

Figure S1. Phage sensitivity to environmental conditions. (A) Temperature and (B) pH, of phages phiIPLA-RODI (black) and phiIPLA-C1C (white). Values represent the mean \pm standard deviation of three independent experiments. Bars having an asterisk are significantly different from the control (ANOVA; $P < 0.05$).



Figure S2: Progressive MAUVE comparison at the nucleotide level of phages belonging to the *Myoviridae* family infecting Staphylococcal species. Coloured blocks surround a region of the genome sequence that aligns and is homologous to part of another genome. Regions with lack of homology are outside these blocks or white inside the blocks. The height of the similarity profile corresponds to the average of conservation in that region of the genome sequence.

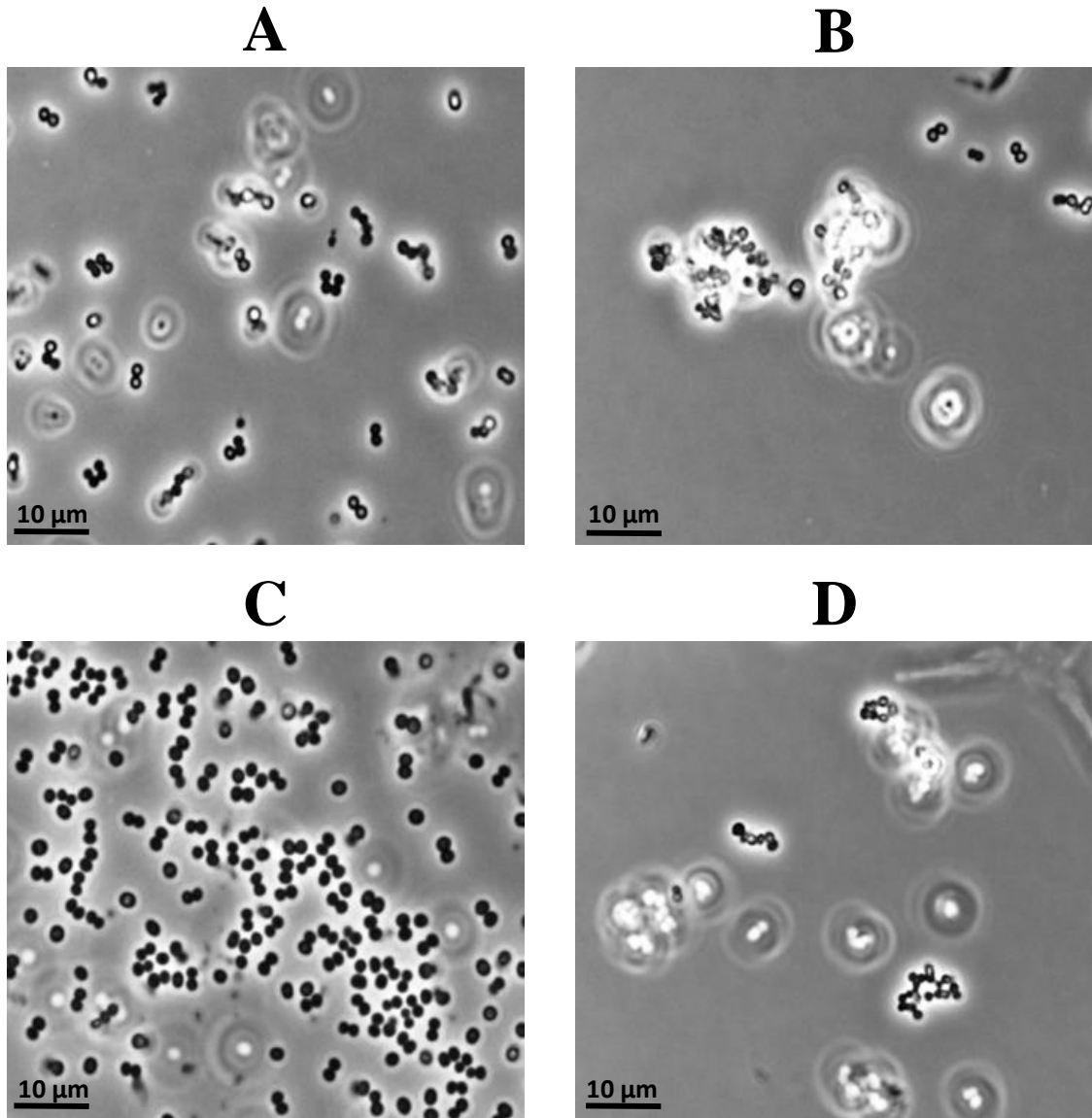


Figure S3. Optical microphotographs of (A) *S. aureus* IPLA16; (B) *S. aureus* IPLA16-R71 resistant to phage phiIPLA-RODI; (C) *S. epidermidis* LO5081 and (D) *S. epidermidis* LO5081-R49 resistant to phage phiIPLA-C1C. Cultures were grown in TSB at 37°C with shaking during 16 h.

<i>orf</i>	From	To	Length	aa	kDa (pI)	Predictive Function	Closes hit (E value)	% aa identity / % similarity	Accession no.	Predicted domain (E value)
1	14	496	483	160	18.25 (3.60)	Terminal repeat-encoded protein	Terminal repeat-encoded protein [<i>Staphylococcus</i> phage phiSA012] (1e-66)	71% (83%)	BAO47048.1	
2	575	739	165	54	6.3 (4.96)	Terminal repeat-encoded protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (7e-28)	98% (98%)	YP_008853972.1	
3	739	1008	270	89	10.1 (5.12)	TreT	Hypothetical protein GH15_015 [<i>Staphylococcus</i> phage GH15] (1e-50)	93% (96%)	YP_007002138.1	
4	1093	1314	222	73	8.65 (4.51)	TreU	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (3e-37)	90% (93%)	YP_008853974.1	
5	1932	1642	291	96	11.59 (4.27)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (3e-62)	99% (98%)	YP_007112845.1	
6	2272	2036	237	78	9.55 (4.59)	BofL	gp ORF004 [<i>Staphylococcus</i> phage A5W] (4e-49)	100% (100%)	ACB88995.1	
7	2759	2274	486	161	19.16 (7.44)	Hypothetical protein	ORF088 [<i>Staphylococcus</i> phage G1] (8e-105)	96% (97%)	YP_241045.1	
8	3179	2772	408	135	16.46 (5.06)	Hypothetical protein	ORF109 [<i>Staphylococcus</i> phage G1] (4e-93)	100% (100%)	YP_241046.1	
9	3610	3179	432	143	17.24 (4.33)	UboA	UboA [<i>Staphylococcus</i> phage Fi200W] (8e-95)	100% (100%)	AFN38459.1	
10	3804	3613	192	63	7.88 (10.21)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (4e-36)	100% (100%)	YP_007112842.1	
11	4286	3801	486	161	18.41 (9.6)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiSA012] (5e-105)	98% (99%)	BAO47055.1	
12	4710	4279	432	143	167.44 (3.95)	Hypothetical protein	Hypothetical protein KgORF2 [<i>Staphylococcus</i> phage K] (5e-97)	99% (100%)	YP_024433.1	
13	5266	4724	543	180	21.55 (9.68)	Nucleotidyl transferase	Hypothetical protein KgORF3 [<i>Staphylococcus</i> phage K] (5e-123)	99% (99%)	YP_024434.1	COG1665 (9.88e-03)
14	5766	5278	489	162	19.5 (9.89)	ribA/ribD-fused hypothetical protein	Hypothetical protein KgORF4 [<i>Staphylococcus</i> phage K] (4e-115)	98% (100%)	YP_024435.1	ribofla_fusion[TIGR02464], (4.99e-75)
15	6177	5779	399	132	16.75 (9.4)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-3] (5e-87)	99% (99%)	YP_008854162.1	
16	6881	6174	708	235	27.62 (4.88)	Phosphatase	Putative protein phosphatase [<i>Staphylococcus</i> phage K] (9e-169)	98% (100%)	YP_024437.1	MPP_PPP_family[cd00144] (9.50e-27)
17	7535	6981	555	184	21.22 (4.33)	Hypothetical protein	Hypothetical protein KgORF7 [<i>Staphylococcus</i> phage K] (1e128)	99% (99%)	YP_024438.1	
18	7868	7551	318	105	11.80 (7.19)	Hypothetical protein	ORF138 [<i>Staphylococcus</i> phage G1] (4e-66)	99% (100%)	YP_241056.1	
19	9402	8854	549	182	21.95 (4.25)	Hypothetical protein	Hypothetical protein KgORF8 [<i>Staphylococcus</i> phage K] (6e-123)	99% (100%)	YP_024439.1	

