Supplemental Information for:

Alterations in gp37 expand the host range of a T4-like phage

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Running title: gp37 replacement expands phage host range

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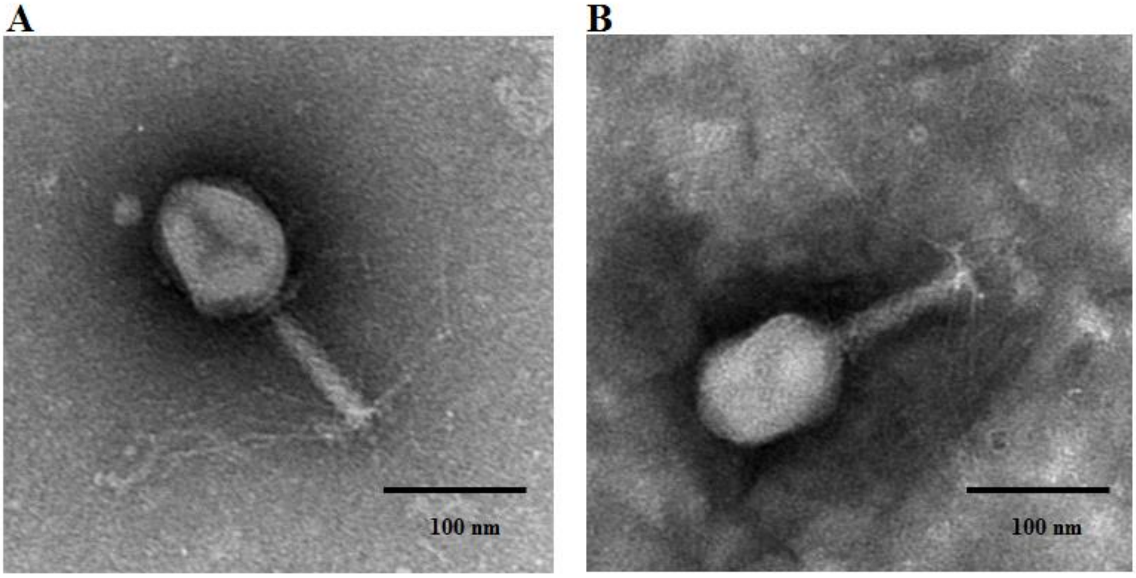

Fig. S1 Electron microscopy images of QL01 and WG01

(A) Electron microscopy image of WG01.

(B) Electron microscopy image of QL01.

The phage filtrate was applied to a copper grid coated with a carbon support film before negative staining with phosphotungstic acid (PTA, 2% w/v). Electron micrographs were generated with an H_7650 (Hitachi, Japan) transmission electron microscope (TEM).

WG01 possessed an icosahedral head and a contractile tail, which exhibited the same morphology as QL01.

