

Supporting Information

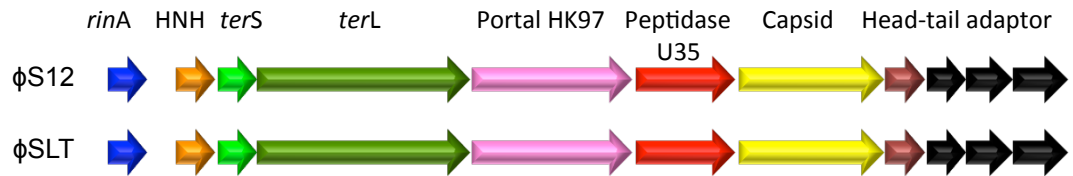
Staphylococcal pathogenicity island DNA packaging system involving *cos*-site packaging and phage-encoded HNH endonucleases

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		cos site	
ϕIPLA35	TATAGCCCCCTGCCCATTTGGCTTAAAATGTTTTTTTCGCCGGGTAC	CGGCGGGGGC	CCTTC 60
ϕ7401PVL	TATAGCCCCCTGCCCATTTGGCTTAAAATGTTTTTTTCGCCGGGTAC	CGGCGGGGGC	CCTTC 60
SaPI_{bov5}	TATAGCCCCCTGCCCATTTGGCTTAAAATGTTTTTTTCGCCGGGTAC	CGGCGGGGGC	CCTTC 60
SaPI_{bov4}	TATAGCCCCCTGCCCATTTGGCTTAAAATGTTTTTTTCGCCGGGTAC	CGGCGGGGGC	CCTTC 60
ϕtp310-2	TATAGCCCCCTGCCCATCGGCTTAAAATGTTTTTTTCGCCGGGTAC	CGGCGGGGGC	CCTTC 60
SaPI_{NN54}	TATAGCCCCCTACCCATCGGCTTAAAATGTTTTTTTCGACGGGTAC	CGGCGGGGGC	CCTTC 60
SaPI_{Ishikawa11}	TATAGCCCCCTACCCATCGGCTTAAAATGTTTTTTTCGACGGGTAC	CGGCGGGGGC	CCTTC 60
ϕ12	TATAGCCCCCTACCCATCGGCTTAAAATGTTTTTTTCGACGGGTAC	CGGCGGGGGC	CCTTC 60
	*****_*****_*****_*****_*****_*****_*****_*****_*****_*****		
ϕIPLA35	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
ϕ7401PVL	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
SaPI_{bov5}	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
SaPI_{bov4}	GCTTGCGACGCGGATAAACTTTTATGAAAGGGG		93
ϕtp310-2	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
SaPI_{NN54}	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
SaPI_{Ishikawa11}	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
ϕ12	GCTTGCAACGCGGATAAACTTTTATGAAAGGGG		93
	*****_*****_*****_*****_*****_*****_*****_*****_*****_*****		

Figure S1. Cos alignment. The predicted SaPI and phage cos sites and their flanking sequences are aligned using ClustalW2. The cos sites are shaded in yellow.

Gram-positive



Gram-negative

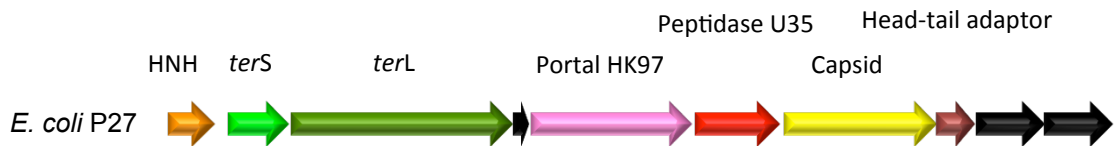


Figure S2. Alignment of selected genes from phage genomes coding for HNH proteins. Genes are coloured according to their sequence and function: *rinA*: blue; *hnh*: orange; *terS*: light green; *terL*: green; portal: pink; peptidase: red; capsid: yellow; head-tail adaptors: brown; hypothetical proteins: black.

PacI **C**GY**C**GI**S**EAG**F** QCLGV**D**R**S**DS**F**EG**Y**SP Q**N**AR**L**AC**F**IC**N**RIKSNI
GS15 **C**HY**C**G EIFPP EEL**T**M**D**HLVPVVRGGKST R**G**N**V**VPAC**K**EC**N**NRKKYL
STL **C**Q**M**CLREDIV**T** DANIV**H**H**I**IYVDEDEFNKALDLD**N**LMSV**C**Y**S**CH**N**KI**H**AN^{HNH}

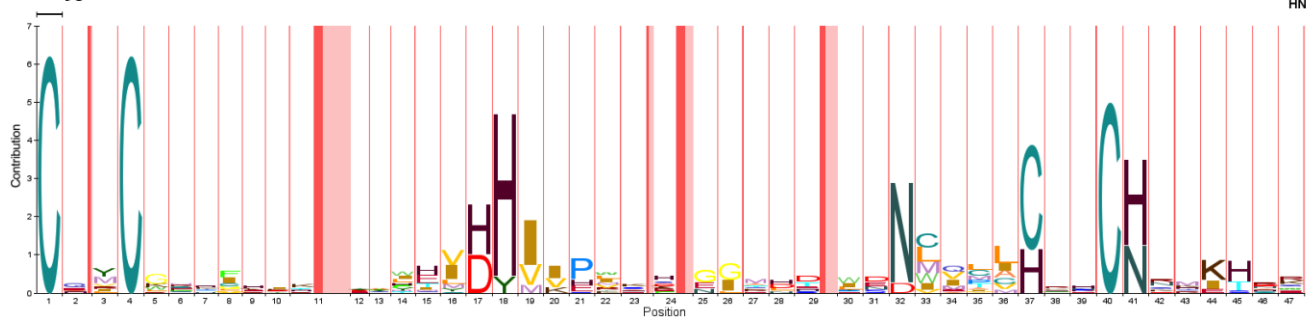


Figure S3. Sequence conservation in HNHs catalytic domains. HMM logo representation of PFAM family HNH (PF01844) (<http://pfam.sanger.ac.uk/family/PF01844.18>) generated by the alignment of 7400 sequences. Each position in the sequence is represented by a stack. The overall height of the stack indicates the sequence conservation at that position, while the height of symbols within the stack indicates the relative frequency of each amino at that position. The sequence corresponding to the HNH domains of ϕ SLT HNH (STL), GS-15 (GS15) and *PacI* are aligned with the HMM logo and the catalytic and Zn-chelating residues displayed as stick in Fig. 3 are highlighted in red and cyan, respectively.