20	9624	9406	219	72	8.41 (4.18)	Hypothetical protein	ORF201 [<i>Staphylococcus</i> phage G1] (3e-43)	100% (100%)	YP_241058.1	
21	9819	9625	195	64	7.64 (4.39)	Hypothetical protein	ORF218 [<i>Staphylococcus</i> phage G1] (1e-37)	100% (100%)	YP_241059.1	
22	10546	9809	738	245	28.67 (5.98)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (1e-171)	99% (99%)	YP_007112830.1	
23	10713	10609	105	34	4.13 (4.37)	Hypothetical protein	ORF437 [<i>Staphylococcus</i> phage G1] (7e-12)	85% (97%)	YP_241061.1	
24	10962	10735	228	75	89.2 (4.31)	Aspartate aminotransferase	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (3e-45)	97% (97%)	YP_008853991.1	PRK05937[PRK05937], (3.65e-03)
25	11350	10964	387	128	14.62 (4.57)	Hypothetical protein	Hypothetical protein GH15_039 [<i>Staphylococcus</i> phage GH15] (6e-89)	100% (100%)	YP_007002162.1	
26	11620	11447	174	57	6.81 (4.94)	Hypothetical protein	Hypothetical protein GH15_040 [<i>Staphylococcus</i> phage GH15] (8e-34)	100% (100%)	YP_007002163.1	
27	12143	11661	483	160	18.98 (4.52)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (8e-108)	98% (100%)	YP_008853994.1	
28	12735	12193	543	180	20.55 (4.60)	Hypothetical protein	Hypothetical protein GH15_042 [<i>Staphylococcus</i> phage GH15] (1e-114)	94% (96%)	YP_007002165.1	
29	13265	12735	531	176	20.51 (3.92)	Hypothetical protein	Hypothetical protein GH15_043 [<i>Staphylococcus</i> phage GH15] (7e-122)	99% (100%)	YP_007002166.1	
30	13432	13268	165	54	6.15 (9.9)	Membrane protein	ORF256 [<i>Staphylococcus</i> phage G1] (1e-26)	94% (98%)	YP_241068.1	
31	13722	13435	288	95	11.29 (9.45)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage JD007] (2e-06)	52% (69%)	YP_007112822.1	
32	14567	13722	846	281	31.77 (4.41)	Hypothetical protein	Hypothetical protein GH15_046 [<i>Staphylococcus</i> phage GH15] (0.0)	98% (99%)	YP_007002169.1	
33	15698	14580	1119	372	42.24 (4.48)	AAA family ATPase	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (0.0)	99% (99%)	YP_008854000.1	PHA02244 ATPase-like protein (0.0)
34	16177	15851	327	108	12.81 (4.52)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (9e-71)	97% (98%)	YP_008854001.1	
35	16586	16170	417	138	16.01 (5.21)	Hypothetical protein	Hypothetical protein GH15_049 [<i>Staphylococcus</i> phage GH15] (8e-94)	99% (99%)	YP_007002172.1	
36	17020	16718	303	100	11.30 (4.58)	NTP-PPase	Hypothetical protein KgORF17 [<i>Staphylococcus</i> phage K] 87e-64)	100% (100%)	YP_024448.1	NTP-PPase_u3[cd11540], (1.92e-24)
37	17208	17020	189	62	7.321 (4.04)	Hypothetical protein	Hypothetical protein GH15_051 [<i>Staphylococcus</i> phage GH15] (2e-34)	100% (100%)	YP_007002174.1	
38	17413	17252	162	53	6.37 (4.39)	Hypothetical protein	ORF259 [<i>Staphylococcus</i> phage G1] (3e-29)	100% (100%)	YP_241076.1	
39	19464	17413	2052	683	79.79 (6.52)	Hypothetical protein	Hypothetical protein GH15_053 [<i>Staphylococcus</i> phage GH15] (0.0)	99% (99%)	YP_007002176.1	
40	19806	19543	264	87	10.26 (4.97)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (2e-52)	98% (97%)	YP_008854007.1	
41	19996	19823	174	57	6.67 (7.15)	Peptidoglycan binding	Hypothetical protein [<i>Staphylococcus</i> phage	98% (100%)	YP_007112812.1	LysM[cd00118], (1.06e-07)

