gp18 (98.9%)	gp18 tail sheath protein
Phage tail fibers	Gp164	163	Gp167 (100%)	163	Gp167 (100%)	163	Gp19 (100%)	gp19 tail tube protein
Phage portal vertex of the head	Gp165	524	Gp168 (99.4%)	524	Gp168 (99.2%)	524	Gp20 (99.4%)	gp20 portal vertex protein of head
Phage prohead core protein	Gp166	79	Gp169 (100%)	79	Gp169 (100%)	79	Gp67 (97.8%)	gp67 prohead core protein, precursor to internal peptides
Phage capsid and scaffold	Gp167	141	Gp170 (100%)	141	Gp170 (100%)	141	Gp68 (100%)	gp68 prohead core protein
Phage prohead assembly (scaffolding) protein	Gp168	212	Gp171 (100%)	212	Gp171 (100%)	212	Gp21 (99.5%)	gp21 prohead core scaffold protein and protease
							Gp21'	gp21' prohead core protease alternate start product
Phage prohead assembly (scaffolding) protein	Gp169	269	Gp172 (99.2%)	269	Gp172 (99.6%)	269	Gp22 (98.8%)	gp22 prohead core scaffold protein
Phage major capsid protein	Gp170	521	Gp173 (96.7%)	521	Gp173 (96.7%)	521	Gp23 (99.2%)	gp23 major head protein
							SegD	SegD homing endonuclease
Phage capsid vertex	Gp171	427	Gp174 (99%)	427	Gp174 (99.3%)	427	Gp24 (99%)	gp24 head vertex protein
RNA ligase, phage-associated	Gp172	334	Gp175 (97.3%)	334	Gp175 (96.7%)	334	RnlB (97.6%)	RnlB RNA ligase 2
Phage protein	Gp173	92	Gp176 (94.5%)	92	Gp176 (96.7%)	92	Gp24.2 (98.9%)	gp24.2 conserved hypothetical protein
Phage protein	Gp174	61	Gp177 (98.1%)	55	Gp177 (100%)	61	Gp24.3 (81.9%)	gp24.3 conserved hypothetical protein
Phage capsid and scaffold	Gp175	376	Gp178 (90.4%)	376	Gp178 (78.5%)	472	Hoc (88.5%)	Hoc head outer capsid protein
Inh inhibitor of gp21 prohead protease	Gp176	225	Gp179 (97.7%)	226	Gp179 (99.1%)	226	Inh (98.2%)	Inh inhibitor of prohead protease gp21

Phage-associated homing endonuclease	Gp177	205					SegE (98.5%)	SegE homing endonuclease
DNA helicase, phage-associated	Gp178	502	Gp180 (98.4%)	503	Gp180 (98.2%)	503	UvsW (99%)	UvsW RNA-DNA and DNA-DNA helicase, ATPase
DNA helicase, phage-associated	Gp179	76	Gp181 (98.6%)	76	Gp181 (97.3%)	76	UvsW (98.6%)	UvsW RNA-DNA and DNA-DNA helicase, ATPase
Phage protein	Gp180	55	Gp182 (100%)	55	Gp182 (100%)	55	UvsY.-2 (100%)	UvsY.-2 conserved hypothetical protein
Phage protein	Gp181	74	Gp183 (100%)	74	Gp183 (94.5%)	74	UvsY.-1 (100%)	UvsY.-1 conserved hypothetical protein
Single stranded DNA-binding protein, phage-associated	Gp182	137	Gp184 (99.2%)	137	Gp184 (100%)	137	UvsY (99.2%)	UvsY recombination, repair and ssDNA binding protein
Phage baseplate wedge subunit (T4-like gp25)	Gp183	132	Gp185 (99.2%)	132	Gp185 (100%)	132	Gp25 (99.2%)	gp25 baseplate wedge subunit
Phage baseplate hub assembly chaperone (T4-like gp26)	Gp184	208	Gp186 (99%)	208	Gp186 (99%)	208	Gp26' Gp26 (99.5%)	gp26' internal in-frame translation initiation gp26 baseplate hub subunit
Phage baseplate	Gp185	249	Gp187 (98.3%)	249	Gp187 (97.9%)	249	Gp51 (95.9%)	gp51 baseplate hub assembly catalyst
Phage baseplate hub subunit	Gp186	391	Gp188 (98.9%)	391	Gp188 (99.4%)	391	Gp27 (99.2%)	gp27 baseplate hub subunit
Phage baseplate hub	Gp187	152	Gp189 (100%)	152	Gp189 (100%)	152	Gp28 (99.3%)	gp28 baseplate hub distal subunit
Phage baseplate hub	Gp188	590	Gp190 (97.4%)	590	Gp190 (98.1%)	590	Gp29 (97.1%)	gp29 baseplate hub subunit, tail length determinant
Phage baseplate tail tube cap (T4-like gp48)	Gp189	364	Gp191 (96.7%)	364	Gp191 (97.8%)	364	Gp48 (98.6%)	gp48 baseplate tail tube cap
Phage tail assembly	Gp190	321	Gp192 (98.7%)	321	Gp192 (100%)	321	Gp54 (97.8%)	gp54 baseplate tail tube initiator
Phage protein	Gp191	96	Gp193 (97.9%)	96	Gp193 (94.7%)	92	Alt.-3 (98.9%)	Alt.-3 conserved hypothetical protein
RNA polymerase-ADP-ribosyltransferase Alt	Gp192	92	Gp194 (98.7%)	685	Gp194 (100%)	92	Alt.-2 (97%)	Alt.-2 hypothetical protein
RNA polymerase-ADP-ribosyltransferase Alt	Gp193	682	Gp195 (96.7%)	684	Gp195 (99.8%)	682	Alt.-1 (98.6%)	Alt.-1 hypothetical protein Alt RNA polymerase ADP-ribosylase
Phage protein	Gp194	62	Gp196 (91.9%)	62	Gp196 (91.9%)	62	Alt.1 (98.3%)	Alt.1 conserved hypothetical protein