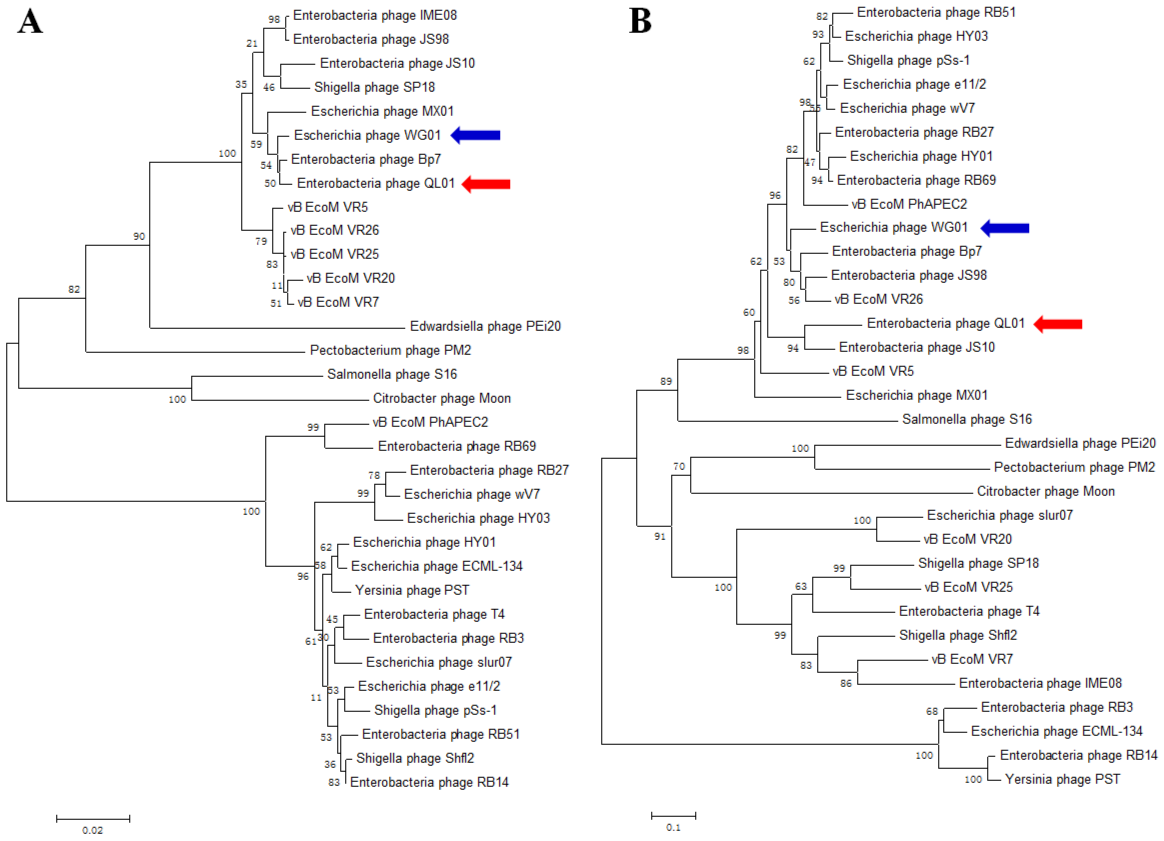

Fig. S2 Phylogenetic trees for the amino acid sequences of gp23 and gp37

A neighbor-joining tree analysis and bootstrap analysis (1000 bootstrap replicates) based on the alignment of the amino acid sequence of gp23 (A) and gp37 (B) of 33 T4-like phages. The numbers at the nodes indicate the bootstrap probabilities of that particular branch. The phylogenetic tree based on gp23 revealed that WG01 shared a close phylogenic relationship with Bp7 and QL01; however, in the distance tree of gp37, WG01 shared a close phylogenic relationship with Bp7, JS98, and vB_EcoM-VR26, but a distant phylogenic relationship with QL01. Moreover, QL01 and JS10 shared a close evolutionary relationship.

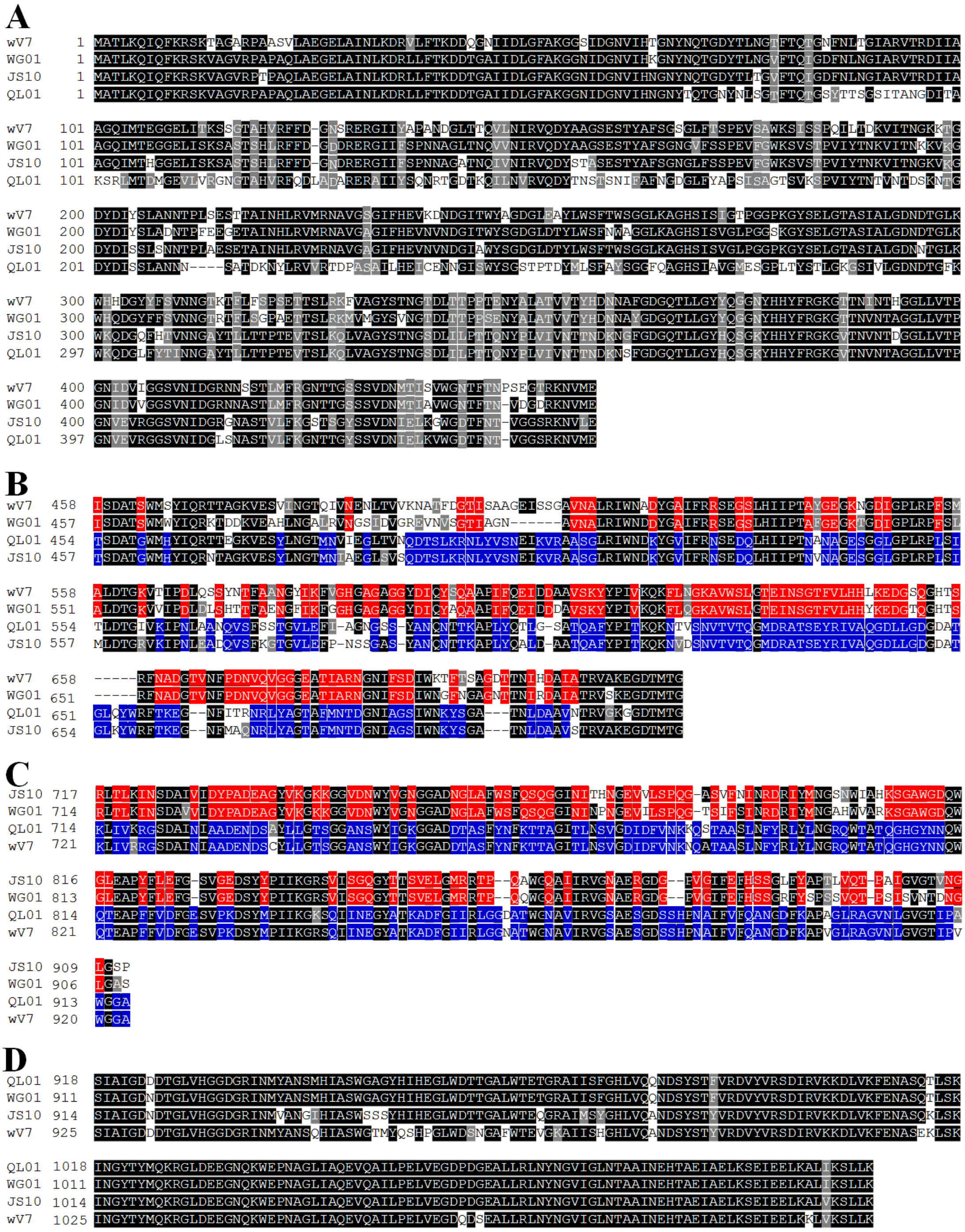

Fig. S3 Alignment results of gp37 of WG01 with other homologous T4-like phages

The different amino acids domains (1–456, 457–713, 714–910, and 911–1100) of WG01 gp37 was compared with the corresponding protein sequences of QL01, JS10, and wV7.

(A) The N-terminal domain (amino acids 1–456) of WG01 gp37 was compared with the corresponding protein sequences of QL01, JS10, and wV7.

(B) The N-terminal domain (amino acids 457−713) of WG01 gp37 was compared with the corresponding protein sequences of QL01, JS10, and wV7.

(C) The WG01 gp37 C-terminal domain (amino acids 714–910) was compared with the corresponding protein sequences of QL01, JS10, and wV7.

(D) The WG01 gp37 C-terminal receptor attachment domain (amino acids 911−1100) was compared with the corresponding protein sequences of QL01, JS10, and wV7.