						protein	JD007] (4e-31)			
42	20581	20003	579	192	21.46 (8.93)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (4e-130)	100% (100%)	YP_008854009.1	
43	21173	20574	600	199	22.58 (4.65)	Nucleoside 2-deoxyribosyltransferase	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (2e-114)	82% (89%)	YP_008854010.1	Nuc_deoxyrib_tr[<i>pfam05014</i>], (3.71e-03)
44	22059	21166	894	297	34.55 (5)	RNA ligase	Putative DNA ligase [<i>Staphylococcus</i> phage GH15] (0.0)	95% (99%)	YP_007002182.1	RNA_ligase[<i>pfam09414</i>], (1.06e-11)
45	22287	22063	225	74	8.15 (9.42)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (6e-40)	100% (100%)	YP_008854012.1	
46	23096	22356	741	246	28.53 (4.96)	PhoH-related protein	Putative PhoH-related protein [<i>Staphylococcus</i> phage K] (0.0)	99% (100%)	YP_024453.1	PhoH[<i>pfam02562</i>], (5.49e-25)
47	23762	23148	615	204	23.08 (3.97)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (1e-142)	99% (99%)	YP_008854014.1	
48	24203	23778	426	141	15.79 (7.15)	Ribonuclease	Putative ribonuclease [<i>Staphylococcus</i> phage GH15] (2e-194)	100% (100%)	YP_007002186.1	
49	24384	24193	192	63	7.47 (5.61)	Hypothetical protein	ORF222 [<i>Staphylococcus</i> phage G1] (3e-37)	100% (100%)	YP_241086.1	
50	25048	24407	642	213	24.58 (3.82)	Hypothetical protein	Hypothetical protein KgORF25 [<i>Staphylococcus</i> phage K] (4e-143)	99% (100%)	YP_024456.1	
51	25268	25038	231	76	8.83 (9.12)	DNA binding protein	ORF187 [<i>Staphylococcus</i> phage G1] (1e-46)	100% (100%)	YP_241088.1	HTH_XRE[<i>cd00093</i>], (3.67e-10)
52	25498	25271	228	75	9.26 (10.21)	Hypothetical protein	ORF190 [<i>Staphylococcus</i> phage G1] (2e-42)	96% (98%)	YP_241089.1	
53	26299	25607	693	230	24.90 (4.75)	Transglycosylase	Putative transglycosylase IsaA [<i>Staphylococcus</i> phage GH15] (4e-167)	100% (100%)	YP_007002191.1	LT_GEWL[<i>cd00254</i>], (3.26e-5)
54	27291	26497	795	264	29.29 (9.28)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (0.0)	100% (100%)	YP_007002192.1	
55	27599	27291	309	102	12.13 (9.31)	Hypothetical protein	Hypothetical protein GH15_070 [<i>Staphylococcus</i> phage GH15] (6e-65)	100% (100%)	YP_007002193.1	
56	28332	27712	621	206	24.55 (9.41)	Hypothetical protein	Hypothetical protein KgORF27 [<i>Staphylococcus</i> phage K] (9e-42)	42% (58%)	YP_024458.1	
57	29885	28395	1491	496	54.81 (9.8)	Endolysin	Putative lysin [<i>Staphylococcus</i> phage GH15] (0.0)	99% (100%)	YP_007002194.1	CHAP[<i>pfam05257</i>], (1.42e-11) Amidase_2[<i>pfam01510</i>], (4.58e-10) SH3b[<i>smart00287</i>], (2.66e-03)
58	30388	29885	504	167	18.11 (3.88)	Holin	Putative holin [<i>Staphylococcus</i> phage GH15] (2e-114)	98% (99%)	YP_007002195.1	Phage_holin_1[<i>pfam04531</i>], (1.28e-31)
59	30658	30473	186	61	7.06 (4.81)	Hypothetical protein	ORF233 [<i>Staphylococcus</i> phage G1] (1e-33)	100% (100%)	YP_241098.1	
60	32429	32211	219	72	8.67 (9.36)	Hypothetical protein	ORF200 [<i>Staphylococcus</i> phage G1] (4e-45)	100% (100%)	YP_241099.1	
61	33118	32909	210	69	7.76 (5.57)	Hypothetical protein	Hypothetical protein GH15_075 [<i>Staphylococcus</i> phage GH15] (1e-40)	100% (100%)	YP_007002198.1	

62	33463	33131	333	110	12.50 (5.08)	Hypothetical protein	Hypothetical protein GH15_076 [<i>Staphylococcus</i> phage GH15] (8e-69)	99% (100%)	YP_007002199.1	
63	33802	33476	327	108	13.01 (5.14)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (1e-69)	98% (99%)	YP_007002200.1	
64	34243	34629	387	128	14.84 (9.31)	Membrane protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (8e-81)	98% (100%)	YP_008854032.1	
65	34607	34885	279	92	10.57 (10.03)	Hypothetical protein	ORF161 [<i>Staphylococcus</i> phage G1] (2e-60)	100% (100%)	YP_241104.1	
66	34882	35292	411	136	15.62 (4.38)	Hypothetical protein	ORF133 [<i>Staphylococcus</i> phage G1] (6e-91)	99% (100%)	YP_241105.1	
67	35307	35657	351	116	13.56 (9.9)	Terminase large subunit	Putative terminase large subunit [<i>Staphylococcus</i> phage GH15] (2e-76)	100% (100%)	YP_007002205.1	
68	35897	36667	771	256	30.01 (9.2)	Group I intron VSR homing endonuclease	Group I intron protein [<i>Staphylococcus</i> phage vB_SauM_Romulus] (7e-134)	89% (94%)	YP_007677505.1	Very-short-patch-repair endonuclease [Replication, recombination, and repair] (3.42e-03)
69	36734	38194	1461	486	56.37 (5.74)	Terminase large subunit	Ter [<i>Staphylococcus</i> phage MSA6] (0.0)	100% (100%)	AFN38730.1	Terminase_GpA[pfam05876] (1.62e-17)
70	38187	39008	822	273	30.6 (4.92)	Hypothetical protein	Hypothetical protein GH15_083 [<i>Staphylococcus</i> phage GH15] (0.0)	96% (99%)	YP_007002206.1	
71	39165	39644	480	159	18.53 (4.62)	Hypothetical protein	Hypothetical protein GH15_085 [<i>Staphylococcus</i> phage GH15] (5e-109)	100% (100%)	YP_007002208.1	
72	39686	40936	1251	416	45.82 (3.89)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (0.0)	94% (95%)	YP_007002209.1	
73	41021	41362	342	113	12.82 (9.61)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (1e-71)	100% (100%)	YP_007002210.1	
74	41372	41752	381	126	14.84 (6.14)	Hypothetical protein	Hypothetical protein KgORF40 [<i>Staphylococcus</i> phage K] (2e-82)	99% (100%)	YP_024470.1	
75	41756	43447	1692	563	64.04 (6.19)	Portal protein	Putative portal protein [<i>Staphylococcus</i> phage GH15] (0.0)	99% (100%)	YP_007002212.1	Phage_portal[pfam04860], (1.99e-14)
76	43641	44414	774	257	28.62 (4.71)	Prohead protease	Hypothetical protein KgORF42 [<i>Staphylococcus</i> phage K] (0.0)	99% (100%)	YP_024472.1	Peptidase_U35[pfam04586], (2.03e-05)
77	44433	45383	951	316	35.74 (4.17)	Hypothetical protein	Hypothetical protein KgORF43 [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024473.1	
78	45499	46890	1392	463	51.27 (4.9)	Capsid protein	Putative capsid protein [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024474.1	
79	46982	47278	297	98	11.28 (9.88)	Hypothetical protein	ORF151 [<i>Staphylococcus</i> phage G1] (1e-59)	100% (100%)	YP_240904.1	
80	47291	48199	909	302	34.16 (4.93)	Hypothetical protein	Hypothetical protein KgORF45 [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024475.1	
81	48213	49091	879	292	33.71 (5.99)	Hypothetical protein	hypothetical protein GH15_095 [<i>Staphylococcus</i> phage GH15] (0.0)	99% (100%)	YP_007002218.1	
82	49091	49711	621	206	23.73 (10.85)	Hypothetical protein	Hypothetical protein GH15_096	99% (100%)	YP_007002219.1	