DNA ligase, phage-associated	Gp195	487	Gp197 (98.3%)	487	Gp197 (99.3%)	487	Gp30 (98.7%)	gp30 DNA ligase
Phage protein	Gp196	89	Gp198 (98.8%)	89	Gp198 (98.8%)	89	Gp30.1 (100%)	gp30.1 conserved hypothetical protein
Phage protein	Gp197	279	Gp199 (97.1%)	278	Gp199 (99.2%)	279	Gp30.2 (97.8%)	gp30.2 conserved hypothetical protein
Phage protein	Gp198	126	Gp200 (97.1%)	126	Gp200 (100%)	126	Gp30.3 (99.2%)	gp30.3 conserved hypothetical protein
							Gp30.3'	gp30.3' hypothetical protein
Phage protein	Gp199	68	Gp201 (89.7%)	68	Gp201 (98.5%)	68	Gp30.4 (95.5%)	gp30.4 conserved hypothetical protein
Phage protein	Gp200	65	Gp202 (98.4%)	65	Gp202 (100%)	65	Gp30.5 (100%)	gp30.5 hypothetical protein
Phage protein	Gp201	95	Gp203 (100%)	95	Gp203 (100%)	95	Gp30.6 (98.9%)	gp30.6 conserved hypothetical protein
Phage protein	Gp202	121	Gp204 (98.3%)	121	Gp204 (100%)	121	Gp30.7 (98.3%)	gp30.7 conserved hypothetical protein
Phage protein	Gp203	110	Gp205 (97.2%)	110	Gp205 (99%)	110	Gp30.8 (98.1%)	gp30.8 conserved hypothetical protein
Phage protein	Gp204	72	Gp206 (100%)	58	Gp206 (100%)	58	Gp30.9 (100%)	gp30.9 conserved hypothetical protein
Phage rIII lysis inhibitor accessory	Gp205	82	Gp207 (100%)	82	Gp207 (100%)	82	rIII (100%)	rIII lysis inhibition accessory protein, rapid lysis phenotype
Phage head assembly chaperone protein	Gp206	111	Gp208 (99.1%)	111	Gp208 (100%)	111	Gp31 (99.1%)	gp31 head assembly cochaperone with GroEL
Phage tail fibers	Gp207	102	Gp209 (99%)	102	Gp209 (100%)	102	Gp31.1 (100%)	gp31.1 conserved hypothetical protein
Phage tail fibers	Gp208	78	Gp210 (94.8%)	78	Gp210 (94.8%)	78	Gp31.2 (98.7%)	gp31.2 hypothetical protein
dCMP deaminase	Gp209	193	Gp211 (100%)	193	Gp211 (100%)	193	dCMP (99.4%)	dCMP deaminase
Phage protein	Gp210	112	Gp212 (97.3%)	112	Gp212 (100%)	112	Cd.1 (99.1%)	Cd.1 hypothetical protein
Phage protein	Gp211	79	Gp213 (98.7%)	78	Gp213 (97.4%)	78	Cd.2 (95.8%)	Cd.2 conserved hypothetical protein
Phage protein					Gp214	175		
Phage protein	Gp212	91	Gp215 (98.9%)	91	Gp215 (97.8%)	91	Cd.3 (98.9%)	Cd.3 conserved hypothetical protein
Phage protein			Gp216	66	Gp216 (95.4%)	66	Cd.4 (96.9%)	Cd.4 conserved hypothetical protein
Phage protein			Gp217	65	Gp217 (95.3%)	65	Cd.5 (100%)	Cd.5 hypothetical protein
3'-phosphatase, 5'-polynucleotide kinase, phage-associated	Gp213	302	Gp218 (93.3%)	301	Gp218 (90.3%)	300	PseT (97.6%)	PseT polynucleotide 5'-kinase and 3'-phosphatase
Phage protein	Gp214	79	Gp219 (61.3%)	106				
Phage protein	Gp215	76	Gp220 (100%)	76	Gp219 (100%)	75	PseT.1 (100%)	PseT.1 conserved hypothetical protein
Phage outer membrane lipoprotein Rz1	Gp216	99	Gp221 (100%)	99	Gp220 (100%)	99	PseT.2 (98.9%)	PseT.2 conserved hypothetical protein

