

1 **Figure S1.** (A) Exponentially growing cells were infected with iEPS5  
2 (MOI, 0.01) and incubated at 37°C. After centrifugation and filtration,  
3 the phage titer in the filtrate was determined by standard overlay  
4 assay. The results are expressed as means and standard deviations of  
5 triplicate assays. (B) One-step growth curve analysis  
6 of *S. Typhimurium* SL1344 infected by iEPS5. E, eclipse period; L,  
7 latent period; B, burst size. Closed squares, non-chloroform-treated  
8 sample; opened circle, chloroform-treated sample. The error bars  
9 indicate standard deviations.

10

11 **Figure S2.** Motility and dotting assay of iEPS5 resistant isolates. (A)  
12 Motility of six candidate mutants was assessed. One micro liter of an  
13 overnight culture of each candidate isolate was spotted in the middle  
14 of a swim plate (LB, 0.3% agar) and incubated at 37°C for 8 h. SL1344  
15 (WT), CH507 ( $\Delta fliC$ ), CH508 ( $\Delta fliB$ ), and CH509 ( $\Delta fliC/\Delta fliB$ ) strains  
16 were used for control. (B) Serially diluted phage was spotted onto  
17 plates of the single flagellin mutants (CH507,  $\Delta fliC$  and CH508  $\Delta fliB$ )  
18 and double mutant (CH509,  $\Delta fliC/\Delta fliB$ ). The serially diluted phages  
19 from  $10^2$  to  $10^9$  PFU/ml were used as indicated inside circle.

20

21 **Figure S3.** Motility and dotting assay were performed using various  
22 mutants, which have different motile phenotypes. SJW2811 (extreme  
23 CW-biased), SJW3076 (CCW-biased), MMTA19 (slow *motA* mutant),  
24 MMTA173 (slow *motA* mutant), MMTB135 (slow *motB* mutant),  
25 MMTB6055 (slow *motB* mutant).

26

27 **Figure S4.** Polyhook structure and unbound form of phage.  
28 Transmission electron micrograph of iEPS5 and polyhook strain  
29 (CH506,  $\Delta$ *filK*). Arrows designate phage, tail fiber, and polyhook  
30 (PH).

31

32 **Figure S5.** Visualization of bacterial cells during infection by SYBR-  
33 gold-labeled EPS7 phage. The SYBR-gold-labeled EPS7 particles  
34 known to use BtuB as a receptor (1) were seen as dots adhered to the  
35 surface of bacteria in contrast to iEPS5 or Chi particles shown  
36 adhered to the flagellar filament in Fig. 5 at 10 min after infection.  
37 The cytosol of the whole bacteria was fluorescent at 1 h after  
38 infection due to the SYBR-gold-labeled EPS7 DNA injected. LM, light

39 microscopy; EFM, epifluorescence microscopy; Merge, LM+EFM,  
40 Magnification = 1,000X.

41

42 **Figure S6.** Phylogenetic analysis of terminase large subunits in iEPS5  
43 with various bacteriophages. Amino acid sequences of terminase  
44 large subunits were compared by ClustalW alignments and the  
45 phylogenetic tree was generated by the neighbor-joining method  
46 with *P* distance values using MEGA5 program.

47

48

49 **Table S1.** The bacterial strains and plasmids used in this study

50

Strain or plasmid	Description	Reference or source <sup>a</sup>
<b>S. Typhimurium</b>		
SL1344	Wild-type	NCTC
CH501	$\Delta$ <i>fliR</i>	This study
CH502	$\Delta$ <i>flgK</i>	This study
CH504	$\Delta$ <i>motA</i>	This study
CH505	$\Delta$ <i>cheY</i>	This study
CH506	$\Delta$ <i>fliK</i>	This study
CH507	$\Delta$ <i>fliC</i>	This study
CH508	$\Delta$ <i>fljB</i>	This study
CH509	$\Delta$ <i>fliC/\Delta</i> <i>fljB</i>	This study
CH511	$\Delta$ <i>fliR/p</i> ACYC- <i>fliR</i>	This study
CH512	$\Delta$ <i>flgK/p</i> ACYC- <i>flgK</i>	This study
CH514	$\Delta$ <i>motA/p</i> UHE- <i>motA</i>	This study
CH515	$\Delta$ <i>cheY/p</i> UHE- <i>cheY</i>	This study
CH516	$\Delta$ <i>fliK/p</i> UHE- <i>fliK</i>	This study
SJW2811	<i>AfliG</i> ( $\Delta$ 169-171) CW-biased	(2)
SJW3076	$\Delta$ <i>cheA</i> to <i>cheZ</i> CCW-biased	(3)
<b>E. coli</b>		
DH5 $\alpha$	<i>supE44 hsdR17 recA1 gyrA96 thi-1 relA1</i>	(4)
EC100D <sup>TM</sup>	<i>pir</i> <sup>+</sup>	Epicentre
<b>Plasmid</b>		
pUHE21-2 <i>lacI</i> <sup>q</sup>	rep <sub>pMB1</sub> Ap <sup>r</sup> <i>lacI</i> <sup>q</sup>	(5)
pACYC184	rep <sub>p15A</sub> Cm <sup>r</sup> Tet <sup>r</sup>	(6)
pKD13	rep <sub>R6K<math>\gamma</math></sub> Ap <sup>r</sup> -FRT Km <sup>r</sup> -FRT	(7)
pKD46	rep <sub>pSC101<sup>ts</sup></sub> Ap <sup>r</sup> P <sub><i>araBAD</i></sub> $\gamma$ $\beta$ <i>exo</i>	(7)
pCP20	rep <sub>pSC101<sup>ts</sup></sub> Ap <sup>r</sup> Cm <sup>r</sup> <i>cI857</i> $\lambda$ P <sub>R</sub> <i>flp</i>	(8)
pACYC- <i>fliR</i>	rep <sub>p15A</sub> Cm <sup>r</sup> Tet <sup>r</sup> <i>fliR</i>	This study
pACYC- <i>flgK</i>	rep <sub>p15A</sub> Cm <sup>r</sup> Tet <sup>r</sup> <i>flgK</i>	This study
pUHE- <i>motA</i>	rep <sub>pMB1</sub> Ap <sup>r</sup> <i>lacI</i> <sup>q</sup> <i>motA</i>	This study
pUHE- <i>cheY</i>	rep <sub>pMB1</sub> Ap <sup>r</sup> <i>lacI</i> <sup>q</sup> <i>cheY</i>	This study
pUHE- <i>fliK</i>	rep <sub>pMB1</sub> Ap <sup>r</sup> <i>lacI</i> <sup>q</sup> <i>fliK</i>	This study