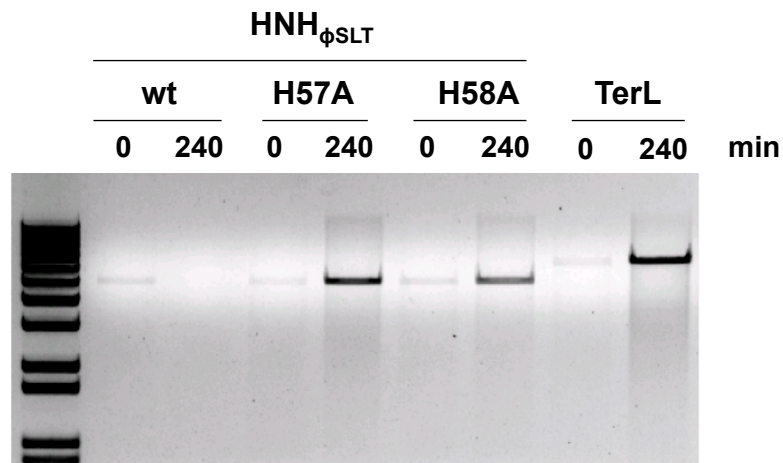


Figure S4. Plasmid DNA from *E. coli* strains expressing the different proteins was extracted and digested with *Bam*HI, which cuts once in the plasmid. Note that absence of plasmid in the sample obtained 240 min after IPTG induction of the wt HNH protein, which is indicative of unspecific nuclease activity. By contrast, neither the HNH mutants nor the TerL proteins showed nuclease activity.

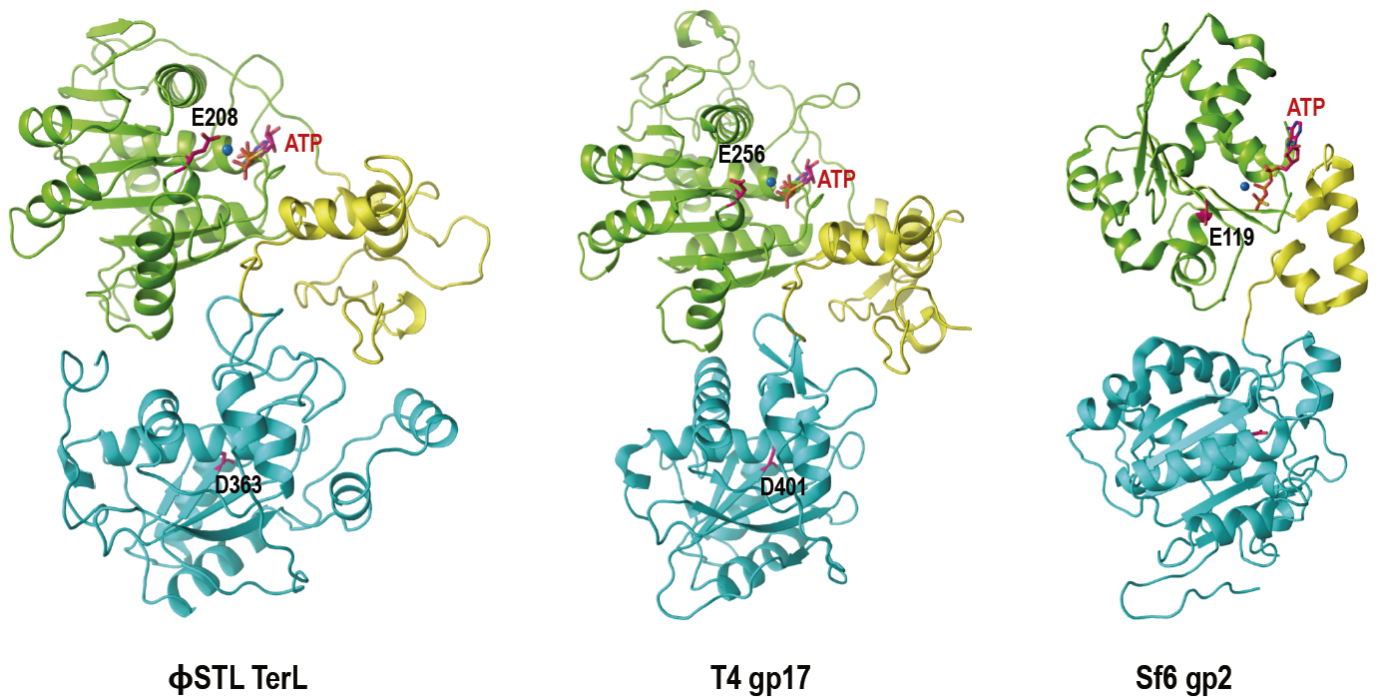
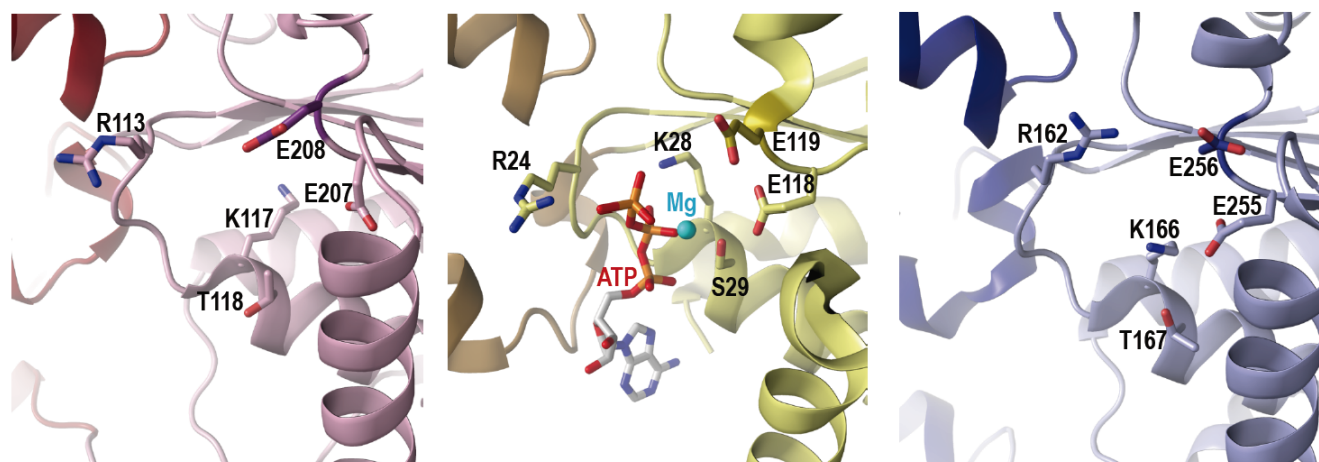


Figure S5. Overall modeled three-dimensional structure of TerL _{ϕ SLT}. The three-dimensional structure of TerL _{ϕ SLT} modeled with I-TASSER is shown in ribbon representation with the motor N-terminal domain colored in yellow (subdomain I) and green (subdomain II) and the nuclease C-terminal domain in cyan. TerL _{ϕ SLT} showed an overall fold that closely resembles to phage T4 gp17 (PDB 3CPE) and distally to phage Sf6 gp2 (PDB 4IEE) large terminases, which structures are shown in ribbon representation a colored as TerL _{ϕ SLT}. Catalytic residues mutated TerL _{ϕ SLT} and the corresponding in T4 gp17 and Sf6 gp2 are shown in stick, labeled and colored in magenta. The ATP molecule present in the Sf6 gp2 structure was placed in TerL _{ϕ SLT} and T4 gp17 structures by superimposition of the corresponding motor domains and are shown in sticks with the carbon atom in magenta.