							[<i>Staphylococcus</i> phage GH15] (9e-148)			
83	49730	50566	837	278	31.76 (4.47)	Hypothetical protein	Hypothetical protein KgORF48 [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024478.1	
84	50568	50783	216	71	8.28 (9.14)	Hypothetical protein	ORF202 [<i>Staphylococcus</i> phage G1] (3e-45)	100% (100%)	YP_240909.1	
85	50810	52573	1764	587	64.43 (4.69)	Major tail sheath protein	Major tail sheath protein [<i>Staphylococcus</i> phage 812] (0.0)	99% (100%)	ABL87117.1	pfam04984: Phage_sheath_1 (1.73e-4)
86	52646	52984	339	112	12.45 (9.01)	Tail tube protein	TmpA [<i>Staphylococcus</i> phage A3R] (4e-73)	98% (99%)	AFN38130.1	
87	53779	54783	1005	334	39.42 (9.17)	Ioh	Ioh [<i>Staphylococcus</i> phage A3R] (3e-39)	35% (51%)	AFN38131.1	
88	54840	54980	141	46	5.39 (11.19)	Hypothetical protein	Hypothetical protein phi_A3R_ORF076 [<i>Staphylococcus</i> phage A3R] (4e-16)	76% (89%)	AFN38132.1	
89	55023	55481	459	152	18.12 (10.02)	Hypothetical protein	Hypothetical protein KgORF51 [<i>Staphylococcus</i> phage K] (9e-105)	97% (100%)	YP_024481.1	
90	55494	55688	195	64	7.15 (9.87)	Hypothetical protein	ORF215 [<i>Staphylococcus</i> phage G1] (3e-34)	100% (100%)	YP_240914.1	
91	55770	56081	312	103	12.25 (5.8)	Hypothetical protein	Hypothetical protein KgORF52 [<i>Staphylococcus</i> phage K] (9e-66)	100% (100%)	YP_024482.1	
92	56213	56671	459	152	18.15 (4.50)	Hypothetical protein	Hypothetical protein KgORF53 [<i>Staphylococcus</i> phage K] (5e-105)	100% (100%)	YP_024483.1	
93	56715	57251	537	178	20.92 (4.01)	Tail morphogenetic protein	Hypothetical protein KgORF54 [<i>Staphylococcus</i> phage K] (1e-125)	100% (100%)	YP_024484.1	
94	57307	61362	4056	1351	143.77 (9.51)	TMP	Tail morphogenetic protein, tape measure protein [<i>Staphylococcus</i> phage phiSA012] (0.0)	99% (100%)	BAO47136.1	TACC[Cdd:pfam05010], (7.75e-06)
95	61441	63867	2427	808	91.25 (6.30)	CHAP domain protein	Hypothetical protein KgORF56 [<i>Staphylococcus</i> phage K] (0.0)	99% (99%)	YP_024486.1	CHAP[pfam05257], (6.45e-17)
96	63881	64768	888	295	34.58 (4.21)	Protease	Hypothetical protein GH15_109 [<i>Staphylococcus</i> phage GH15] (0.0)	99% (99%)	YP_007002232.1	IPR000064 Endopeptidase (0.00054)
97	64768	67314	2547	848	95.99 (4.61)	Glycerophosphoryl diester phosphatase	Glycerophosphoryl diester phosphodiesterase [<i>Staphylococcus</i> phage JD007] (0.0)	99% (99%)	YP_007112758.1	GDPD_SaGlpQ_like[cd08601] (6.54e-69)
98	67421	68212	792	263	29.32 (8.75)	Hypothetical protein	Hypothetical protein KgORF59 [<i>Staphylococcus</i> phage K] (0.0)	99% (100%)	YP_024489.1	
99	68212	68736	525	174	19.95 (4.24)	Hypothetical protein	ORF078 [<i>Staphylococcus</i> phage G1] (3e- 121)	100% (100%)	YP_240925.1	
100	68736	69440	705	234	26.58 (4.44)	Baseplate protein	Putative bacteriophage baseplate protein [<i>Staphylococcus</i> phage K] (6e-171)	100% (100%)	YP_024491.1	
101	69455	70501	1047	348	39.2 (4.53)	Baseplate protein	Hypothetical protein KgORF62 [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024492.1	LysM[cd00118] (4.35e-03) [COG3628], Phage baseplate assembly protein W (2.23e- 04)

102	70522	73587	3066	1021	116.45 (4.76)	Hypothetical protein	Hypothetical protein KgORF63 [Staphylococcus phage K] (0.0)	90% (94%)	YP_024493.1	IPR006949 Baseplate assembly protein J-like (4.5e-26)
103	73698	74219	522	173	19.23 (5.12)	Baseplate protein	Hypothetical protein KgORF64 [Staphylococcus phage K] (4e-122)	100% (100%)	YP_024494.1	Phage-Gp8[pfam09215], (1.40e-03)
104	74240	77698	3459	1152	129.33 (4.84)	Adsorption-associated tail protein	Adsorption-associated tail protein [Staphylococcus phage JD007] (0.0)	99% (99%)	YP_007112751.1	
105	77747	77905	159	52	62.8 (9.20)	Hypothetical protein	ORF262 [Staphylococcus phage G1] (9e-27)	100% (100%)	YP_240931.1	
106	77906	79825	1920	639	72.4 (6.22)	Carbohydrate binding domain protein	Hypothetical protein [Staphylococcus phage JD007] (0.0)	97% (98%)	YP_007112749.1	IPR003305Carbohydrate-binding, (5.4e-07)
107	79847	80218	372	123	14.49 (4.58)	Hypothetical protein	Hypothetical protein [Staphylococcus phage JD007] (7e-83)	100% (100%)	YP_007112748.1	
108	80225	81601	1377	458	50.49 (5.64)	Hypothetical protein	Hypothetical protein [Staphylococcus phage JD007] (0.0)	98% (98%)	YP_007112747.1	
109	81691	83439	1749	582	67.23 (5.46)	DNA helicase	Putative helicase [Staphylococcus phage K] (0.0)	99% (100%)	YP_024499.1	Helicase, C-terminal (IPR001650) (7.6e-15)
110	83451	85064	1614	537	63.14 (8.28)	Rep protein	Putative Rep protein [Staphylococcus phage GH15] (0.0)	99% (99%)	YP_007002246.1	HTH_ARSR[cd00090] (1.49e-04)
111	85057	86499	1443	480	54.58 (5.38)	ATPase	Putative ATPase [Staphylococcus phage K] (0.0)	99% (99%)	YP_024501.1	IPR003593 AAA+ ATPase domain (1.4e-05)
112	86578	86997	420	139	16.18 (5.39)	Hypothetical protein				
113	86997	88022	1026	341	39.34 (4.76)	Exonuclease	Hypothetical protein [Staphylococcus phage S25-4] (0.0)	96% (98%)	YP_008854079.1	MPP_Mre11_N[cd00840], (9.51e-25)
114	88022	88399	378	125	15.17 (4.81)	Hypothetical protein	Hypothetical protein KgORF73 [Staphylococcus phage K] (9e-72)	84% (92%)	YP_024503.1	
115	88399	90318	1920	639	73.34 (4.96)	ATPase	Hypothetical protein [Staphylococcus phage S25-4] (0.0)	98% (99%)	YP_008854081.1	ABC_ATPase[cd00267], (1.18e-04)
116	90318	90914	597	198	23.20 (5.96)	Hypothetical protein	Hypothetical protein [Staphylococcus phage JD007] (5e-140)	98% (99%)	YP_007112958.1	
117	90929	91996	1068	355	41.04 (8.50)	DNA Primase	Putative primase [Staphylococcus phage K] (0.0)	99% (99%)	YP_024506.1	TOPRIM_DnaG_primases[cd03364], (2.75e-07)
118	92062	92400	339	112	12.88 (3.98)	Hypothetical protein	ORF127 [Staphylococcus phage G1] (1e-69)	98% (99%)	YP_240943.1	
119	92400	92852	453	150	17.10 (4.69)	Hypothetical protein	Hypothetical protein phi_676Z_ORF107 [Staphylococcus phage 676Z] (2e-96)	95% (99%)	AFN38356.1	
120	92839	93447	609	202	23.64 (5.36)	Resolvase	Resolvase [Staphylococcus phage JD007] (4e-146)	99% (100%)	YP_007112954.1	tRNA endonuclease-like domain (IPR011856)(4.6e-06)
121	93437	93856	420	139	15.75 (10.18)	Ribonucleotide reductase flavodoxin	gp ORF109 [Staphylococcus phage A5W] (9e-92)	98% (98%)	ACB89102.1	nrdI[PRK03600],(2.13e-25)
122	93871	95985	2115	704	80.30 (5.39)	Ribonucleotide reductase	Putative ribonucleotide reductase large	99% (99%)	YP_007002258.1	Ribonuc_red_lgC[pfam02867], (6.96e-176)