The black boxes represent the same amino acids. Grey boxes represent the amino acids in the same classification. In (B) and (C), the amino acid sequences exhibited a higher homology with the corresponding parts of WG01 marked with red boxes. The amino acid sequences exhibiting a lower homology with the corresponding parts of WG01 are marked with blue boxes.

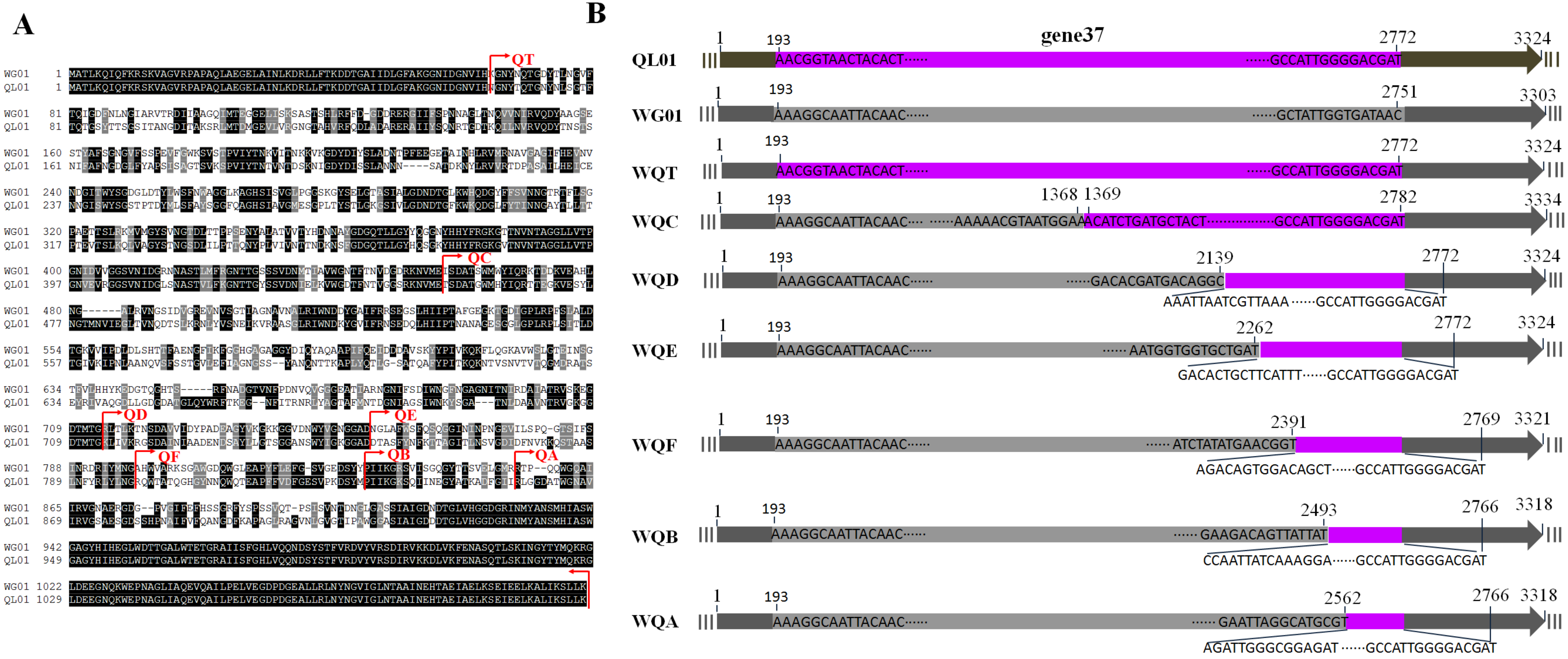
A
B
WG01
QL01
QT
QC
QD
QE
QF
QB
QA
gene37
QL01
1
193
2772
3324
AACGGTAACTACACT······
······GCCATTGGGGACGAT
WG01
1
193
2751
3303
AAAGGCAATTACAAC······
······GCTATTGGTGATAAC
WQT
1
193
2772
3324
AACGGTAACTACACT······
······GCCATTGGGGACGAT
WQC
1
193
1368 1369
2782
3334
AAAGGCAATTACAAC····
······AAAAACGTAATGGAAACATCTGATGCTACT················GCCATTGGGGACGAT
WQD
1
193
2139
2772
3324
AAAGGCAATTACAAC······
······GACACGATGACAGGC
AAATTAATCGTTAAA ······GCCATTGGGGACGAT
WQE
1
193
2262
2772
3324
AAAGGCAATTACAAC······
······ AATGGTGGTGCTGAT
GACACTGCTTCATTT······GCCATTGGGGACGAT
WQF
1
193
2391
2769
3321
AAAGGCAATTACAAC······
······ ATCTATATGAACGGT
AGACAGTGGACAGCT······GCCATTGGGGACGAT
WQB
1
193
2493
2766
3318
AAAGGCAATTACAAC······
······ GAAGACAGTTATTAT
CCAATTATCAAAGGA······GCCATTGGGGACGAT
WQA
1
193
2562
2766
3318
AAAGGCAATTACAAC······
······ GAATTAGGCATGCGT
AGATTGGGCGGAGAT ······GCCATTGGGGACGAT

Fig. S4 Comparison and recombination positions between QL01 and WG01 on gene37

(A)Alignment results of gp37 from WG01 and QL01

The gp37 of WG01 exhibited a relatively low degree of sequence conservation with 59% identity associated with QL01. A high identity (100%) of the amino acid alignment in the first 64 aa of the gp37 N-terminal domain and the first 183 aa of gp37 C-terminal domain between WG01 and QL01 was observed. In contrast, minimal homology was observed in the other regions of gp37. The positions of the initiation sites for the different recombinant fragments and the name of the DNA fragments are indicated above the sequence.