ATPase motif

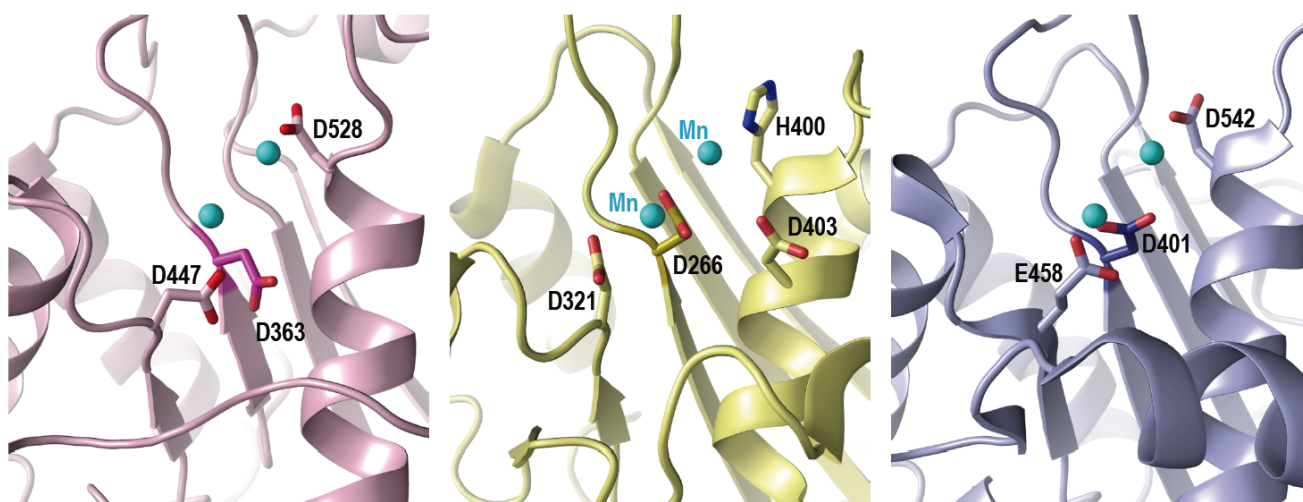


ϕ SLT

Sf6 gp2

T4 gp17

Nuclease



ϕ SLT

SPP1

T4 gp17

Figure S6. ATPase and nuclease active sites of TerL _{ϕ SLT}. Close view of the ATPase (upper) and nuclease (lower) active sites of TerL _{ϕ SLT}, Sf6 gp2 and T4 gp17 with catalytically important residues are shown as sticks. ATP molecule found in the ATPase site of Sf6 gp2 is shown in sticks with carbon atom in white. Cations found in Sf6 gp2 structure or modeled in the nuclease site of TerL _{ϕ SLT} and T4 gp17 structures are shown as cyan spheres. In TerL _{ϕ SLT} active site, the catalytic residues mutated in this work, Glu208 and Asp363, are highlighted in darker hues. Glu208 in the ATPase active site would correspond to the general base that polarises a water molecule for ATP nucleophilic attack. Asp363 is one of the three acidic residues forming the catalytic triad.

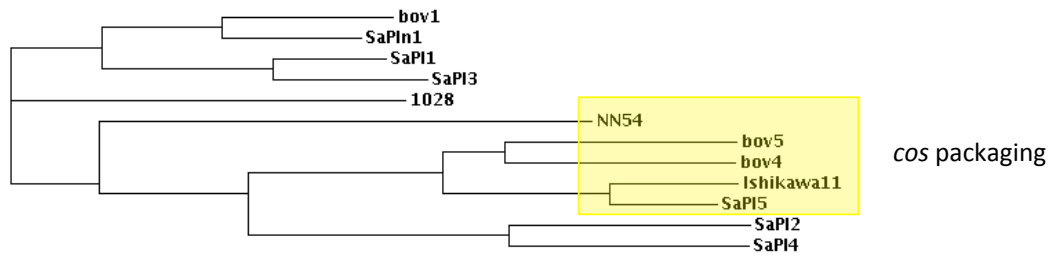


Figure S7. Bootstrapped Neighbor-Joining tree of different SaPIs. The tree was generated using ClustalW2 version. Shaded in yellow are the *cos*-type SaPIs.

Table S1. Role of the different cloned *cos* sites in pCU1 transfer^a.

Donor strain	Phage	Cloned site <i>cos</i> ^b	Plasmid titre ^c
JP10974	φ12	Empty vector	< 10
JP10968	φ12	φ12	2 x 10 ³
JP10878	φ12	φ12 Δ <i>cos</i>	< 10
JP10907	φ12	φSLT	6 x 10 ²
JP10879	φ12	φSLT Δ <i>cos</i>	< 10
JP10875	φ12	SaPIbov5	1 x 10 ³
JP10876	φ12	SaPIbov5 Δ <i>cos</i>	< 10
JP10908	φ12	φP27 ^d	< 10
JP10880	φ12	φP27 Δ <i>cos</i>	< 10
JP11204	φ11	Empty vector	6.2 x 10 ³
JP11196	φ11	φ12	5 x 10 ³
JP11197	φ11	φ12 Δ <i>cos</i>	9.6 x 10 ³
JP11198	φ11	φSLT	2.4 x 10 ³
JP11199	φ11	φSLT Δ <i>cos</i>	9.6 x 10 ³
JP11200	φ11	SaPIbov5	3.1 x 10 ³
JP11201	φ11	SaPIbov5 Δ <i>cos</i>	7 x 10 ³
JP11202	φ11	φP27 ^d	2.1 x 10 ³
JP11203	φ11	φP27 Δ <i>cos</i>	1.1 x 10 ³

^aThe means of results from three independent experiments are shown. Variation was within ±5% in all cases.

^bIn addition to the *cos* site, the cloned DNA contains ~50 pb of the flanking region to the *cos* site. The fragment cloned in the Δ*cos* plasmids are mutant in the *cos* site (maintaining the flanking sequences).

^cNo. of transductants/ml induced culture, using RN4220 as recipient strain.

^dφP27 is an *E. coli* phage carrying a completely different *cos* site.

Table S2. Effect of ϕ SLT mutations on phage titre^a.