Phage spanin Rz	Gp217	117	Gp222 (94%)	117	Gp221 (90.6%)	117	PseT.3 (90.6%)	PseT.3 conserved hypothetical predicted membrane protein
Phage alc transcription terminator	Gp218	167	Gp223 (98.2%)	167	Gp222 (98.1%)	167	Alc (96.9%)	Alc inhibitor of host transcription
RNA ligase, phage-associated #T4-like RnlA	Gp219	374	Gp224 (99.4%)	374	Gp223 (98.4%)	374	RnlA (98.9%)	RnlA RNA ligase 1 and tail fiber attachment catalyst
Phage endonuclease	Gp220	136	Gp225 (99.2%)	136	Gp224 (99.2%)	136	DenA (99.2%)	DenA endonuclease II
Ribonucleotide reductase of class Ia (aerobic), beta subunit	Gp221	156	Gp226 (100%)	392	Gp225 (99.3%)	392	NrdB (99.3%)	NrdB aerobic NDP reductase, small subunit
Phage-associated homing endonuclease	Gp222	269					I-TevIII (95.5%)	I-TevIII homing endonuclease (defective)
Ribonucleotide reductase of class Ia (aerobic), beta subunit	Gp223	225					NrdB (86%)	NrdB aerobic NDP reductase, small subunit
Ribonucleotide reductase of class Ia (aerobic), alpha subunit	Gp224	329	Gp227 (99.3%)	754	Gp226 (98.4%)	329	Nrd.1 NrdA (97.3%)	Nrd.1 hypothetical protein NrdA aerobic NDP reductase, large subunit
Phage-associated homing endonuclease	Gp225	236			Gp227 (99.5%)	236	MobE (45.3%)	MobE homing endonuclease
Ribonucleotide reductase of class Ia (aerobic), alpha subunit	Gp226	477			Gp228 (99.7%)	477	NrdA (99.7%)	NrdA aerobic NDP reductase, large subunit
undefined product					Gp229	108	NrdA.1 (96.3%)	NrdA.1 conserved hypothetical protein
Phage protein	Gp227	87	Gp228 (95.4%)	87	Gp230 (94.2%)	87	NrdA.2 (96.5%)	NrdA.2 conserved hypothetical protein
Thymidylate synthase	Gp228	104	Gp229 (71.4%)	104	Gp231 (100%)	104	dTMP (74%)	dTMP (thymidylate) synthase
Phage-associated homing endonuclease	Gp229	245	Gp230 (99.1%)	245	Gp232 (99.5%)	245	I-TevI (99.5%)	I-TevI homing endonuclease
Thymidylate synthase	Gp230	183	Gp231 (92.9%)	183	Gp233 (93.4%)	183	dTMP (90.7%)	dTMP (thymidylate) synthase
hypothetical protein	Gp231	68	Gp232 (98.5%)	68	Gp234 (98.5%)	68		
Dihydrofolate reductase, phage-associated	Gp232	193	Gp233 (98.9%)	193	Gp235 (98.4%)	193	Frd (97.9%)	Frd dihydrofolate reductase
Phage protein	Gp233	81	Gp234 (98.7%)	81	Gp236 (100%)	81		
Phage protein	Gp234	41	Gp235 (100%)	80	Gp237 (100%)	80	Frd.1 (100%)	Frd.1 conserved hypothetical protein