51 <sup>a</sup> NCTC, National Collection of Type Cultures

52 **Table S2.** Oligonucleotide used for the construction of stains and  
 53 plasmids  
 54

Primer name	Sequence (5' → 3')	Purpose
<i>fliR</i> -lamb-F	ATTACGTGCGCACTCTGTTTCAGCAATTTACCTTATATCA TCGGATAAACAGAACGTGTAGGCTGGAGCTGCTTCG	λ Red deletion of <i>fliR</i>
<i>fliR</i> -lamb-R	TTTAAAATTTATTTTCGGATAAACCTTAGTAAAACAGGA TAAAAATTATGGGTTAATTCCGGGGATCCGTCGACC	
<i>flgK</i> -lamb-F	GCCGATAACAACGAGTATTGAAGGATTA AGGAACCATCTGTAGGCTGGAGCTGCTTCG	λ Red deletion of <i>flgK</i>
<i>flgK</i> -lamb-R	TACATCATCTGGGTAAGTATGATACGCATGTCA TCCTTCTCCTATTCCGGGGATCCGTCGACC	
<i>motA</i> -lamb-F	CTGCGCATCCTGTCATAGTCAACAGCGGAA GGATGATGCTGTAGGCTGGAGCTGCTTCG	λ Red deletion of <i>motA</i>
<i>motA</i> -lamb-R	CTGCGGCGTTTTACGACGACAATGGGATGA GCCTGATTTTATTCCGGGGATCCGTCGACC	
<i>cheY</i> -lamb-F	TGGCGAAAATCAGTGCCGGACAGGCGATACGTATTTG AACCAGGAGTAGTATTTTTGTAGGCTGGAGCTGCTTCG	λ Red deletion of <i>cheY</i>
<i>cheY</i> -lamb-R	TCCTGCTGAGCCTTCATCAGCAGGCTTGATAGATGGTT GCATCATCATCGCATCCATTCCGGGGATCCGTCGACC	
<i>fliK</i> -lamb-F	TCTGGCGCTCCTGGCGGGCGGTTAGGCGC AGACGGCGCATGTAGGCTGGAGCTGCTTCG	λ Red deletion of <i>fliK</i>
<i>fliK</i> -lamb-R	GCCGCTTCCGCCAACTGGGTGCGCAACAT GGGCAGGGCGATTCCGGGGATCCGTCGACC	
<i>fliR</i> -pACYC-F	TCCAGCAATTAAGCTTATATCATCG	Complementation of <i>fliR</i> gene in pACYC184
<i>fliR</i> -pACYC-R	ATATCCTGGTGCATGCTTTTTAAAA	
<i>flgK</i> -pACYC-F	ACGAGTATTGAAAGCTTAAAAGGAAC	Complementation of <i>flgK</i> gene in pACYC184
<i>flgK</i> -pACYC-R	ACTGATACGCATGCCATCCTTC	
<i>motA</i> -pUHE-F	CCCGACTGCGAATTCGTGCATAGT	Overexpression of <i>motA</i> gene in pUHE21-2 <i>lacI</i> <sup>q</sup>
<i>motA</i> -pUHE-R	GGGACTCCGGATCCAAATCC	
<i>cheY</i> -pUHE-F	GCGATACGAATTCGAACCAGG	Overexpression of <i>cheY</i> gene in pUHE21-2 <i>lacI</i> <sup>q</sup>
<i>cheY</i> -pUHE-R	TTGATAGATGGATCCATCATCATC	
<i>fliK</i> -pUHE-F	CGTGCAGCAATGAGGAATTCGGA	Overexpression of <i>fliK</i> gene in pUHE21-2 <i>lacI</i> <sup>q</sup>
<i>fliK</i> -pUHE-R	GGATAATCATGGATCCTCTGGCG	

55

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
01	-	551	802	252	84	9.4	11.2	hypothetical protein				
02	-	795	1046	252	84	9.4	10.1	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	2e-31	167	YP_007007078.1
03	-	1039	1245	207	69	7.3	4.9	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	1e-08	62	YP_007007076.1
04	-	1298	2458	1161	387	43.5	5.2	hypothetical protein				
05	-	2584	2805	222	74	7.7	9.2	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	3e-18	71	YP_007007071.1
06	-	2802	3350	549	183	20.3	5.5	hypothetical protein	hypothetical protein MetexDRAFT_0343 [ <i>Methylobacterium extorquens</i> DSM 13060]	1e-07	116	ZP_12695608.1
07	-	3361	3564	204	68	7.4	9.9	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	7e-08	61	YP_007007068.1
08	-	3576	4199	624	208	24.4	5.0	hypothetical protein	hypothetical protein HMPREF9944_00383 [ <i>Prevotella maculosa</i> OT 289]	1e-17	196	ZP_09552119.1
09	-	4202	4402	201	67	7.8	11.0	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	6e-27	67	YP_007007066.1
10	-	4417	4956	540	180	20.0	9.4	hypothetical protein				
11	-	4975	5232	258	86	10.0	7.7	hypothetical protein	hypothetical protein PP1_003 [ <i>Pectobacterium</i> phage PP1]	6e-10	74	YP_007010646.1
12	+	5993	6364	372	124	13.5	5.4	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	2e-52	127	YP_007007063.1