ϕ SLT	Complemented ^b	Phage transductants ^c
Wild type	Empty vector	5.0×10^5
Δhnh		< 10
Δhnh	pCN51- <i>hnh</i> _{ϕSLT}	1.9×10^3
HNH H57A		< 10
HNH H57A	pCN51- <i>hnh</i> _{ϕSLT}	2.2×10^2
HNH H58A		< 10
HNH H58A	pCN51- <i>hnh</i> _{ϕSLT}	1.3×10^2
$\Delta terS$		< 10
$\Delta terS$	pCN51- <i>terS</i> _{ϕSLT}	1.6×10^6
$\Delta terL$		< 10
$\Delta terL$	pCN51- <i>terL</i> _{ϕSLT}	4.6×10^5
TerL E208A		< 10
TerL E208A	pCN51- <i>terL</i> _{ϕSLT}	1.0×10^4
TerL D363A		< 10
TerL D363A	pCN51- <i>terL</i> _{ϕSLT}	1.1×10^4
$\Delta Portal$		< 10
$\Delta Portal$	pCN51-p40 _{ϕSLT}	1.2×10^5
Δ Prohead protease		< 10
Δ Prohead protease	pCN51-p41 _{ϕSLT}	2.4×10^4
Δ Major capsid protein		< 10
Δ Major capsid protein	pCN51- p42 _{ϕSLT}	1.4×10^5
Tail protein		< 10
Tail protein	pCN51- p47 _{ϕSLT}	2.8×10^5

^aThe means of results from three independent experiments are shown. Variation was within $\pm 5\%$ in all cases.

^bComplemented in donor strain.

^cNo. of transductants/ml induced culture, using RN4220 as recipient strain.

Table S3. Effect of ϕ P27 mutations on phage titre^a.

ϕ P27	Mutant in	Complemented ^b	Transductant titre ^c
Wild type		Empty vector	1.8×10^8
Δ ORF34	<i>hnh</i>		< 10
Δ ORF34	<i>hnh</i>	pBAD18- <i>hnh</i> _{ϕP27}	1.6×10^7
Δ ORF35	<i>terS</i>		< 10
Δ ORF35	<i>terS</i>	pBAD18- <i>terS</i> _{ϕP27}	1.5×10^5
Δ ORF36	<i>terL</i>		< 10
Δ ORF36	<i>terL</i>	pBAD18- <i>terL</i> _{ϕP27}	4.7×10^6
Δ ORF38	Portal		< 10
Δ ORF38	Portal	pBAD18-p38 _{ϕP27}	2.8×10^3
Δ ORF39	Prohead protease		< 10
Δ ORF39	Prohead protease	pBAD18-p39 _{ϕP27}	2.2×10^5
Δ ORF40	Major capsid		< 10
Δ ORF40	Major capsid	pBAD18-p40 _{ϕP27}	5.5×10^6
Δ ORF47	Tail protein		< 10
Δ ORF47	Tail protein	pBAD18-p47 _{ϕP27}	1.2×10^6

^aThe means of results from three independent experiments are shown. Variation was within $\pm 5\%$ in all cases.

^bComplemented in donor strain.

^cNo. of transductants/ml induced culture, using MG1655 as recipient strain.

Table S4. Strains used in this study.

Strains	Description	Reference
RN4220	Restriction-defective derivative of RN450	(1)
RN451	RN450 lysogenic for ϕ 11	(2)
RN10359	RN450 lysogenic for 80 α	(3)
JP10435	RN4220 lysogenic for ϕ 12	This work
JP1794	RN451 SaPIbov1 <i>tst::tetM</i>	(4)
JP7085	RN451 SaPIbov5 <i>tetM</i>	This work
JP3603	RN10359 SaPIbov1 <i>tst::tetM</i>	(4)
JP7084	RN10359 SaPIbov5 <i>tetM</i>	This work
JP11041	JP10435 SaPIbov1 <i>tst::tetM</i>	This work
JP11010	JP10435 SaPIbov5 <i>tetM</i>	This work
JP11215	RN4220 SaPIbov5 <i>tetM</i> Δ cos site	This work
JP11229	JP10435 SaPIbov5 <i>tetM</i> Δ cos site	This work
JP11228	RN451 SaPIbov5 <i>tetM</i> Δ cos site	This work
JP3377	RN451 Δ terS	(4)
JP3378	JP3377 SaPIbov1 <i>tst::tetM</i>	(4)
JP10764	JP3377 SaPIbov5 <i>tetM</i>	This work
JP11401	JP10764 pJP1570	This work
JP10971	JP10435 Δ hnh	This work
JP11011	JP10971 SaPIbov5 <i>tetM</i>	This work
JP11406	JP11011 pJP1514	This work
LUG1170	SH1000 ϕ SLT	(5)
JP11195	LUG1170 SaPIbov1 <i>tst::tetM</i>	This work
JP11194	LUG1170 SaPIbov5 <i>tetM</i>	This work
JP11230	LUG1170 SaPIbov5 <i>tetM</i> Δ cos site	This work
JP11402	LUG1170 ϕ SLT Δ hnh	This work
JP11403	JP11402 SaPIbov5 <i>tetM</i>	This work
JP11404	JP11402 pJP1077	This work
JP11405	JP11403 pJP1077	This work
JP10817	RN4220 pJP1523	This work
JP10818	RN4220 pJP1524	This work
JP6847	RN4220 pJP836	This work
JP6848	RN4220 pJP837	This work
JP5011	RN4220 lysogenic for ϕ SLT <i>pvl::tetM</i>	(6)
JP8240	JP5011 ϕ SLT Δ hnh	This work
JP9104	JP5011 ϕ SLT Δ terS	This work
JP9105	JP5011 ϕ SLT Δ terL	This work
JP9106	JP5011 ϕ SLT Δ ORF40	This work
JP9107	JP5011 ϕ SLT Δ ORF41	This work
JP9108	JP5011 ϕ SLT Δ ORF42	This work
JP9951	JP5011 ϕ SLT Δ ORF47	This work
JP9666	JP5011 ϕ SLT HNH H57A	This work
JP9667	JP5011 ϕ SLT HNH H58A	This work
JP10934	JP5011 ϕ SLT TerL E208A	This work
JP10976	JP5011 ϕ SLT TerL D363A	This work
JP11367	JP5011 pCN51	This work
JP9059	JP8240 pJP1077	This work
JP9119	JP9104 pJP1245	This work