(B)The recombination positions between QL01 and WG01 on gene37

Gene37 diagrams of the QL01, WG01, and WG01 derivatives (WQT, WQC, WQD, WQE WQF, WQB, and WQA) are displayed. The nucleic acid sequences of the changes are indicated on or in the diagram. The recombination positions between QL01 and WG01 on the gene37 locus are indicated above the diagrams. The color gray represents WG01, which was modified in this study. The color mauve represents the exchanged regions which are derived from QL01. For example, in WQT, the region from 193 to 2772 was the exchanged region from QL01.

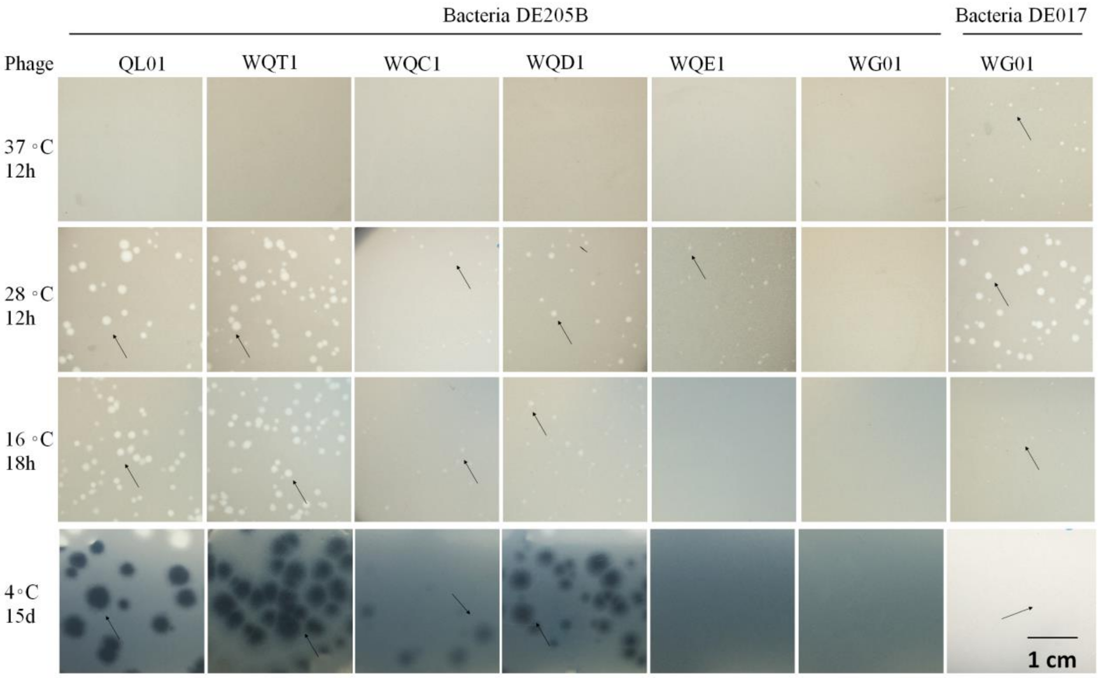

Fig. S5 Growth characteristics of WG01, QL01, and WG01 derivatives

The results of the growth characteristics for WG01, QL01, WQT1, WQC1, WQD1, and WQE1 were displayed. On the lawn of DE205B, QL01, WQT1, WQC1, and WQD1 all formed plaques at 28 ℃, 16 ℃, and 4 ℃, rather than at 37 ℃; WQE1 only formed plaques at 28 ℃. WG01 could not infect DE205B, but could form plaques at 37 ℃, 28 ℃, 16 ℃ and 4 ℃ with DE017.

Table S1 strains used in phage isolation and host range analysis of recombinant phages

Strains	WQT2	WQT3	WQT4	WQT5	WQT6	WQT7	WQT8	WQT9	WQT10	WQT11	WQT12	QL01	WQC	WQD	WQE	WG01	WQT1
DE001	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
DE002	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE003	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE005	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE007	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE008	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE010	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE011	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE013	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE015	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE017	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE018	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+
DE019	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE020	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE021	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE022	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE023	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE028	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE032	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE034	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE037	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+

DE041	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE044	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE046	-	-	-	-	-	+	-	-	-	-	-	-	-	+	-	-	-
DE049	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE050	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE054	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE056	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE060	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE061	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE064	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE065	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE069	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE070	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE071	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE072	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE074	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE075	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE077	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE083	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE085	-	-	-	-	-	+	-	-	-	-	-	-	-	+	-	-	-
DE094	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE098	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE101	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-
DE102	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	-
DE104	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+
DE119	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-

DE120	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE123	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
DE127	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE129	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE132	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE137	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE144	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE147	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-
DE148	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE158	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE160	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE167	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE169	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE172	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE182	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE183	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE186	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE192	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE197	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE205B	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE207	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE209	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE217	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE235	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE241	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-
DE242	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

DE248	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE257	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE278	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE283	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	+
DE295	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE296	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE301	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE302	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE303	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	+
DE312	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	-
DE316	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	+
DE322	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+
DE327	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE353	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-
DE365	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE373	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE376	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE384	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE388	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE389	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE400	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE402	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE404	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE407	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	-	+
DE414	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE419	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+

DE426	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE432	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE452	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+
DE458	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE464	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
XM	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
HX01	-	-	-	-	-	+	-	-	-	-	-	+	-	+	-	-	-
HX04	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
NT-1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
MC1061	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+
MG1655	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
O157:H7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RS218	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
5155	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Host range	49	49	49	49	49	52	49	49	49	49	49	50	47	63	28	22	46