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
13	+	6436	6876	441	147	16.4	5.2	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	4e-27	150	YP_007007062.1
14	+	6863	7198	336	112	12.3	9.8	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	3e-26	115	YP_007007061.1
15	+	7185	7526	342	114	12.7	5.1	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	4e-10	123	YP_007007060.1
16	+	7507	8583	1077	359	40.1	5.0	putative recombination -associated protein RdgC	recombination-associated protein [ <i>Staphylococcus</i> phage SA1]	0.0	358	ACZ55522.1
17	+	8586	8819	234	78	9.1	10.1	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	3e-26	87	YP_007007058.1
18	+	8824	9099	276	92	10.9	5.7	hypothetical protein	hypothetical protein Redjac_0170 [ <i>Providencia</i> phage Redjac]	5e-29	92	YP_006906001.1
19	+	9295	10035	741	247	28.1	5.4	hypothetical protein	hypothetical protein Redjac_0160 [ <i>Providencia</i> phage Redjac]	5e-87	246	YP_006906000.1
20	+	10032	10706	675	225	24.9	7.5	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	1e-22	201	YP_007007055.1
21	+	10703	11803	1101	367	40.7	5.5	hypothetical protein				
22	+	11803	12507	705	235	27.0	6.5	putative N-6-adenine- methyltransferase	DNA methyltransferase [ <i>Enterobacter</i> phage Enc34]	8e-135	234	YP_007007051.1
23	+	12585	13559	975	325	37.0	5.6	hypothetical protein	hypothetical protein Redjac_0130 [ <i>Providencia</i> phage Redjac]	2e-39	344	YP_006905997.1

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
24	+	13570	13764	195	65	7.2	9.3	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	4e-11	64	YP_007007049.1
25	+	13767	13982	216	72	8.1	5.5	hypothetical protein	hypothetical protein MTE1_07137 [ <i>Klebsiella pneumoniae</i> JHCK1]	3e-12	77	ZP_19006088.1
26	+	13972	14226	255	85	9.9	9.3	hypothetical protein	hypothetical protein PA13_02472 [ <i>Pseudomonas aeruginosa</i> 138244]	6e-29	89	ZP_11910685.1
27	+	14208	14720	513	171	19.6	9.2	hypothetical protein				
28	+	14801	15082	282	94	10.3	5.7	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	6e-17	96	YP_007007048.1
29	+	15079	15390	312	104	12.1	5.9	hypothetical protein				
30	+	15387	15839	453	151	17.4	10.5	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	7e-18	162	YP_007007047.1
31	+	15841	16554	714	238	27.6	9.5	hypothetical protein	hypothetical protein [ <i>Staphylococcus</i> phage SA1]	5e-138	211	ACZ55544.1
32	+	16630	16914	285	95	11.3	7.6	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	4e-36	95	YP_007007043.1
33	+	16911	17372	462	154	17.3	6.2	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	6e-27	144	YP_007007041.1
34	-	17373	17576	204	68	7.5	5.4	hypothetical protein	putative Rz1 protein [ <i>Enterobacter</i> phage Enc34]	1e-29	68	YP_007007040.1
35	+	17578	17748	171	57	6.6	7.6	hypothetical protein				
36	-	17754	18467	714	238	25.8	9.2	lysis protein A	lysis protein A [ <i>Salmonella</i> phage iEPS5]	2e-171	237	AEB40057.1



**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
37	-	18471	18809	339	113	12.6	7.4	lysis protein B	lysis protein B [ <i>Salmonella</i> phage iEPS5]	3e-73	112	AEB40058.1
38	-	18874	21069	2196	732	81.4	7.7	hypothetical protein	hypothetical protein [ <i>Staphylococcus</i> phage SA1]	0.0	611	ACZ55502.1
39	-	21079	22305	1227	409	44.9	6.7	hypothetical protein	hypothetical protein Redjac_0070 [ <i>Providencia</i> phage Redjac]	4e-50	406	YP_006905991.1
40	-	22320	23339	1020	340	37.0	5.4	hypothetical protein	hypothetical protein Redjac_0060 [ <i>Providencia</i> phage Redjac]	0.0	339	YP_006905990.1
41	-	23353	24315	963	321	34.9	5.0	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	0.0	320	YP_007007033.1
42	-	24326	25333	1008	336	36.6	5.5	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	2e-162	331	YP_007007032.1
43	-	25343	26083	741	247	27.3	5.2	hypothetical protein	tail fiber protein [ <i>Providencia</i> phage Redjac]	7e-139	246	YP_006905987.1
44	-	26083	29973	3891	1297	143.3	5.1	hypothetical protein	tail assembly protein [ <i>Providencia</i> phage Redjac]	0.0	1287	YP_006905986.1
45	-	29963	30202	240	80	9.2	9.6	hypothetical protein	tail assembly protein [ <i>Enterobacter</i> phage Enc34]	2e-30	77	YP_007007028.1
46	-	30202	30432	231	77	8.4	10.4	putative tail assembly protein 1	tail assembly protein [ <i>Enterobacter</i> phage Enc34]	2e-32	78	YP_007007027.1
47	-	30444	31262	819	273	29.5	5.4	putative tail assembly protein 2	conserved tail assembly protein [ <i>Providencia</i> phage Redjac]	3e-162	272	YP_006905985.1
48	-	31272	32960	1689	563	63.1	5.4	hypothetical protein	hypothetical protein [ <i>Staphylococcus</i> phage SA1]	0.0	562	ACZ55504.1