Strains	Description	Reference
JP9120	JP9105 pJP1246	This work
JP9121	JP9106 pJP1247	This work
JP9122	JP9107 pJP1248	This work
JP9123	JP9108 pJP1249	This work
JP10024	JP9951 pJP1520	This work
JP9959	JP9666 pJP1077	This work
JP9960	JP9667 pJP1077	This work
JP11307	JP10934 pJP1246	This work
JP11308	JP10976 pJP1246	This work
JP11074	JP10971 pJP1514	This work
JP11204	RN451 pCU1	This work
JP11198	RN451 pJP1525	This work
JP11199	RN451 pJP1526	This work
JP11196	RN451 pJP1527	This work
JP11197	RN451 pJP1528	This work
JP11200	RN451 pJP1529	This work
JP11201	RN451 pJP1530	This work
JP11202	RN451 pJP1531	This work
JP11203	RN451 pJP1532	This work
JP10974	JP10435 pCU1	This work
JP10907	JP10435 pJP1525	This work
JP10879	JP10435 pJP1526	This work
JP10968	JP10435 pJP1527	This work
JP10878	JP10435 pJP1528	This work
JP10875	JP10435 pJP1529	This work
JP10876	JP10435 pJP1530	This work
JP10908	JP10435 pJP1531	This work
JP10880	JP10435 pJP1532	This work
JP9818	STEC strain 2771/97 ϕ P27	(7)
JP10045	JP9818 ϕ P27 <i>stx::tetA</i>	This work
JP10363	<i>E. coli</i> strain MG1655	Lab strain
JP10819	JP10363 ϕ P27 <i>stx::tetA</i>	This work
JP10960	JP10819 ϕ P27 Δ ORF34	This work
JP10961	JP10819 ϕ P27 Δ ORF35	This work
JP10962	JP10819 ϕ P27 Δ ORF36	This work
JP10963	JP10819 ϕ P27 Δ ORF38	This work
JP10964	JP10819 ϕ P27 Δ ORF39	This work
JP10965	JP10819 ϕ P27 Δ ORF40	This work
JP10967	JP10819 ϕ P27 Δ ORF47	This work
JP11327	JP10819 pBAD18	This work
JP11328	JP10960 pJP1539	This work
JP11329	JP10961 pJP1540	This work
JP11330	JP10962 pJP1541	This work

Strains	Description	Reference
JP11331	JP10963 pJP1542	This work
JP11332	JP10964 pJP1543	This work
JP11333	JP10965 pJP1544	This work
JP11334	JP10967 pJP1545	This work
JP10025	BL21 (DE3) pJP1533	This work
JP10566	BL21 (DE3) pJP1534	This work
JP10567	BL21 (DE3) pJP1535	This work
JP10317	BL21 (DE3) pJP1253	This work

Table S5. Plasmids used in this study.

Plasmid	Description	Reference
pMAD	Vector for efficient allelic replacement	(8)
pJP1510	pMAD derivative, deletion of ϕ 12 <i>hnh</i>	This work
pJP1076	pMAD derivative, deletion of ϕ SLT ORF 37	This work
pJP1240	pMAD derivative, deletion of ϕ SLT ORF 38	This work
pJP1241	pMAD derivative, deletion of ϕ SLT ORF 39	This work
pJP1242	pMAD derivative, deletion of ϕ SLT ORF 40	This work
pJP1243	pMAD derivative, deletion of ϕ SLT ORF 41	This work
pJP1244	pMAD derivative, deletion of ϕ SLT ORF 42	This work
pJP1509	pMAD derivative, deletion of ϕ SLT ORF 47	This work
pJP1254	pMAD derivative, mutation H57A in ϕ SLT ORF 37	This work
pJP1255	pMAD derivative, mutation H58A in ϕ SLT ORF37	This work
pJP1512	pMAD derivative, mutation E208A in ϕ SLT ORF 39	This work
pJP1513	pMAD derivative, mutation D363A in ϕ SLT ORF39	This work
pJP730	pMAD derivative, insertion of the <i>tetM</i> cassette into SaPIbov5	(9)
pJP1557	pMAD derivate, deletion <i>cos</i> site SaPIbov5	This work
pCN51	Expression vector	(10)
pJP1514	pCN51- <i>hnh</i> ϕ 12	This work
pJP1077	pCN51- <i>hnh</i> ϕ SLT	This work
pJP1245	pCN51- <i>terS</i> ϕ SLT	This work
pJP1246	pCN51- <i>terL</i> ϕ SLT	This work
pJP1247	pCN51-p40 ϕ SLT	This work
pJP1248	pCN51-p41 ϕ SLT	This work
pJP1249	pCN51-p42 ϕ SLT	This work
pJP1520	pCN51-p47 ϕ SLT	This work
pJP1570	pCN51- <i>terS</i> ϕ 11	This work
pCN42	Used in transcriptional fusions to the staphylococcal β -lactamase <i>blaZ</i> . Contains the <i>Pcad</i> promoter	(10)
pJP1523	Transcriptional analysis of ϕ 12 <i>hnh</i> in presence of RinA, pCN42 derivate	This work
pJP1524	Transcriptional analysis of ϕ 12 <i>hnh</i> in absence of RinA, pCN42 derivate	This work
pJP836	Transcriptional analysis of ϕ SLT <i>hnh</i> in presence of RinA, pCN42 derivate	This work
pJP837	Transcriptional analysis of ϕ SLT <i>hnh</i> in absence of RinA, pCN42 derivate	This work
pKD46	Plasmid with Red system of lambda phage.	(11)
pCP20	Plasmid for cassette replacement using FRTs in <i>E. coli</i> .	(11)
pBAD18	Expression vector	(12)
pJP1539	pBAD18- <i>hnh</i> ϕ 27	This work
pJP1540	pBAD18- <i>terS</i> ϕ 27	This work
pJP1541	pBAD18- <i>terL</i> ϕ 27	This work
pJP1542	pBAD18-p38 ϕ 27	This work
pJP1543	pBAD18-p39 ϕ 27	This work
pJP1544	pBAD18-p40 ϕ 27	This work
pJP1545	pBAD18-p47 ϕ 27	This work
pCU1	Cm ^r . Cloning vector	(13)
pJP1525	pCU1 <i>cos</i> site ϕ SLT	This work
pJP1526	pCU1 Δ <i>cos</i> site ϕ SLT	This work
pJP1527	pCU1 <i>cos</i> site ϕ 12	This work
pJP1528	pCU1 Δ <i>cos</i> site ϕ 12	This work
pJP1529	pCU1 <i>cos</i> site ϕ SaPIbov5	This work
pJP1530	pCU1 Δ <i>cos</i> site ϕ SaPIbov5	This work

Plasmid	Description	Reference
pJP1531	pCU1 <i>cos</i> site ϕ P27	This work
pJP1532	pCU1 Δ <i>cos</i> site ϕ P27	This work
pJP1533	Expression in <i>E. coli</i> of His-HNH ϕ SLT, pPROEX HTa derivative	This work
pJP1534	Expression in <i>E. coli</i> of His-HNH H57A mutant ϕ SLT, pPROEX HTa derivative	This work
pJP1535	Expression in <i>E. coli</i> of His-HNH H58A mutant ϕ SLT, pPROEX HTa derivative	This work
pJP1253	Expression in <i>E. coli</i> of His-terL ϕ SLT, pPROEX HTa derivative	This work

Table S6. Primers used in this study.