						large subunit	subunit [<i>Staphylococcus</i> phage GH15] (0.0)			
123	95999	97048	1050	349	40.45 (4.5)	Ribonucleotide reductase small subunit	Ribonucleoside-diphosphate beta subunit [<i>Staphylococcus</i> phage JD007] (0.0)	98% (99%)	YP_007112951.1	RNRR2[cd01049], (1.58e-59)
124	97066	97395	330	109	12.48 (4.39)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (2e-69)	96% (97%)	YP_007112950.1	
125	97379	97699	321	106	12.04 (4.57)	Thioredoxin-like protein	Thioredoxin-like protein [<i>Staphylococcus</i> phage K] (4e-68)	99% (100%)	YP_024513.1	TRX_family[cd02947], (7.08e-08)
126	97906	98502	597	198	23.59 (6.25)	Hypothetical protein	Hypothetical protein GH15_139 [<i>Staphylococcus</i> phage GH15] (2e-140)	100% (100%)	YP_007002262.1	
127	98512	98817	306	101	11.92 (5.62)	Integration host factor	Putative integration host factor [<i>Staphylococcus</i> phage K] (5e-66)	100% (100%)	YP_024515.1	HU_IHF[cd00591], (7.28e-08)
128	98893	102111	3219	1072	124.57 (5.21)	DNA polymerase	DNA polymerase I [<i>Staphylococcus</i> phage phiSA012] (0.0)	99% (99%)	BAO47171.1	DNA_pol_A_pol_I_C[cd08637] (5.79e-80)
129	102181	102423	243	80	9.26 (3.83)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (2e-48)	98% (100%)	YP_008854095.1	
130	102440	102922	483	160	18.94 (5.12)	Hypothetical protein	Hypothetical protein GH15_143 [<i>Staphylococcus</i> phage GH15] (2e-113)	99% (100%)	YP_007002266.1	
131	103009	104280	1272	423	47.01 (4.44)	Hypothetical protein	Hypothetical protein GH15_144 [<i>Staphylococcus</i> phage GH15] (0.0)	98% (99%)	YP_007002267.1	
132	104340	105596	1257	418	46.76 (4.95)	DNA repair protein	Putative DNA repair protein [<i>Staphylococcus</i> phage GH15] (0.0)	99% (100%)	YP_007002268.1	recA[cd00983] (1.49e-36)
133	105600	105953	354	117	13.38 (4.89)	Hypothetical protein	ORF121 [<i>Staphylococcus</i> phage G1] (6e-79)	100% (100%)	YP_240963.1	
134	105940	106602	663	220	26.60 (5.07)	Sigma factor	Putative sigma factor [<i>Staphylococcus</i> phage K] (1e-155)	100% (100%)	YP_024522.1	
135	106730	107362	633	210	23.21 (4.46)	Putative Ig-like protein	Hypothetical protein KgORF95 [<i>Staphylococcus</i> phage K] (3e-149)	99% (100%)	YP_024523.1	
136	107385	107897	513	170	17.83 (4.13)	Major tail protein	Putative major tail protein [<i>Staphylococcus</i> phage K] (4e-113)	99% (100%)	YP_024524.1	Big_2[pfam02368], (1.65e-05)
137	107912	108139	228	75	7.81 (4.17)	Tail protein	ORF189 [<i>Staphylococcus</i> phage G1] (9e-45)	100% (100%)	YP_240967.1	
138	108235	108495	261	86	10.27 (5.52)	Hypothetical protein	Hypothetical protein GH15_151 [<i>Staphylococcus</i> phage GH15] (8e-55)	100% (100%)	YP_007002274.1	
139	108499	109254	756	251	29.15 (4.21)	Hypothetical protein	Hypothetical protein KgORF97 [<i>Staphylococcus</i> phage K] (8e-180)	100% (100%)	YP_024525.1	
140	109247	110497	1251	416	47.56 (5.64)	DNA polymerase	DNA polymerase [<i>Staphylococcus</i> phage JD007] (0.0)	99% (100%)	YP_007112932.1	
141	110511	110879	369	122	13.99 (5.56)	Hypothetical protein	Hypothetical protein KgORF99 [<i>Staphylococcus</i> phage K] (2e-80)	100% (100%)	YP_024527.1	
142	110866	111177	312	103	12.01 (4.43)	Hypothetical protein	Hypothetical protein KgORF100	100% (100%)	YP_024528.1	

							[<i>Staphylococcus</i> phage K] (7e-68)			
143	111241	111777	537	178	20.78 (6.39)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage phiSA012] (3e-126)	99% (100%)	BAO47187.1	
144	111770	112537	768	255	30.04 (9.83)	Hypothetical protein	Hypothetical protein KgORF101 [<i>Staphylococcus</i> phage K] (0.0)	100% (100%)	YP_024529.1	
145	112515	112961	447	148	17.33 (10.63)	Hypothetical protein	Hypothetical protein KgORF102 [<i>Staphylococcus</i> phage K] (4e-103)	100% (100%)	YP_024530.1	
146	112961	113824	864	287	32.35 (5.40)	Hypothetical protein	ORF036 [<i>Staphylococcus</i> phage G1] (0.0)	100% (100%)	YP_240976.1	
147	114196	114927	732	243	28.35 (5.05)	Hypothetical protein	Hypothetical protein KgORF103 [<i>Staphylococcus</i> phage K] (1e-172)	100% (100%)	YP_024531.1	
148	114945	115403	459	152	17.84 (4.62)	Hypothetical protein	Hypothetical protein GH15_161 [<i>Staphylococcus</i> phage GH15] (2e-105)	100% (100%)	YP_007002284.1	
149	115468	115911	444	147	17.50 (5.96)	Hypothetical protein	Hypothetical protein KgORF105 [<i>Staphylococcus</i> phage K] (2e-98)	100% (100%)	YP_024533.1	
150	115928	116632	705	234	27.36 (4.37)	Hypothetical protein	Hypothetical protein KgORF106 [<i>Staphylococcus</i> phage K] (4e-167)	99% (100%)	YP_024534.1	
151	116694	117092	399	132	15.42 (9.30)	Hypothetical protein	Hypothetical protein KgORF107 [<i>Staphylococcus</i> phage K] (6e-90)	100% (100%)	YP_024535.1	
152	117239	117481	243	80	9.39 (9.79)	Hypothetical protein	ORF182 [<i>Staphylococcus</i> phage G1] (3e-48)	100% (100%)	YP_240982.1	
153	117486	118043	558	185	21.67 (9.88)	Membrane protein	Hypothetical protein PhageK_168 [<i>Staphylococcus</i> phage K] (2e-130)	99% (100%)	AHB80083.1	
154	118079	118255	177	58	6.98 (4.37)	Hypothetical protein	ORF240 [<i>Staphylococcus</i> phage G1] (2e-32)	100% (100%)	YP_240984.1	
155	118248	118496	249	82	9.04 (9.72)	Membrane protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (1e-46)	94% (98%)	YP_007112917.1	
156	118489	118722	234	77	88.93 (7.61)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-3] (5e-42)	90% (96%)	YP_008854298.1	
157	118804	119448	645	214	25.20 (5.49)	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	Putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [<i>Staphylococcus</i> phage GH15] (1e-145)	98% (99%)	YP_007002293.1	
158	119464	119712	249	82	9.04 (9.72)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (1e-35)	94% (100%)	YP_008854124.1	
159	119724	119900	177	58	6.9 (10.19)	Hypothetical protein	Hypothetical protein phi_676Z_ORF149 [<i>Staphylococcus</i> phage 676Z] (1e-30)	98% (98%)	AFN38398.1	
160	119893	120189	297	98	11.47 (8.99)	Hypothetical protein	Hypothetical protein GH15_172 [<i>Staphylococcus</i> phage GH15] (3e-62)	98% (99%)	YP_007002295.1	
161	120237	120419	183	60	7.13 (9.35)	Membrane protein	ORF219 [<i>Staphylococcus</i> phage G1] (2e-32)	98% (100%)	YP_240988.1	
162	120432	120803	372	123	14.34 (3.99)	Hypothetical protein	Hypothetical protein GH15_174 [<i>Staphylococcus</i> phage GH15] (3e-75)	93% (97%)	YP_007002297.1	