Phage protein	Gp235	126	Gp236 (64.3%)	128	Gp238 (40.9%)	128	Frd.2 (65.1%)	Frd.2 conserved hypothetical protein
Phage protein	Gp236	75	Gp237 (90.6%)	75	Gp239 (81.5%)	76	Frd.3 (94.6%)	Frd.3 hypothetical protein
Single stranded DNA-binding protein, phage-associated	Gp237	302	Gp238 (98%)	302	Gp240 (98.3%)	302	Gp32 (98%)	gp32 single-stranded DNA binding protein
Phage DNA helicase loader	Gp238	217	Gp239 (100%)	212	Gp241 (100%)	217	SegG Gp59 (100%)	SegG homing endonuclease gp59 loader of gp41 DNA helicase
Transcriptional regulator	Gp239	112	Gp240 (100%)	112	Gp242 (100%)	112	Gp33 (100%)	gp33 late promoter transcription accessory protein
Phage double-stranded DNA binding protein #T4- like dsbA, late transcriptional regulation	Gp240	89	Gp241 (100%)	89	Gp243 (100%)	89	DsbA (100%)	dsDNA binding protein, late transcription
Phage ribonuclease H	Gp241	305	Gp242 (99%)	305	Gp244 (99%)	305	Gprnh (99%)	RNaseH ribonuclease
Phage long tail fiber proximal subunit	Gp242	1290	Gp243 (93.3%)	1289	Gp245 (93.2%)	1290	Gp34 (93.8%)	gp34 long tail fiber, proximal subunit
Phage tail connector protein	Gp243	372	Gp244 (94.8%)	371	Gp246 (95.4%)	371	Gp35 (94.8%)	gp35 hinge connector of long tail fiber, proximal connector
Phage tail fibers (Phage tail connector protein in fPS-65&90)	Gp244	218	Gp245 (60.7%)	216	Gp247 (67.6%)	229	Gp36 (80.5%)	gp36 hinge connector of long tail fiber, distal connector
Phage tail fibers	Gp245	1018	Gp246 (65.2%)	994	Gp248 (74.1%)	988	Gp37 (34.5%) Gp38	gp37 long tail fiber, distal subunit gp38 distal long tail fiber assembly catalyst
Phage tail fibers	Gp246	259	Gp247 (69%)	260	Gp249 (95.7%)	259		
Phage holin	Gp247	218	Gp248 (97.7%)	218	Gp250 (97.2%)	246	T	holin lysis mediator
Phage anti-sigma factor	Gp248	90	Gp249 (98.8%)	90	Gp251 (100%)	90	AsiA (100%)	AsiA anti-sigma 70 protein
Phage anti-sigma factor	Gp249	50	Gp250 (93%)	44	Gp252 (100%)	50	AsiA.1 (96%)	AsiA.1 hypothetical protein
Phage anti-restriction nuclease	Gp250	92	Gp251 (96.7%)	92	Gp253 (98.9%)	92	Arn (97.8%)	Arn inhibitor of MrcBC restriction endonuclease (anti-restriction nuclease)
Phage protein	Gp251	39	Gp252 (97.4%)	39	Gp254 (97.4%)	39		
Phage anti-restriction nuclease	Gp252	43	Gp253 (97.6%)	43	Gp255 (97.6%)	43	Arn.1 (95.3%)	Arn.1 conserved hypothetical protein
Phage anti-restriction nuclease	Gp253	98	Gp254 (96.9%)	98	Gp256 (98.9%)	98	Arn.2 (98.9%)	Arn.2 conserved hypothetical protein