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
49	-	32966	37261	4296	1432	153.9	9.3	putative tape measure protein	tape measure protein [ <i>Providencia</i> phage Redjac]	0.0	1435	YP_006906025.1
50	-	37254	37451	198	66	7.3	10.0	hypothetical protein	pre-tape measure frameshift protein [ <i>Enterobacter</i> phage Enc34]	4e-29	227	YP_007007021.1
51	-	37496	37957	462	154	16.7	5.6	hypothetical protein	pre-tape measure frameshift protein [ <i>Enterobacter</i> phage Enc34]	1e-49	227	YP_007007021.1
52	-	38054	39193	1140	380	40.3	4.9	bacterial Ig-like domain-containing protein	hypothetical protein [ <i>Staphylococcus</i> phage SA1]	0.0	379	ACZ55519.1
53	-	39207	39710	504	168	19.0	6.2	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	1e-89	168	YP_007007019.1
54	-	39707	40333	627	209	22.5	10.6	hypothetical protein	hypothetical protein [ <i>Staphylococcus</i> phage SA1]	3e-139	208	ACZ55545.1
55	-	40333	40698	366	122	13.5	5.4	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	6e-66	120	YP_007007017.1
56	-	40701	40994	294	98	10.7	7.4	hypothetical protein	hypothetical protein Redjac_0360 [ <i>Providencia</i> phage Redjac]	6e-20	90	YP_006906020.1
57	-	41056	42120	1065	355	40.0	6.1	major capsid protein E	capsid protein [ <i>Staphylococcus</i> phage SA1]	0.0	354	ACZ55524.1
58	-	42133	42552	420	140	14.5	5.2	putative decorator protein D	phage structural protein [ <i>Enterobacter</i> phage Enc34]	3e-77	139	YP_007007014.1
59	-	42567	43853	1287	429	45.3	4.8	putative prohead protease ClpP	prohead protease ClpP [ <i>Staphylococcus</i> phage SA1]	0.0	438	ACZ55516.1

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
60	-	43880	45559	1680	560	62.3	5.9	putative lambda family portal protein B	phage portal protein [ <i>Staphylococcus</i> phage SA1]	0.0	559	ACZ55505.1
61	-	45556	45810	255	85	9.5	7.4	putative head-to-tail joining protein W	head-to-tail joining protein [ <i>Enterobacter</i> phage Enc34]	2e-31	83	YP_007007011.1
62	-	45821	47896	2076	692	78.0	6.0	putative terminase large subunit	terminase large subunit [ <i>Providencia</i> phage Redjac]	0.0	691	YP_006906015.1
63	-	47886	48455	570	190	21.6	5.6	putative terminase small subunit	terminase small subunit [ <i>Enterobacter</i> phage Enc34]	1e-114	191	YP_007007009.1
64	-	48442	49917	1476	492	56.8	6.0	SNF2 domain -containing protein	helicase [ <i>Staphylococcus</i> phage SA1]	0.0	491	ACZ55509.1
65	-	49964	50251	288	96	11.2	9.8	VRR-NUC domain -containing protein	VRR-NUC domain protein [ <i>Enterobacter</i> phage Enc34]	9e-40	95	YP_007007007.1
66	-	50253	52292	2040	680	77.6	8.6	putative DNA polymerase	DNA polymerase I [ <i>Staphylococcus</i> phage SA1]	0.0	645	ACZ55501.1
67	-	52359	52955	597	199	22.6	5.4	hypothetical protein	conserved phage protein [ <i>Staphylococcus</i> phage SA1]	5e-141	198	ACZ55548.1
68	-	53010	54347	1338	446	50.5	5.1	hypothetical protein	conserved phage protein [ <i>Staphylococcus</i> phage SA1]	0.0	445	ACZ55515.1
69	-	54340	54765	426	142	15.5	10.4	hypothetical protein	hypothetical protein [ <i>Enterobacter</i> phage Enc34]	3e-15	107	YP_007007003.1
70	-	54731	55147	417	139	14.3	5.4	hypothetical protein	hypothetical protein Redjac_0260 [ <i>Providencia</i> phage Redjac]	9e-35	125	YP_006906010.1

**Table S3.** Features of bacteriophage iEPS5 ORFs, gene products, and functional assignments (continued)

ORF	Gene Strand	Left end	Right end	Length (nt)	No. amino acids	Size (kDa)	pI	Predictive function	Best hit	e-value	No. amino acids	Accession no.
71	+	55444	55671	228	76	8.4	7.6	hypothetical protein	putative transcriptional regulator [ <i>Enterobacter</i> phage Enc34]	1e-25	93	YP_007007001.1
72	+	55668	58253	2586	862	98.7	5.5	putative primase	DNA primase [ <i>Enterobacter</i> phage Enc34]	0.0	864	YP_007007000.1
73	-	58289	58612	324	108	12.3	8.5	HTH domain -containing protein	helix-turn-helix domain protein [ <i>Desulfovibrio</i> sp. FW1012B]	1e-05	110	ZP_09132024.1