+, clear lysis; -, no reaction

Table S2 T4-like phages that showed homology with the genome sequence of QL01

Phage	Host strain	RefSeq	Size (bp)	Query %	Ident %
Enterobacteria phage WG01	*Escherichia coli*	NC_031928.1	169936	100	100
Enterobacteria phage Bp7	*Escherichia coli*	NC_019500.1	168066	92	98
Enterobacteria phage JS98	*Escherichia coli*	NC_010105.1	170523	94	92
Enterobacteria phage QL01	*Escherichia coli*	NC_028847.1	170527	95	98
Enterobacteria phage JS10	*Escherichia coli*	NC_012741.1	171451	93	93
Enterobacteria phage MX01	*Escherichia coli*	NC_031934.1	168929	93	94
Enterobacteria phage vB_EcoM_VR5	*Escherichia coli*	NC_028881.1	170473	90	90
Enterobacteria phage IME08	*Escherichia coli*	NC_014260.1	172253	91	92
Enterobacteria phage vB_EcoM_VR20	*Escherichia coli*	NC_028894.1	170336	76	79
Enterobacteria phage vB_EcoM_VR25	*Escherichia coli*	NC_028925.1	170822	74	79
Shigella phage SP18	*Shigella sonnei*	NC_014595.1	170605	76	77
Enterobacteria phage vB_EcoM_VR26	*Escherichia coli*	NC_028957.1	171541	74	81
Enterobacteria phage vB_EcoM_VR7	*Escherichia coli*	NC_014792.1	169285	72	80
Edwardsiella phage PEi20	*Edwardsiella ictaluri*	NC_028683.1	177643	52	80
Pectobacterium bacteriophage PM2	*Pectobacterium carotovorum subsp. Carotovorum*	NC_028940.1	170286	51	78
Escherichia phage slur07	*Escherichia coli*	NC_028780.1	167124	48	76
Escherichia phage ECML-134	*Escherichia coli*	NC_025449.1	166783	48	75
Escherichia phage HY01	*Escherichia coli*	NC_027349.1	166977	50	76
Shigella phage pSs-1	*Shigella sonnei*	NC_025829.1	164999	49	75
Enterobacteria phage T4	*Escherichia coli*	NC_000866.4	168903	46	76
Enterobacteria phage RB27	*Escherichia coli*	NC_025448.1	165179	48	76
Yersinia phage PST	*Yersinia pseudotuberculosis*	NC_027404.1	167785	49	76
Enterobacteria phage RB3	*Escherichia coli*	NC_025419.1	168402	44	76
Enterobacteria phage RB14	*Escherichia coli*	NC_012638.1	165429	48	76
Escherichia phage wV7	*Escherichia coli*	NC_019505.1	166452	49	75
Shigella phage Shfl2	*Shigella flexneri*	NC_015457.1	165919	48	75
Escherichia phage HY03	*Escherichia coli*	NC_031047.1	170770	47	75
Escherichia phage e11/2	*Escherichia coli*	NC_024125.2	168470	48	75
Escherichia phage vB_EcoM_PhAPEC2	*Escherichia coli*	NC_024794.1	167318	57	75
Enterobacteria phage RB69	*Escherichia coli*	NC_004928.1	167560	58	75

Enterobacteria phage RB51	*Escherichia coli*	NC_012635.1	168394	50	75
Citrobacter phage Moon	*Citrobacter freundii*	NC_027331.1	170341	41	75
Salmonella phage S16	*Salmonella enterica*	NC_020416.1	160221	33	72

Table S3. Comparison results for WG01 and QL01

QL01 ORF	WG01 ORF	WG01 protein identity with the proteins of QL01		Protein (from NCBI) identity with either WG01 or QL01 proteins			Product
		query	iden	phage	query	iden	
1	1	100	99				rIIA protects from prophage-induced early lysis
2	2	100	99				hypothetical protein
3	3	100	99				hypothetical protein
4	4	100	96				hypothetical protein
5	5	100	100				topoisomerase II large subunit
6	6	100	100				hypothetical protein
7	7	100	100				hypothetical protein
8	8	100	99				putative RNA metabolism modulator
9	9	100	100				modifier of suppressor tRNAs
10	10	100	87				modifier of transcription
11	11	100	97				hypothetical protein
12	12	100	97				hypothetical protein
13	13	100	99				hypothetical protein
14	14	100	97				hypothetical protein
15	15	100	99				DNA helicase
16	16	100	100				hypothetical protein
17	17	100	99				putative Srd anti-sigma factor
18	18	100	99				hypothetical protein
19	19	100	99				hypothetical protein
-	20	-	-	Shigella phage SP18_gp021	100	59	hypothetical protein

20	21	100	97	hypothetical protein
21	22	100	88	hypothetical protein
22	23	100	93	hypothetical protein
23	24	100	98	Srh transcription modulator
24	25	81	92	hypothetical protein
25	26	100	100	hypothetical protein
26	27	100	92	hypothetical protein
27	28	100	100	dCTPase
28	29	100	100	hypothetical protein
29	30	100	100	hypothetical protein
30	31	100	100	hypothetical protein
31	32	100	100	hypothetical protein
32	33	100	99	hypothetical protein
33	34	100	96	spackle periplasmic protein
34	35	100	99	hypothetical protein
35	36	100	98	hypothetical protein
36	37	100	97	discriminator of mRNA degradation
37	38	100	100	hypothetical protein
38	39	100	100	DNA primase-helicase subunit
39	40	100	100	hypothetical protein
40	41	100	100	UvsX RecA-like recombination protein
41	42	100	99	hypothetical protein
42	43	100	100	hypothetical protein
43	44	100	100	hypothetical protein
44	45	100	100	hypothetical protein
45	46	100	100	hypothetical protein