Plasmid	Oligonucleotides	Sequence (5'-3')
pJP1510	phi12-1mB	CGCGGATCCGCATCATACGATATTAAGCCA
	phiSLTp37-1c	GTATTGATATGACTTACGACC
	phiSLTp37-2m	GGTCGTAAGTCATATCAATACCTAATGTCAGTTTGTATAGC
	phiSLTp37-3cE	CCGGAATTCCTTCATCAAATACCCATTTACC
pJP1076	phiSLT-p36-5mB	CGCGGATCCTTGCAGAATAAAGAACTAACG
	phiSLTp37-1c	GTATTGATATGACTTACGACC
	phiSLTp37-2m	GGTCGTAAGTCATATCAATACCTAATGTCAGTTTGTATAGC
	phiSLTp37-3cE	CCGGAATTCCTTCATCAAATACCCATTTACC
pJP1240	phiSLTp37-4mB	CGCGGATCCTAAGTAAACGAGGCACATCGC
	phiSLTp36-10c	TAAC TTCATATAAAGACCCCC
	phiSLTp38-4m	GGGGGTCTTTATATGAAGTTACAAGAAGAAGGTGGTTTTGGT
	phiSLTp38-5cE	CCGGAATTCCAACTTATCACTGTCTGAAGC
pJP1241	phiSLTp37-4mB	CGCGGATCCTAAGTAAACGAGGCACATCGC
	phiSLTp39-1c	CATTTAAACTTTAATAGTCACC
	phiSLTp39-2m	GGTGACTATTAAGTTTTAAATGAGTGGTGAAGGAAACATAGAG
	phiSLTp39-3cE	CCGGAATTCACATCAATCGGACTAATGCC
pJP1242	phiSLTp40-1mB	CGCGGATCCTTCGCTAATAACGACGAAATG
	phiSLTp40-2c	AATTTTTCTTTATGCGTGTGAC
	phiSLTp40-3m	GTCACACGCATAAAGAAAAATTTTATACCCAATTGACACGCCAC
	phiSLTp40-4cE	CCGGAATTCCTTAGGTGTTCAACCAATTC
pJP1243	phiSLTp41-1mB	CGCGGATCCTTTGATAATGCAGTAAGAACC
	phiSLTp41-2c	CCTTTACTTTTTGATTTTCTTTTC
	phiSLTp41-3m	GAAAAGAAAATCAAAAAGTAAAGGGAAAAAATTAACGCGAATGC
	phiSLTp41-4cE	CCGGAATTC TACTAAATCTACATCTGATCC
pJP1244	phiSLTp41-5mB	CGCGGATCCTTATACCCAATTGACACGCCAC
	phiSLTp42-1c	TTCATATAATGTCGGCATTTC
	phiSLTp42-2m	GAAATGCCGACATTATATGAAGATCAGCAACGTACATTAGAC
	phiSLTp42-3cE	CCGGAATTC TAAAGCTCTATCACTCTTAGC
pJP1509	phiSLTp47-1mB	CGCGGATCCTTTAAAGATACGGGTGCTAGC
	phiSLTp47-2c	ATAAGAACC TTGCTTCTGTC
	phiSLTp47-3m	CAGAAGGACAAGGTTCTTATGACAGTGAAGATCATT CAGAG
	phiSLTp47-4cE	CCGGAATTC TGCTTCGCCCATTTGTCACATC
pJP1254	phiSLT-p36-5mB	CGCGGATCCTTGCAGAATAAAGAACTAACG
	phiSLTp37-15c	AAAATCTTCGTCGACATAAATAATGTGTGCTACAATGTTTGCATC
	phiSLTp37-14m	GATGCAAACATTGTAGCACACATTATTTATGTCGACGAAGATTTT
	phiSLTp37-3cE	CCGGAATTCCTTCATCAAATACCCATTTACC
pJP1255	phiSLT-p36-5mB	CGCGGATCCTTGCAGAATAAAGAACTAACG
	phiSLTp37-17c	AAAATCTTCGTCGACATAAATAATTGCATGTACAATGTTTGCATC
	phiSLTp37-16m	GATGCAAACATTGTACATGCAATTATTTATGTCGACGAAGATTTT
	phiSLTp37-3cE	CCGGAATTCCTTCATCAAATACCCATTTACC

Plasmid	Oligonucleotides	Sequence (5'-3')
pJP1512	phiSLTp39-26mS	ACGCGT <u>TCGAC</u> TCTATGGGTTTAACTGCAGCA
	phiSLTp39-23c	GAAATCAATTTATAATCTTTGAATTCATGAATTGCATCAAAAAATCCCAT ATGTGATTT
	phiSLTp39-22m	AAATACACATATGGGTATTTTTGATGCAATTCATGAATTCAAAGATTATA AATTGATTTT
	phiSLTp39-27cB	CGCGGATCCCTCTTTTGCGATAACATTAC
pJP1513	phiSLTp39-4mB	CGCGGATCCCTCTATGGGTTTAACTGCAGCA
	phiSLTp39-25c	TAAAGTCTCTGTTTCTGATAATGCATAACCTATAGTACATGGTCGACC TTCCAATCATCTAAGGAAAT
	phiSLTp39-24m	ATTCCTTAGATGAGTTGGAAGGTCGACCATGTAATAGGTTATGCAT TATCAGAAACAGAGGACTTTA
	phiSLTp39-5cE	CCGGAATTCCTCTTTTGCGATAACATTAC
pJP1557	SaPIbov5-45mB	CGCGGATCCGAGGGACATATCTATACAGAG
	SaPIbov5-46c	CGCGTTGCAAGCGAAGGGTTTTTTTTTTTACCCGGCGAAAAACATTTT AAGCCCATGGGCAGGGGGCTATATTTTTTAT
	SaPIbov5-47m	ATAAAAAATATAGCCCCCTGCCCATGGGCTTAAAAATGTTTTTTCGCCG GGTAAAAAACCCTTCGCTTGCAACGCG
	SaPIbov5-48cE	CCGGAATTCATCATCTCCGTCACATTAC
pJP1514	phi12p28-1mB	CGCGGATCCGGCACATCGCTATGCGGTGTG
	phi12p28-2cE	CCGGAATTCAGGGGGCTATAAAAAATAATTA
pJP1077	phiSLTp37-4mB	CGCGGATCCTAAGTAAACGAGGCACATCGC
	phiSLTp36-4cE	CCGGAATTCAAACATTTTAAGCCGATGGGC
pJP1245	phiSLTp38-6mB	CGCGGATCCGAGAGGCCAAACGCTAGC
	phiSLTp38-7cE	CCGGAATTCGTTGTTAATAGTTTTGGTGAAGG
pJP1246	phiSLTp39-4mB	CGCGGATCCCTCTATGGGTTTAACTGCAGCA
	phiSLTp39-5cE	CCGGAATTCCTCTTTTGCGATAACATTAC
pJP1247	phiSLTp40-5mB	CGCGGATCCAGTGGTGAAGGAAACATAGAG
	phiSLTp40-6cE	CCGGAATTCCTTTACTTTTTGATTTCTTTTC
pJP1248	phiSLTp41-5mB	CGCGGATCCTTATACCCAATTGACACGCCAC
	phiSLTp41-6cE	CCGGAATTCATATAATGTGGCATTTC
pJP1249	phiSLTp42-4mB	CGCGGATCCCCTAAAGAAAGTATGTCACTAG
	phiSLTp42-5cE	CCGGAATTCGCTGATTTAGCCTTAGCTG
pJP1520	phiSLTp47-5mS	ACGCGT <u>CGACC</u> AGCGCATCGAATAGGTGTG
	phiSLTp47-6cB	CGCGGATCCCTGCTACTTCAACATTTTGGG
pJP1570	orf29phi11-21mB	CGCGGATCCTGGGTTGGCTGATTATAGCC
	orf29phi11-22cE	CCGGAATTCGTTAAAGTTTAATTTAACTTTTCG
pJP1523	phi12p27-1mS	ACGCGT <u>CGAC</u> GGGCACATTATTGTTTGGT
	phi12p27-4cB	CGCGGATCCTCTTACGTAAACACATTGAC