**Table S4.** Adsorption assay of iEPS5 to several strains and cognate adsorption constant (*k*)

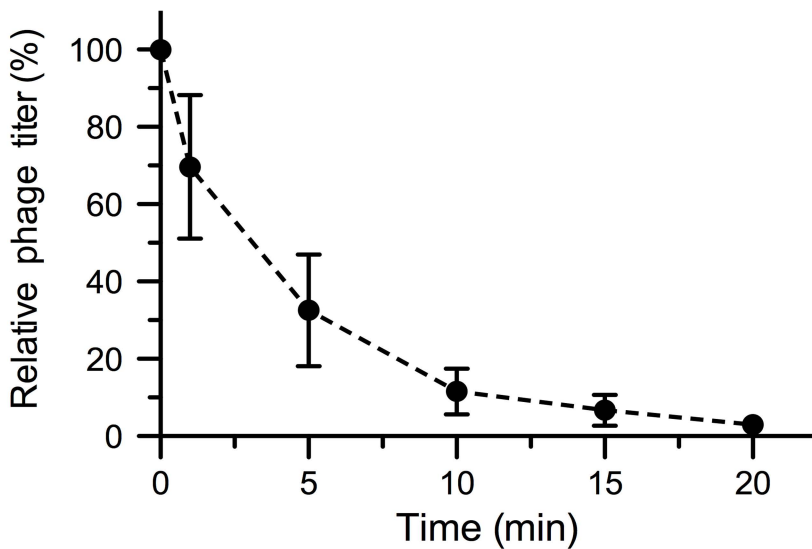
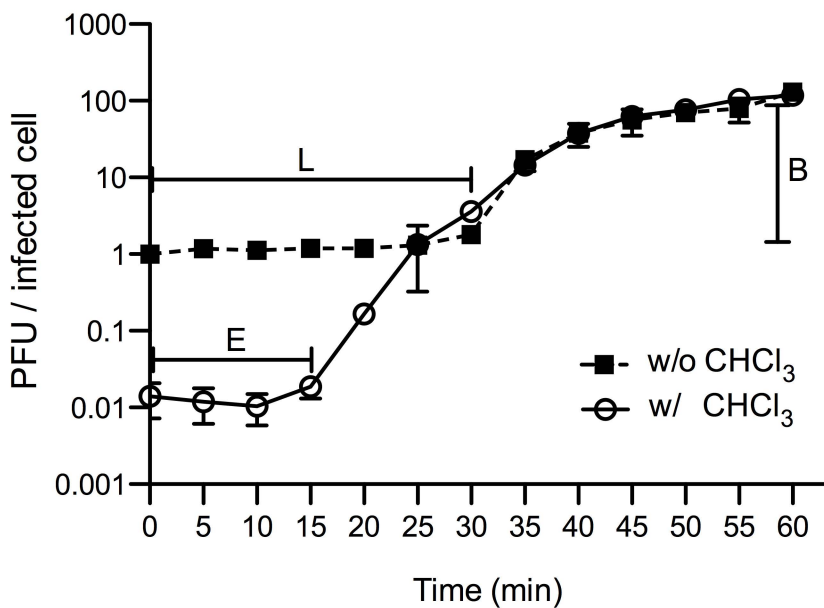
Strain	<i>k</i> <sup>a</sup>	Strain	<i>k</i> <sup>a</sup>	Strain	<i>k</i> <sup>a</sup>
WT	1.924E-09	WT	2.008E-09	WT	1.959E-09
<i>ΔmotA</i>	2.457E-11	<i>ΔcheY</i>	1.628E-09	<i>ΔfliK</i>	5.123E-11
<i>ΔfliR</i>	7.423E-11	<i>ΔcheY</i> / pUHE- <i>cheY</i> No IPTG	1.433E-09	<i>ΔfliK</i> / pUHE- <i>fliK</i> No IPTG	1.15E-10
<i>ΔflgK</i>	2.431E-11	<i>ΔcheY</i> / pUHE- <i>cheY</i> 500 μM IPTG	2.789E-10	<i>ΔfliK</i> / pUHE- <i>fliK</i> 100 μM IPTG	3.645E-10
SJW3076	1.413E-09	<i>ΔcheY</i> / pUHE- <i>cheY</i> 1 mM IPTG	1.012E-10	<i>ΔfliK</i> / pUHE- <i>fliK</i> 200 μM IPTG	4.914E-10
SJW2811	2.31E-11	<i>ΔcheY</i> / pUHE- <i>cheY</i> 2 mM IPTG	4.071E-11	<i>ΔfliK</i> / pUHE- <i>fliK</i> 500 μM IPTG	9.325E-10