46	47	100	100				hypothetical protein
47	48	100	100				immunity to superinfection membrane protein
48	49	100	99				DNA polymerase
49	50	100	99				hypothetical protein
50	51	100	100				translational repressor protein
51	52	100	99				clamp loader subunit DNA polymerase
52	53	100	99				hypothetical protein
53	54	100	100				sliding clamp DNA polymerase accessory protein
54	55	100	100				hypothetical protein
55	56	100	100				hypothetical protein
56	57	100	99				hypothetical protein
57	58	100	100				hypothetical protein
58	59	100	100				hypothetical protein
59	60	100	97				recombination endonuclease subunit
60	-	-	-	BP7_0131	55	61	N-terminal catalytic GIY-YIG domain of bacteriophage T4 segABCDEFG gene encoding proteins
-	61	-	-	JS98_058	100	98	gp47.1 hypothetical predicted membrane protein
61	62	100	100				hypothetical protein
62	63	100	100				hypothetical protein
63	64	100	100				hypothetical protein
64	65	100	100				hypothetical protein
65	66	100	99				hypothetical protein
66	67	100	97				hypothetical protein
67	68	100	100				hypothetical protein
68	69	100	99				hypothetical protein

69	70	100	100				hypothetical protein
70	71	100	88				hypothetical protein
71	72	100	100				hypothetical protein
72	73	100	100				hypothetical protein
73	74	100	68				hypothetical protein
74	75	100	100				hypothetical protein
75	76	100	100				hypothetical protein
76	77	100	100				putative membrane protein
77	78	100	100				hypothetical protein
78	79	100	100				hypothetical protein
79	80	100	100				hypothetical protein
80	81	100	100				hypothetical protein
81	82	100	100				hypothetical protein
82	83	100	100				thioredoxin
83	84	100	100				hypothetical protein
84	85	100	99				hypothetical protein
85	86	100	99				hypothetical protein
86	87	100	97				hypothetical protein
87	88	100	100				hypothetical protein
88	89	100	100				hypothetical protein
89	90	100	100				hypothetical protein
90	91	100	81				hypothetical protein
91	92	100	98				hypothetical protein
-	93	-	-	Edwardsiella phage PEi20_098, Edwardsiella phage PEi26_098	96	51	hypothetical protein
92	94	100	91				hypothetical protein

93	95	98	99				hypothetical protein
94	96	100	100				hypothetical protein
95	97	100	100				hypothetical protein
96	98	100	95				hypothetical protein
97	99	100	100				hypothetical protein
98	100	100	100				hypothetical protein
99	101	100	100				hypothetical protein
100	102	100	100				hypothetical protein
101	103	100	100				thymidine kinase
102	104	100	59				hypothetical protein
103	105	100	100				hypothetical protein
104	106	100	99				hypothetical protein
105	107	100	100				valyl-tRNA synthetase modifier
106	108	100	98				hypothetical protein
107	109	100	98				site-specific RNA endonuclease
108	-	-	-	Edwardsiella phage PEi26_122	100	88	conserved hypothetical protein
109	110	100	98				hypothetical protein
110	111	100	100				hypothetical protein
111	112	100	100				hypothetical protein
112	113	100	99				hypothetical protein
113	144	97	51				IP7
-	114	-	-	-	-	-	hypothetical protein
-	115	-	-	Escherichia phage Av-05_183	94	37	hypothetical protein
114	116	100	99				endonuclease V N-glycosylase UV repair enzyme
115	117	100	99				internal head protein
116	118	100	100				hypothetical protein

117	119	100	99	hypothetical protein
118	120	100	100	nudix hydrolase
119	121	100	100	hypothetical protein
120	122	100	53	putative membrane protein
121	123	100	93	hypothetical protein
122	124	100	100	hypothetical protein
123	125	100	99	hypothetical protein
124	126	100	100	hypothetical protein
125	127	100	100	hypothetical protein
126	128	100	100	hypothetical protein
127	129	100	100	hypothetical protein
128	130	100	100	hypothetical protein
129	131	100	100	hypothetical protein
130	132	100	100	hypothetical protein
131	133	100	99	hypothetical protein
132	134	100	77	hypothetical protein
133	135	100	98	hypothetical protein
134	136	100	97	hypothetical protein
135	137	100	99	hypothetical protein
136	138	100	99	hypothetical protein
137	139	100	100	hypothetical protein
138	140	100	99	hypothetical protein
139	141	100	100	hypothetical protein
140	142	100	92	hypothetical protein
141	143	100	69	hypothetical protein
142	145	100	98	hypothetical protein

143	146	100	91				hypothetical protein
-	147	-	-	Citrobacter phage Merlin_166	95	53	hypothetical protein
144	148	100	99				hypothetical protein
145	149	100	100				chaperone for tail fiber formation
146	150	100	100				hypothetical protein
147	151	100	99				tail completion and sheath stabilizer protein
148	-	-	-	vB_EcoM_VR25_162	100	62	hypothetical protein
149	152	100	98				DNA end protector protein
150	153	100	100				head completion protein
151	154	100	100				hypothetical protein
152	155	95	95				baseplate hub subunit and tail lysozyme
153	-	-	-	IME08_142	100	95	5.1 gene product
154	-	-	-	IME08_143	100	100	5.4 gene product
-	156	-	-	Bp7_254	100	100	hypothetical protein
155	157	100	100				baseplate wedge subunit
156	158	100	99				baseplate wedge initiator
157	159	100	100				baseplate wedge subunit
158	160	100	100				baseplate wedge tail fiber
159	161	100	99				baseplate wedge subunit and tail pin
160	162	100	100				baseplate wedge subunit and tail pin
161	163	100	100				short tail fibers protein
162	164	100	99				fibritin neck whiskers
163	165	100	100				neck protein
164	166	100	100				neck protein
165	167	100	100				tail sheath stabilizer and completion protein
166	168	100	97				terminase DNA packaging enzyme small subunit