Plasmid	Oligonucleotides	Sequence (5'-3')
pJP1524	phi12p27-1mS	ACGCGT <u>CGAC</u> GGGCACATTATTGTTTGGT
	phi12p27-2c	AGCTCTTTCGTTGGGTAA
	phi12p27-3m	TTAACCCAACGAAAGAGCTGAACTTTGTAAAGCGGTAG
	phi12p27-4cB	CGCGGATCCTCTTCACGTAACACATTTGAC
pJP836	phiSLTp36-7mB	CGCGGATCCGACATTAAGTTGCTTATAGCG
	phiSLTp36-8cE	CCGGAATTCCTCTCTTAACTTCTCCATGC
pJP837	phiSLTp36-7mB	CGCGGATCCGACATTAAGTTGCTTATAGCG
	phiSLTp36-2c	GATATCATATATTGTGTTCCC
	phiSLTp36-3m	GGAACACAATATATGATATCAACTTTGTAAAGCGGTAGCG
	phiSLTp36-8cE	CCGGAATTCCTCTCTTAACTTCTCCATGC
pJP1539	phiP27-HNH-15mXba1	GCTCTAGAAAGTAACAGGCATTACAGCAGC
	phiP27-HNH-16cH	CCCAAGCTTTCACCTGATTGTTTCGCGCG
pJP1540	phiP27-terS-15mXba1	GCTCTAGAAATTTTACACCCGCGAAATT
	phiP27-terS-16cH	CCCAAGCTTTCATAGGTTTTTAAATGGATTATCGC
pJP1541	phiP27-terL-15mXba1	GCTCTAGAGGGAGCGATAATCCATTTAAAA
	phiP27-terL-16cH	CCCAAGCTTTTAAAGCGAACGGATCCCGTA
pJP1542	phiP27p38-5mXba1	GCTCTAGAGCAGATATCTCGACCGTACA
	phiP27p38-6cH	CCCAAGCTTTCAGACGCTGTTTTGTCTGC
pJP1543	phiP27p39-6mXba1	GCTCTAGAGATGAACATGACCACCAGTCC
	phiP27p39-5cH	CCCAAGCTTTTAAAATTTAAGATTTTTCAGTGCATTC
pJP1544	phiP27p40-5mXba1	GCTCTAGACGCACTGAATGCACTGAAAAA
	phiP27p40-6cH	CCCAAGCTTTTACGCAGCGGCTTTCTGG
pJP1545	phiP27p47-5mXba1	GCTCTAGATATTTTCGCAGTTTACAGAAGT
	phiP27p47-6cH	CCCAAGCTTTTAAACGCCTGAAAGGTGAATA
pJP1525	phiSLT-45mH	CCCAAGCTTTTTTATGCCCCCTGCC
	phiSLT-46cB	CGCGGATCCGACCCCCTTTCATGAAAAAT
pJP1526	phiSLT-50mE	CCGGAATTCCCCCCTGCCATCGGCTTAAATGTTTTTCGCCGGT AAAAAAAAAACCAAACGCTAGCAACGCGGA
	phiSLT-51cB	CGCGGATCCCCCTTTCATGAAAAATTTATCCGCGTTGCTAGCGTTG GTTTTTTTTTACC CGCGGAAAAACATTT
pJP1527	phi12-7mE	CCGGAATTCGCCCCCTACCCATCGGCTTAAATGTTTTTCGACGGT ACCGCGGGGGCCCTTCGCTTGCAACGCGGA
	phi12-8cB	CGCGGATCCCCCTTTCATAAAAGTTTATCCGCGTTGCAAGCGAAG GCCCCGCGGTTACCGTCGAAAAACATTT