Phage anti-restriction nuclease	Gp254	152	Gp255 (82.3%)	153	Gp257 (96.7%)	153	Arn.3 (98%)	Arn.3 conserved hypothetical protein
Phage anti-restriction nuclease	Gp255	109	Gp256 (99%)	109	Gp258 (100%)	109	Arn.4 (100%)	Arn.4 conserved hypothetical protein
Phage transcriptional regulator of middle promoters	Gp256	211	Gp257 (99.5%)	211	Gp259 (98.5%)	211	MotA (97.6%)	MotA activator of middle period transcription
Transcriptional regulator	Gp257	49	Gp258 (91.8%)	49	Gp260 (100%)	49	MotA.1 (97.9%)	MotA.1 hypothetical predicted periplasmic protein
DNA topoisomerase, phage-associated	Gp258	442	Gp259 (98.6%)	442	Gp261 (99.3%)	442	Gp52 (99.5%)	gp52 topoisomerase II, medium subunit
undefined product					Gp262	52	Gp52.1 Ac (97%) Stp	gp52.1 conserved hypothetical predicted membrane protein Ac acridine resistance protein Stp activator of host PrrC lysyl-tRNA endonuclease
Phage protein	Gp259	152	Gp260 (97.3%)	152	Gp263 (97.3%)	152	Ndd (96.7%)	Ndd nucleoid disruption protein
Phage protein	Gp260	71	Gp261 (98.5%)	71	Gp264 (95.7%)	71	Ndd.1 (97.1%)	Ndd.1 conserved hypothetical protein
Phage protein	Gp261	41	Gp262 (92.6%)	41	Gp265 (90.2%)	41	Ndd.2 (88.8%)	Ndd.2 hypothetical predicted outer membrane protein
Phage protein	Gp262	65	Gp263 (96.9%)	65	Gp266 (100%)	65	Ndd.2a (95%) Ndd.3 Ndd.4 Ndd.5 Ndd.6	Ndd.2a hypothetical predicted periplasmic protein Ndd.3 hypothetical predicted inner membrane protein Ndd.4 hypothetical predicted inner membrane protein Ndd.5 hypothetical predicted outer membrane protein Ndd.6 conserved hypothetical predicted outer membrane protein
hypothetical protein	Gp263	37	Gp264 (94.5%)	37	Gp267 (94.5%)	37	Inh (46.6%)	Inh inhibitor of prohead protease gp21
Phage protein	Gp264	87	Gp265 (56.3%)	87	Gp268 (97.7%)	87		
Phage endonuclease putative protein	Gp265	185	Gp266 (97.3%)	185	Gp269 (98.3%)	185	DenB (99.4%)	DenB DNA endonuclease IV
Phage rIIB lysis inhibitor	Gp266	64	Gp267 (95.3%)	64	Gp270 (100%)	64	DenB.1 (96.8%)	DenB.1 hypothetical protein
	Gp267	312	Gp268 (97.4%)	312	Gp271 (97.7%)	312	rIIB (98%)	rIIB protector from prophage-induced early lysis

Supplementary Figures

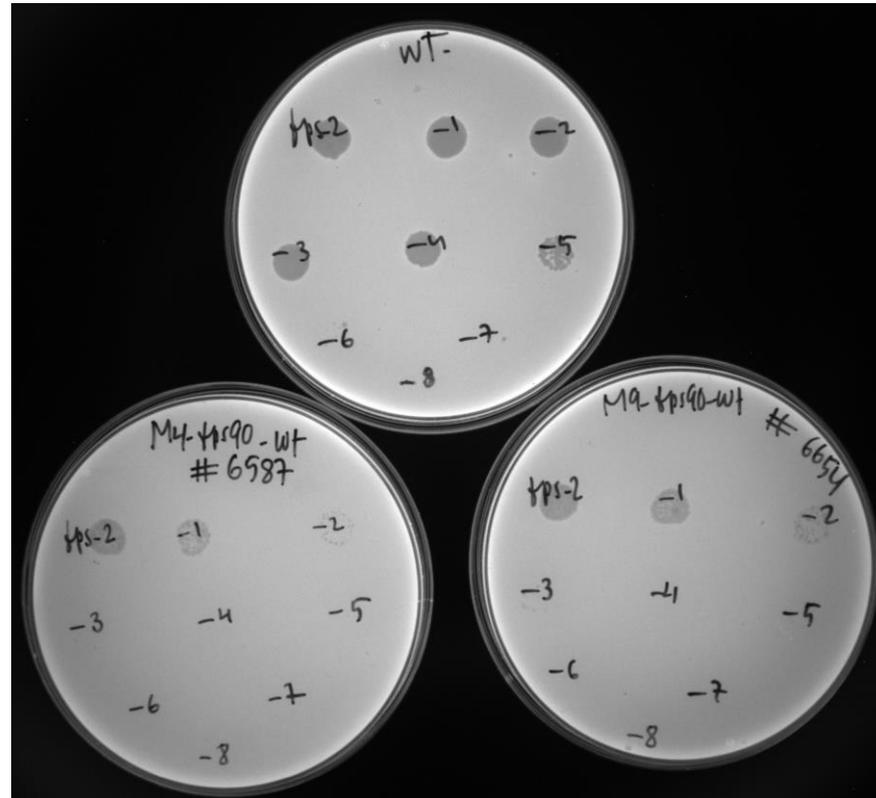


Figure S1. The EOP test of fPS-2 with M4-fps90-wt and M9-fps90-wt strains to determine whether the OmpF protein is required by fPS-2 for full infection. As seen in the plates, there is about 4 logs reduction in the EOP of the phage on the mutant strains compared to the wild-type strain, suggesting that the OmpF is required by fPS-2 for full infection.