167	169	100	100				terminase DNA packaging enzyme large subunit
168	170	100	98				tail sheath protein
169	-	-	-	Klebsiella phage PKO111_028	99	65	hypothetical protein
170	171	100	100				hypothetical protein
171	-	-	-	Bp7_237	100	100	hypothetical protein
172	172	100	100				hypothetical protein
173	173	100	100				prohead core protein precursor
174	174	100	100				prohead core protein
175	175	100	100				prohead core scaffold protein and protease
176	176	100	99				prohead core scaffold protein
177	177	100	99				major head protein
178	178	100	100				hypothetical protein
179	179	100	99				head vertex protein
180	180	100	100				head vertex protein
181	181	100	84				RNA ligase 2
182	182	100	100				hypothetical protein
183	183	100	98				head outer capsid protein
184	184	100	99				inhibitor of prohead protease
185	185	100	100				hypothetical protein
186	186	100	100				hypothetical protein
187	187	100	100				hypothetical protein
188	188	100	100				hypothetical protein
189	189	100	100				UvsY recombination repair and ssDNA binding protein
190	190	100	100				baseplate hub subunit
191	191	100	99				baseplate hub subunit

192	192	100	100				baseplate hub assembly catalyst
193	193	100	100				aseplate hub subunit
194	194	100	100				hypothetical protein
195	195	100	99				baseplate hub subunit
196	196	100	99				baseplate tail tube cap
197	197	100	96				baseplate tail tube initiator
198	198	100	98				hypothetical protein
199	199	100	98				RNA polymerase ADP-ribosylase
200	200	100	46				RNA polymerase ADP-ribosylase
201	200	99	99				RNA polymerase ADP-ribosylase
201	201	94	41				RNA polymerase ADP-ribosylase
202	202	100	98				hypothetical protein
203	203	100	99				DNA ligase
204	204	100	100				hypothetical protein
205	205	100	99				hypothetical protein
206	206	100	99				hypothetical protein
207	207	100	57				hypothetical protein
207	208	100	97				hypothetical protein
208	209	100	98				hypothetical protein
209	-	-	-	vB_EcoM_VR5_207	97	92	hypothetical protein
210	210	100	99				hypothetical protein
211	211	100	98				hypothetical protein
212	212	100	100				hypothetical protein
213	213	100	100				hypothetical protein
214	214	100	99				hypothetical protein
215	215	100	100				head assembly cochaperone with GroEL

216	216	100	100				hypothetical protein
217	217	100	100				hypothetical protein
218	218	100	99				hypothetical protein
219	219	100	99				hypothetical protein
220	220	100	88				hypothetical protein
221	221	100	97				hypothetical protein
222	222	100	100				hypothetical protein
223	223	100	100				hypothetical protein
224	-	-	-	RB14_217	100	78	hypothetical protein
225	224	100	97				PseT polynucleotide 5'-kinase and 3'-phosphatase
226	225	100	100				hypothetical protein
227	226	100	100				hypothetical protein
228	227	100	100				hypothetical protein
229	228	100	99				putative membrane protein
230	229	100	100				hypothetical protein
231	230	100	100				hypothetical protein
232	231	100	100				hypothetical protein
233	232	100	99				hypothetical protein
234	233	100	99				aerobic NDP reductase small subunit
235	234	100	99				aerobic NDP reductase large subunit
236	235	74	99				hypothetical protein
237	236	100	100				dTMP thymidylate synthase
238	237	100	95				dihydrofolate reductase
239	238	100	100				hypothetical protein
240	239	100	100				hypothetical protein
241	240	100	100				hypothetical protein

242	241	100	96				hypothetical protein
243	242	100	100				hypothetical protein
244	243	100	98				hypothetical protein
245	244	100	100				late promoter transcription accessory protein
246	245	100	100				hypothetical protein
247	246	100	99				RNaseH ribonuclease
248	247	100	98				long tail fiber proximal subunit
249	248	100	99				long tail fiber proximal connector
250	249	100	99				long tail fiber distal connector
251	250	100	58				long tail fiber distal subunit
252	251	100	99				tail fiber adhesin
253	252	100	100				hypothetical protein
254	253	100	100				anti-sigma 70 protein
255	254	100	93				hypothetical protein
256	255	100	97				hypothetical protein
257	256	100	98				hypothetical protein
258	257	100	85				hypothetical protein
259	-	-	-	RB32_252	100	90	hypothetical protein
-	258	-	-	Bp7_151	100	100	hypothetical protein
260	259	100	75				hypothetical protein
261	260	100	100				hypothetical protein
262	261	100	100				hypothetical protein
263	262	99	98				topoisomerase II medium subunit
264	263	100	100				hypothetical protein
265	264	100	98				putative membrane protein
266	265	100	100				nucleoid disruption protein

267	266	100	100				hypothetical protein
268	267	100	100				hypothetical protein
269	268	100	100				putative inner membrane
270	269	100	98				hypothetical protein
271	-	-	-	-	-	-	hypothetical protein
272	270	100	100				hypothetical protein
273	271	100	99				hypothetical protein
274	272	100	100				hypothetical protein
275	273	100	93				hypothetical protein

Table S4. The DNA sequences of chimeric phages and mutants from the WQT chimeric phage