Plasmid	Oligonucleotides	Sequence (5'-3')
pJP1528	phi12-9mE	<u>CCGGAATTC</u> GCCCCCTACCCATCGGCTTAAATGTTTTTTCGACGGGT AAAAAAAAAACCCCTTCGCTTGCAACGCGGA
	phi12-10mB	CGCGGAT <u>CCCCCCTTT</u> CATAAAAGTTTATCCGCGTTGCAAGCGAAGG GTTTTTTTTTACCCTCGAAAAACATT
pJP1529	SaPIbov5-41mE	<u>CCGGAATTC</u> GCCCCCTGCCATTGGCTTAAATGTTTTTTCGCCGGGT ACCGGCGGGGGCCCTTCGCTTGCAACGCGGA
	SaPIbov5-42cB	CGCGGAT <u>CCCCCCTTT</u> CATAAAAGTTTATCCGCGTTGCAAGCGAAGG GCCCCGCCGGTACCCTCGAAAAACATT
pJP1530	SaPIbov5-43mE	<u>CCGGAATTC</u> GCCCCCTGCCATTGGCTTAAATGTTTTTTCGCCGGGT AAAAAAAAAACCCCTTCGCTTGCAACGCGGA
	SaPIbov5-44cB	CGCGGAT <u>CCCCCCTTT</u> CATAAAAGTTTATCCGCGTTGCAAGCGAAGG GTTTTTTTTTACCCTCGAAAAACATT
pJP1531	hip27-18mE	<u>CCGGAATTC</u> AGGGGCGGGTCAAATCCCTGCAACCCTGGCTGTCCGG GACCGCCCGCCCCGTCAAATTTTACACCCGCG
	hip27-19cB	CGCGGAT <u>CCAATCCT</u> GAAATTTTAAATTCGCGGGTGAAAAATTTGAC GGGGCGGGCGGTCCCGGACAGCCAGGGTTG
pJP1532	hip27-16mE	<u>CCGGAATTC</u> AGGGGCGGGTCAAATCCCTGCAACCCTGGCTGTCCGG GACAAAAAAAAAGTCAAATTTTACACCCGCG
	hip27-17cB	CGCGGAT <u>CCAATCCT</u> GAAATTTTAAATTCGCGGGTGAAAAATTTGAC TTTTTTTTTGTCCCGGACAGCCAGGGTTG
pJP1533	phiSLTp37-9mB	CGCGGAT <u>CCGAT</u> GACCAAGCATAATAACATT
	phiSLTp37-10cE	<u>CCGGAATTC</u> TAAATTTTGAAGCTCTAATTTTC
pJP1534	phiSLTp37-9mB	CGCGGAT <u>CCGAT</u> GACCAAGCATAATAACATT
	phiSLTp37-10cE	<u>CCGGAATTC</u> TAAATTTTGAAGCTCTAATTTTC
pJP1535	phiSLTp37-9mB	CGCGGAT <u>CCGAT</u> GACCAAGCATAATAACATT
	phiSLTp37-10cE	<u>CCGGAATTC</u> TAAATTTTGAAGCTCTAATTTTC
pJP1253	phiSLTp39-7mB	CGCGGAT <u>CCGGT</u> GGTTTTGGTGACTATTAAG
	phiSLTp39-8cE	<u>CCGGAATTC</u> TAAACGCATTATGTCTTTAATAC

*Underlined is shown the sequence recognized by the restriction enzymes used.

ϕ P27 Mutagenesis	Oligonucleotides	Sequence (5'-3')
ϕ P27 <i>stx::tetA</i>	hip27-1m	GGGTCTGGTACTGATTACCTTAGCCAAAAGGAATATATGTATATGAAG TGTATATTGTTACGCTGTTAACTACTTTACTT
	hip27-2c	TGCGTCCAGAAACAAAAGACGCGCATAAATAAACCGTAGATTCTCAGT TAAACTTCACCTGGTATCAAGAGGGTCATTA
ϕ P27 <i>stx::tetA</i> <i>hnh::clor</i>	hip27-HNH-1m	TTCAGTGAGGGGCTGCGATAATGCCGGTATTAAGGAGATTCCAATGC CATCACGAATACCTGTGTAGGCTGGAGCTGCTTC
	hip27-HNH-2c	ATTTGACCCGCCCTCCCCACAAGTGAGAATAATTATCACCTGATTTCG TTCGCGCGTGTATATGAATATCCTCCTTA
ϕ P27 <i>stx::tetA</i> <i>terS::clor</i>	hip27-terS-5m	CCGCGAAATTAATAATTTAGGATTTGACATGTCAGGAAATCTGTTGC GCCCCGAAGAGTGTGTAGGCTGGAGCTGCTTC
	hip27-terS-6c	TTTTTTCGTGTCATAGGTTTTTAAATGGATTATCGCTCCCCTGCTTCGG CGTCATAAGCCCATATGAATATCCTCCTTA

φP27 Mutagenesis	Oligonucleotides	Sequence (5'-3')
φP27 <i>stx::tetA</i> <i>terL::clor</i>	phip27-terL-6m	CACGAAAAAATTACGTGAACGTTAACGCCGCAAATCAGTATGCACGTG ACGTGGTTCGCGTGTGTAGGCTGGAGCTGCTTC
	phip27-terL-7c	GCGCGAGAATCAGCATGATCATAATTACCTCAGTTAAAGCGAACGGAT CCCGTAGGACTCCATATGAATATCCTCCTTA
φP27 <i>stx::tetA</i> <i>orf38::clor</i>	phip27-p38-1m	ACACGGCAGTCTGTCCGGCGGAGGTAAATAGTGTCTTTTCGGGGTTAT TTCAACGAAAAATGTGTAGGCTGGAGCTGCTTC
	phip27-p38-2c	ACTGACGGATTTTCAGGTTACGCGGTATATCAAGACGCTGTTTTGTCTG CATCTCCACTCTCCATATGAATATCCTCCTTA
φP27 <i>stx::tetA</i> <i>orf39::clor</i>	phip27-p39-1m	TGACAACGGTAAGAAAAAGGAGAGTGGAGATGCAGACAAAACAGCGT CTTGATATACCGCTGTGTAGGCTGGAGCTGCTTC
	phip27-p39-2c	TCTTTAACATCAGCCATTATTTTCTCCTGGTTAAAATTTAAGATTTTCA GTGCATTGAGCATATGAATATCCTCCTTA
φP27 <i>stx::tetA</i> <i>orf40::clor</i>	phip27-p40-1m	TGAAAAATCTTAAATTTTAACCAGGAGAAAATAATGGCTGATGTTAAAG ATGTGGAACAGTGTGTAGGCTGGAGCTGCTTC
	phip27-p40-2c	GCCCCGCATTACGCGGGCACAAAAAAACC GCATTACGCAGCGGCTT TCTGGCGGGTTGCCATATGAATATCCTCCTTA
φP27 <i>stx::tetA</i> <i>orf47::clor</i>	phip27-p47-1m	GAAGTGAAGCCGAGGCCGTCCGCATTAACGAGGAGATGAAGCATGG CTGACAGTTTTTCATGTGTAGGCTGGAGCTGCTTC
	phip27-p47-2c	AAGGTAAGGAAGGAAAATCCATTCTGATACCCCATTATTAACGCCTGA AAGGTGAATACCCATATGAATATCCTCCTTA

Southern blot	Oligonucleotides	Sequence (5'-3')
SaPIbov1 / SaPIbov5 probe	SaPIbov1-112mE	CCGGAATTCAATTGCTGAGGCAAACTTC
	SaPIbov1-113cB	CGCGGATCCCTAATTCTCCACGTCTAAAGC
φSLT probe (<i>rinA</i>)	phiSLTp36-1mB	CGCGGATCCATCAGAGCTGAAGTTTCATGG
	phiSLTp36-2c	GATATCATATATTGTGTTCCC
φSLT probe (<i>terS</i>)	phiSLTp38-9mB	CGCGGATCCGATGAAAGGGGTCTTTATATG
	phiSLTp37-5c	AATAAAATGTTGCCAAGGCTG
φP27 probe (<i>terS-terL</i>)	phip27-terL-2c	CGCGTTGGGATTACGGTAGAG
	phiP27-terS-7c	CACTCCCCTTTGGTGT

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