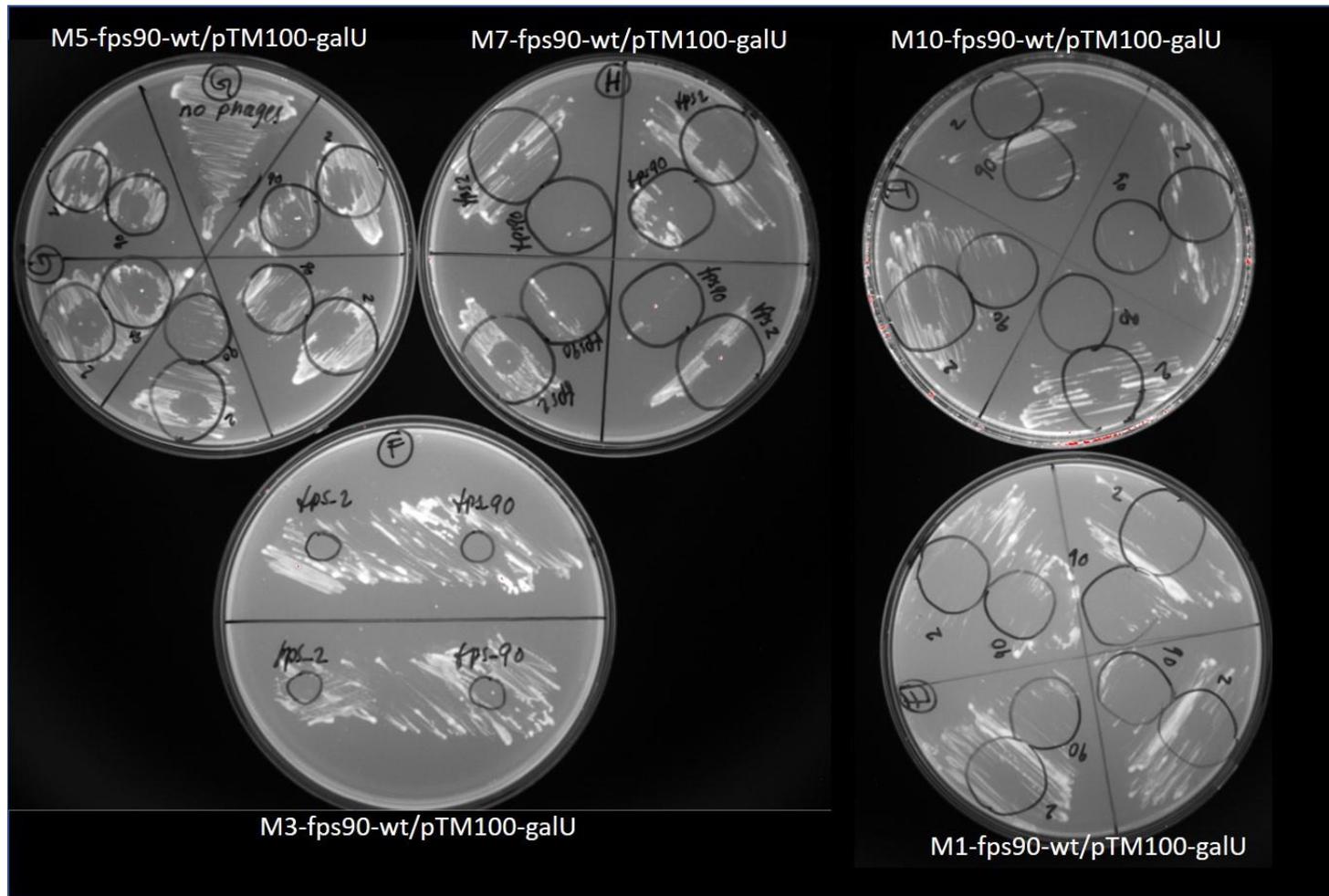


Figure S2. Spot assay to test the sensitivity of the *galU*-complemented spontaneous phage-resistant mutant strains to fPS-2 and fPS-90. The complemented strains are M1-90/*galU*, M3-90/*galU*, M5-90/*galU*, M7-90/*galU* and M10-90/*galU* were abbreviated on the plates as E, F, G, H and I, respectively. The lysis on the bacterial lawn indicated that the complemented strains have retained their sensitivity to the phages when complemented with the wild *galU* gene.