163	120816	121163	348	115	12.97 (4.37)	Hypothetical protein	Hypothetical protein GH15_175 [<i>Staphylococcus</i> phage GH15] (4e-76)	99% (100%)	YP_007002298.1	
164	121169	121441	273	90	9.99 (4.03)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (4e-53)	98% (99%)	YP_007002299.1	
165	121511	121816	306	101	12.14 (9.61)	Hypothetical protein	ORF140 [<i>Staphylococcus</i> phage G1] (8e-67)	100% (100%)	YP_240992.1	
166	121831	122181	351	116	136.67 (10.24)	Hypothetical protein	Hypothetical protein GH15_178 [<i>Staphylococcus</i> phage GH15] (2e-75)	100% (100%)	YP_007002301.1	
167	122215	122394	180	59	7.3 (7.17)	Hypothetical protein	Hypothetical protein GH15_180 [<i>Staphylococcus</i> phage GH15] (1e-33)	97% (100%)	YP_007002303.1	
168	122620	123030	411	136	15.32 (4.37)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (9e-86)	94% (99%)	YP_007002304.1	
169	123032	123256	225	74	8.51 (6.54)	Hypothetical protein	Hypothetical protein GH15_198 [<i>Staphylococcus</i> phage GH15] (5e-44)	96% (100%)	YP_007002321.1	
170	123269	123469	201	66	7.60 (4.90)	Hypothetical protein	ORF211 [<i>Staphylococcus</i> phage G1] (5e-41)	100% (100%)	YP_241008.1	
171	123470	123760	291	96	11.13 (9.48)	Membrane protein	Putative membrane protein [<i>Staphylococcus</i> phage GH15] (6e-59)	100% (100%)	YP_007002323.1	
172	123853	124146	294	97	11.41 (6.15)	Hypothetical protein	Hypothetical protein GH15_201 [<i>Staphylococcus</i> phage GH15] (1e-63)	100% (100%)	YP_007002324.1	
173	124143	125051	909	302	34.92 (4.98)	Phosphoribosyl pyrophosphate synthetase	Putative ribose-phosphate pyrophosphokinase [<i>Staphylococcus</i> phage GH15] (0.0)	96% (98%)	YP_007002325.1	ibP_PPkin[TIGR01251], (7.63e-17)
174	125069	126538	1470	489	56.04 (5.05)	Nicotinamide phosphoribosyltransferase	Nicotinamide phosphoribosyl transferase [<i>Staphylococcus</i> phage phiSA012] (0.0)	98% (98%)	BAO47229.1	NAPRTase_PncB[cd01567], (3.65e-95)
175	126629	126940	312	103	11.87 (9.34)	Hypothetical protein				
176	126957	127190	234	77	9.27 (4.56)	Hypothetical protein				
177	127270	127464	195	64	7.41 (4.46)	Hypothetical protein	Hypothetical protein GH15_196 [<i>Staphylococcus</i> phage GH15] (5e-20)	65% (80%)	YP_007002319.1	
178	127478	127801	324	107	12.53 (6.37)	Hypothetical protein				
179	127814	128176	363	120	14.21 (4.51)	Hypothetical protein				
180	128176	128415	240	79	9.28 (4.16)	Hypothetical protein	Hypothetical protein GH15_212 [<i>Staphylococcus</i> phage GH15] (5e-07)	54% (70%)	YP_007002335.1	
181	128488	128898	411	136	16.29 (4.72)	Hypothetical protein	ORF113 [<i>Staphylococcus</i> phage G1] (6e-78)	94% (97%)	YP_241014.1	
182	128903	129157	255	84	9.88 (4.38)	Hypothetical protein	Hypothetical protein PhageK_205 [<i>Staphylococcus</i> phage K] (7e-40)	78% (92%)	AHB80120.1	Clr2[Cdd:pfam10383], (9.04e-03)
183	129261	129659	399	132	15.12 (5.15)	Hypothetical protein				
184	129673	130101	429	142	16.52 (4.31)	Hypothetical protein				
185	130103	130378	276	91	10.70 (4.57)	Hypothetical protein	Hypothetical protein GH15_213	72% (88%)	YP_007002336.1	