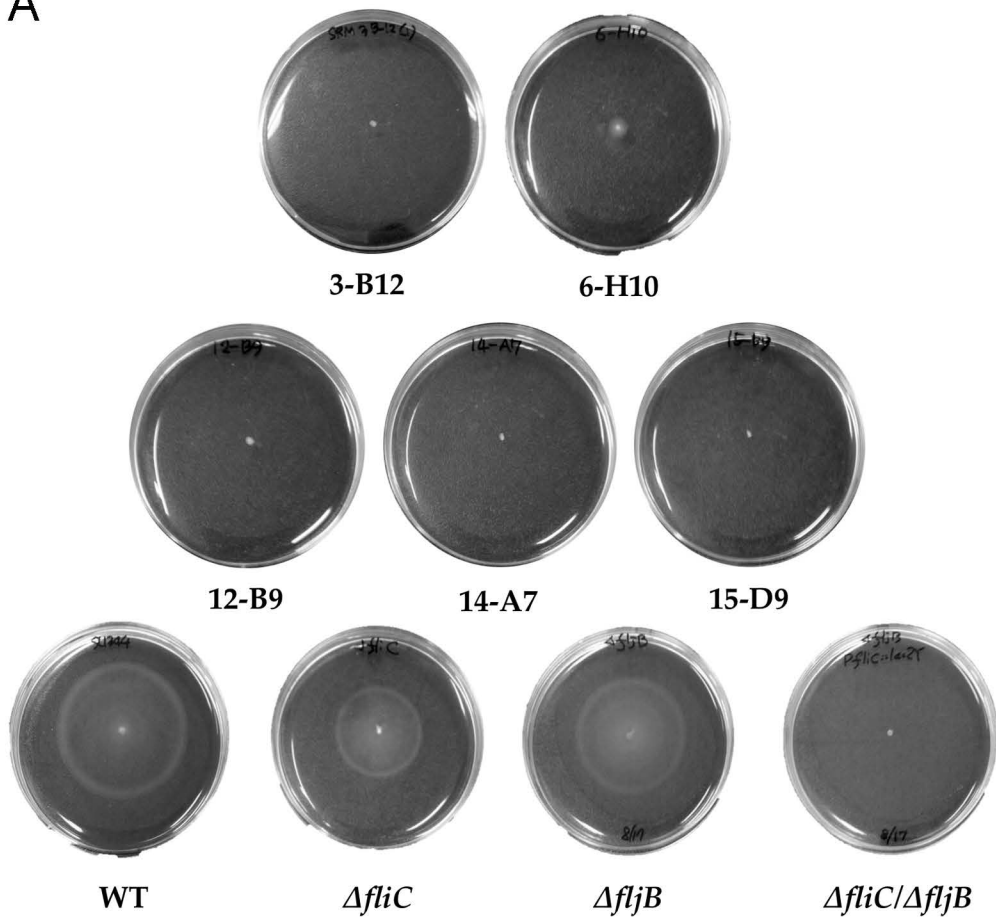
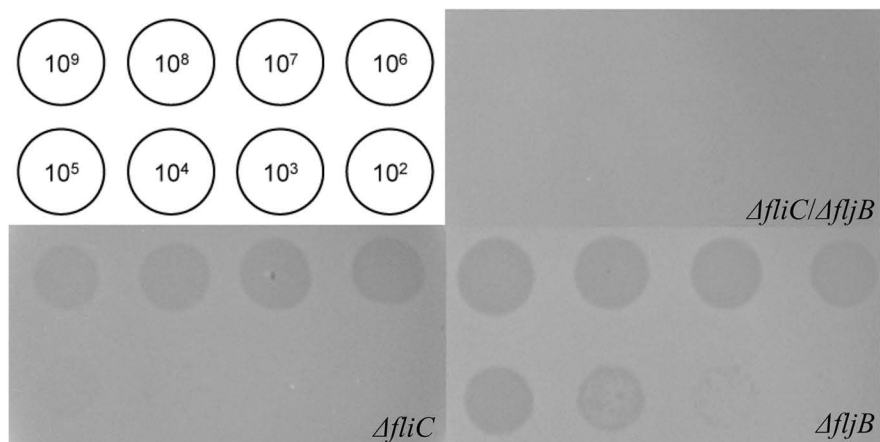
<sup>a</sup> Adsorption constant was calculated by the following formula: constant  $k = -\ln (P_t/P_0)/Nt$ ;

$P_t$  = phage titer at the time  $t$  (PFU/ml),  $P_0$  = initial phage titer (PFU/ml),  $N$  = bacterial density (CFU/ml) and  $t$  =time (min).

## References

1. **Hong J, Kim KP, Heu S, Lee SJ, Adhya S, Ryu S.** 2008. Identification of host receptor and receptor-binding module of a newly sequenced T5-like phage EPS7. *FEMS Microbiol. Lett.* 289:202-209.
2. **Togashi F, Yamaguchi S, Kihara M, Aizawa SI, Macnab RM.** 1997. An extreme clockwise switch bias mutation in *fliG* of *Salmonella typhimurium* and its suppression by slow-motile mutations in *motA* and *motB*. *J. Bacteriol.* 179:2994-3003.
3. **Magariyama Y, Yamaguchi S, Aizawa S.** 1990. Genetic and behavioral analysis of flagellar switch mutants of *Salmonella typhimurium*. *J. Bacteriol.* 172:4359-4369.
4. **Hanahan D.** 1983. Studies on transformation of *Escherichia coli* with plasmids. *J. Mol. Biol.* 166:557-580.
5. **Soncini FC, Vescovi EG, Groisman EA.** 1995. Transcriptional autoregulation of the *Salmonella typhimurium* *phoPQ* operon. *J. Bacteriol.* 177:4364-4371.
6. **Chang AC, Cohen SN.** 1978. Construction and characterization of amplifiable multicopy DNA cloning vehicles derived from the P15A cryptic miniplasmid. *J. Bacteriol.* 134:1141-1156.
7. **Datsenko KA, Wanner BL.** 2000. One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products. *Proc. Natl. Acad. Sci. U. S. A.* 97:6640-6645.
8. **Doublet B, Douard G, Targant H, Meunier D, Madec JY, Cloeckert A.** 2008. Antibiotic marker modifications of lambda Red and FLP helper plasmids, pKD46 and pCP20, for inactivation of chromosomal genes using PCR products in multidrug-resistant strains. *J. Microbiol. Meth.* 75:359-361.