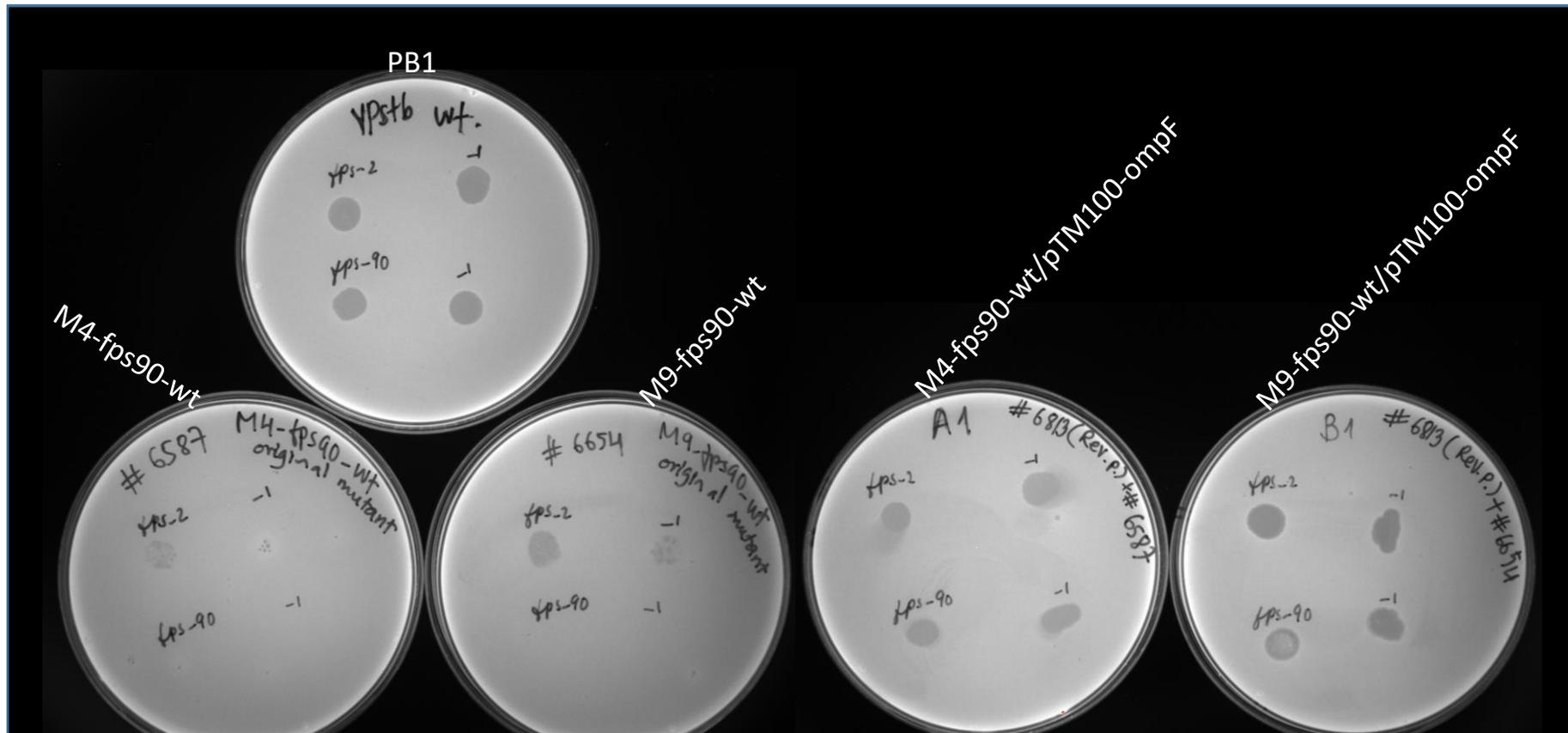


Figure S3. The complementation of the phage-resistant mutant strains M4-fps90-wt and M9-fps90-wt with the plasmid pTM100-ompF carrying the intact *ompF* gene of *Y. pseudotuberculosis* strain PB1. Ten μ l drops of undiluted and 1:10 diluted stocks of the phages fPS-2 and fPS-90 were pipetted on soft-agar plates containing the indicated strains. PB1 is the wild type parental *Y. pseudotuberculosis* strain PB1. The results demonstrate that phage fPS-90 could infect and lyse both the complemented strains indicating that the intact *ompF* gene was able to complement *in trans* both of the strains. Note also that the complemented strains were more efficiently infected by fPS-2.