							[<i>Staphylococcus</i> phage GH15] (4e-32)			
186	130392	130781	390	129	14.35 (5.03)	Hypothetical protein				
187	130897	131523	627	208	23.19 (4.24)	Hypothetical protein	Putative uncharacterized protein [<i>Staphylococcus equorum</i>] (3e-20)	36% (46%)	WP_002512196.1	
188	131604	131720	117	38	4.51 (10.52)	Hypothetical protein				
189	131734	132135	402	133	16.03 (8.85)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage phiSA012] (8e-45)	59% (77%)	YP_024544.1	
190	132167	132376	210	69	8.33 (4.04)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus epidermidis</i>] (2e-07)	47% (65%)	WP_002493393.1	
191	132376	132732	357	118	13.49 (5.03)	Hypothetical protein				
192	133332	133631	300	99	11.56 (4.18)	TreA	gp ORF182 [<i>Staphylococcus</i> phage A5W] (1e-62)	96% (100%)	ACB89175.1	
193	133647	133832	186	61	6.67 (7.68)	TreB	ORF231 [<i>Staphylococcus</i> phage G1] (3e-25)	87% (93%)	YP_241023.1	
194	133939	134226	288	95	10.82 (4.43)	TreC	TreC [<i>Staphylococcus</i> phage A3R] (5e-60)	99% (100%)	AFN38033.1	
195	134226	134552	327	108	12.61 (4.07)	TreE	Hypothetical protein KgORF117 [<i>Staphylococcus</i> phage K] (9e-70)	99% (99%)	YP_024545.1	
196	134567	134860	294	97	11.62 (4.43)	TreE	TreE [<i>Staphylococcus</i> phage A3R] (3e-61)	97% (98%)	AFN38035.1	
197	134864	135049	186	61	7.44 (8.98)	TreF	ORF175 [<i>Staphylococcus</i> phage G1] (8e-35)	100% (100%)	YP_241027.1	
198	135186	135479	294	97	11.62 (4.43)	TreE	TreE [<i>Staphylococcus</i> phage A3R] (3e-61)	97% (98%)	<u>AFN38035.1</u>	
199	135483	135740	258	85	10.23 (6.10)	TreF	ORF175 [<i>Staphylococcus</i> phage G1] (4e-54)	100% (100%)	YP_241027.1	Peptidase_C26[pfam07722], (5.58e-03)
200	135828	136067	240	79	9.13 (4.63)	Hypothetical protein	gp ORF187 [<i>Staphylococcus</i> phage A5W] (2e-45)	94% (96%)	ACB89180.1	
201	136078	136425	348	115	13.59 (4.76)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (1e-71)	91% (99%)	YP_007112864.1	
202	136968	136630	339	112	13.47 (4.33)	Hypothetical protein	ORF128 [<i>Staphylococcus</i> phage G1] (3e-70)	98% (100%)	YP_241030.1	
203	137279	137587	309	102	11.79 (4.63)	TreJ	ORF145 [<i>Staphylococcus</i> phage G1] (8e-68)	99% (99%)	YP_241031.1	
204	137793	138077	285	94	10.98 (8.90)	TreK	gp ORF190 [<i>Staphylococcus</i> phage A5W] (1e-60)	97% (98%)	ACB89183.1	
205	138152	138343	192	63	7.67 (9.90)	Hypothetical protein	Hypothetical protein GH15_004 [<i>Staphylococcus</i> phage GH15] (4e-37)	100% (100%)	YP_007002127.1	
206	139325	138843	483	160	19.42 (9.61)	HNH homing endonuclease	ORF085 [<i>Staphylococcus</i> phage G1] (4e-93)	85% (89%)	YP_241035.1	HNH_3[pfam13392](1.26e-11)
207	139493	139651	159	52	60.56 (10.90)	TreN	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (2e-26)	100% (100%)	YP_008853962.1	
208	139724	139870	147	48	5.61 (9.82)	Hypothetical protein				

209	140036	140359	324	107	12.35 (4.97)	TreP	Hypothetical protein GH15_006 [<i>Staphylococcus</i> phage GH15] (2e-65)	93% (96%)	YP_007002129.1	
210	140445	140840	396	131	15.39 (4.30)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-3] (4e-66)	75% (87%)	YP_008854145.1	
211	141309	141530	222	73	8.46 (3.96)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage S25-4] (5e-45)	100%(100%)	YP_008853966.1	
212	141789	141953	165	54	6.42 (4.67)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus</i> phage JD007] (4e-29)	100% (100%)	YP_007112853.1	
213	142033	142269	237	78	9.00 (4.03)	Hypothetical protein	hypothetical protein [<i>Staphylococcus</i> phage S25-4] (9e-39)	85% (97%)	YP_008853969.1	

Table S1: Features of bacteriophage phiIPLA-RODI *orfs*, gene products (gp) and functional assignments.

orf	From	To	Length	aa	kDa (pI)	Predictive Function	Closes hit (E value)	% aaidentity / % similarity	Accession no.	Predicted domain (E value)
1	1	216	216	71	8.43 (10.51)	Hypothetical protein	ORF151 [<i>Staphylococcus</i> phage Twort] (2e-39)	87% (98%)	YP_238726.1	
2	621	2168	1548	515	59.78 (5.76)	Terminase large subunit	Terminase large subunit [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48129.1	Terminase_GpA[pfam05876], Phage terminase large subunit (GpA) (1.39e-20)
3	2182	2985	804	267	30.63 (4.98)	Hypothetical protein	Hypothetical protein SEP1_002 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48131.1	
4	2972	3133	162	53	6.56 (9.53)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-26)	100% (100%)	AGR48132.1	
5	3147	3638	492	163	19.21 (4.68)	Hypothetical protein	Hypothetical protein SEP1_004 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-110)	99% (100%)	AGR48133.1	
6	3715	4101	387	128	14.85 (9.57)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-44)	100% (100%)	AGR48134.1	
7	4082	4453	372	123	14.57 (4.84)	Hypothetical protein	Hypothetical protein SEP1_006 [<i>Staphylococcus</i> phage phiIBB-SEP1](1e-82)	99% (100%)	AGR48135.1	
8	4455	6146	1692	563	64.21 (5.85)	Portal protein	Portal protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48136.1	Phage_portal[pfam04860], Phage portal protein (4.87e-15)
9	6288	7058	771	256	28.70 (4.92)	Prohead protease	Hypothetical protein SEP1_008 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48137.1	Peptidase_U35[pfam04586], Caudovirus prohead protease (6.91e-06)
10	7061	8074	1014	337	38.40 (4.27)	Hypothetical protein	Hypothetical protein SEP1_009 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (98%)	AGR48138.1	
11	8201	9592	1392	463	51.28 (4.89)	Major capsid protein	Major capsid protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48139.1	
12	9692	9958	267	88	10.12 (10.00)	Hypothetical protein	Hypothetical protein SEP1_011 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-51)	99% (100%)	AGR48140.1	
13	9968	10876	909	302	33.99 (4.65)	Hypothetical protein	Hypothetical protein SEP1_012 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48141.1	
14	10890	11765	876	291	33.45 (5.82)	Capsid protein	Hypothetical protein SEP1_013 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	98% (99%)	AGR48142.1	
15	11765	12400	636	211	24.29 (11.22)	Hypothetical protein	Hypothetical protein SEP1_014 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-41)	95% (96%)	AGR48143.1	
16	12416	13273	858	285	32.27 (4.46)	Hypothetical protein	Hypothetical protein SEP1_015 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (98%)	AGR48144.1	
17	13248	13469	222	73	8.25 (9.31)	Hypothetical protein	Hypothetical protein SEP1_016 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-45)	100% (100%)	AGR48145.1	
18	13489	15273	1785	594	65.59 (4.72)	Major tail sheath	Tail sheath protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48146.1	Phage_sheath_1[pfam04984], Phage tail sheath protein (1.83e-05)
19	15333	15698	366	121	13.53 (9.04)	Hypothetical protein	Hypothetical protein SEP1_018 [<i>Staphylococcus</i> phage phiIBB-SEP1] (6e-	97% (98%)	AGR48147.1	