**A****B****FIG S1**

**A****B**



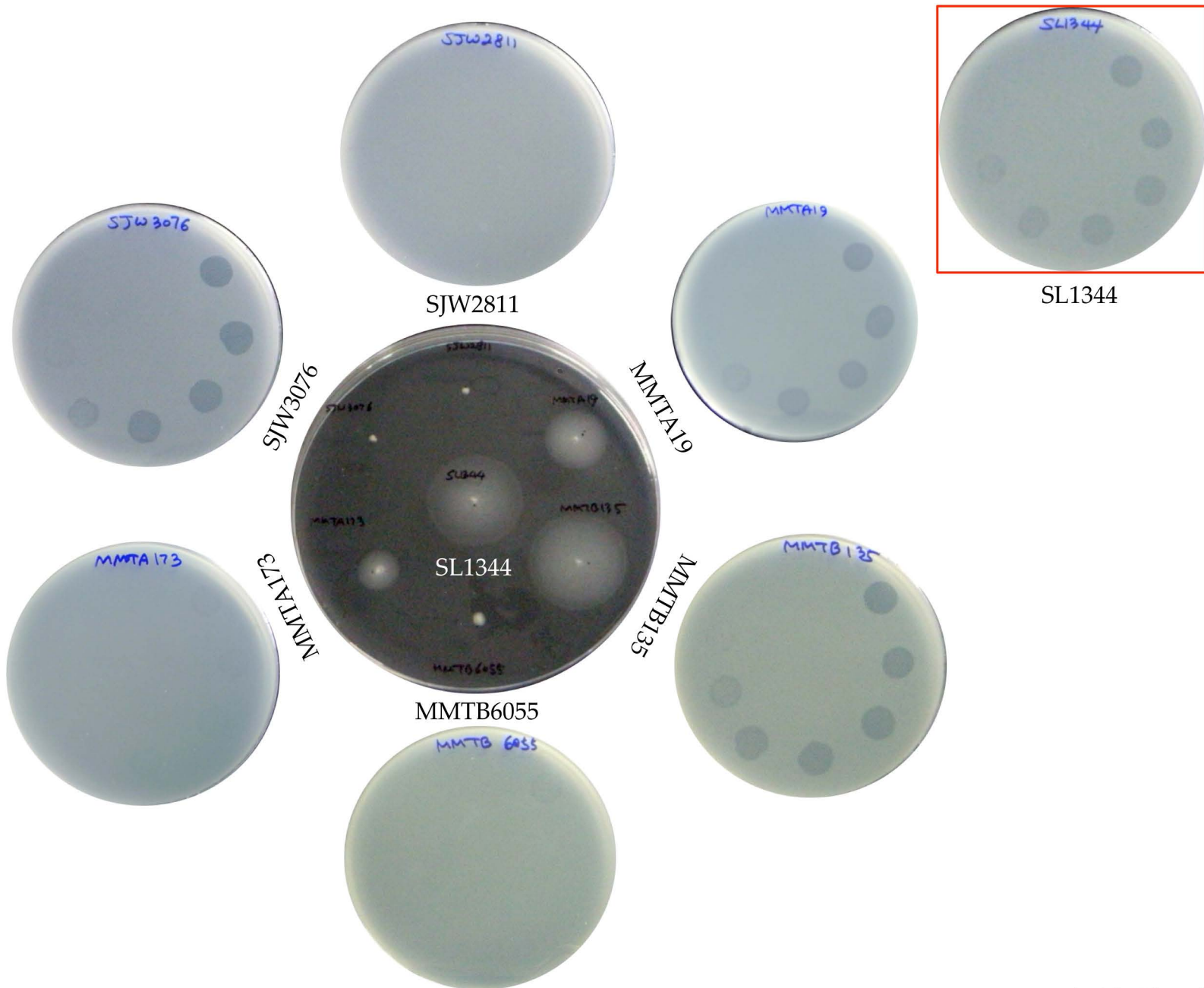


FIG S3

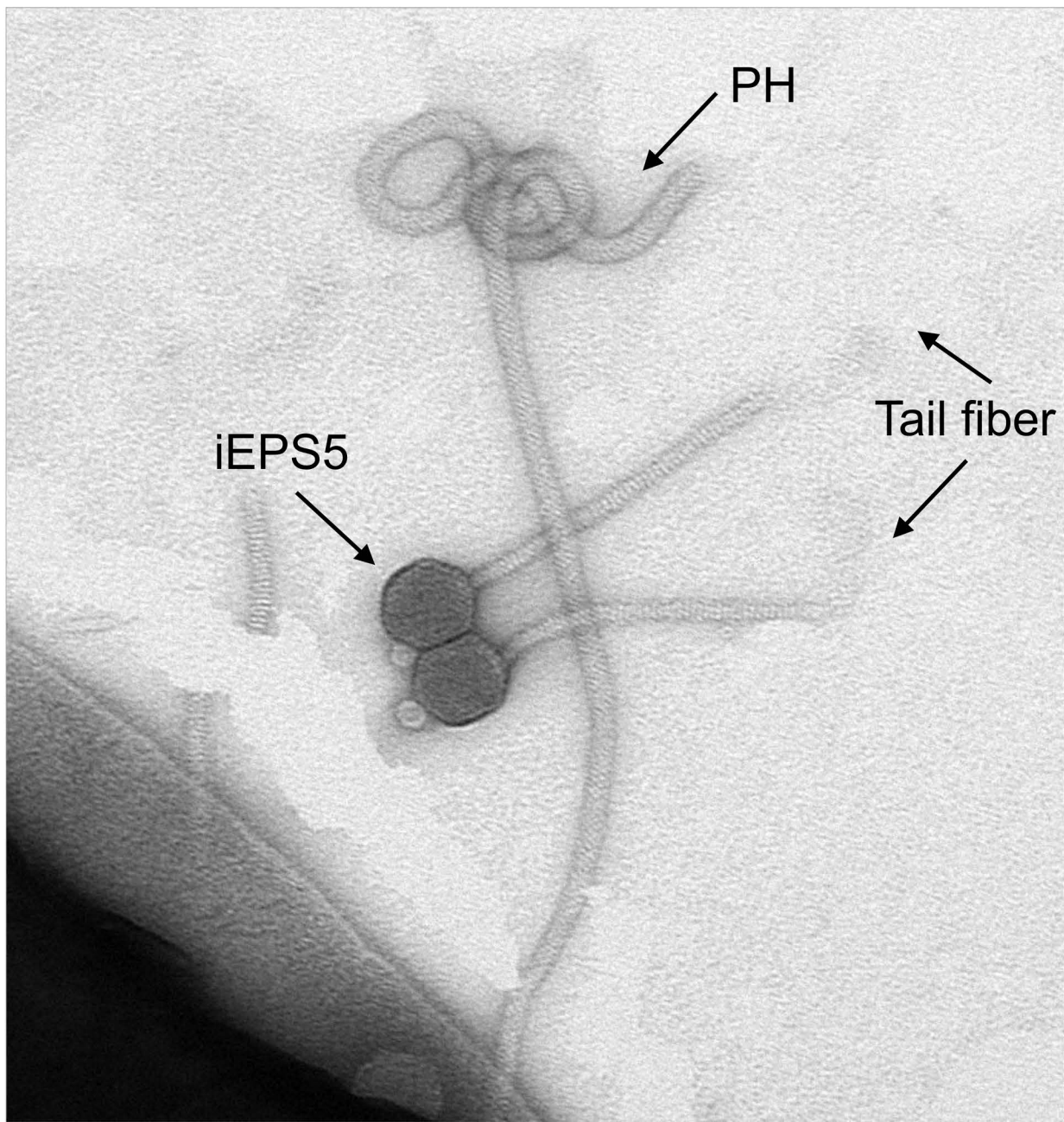