References

1. Burrows, T.W.; Bacon, G.A. V and W antigens in strains of *Pasteurella pseudotuberculosis*. *Br. J. Exp. Pathol.* **1960**, *41*, 38-44.
2. Skurnik, M. Lack of correlation between the presence of plasmids and fimbriae in *Yersinia enterocolitica* and *Yersinia pseudotuberculosis*. *J. Appl. Bact.* **1984**, *56*, 355-363.
3. Bölin, I.; Norlander, L.; Wolf-Watz, H. Temperature-inducible outer membrane protein of *Yersinia pseudotuberculosis* and *Yersinia enterocolitica* is associated with the virulence plasmid. *Infect. Immun.* **1982**, *37*, 506-512.
4. Kiljunen, S.; Datta, N.; Dentovskaya, S.V.; Anisimov, A.P.; Knirel, Y.A.; Bengoechea, J.A.; Holst, O.; Skurnik, M. Identification of the lipopolysaccharide core of *Yersinia pestis* and *Yersinia pseudotuberculosis* as the receptor for bacteriophage fA1122. *J. Bacteriol.* **2011**, *193*, 4963-4972.
5. Kenyon, J.J.; Duda, K.A.; De Felice, A.; Cunneen, M.M.; Molinaro, A.; Laitinen, J.; Skurnik, M.; Holst, O.; Reeves, P.R.; De Castro, C. Serotype O:8 isolates in the *Yersinia pseudotuberculosis* complex have different O-antigen gene clusters and produce various forms of rough LPS. *Innate Immun.* **2016**, *22*, 205-217.
6. Tsubokura, M.; Aleksic, S. A simplified antigenic scheme for serotyping of *Yersinia pseudotuberculosis*: Phenotypic characterization of reference strains and preparation of O and H factor sera. *Contrib. Microb. Immunol.* **1995**, *13*, 99-105.
7. Kondakova, A.N.; Sevillano, A.M.; Shaikhutdinova, R.Z.; Lindner, B.; Komandrova, N.A.; Dentovskaya, S.V.; Shashkov, A.S.; Anisimov, A.P.; Skurnik, M.; Knirel, Y.A. Revision of the O-polysaccharide structure of *Yersinia pseudotuberculosis* O:1a; confirmation of the function of WbyM as paratransferase. *Carbohydr. Res.* **2012**, *350*, 98-102.
8. Laukkanen-Ninios, R.; Didelot, X.; Jolley, K.A.; Morelli, G.; Sangal, V.; Kristo, P.; Brehony, C.; Imori, P.F.; Fukushima, H.; Siitonen, A., *et al.* Population structure of the *Yersinia pseudotuberculosis* complex according to multilocus sequence typing. *Environ Microbiol* **2011**, *13*, 3114-3127.
9. Ben-Gurion, R.; Hertman, I. Bacteriocin-like material produced by *Pasteurella pestis*. *J. Gen. Microbiol.* **1958**, *19*, 289-297.
10. Portnoy, D.A.; Falkow, S. Virulence-associated plasmids from *Yersinia enterocolitica* and *Yersinia pestis*. *J. Bacteriol.* **1981**, *148*, 877-883.
11. Garcia, E.; Nedialkov, Y.A.; Elliott, J.; Motin, V.L.; Brubaker, R.R. Molecular characterization of KatY (antigen 5), a thermoregulated chromosomally encoded catalase-peroxidase of *Yersinia pestis*. *J. Bacteriol.* **1999**, *181*, 3114-3122.
12. Korhonen, T.K.; Väisänen, V.; Saxén, H.; Hultberg, H.; Svenson, S.B. P-Antigen-Recognizing Fimbriae from Human Urupathogenic *Escherichia coli* Strains. *Infect. Immun.* **1982**, *37*, 286-291.
13. Grant, S.G.; Jessee, J.; Bloom, F.R.; Hanahan, D. Differential plasmid rescue from transgenic mouse DNAs into *Escherichia coli* methylation-restriction mutants. *Proc. Natl. Acad. Sci. USA* **1990**, *87*, 4645-4649.
14. Figurski, D.H.; Helinski, D.R. Replication of an origin-containing derivative of plasmid RK2 dependent on a plasmid function provided in trans. *Proc. Natl. Acad. Sci. USA* **1979**, *76*, 1648-1652.
15. Babic, A.; Guerout, A.M.; Mazel, D. Construction of an improved RP4 (RK2)-based conjugative system. *Res. Microbiol.* **2008**, *159*, 545-549.
16. Wang, Q.; Torzewska, A.; Ruan, X.; Wang, X.; Rozalski, A.; Shao, Z.; Guo, X.; Zhou, H.; Feng, L.; Wang, L. Molecular and genetic analyses of the putative *Proteus* O antigen gene locus. *Appl. Environ. Microb.* **2010**, *76*, 5471-5478.
17. Mayer, H.; Schmidt, G. Chemistry and biology of the enterobacterial common antigen (ECA). *Curr. Top. Microbiol. Immunol.* **1979**, *85*, 99-153.

18. Noszczyńska, M.; Kasperkiewicz, K.; Duda, K.A.; Podhorodecka, J.; Rabsztyn, K.; Gwizdała, K.; Swierżko, A.S.; Radziejewska-Lebrecht, J.; Holst, O.; Skurnik, M. Serological characterization of the enterobacterial common antigen substitution of the lipopolysaccharide of *Yersinia enterocolitica* O : 3. *Microbiology* **2015**, *161*, 219-227.