WQT2

ATGGCTACTTTAAAGCAAATCCAATTTAAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCAGTTGGCTGAAGGCGAACTGGCTATTAACTTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAGCGATTATCGACCTTGGCTTTGCTAAGGGTGGAAATATCGATGGTAATGTTATTCATAAAGGCAATTACAACCAAACCGGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTATAACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGTGGCAATGGTACCGCACATGTTCGATTCCAGGATTTAGCTGATGCGCGCGAAAGAGCTATAATTTATTCTCAAAACCGTACTGGGGATACCAAGCAAATCTTGAACGTTCGTGTTCAGGATTACACTAATTCGACATCTAATATTTTTGCATTCAACGGCGACGGTTTATTTTATGCTCCGTCTATTTCCGCCGGAACATCAGTAAAATCTCCGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGCAAATAATAATTCTGCCACGGATAAAAACTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACTTCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCTTTTGCTTATTCCGGTGGTTTTCAAGCAGGTCATTCGATTGCAGTAAGTATGGAATCAGGGCCTTTGACATATTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACGGCCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACAACTCCAACTGAAGTTACAAGCCTTAAACAGTTAGTTGCGGGTTATTCAACCAACGGTTCTGATTTAATTCTTCCTACAACTCAAAACTATCCATTAGTTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACTCTTTTAGGTTATCACCAGAGCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTTGGTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTCGGTTAATATTGATGGTCTCAGTAATGCTTCTACAGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGACACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCATTATATTCAACGAACTACAGAAGGTAAAGTCGAATCCTATTTAAATGGTACCATGAATGTAATTGAAGGATTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAAGTTCGCGCTGCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTTATTTTTCGAAATTCGGAAGACCAACTGCATATTATTCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCCATTACGACCGTTAAGTATTACATTAGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTATTGGAATTCATCGCCGGTAACGGTTCATCTTATGCTAACCAGAACACAACTAAAGCTCCATTGTATCAAACGCTTGGTTCTGCGACTCAAGCATTCTATCCTATTACTAAGCAGAAAAATACAGTTTCTAACGTAACTGTTACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATGGTGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACTTTATAACTCGGAACCGCTTATATGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGCTACTAACCTTGATGCTGCAGTGAATACTCGTGTTGGTAAAGGCGGCGATACAATGACTGGCAAATTAATCGTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAACATCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACACTGCTTCATTTTATAATTTCAAAACTACCGCAGGAATTACTCTTAATAGTGTAGGCGATATTGATTTTAATGTTAAAAAACAATCTACTGCAGCTTCATTAAATTTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGATATAATAATCAATGGCAAACAGAAGCCCCATTCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGTTATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAACGAAGGATATGCCACAAAGGCAGATTTTGGTATTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGAGATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTCGCGCTGGTGTTAACTTGGGTGTCGGTACAATTCCAGCATGGGGCGGAGCATCTATCGCCATTGGGGAC

GATGACACCGGCTTGGTCCATGGCGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCAAGCTGGGGAGCTGGTTACCATATCCATGAAGGTCTTTGGGATACCACTGGTGCCTTGTGGACTGAAACAGGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCGTGACGTTTATGTTCGTTCTGATATTCGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTTCAAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAACCTAATGCCGGTTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCCTGACGGTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAATTGGTTTAAATACAGCTGCAATCAATGAGCACACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAAATCATTGTTAAAATAA

WQT3

ATGGCTACTTTAAAGCAAATCCAATTTAAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCAGTTGGCTGAAGGCGAACTGGCTATTAACTTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAGCGATTATCGACCTTGGCTTTGCTAAGGGTGGAAATATCGATGGTAATGTTATTCATAAAGGCAATTACAACCAAACCGGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTATAACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGTGGCAATGGTACCGCACATGTTCGATTCCAGGATTTAGCTGATGCGCGCGAAAGAGCTATAATTTATTCTCAAAACCGTACTGGGGATACCAAGCAAATCTTGAACGTTCGTGTTCAGGATTACACTAATTCGACATCTAATATTTTTGCATTCAACGGCGACGGTTTATTTTATGCTCCGTCTATTTCCGCCGGAACATCAGTAAAATCTCCGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGCAAATAATAATTCTGCCACGGATAAAAACTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACTTCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCTTTTGCTTATTCCGGTGGTTTTCAAGCAGGTCATTCGATTGCAGTAGGTATGGAATCAGGGCCTTTGACATATTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACGGCCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACAACTCCAACTGAAGTTACAAGCCTTAAACAGTTAGTTGCGGGTTATTCAACCAACGGTTCTGATTTAATTCTTCCTACAACTCAAAACTATCCATTAGTTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACTCTTTTAGGTTATCACCAGAGCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTTGGTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTCGGTTAATATTGATGGTCTCAGTAATGCTTCTACAGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGACACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCATTATATTCAACGAACTACAGAAGGTAAAGTCGAATCCTATTTAAATGGTACCATGAATGTAATTGAAGGATTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAAGTTCGCGCTGCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTTATTTTTCGAAATTCGGAAGACCAACTGCATATTATTCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCCATTACGACCGTTAAGTATTACATTAGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTATTGGAATTCATCGCCGGTAACGGTTCATCTTATGCTAACCAGAACACAACTAAAGCTCCATTGTATCAAACGCTTGGTTCTGCGACTCAAGCATTCTATCCTATTACTAAGCAGAAAAATACAGTTTCTAACGTAACTGTTACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATGGTGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACTTTATAACTCGGAACCGCTTATATGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGCTACTAACCTTGATGCTGCAGTGAATACTCGTGTTGGTAAAGGCGGCGATACAATGACTGGCAAATTAATCGTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAACATCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACACTGCTTCATTTTATAATTTC

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WQT4

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WQT9

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WQT10

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WQT11

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WQT12

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WQC1

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WQD1

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WQE1

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WQT1

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CTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAAATCATTGTTAAAAT
AA

Yellow and green color: nucleic acid mutation which occurred didn’t cause amino acid substitution

Red color: nucleic acid mutation which occurred caused amino acid substitution.