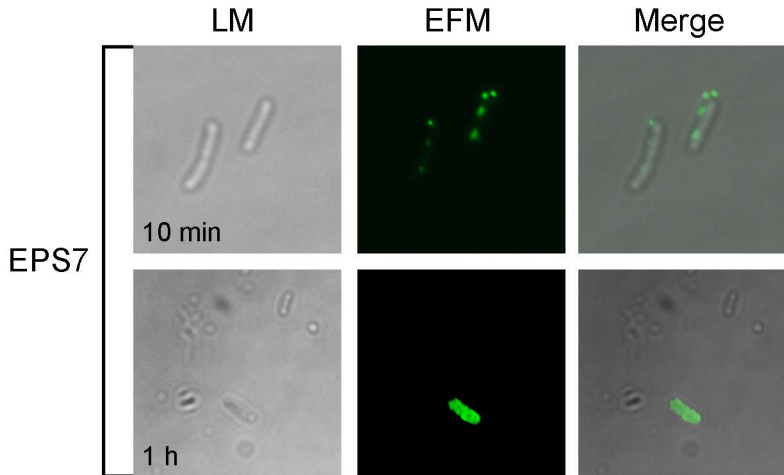
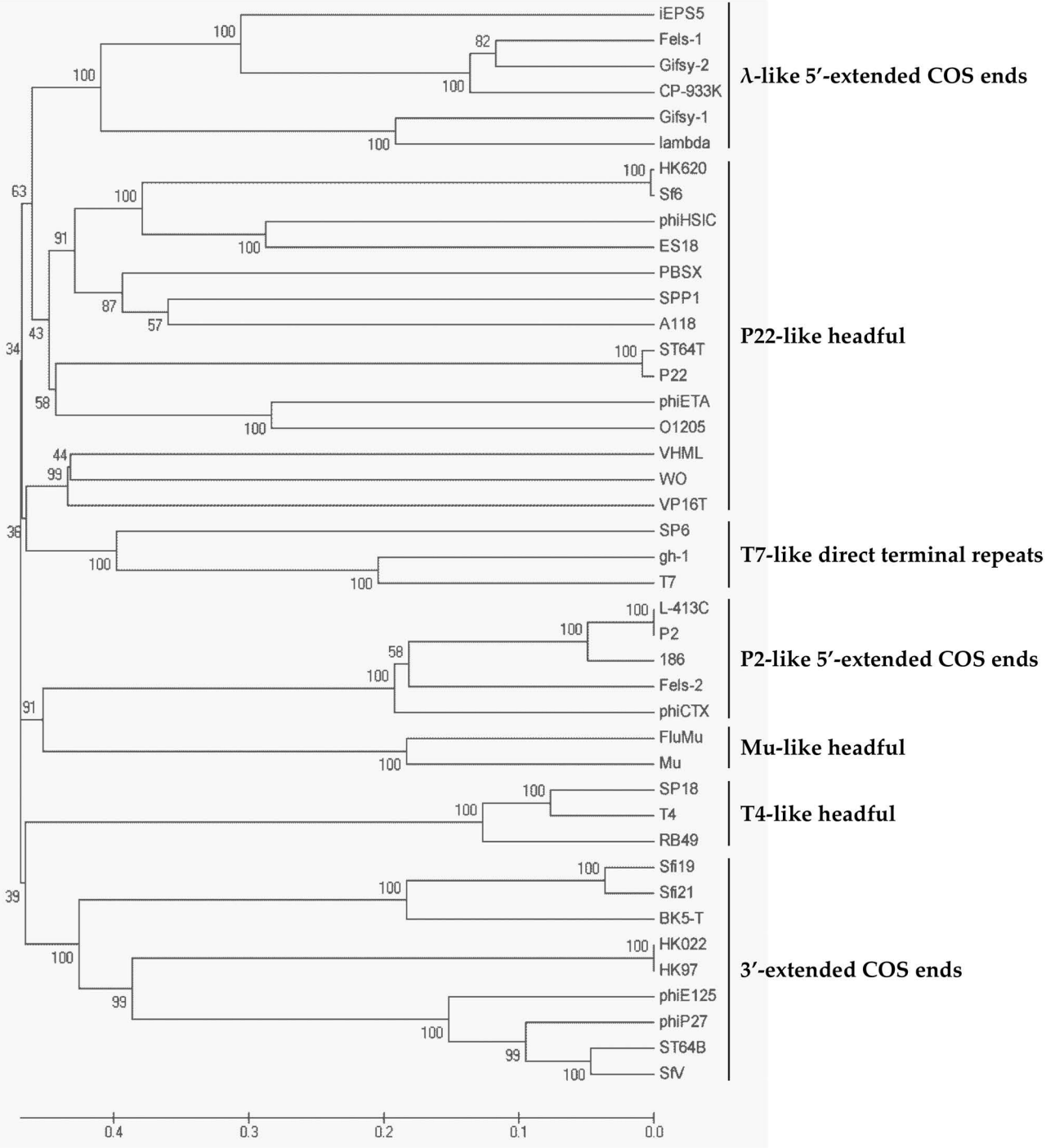


FIG S4



FIGS5



substitution/site