							148)			
20	16510	17448	939	312	36.68 (9.42)	Hypothetical protein	ORF018 [<i>Staphylococcus</i> phage Twort] (3e-92)	50% (66%)	YP_238556.1	
21	17505	17639	135	44	5.45 (11.18)	Hypothetical protein	Hypothetical protein SEP1_022 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-19)	93% (95%)	AGR48150.1	
22	17639	18100	462	153	18.17 (9.72)	Hypothetical protein	Hypothetical protein SEP1_023 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-102)	96% (98%)	AGR48151.1	
23	18105	18302	198	65	7.59 (4.55)	Hypothetical protein	Hypothetical protein SEP1_024 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-32)	97% (98%)	AGR48152.1	
24	18368	18661	294	97	11.69 (5.82)	Hypothetical protein	Hypothetical protein SEP1_025 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-60)	100% (100%)	AGR48153.1	
25	18787	19197	411	136	16.00 (4.53)	Hypothetical protein	Hypothetical protein SEP1_026 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-93)	100% (100%)	AGR48154.1	
26	19229	19738	510	169	20.17 (4.03)	Hypothetical tail protein	Hypothetical protein SEP1_027 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-117)	100% (100%)	AGR48155.1	
27	19793	23110	3318	1105	118.12 (10.11)	Tail lysin	Tail lysin [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48156.1	SMC_prok_A[TIGR02169], chromosome segregation protein SMC (7.96e-03)
28	23855	24436	582	193	21.17 (9.72)	Glucosaminidase	Tail lysin [<i>Staphylococcus</i> phage phiIBB-SEP1] (6e-131)	100% (100%)	AGR48156.1	Glucosaminidase[pfam01832], Mannosyl-glycoproteinendo-beta-N-acetylglucosaminidase (2.51e-09)
29	24499	25296	798	265	28.59 (9.34)	Lytic transglycosylase	SLT-domain containing protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48157.1	SLT[pfam01464], Transglycosylase SLT domain (7.70e-06)
30	25353	27959	2607	868	98.03 (5.88)	Amidase	Putative N-acetylmuramoyl-L-alanine amidase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48158.1	CHAP[pfam05257], CHAP domain (1.28e-21)
31	27974	28882	909	302	35.68 (4.24)	Endopeptidase	Hypothetical protein SEP1_032 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48159.1	IPR000064 Endopeptidase, NLPC/P60 domain(4.1e-05)
32	28885	31038	2154	717	81.76 (4.63)	Chromosome segregation protein	Hypothetical protein SEP1_033 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	98% (99%)	AGR48160.1	PRK01156 chromosome segregation protein (9.17e-05)
33	31059	31727	669	222	24.91 (4.94)	Phage-related replication protein	Hypothetical protein SEP1_034 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-158)	99% (99%)	AGR48161.1	COG4195 Phage-related replication protein (3.31e-47)
34	31841	32638	798	265	26.69 (9.53)	Hypothetical protein	Hypothetical protein SEP1_035 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48162.1	
35	32638	33162	525	174	20.54 (5.08)	Hypothetical protein	Hypothetical protein SEP1_036 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-120)	100% (100%)	AGR48163.1	
36	33162	33866	705	234	27.13 (4.72)	Baseplate wedge subunit	Baseplate wedge subunit [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-160)	93% (99%)	AGR48164.1	COG3628[COG3628], Phage baseplate assembly protein W (1.91e-07)

37	33880	34926	1047	348	39.65 (4.69)	Baseplate J protein	Baseplate J protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48165.1	Baseplate_J[pfam04865], Baseplate J-like protein (8.10e-05)
38	34943	37600	2658	885	102.93 (4.63)	Hypothetical protein	Hypothetical protein SEP1_039 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48166.1	
39	37724	38245	522	173	19.41 (5.67)	Baseplate protein	Hypothetical protein SEP1_040 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-123)	99% (99%)	AGR48167.1	Phage-Gp8[pfam09215], Bacteriophage T4, Gp8 (3.48e-03)
40	38266	41721	3456	1151	129.16 (5.29)	Tail protein	Hypothetical protein SEP1_041 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	98% (99%)	AGR48168.1	
41	41781	41933	153	50	5.95 (9.22)	Hypothetical protein	Hypothetical protein SEP1_042 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-16)	94% (98%)	AGR48169.1	
42	41939	43867	1929	642	73.16 (5.06)	Hypothetical protein	Hypothetical protein SEP1_043 [<i>Staphylococcus</i> phage phiIBB-SEP1](0.0)	83% (91%)	AGR48170.1	PHA01818[PHA01818]
43	43880	44272	393	130	15.11 (4.22)	Methyltransferase subunit G	Hypothetical protein SEP1_044 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-76)	95% (96%)	AGR48171.1	DUF2977[pfam11192], Protein of unknown function (DUF2977) (4.56e-06) PRK01026[PRK01026], tetrahydromethanopterin S-methyltransferase subunit G (8.57e-03)
44	44279	45649	1371	456	50.94 (6.50)	Hypothetical protein	Hypothetical protein SEP1_045 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48172.1	PHA01818[PHA01818], Hypothetical protein (3.54e-116)
45	45741	48743	3003	1000	115.97 (7.86)	DNA helicase	ORF006 [<i>Staphylococcus</i> phage Twort] (0.0)	83% (92%)	YP_238583.1	HELICc[cd00079], Helicase superfamily c-terminal domain (7.70e-12) Hint[cd00081], Hedgehog/Intein domain (8.98e-12)
46	48759	50372	1614	537	63.52 (9.26)	Rep protein	Transcriptional regulator [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	98% (99%)	AGR48174.1	IPR011991 Winged helix-turn-helix DNA-binding domain (2.2e-05)
47	50386	51492	1107	368	43.67 (10.47)	Transposase	Transposase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	80% (91%)	AGR48183.1	OrfB_IS605[pfam01385], Probable transposase (4.42e-10) HTH_OrfB_IS605[pfam12323], Helix-turn-helix domain (1.38e-07) tspaseT_teng_C[TIGR01766], transposase, IS605 OrfB family, central region (1.42e-05)
48	51717	53117	1401	466	53.76 (5.32)	Helicase	DNA helicase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48175.1	GP4d_helicase[cd01122] (7.91e-06)
49	53189	53494	306	101	11.78 (4.38)	Hypothetical protein	Hypothetical protein SEP1_049 [<i>Staphylococcus</i> phage phiIBB-SEP1] (6e-63)	100% (100%)	AGR48176.1	
50	53494	54057	564	187	22.133 (5.15)	Hypothetical protein	Hypothetical protein SEP1_050 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-127)	100% (100%)	AGR48177.1	PTZ00211[PTZ00211], ribonucleoside-diphosphate reductase small subunit (2.12e-03)
51	54057	55091	1035	344	39.78 (4.86)	Exonuclease	DNA repair exonuclease [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48178.1	MPP_Mre11_N[cd00840], Mre11 nuclease, N-terminal metallophosphatase domain (1.35e-24)
52	55169	55558	390	129	15.42 (4.66)	Hypothetical protein	Hypothetical protein KgORF73	81% (93%)	YP_024503.1	PHA02275[PHA02275], Hypothetical

							[<i>Staphylococcus</i> phage K] (2e-70)			protein (1.74e-24)
53	55551	57464	1914	637	73.95 (5.12)	Exonuclease	Putative exonuclease [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	YP_007677555.1	ABC_ATPase[cd00267], ATP-binding cassette transporter nucleotide-binding domain (2.14e-05) ABC_sbcCD[cd03279], ATP-binding cassette domain of sbcCD (1.11e-13)
54	57471	58070	600	199	23.58 (9.51)	Hypothetical protein	Hypothetical protein SEP1_054 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-140)	100% (100%)	AGR48181.1	
55	58082	59137	1056	351	40.53 (7.63)	DNA primase	Primase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48182.1	TOPRIM_DnaG_primases[cd03364], TOPRIM_DnaG_primases (1.69e-09) ZnF_CHCC[smart00400], zinc finger (1.80e-06)
56	59199	59510	312	103	11.92 (3.83)	Hypothetical protein	Hypothetical protein SEP1_057 [<i>Staphylococcus</i> phage phiIBB-SEP1] (6e-64)	99% (100%)	AGR48184.1	
57	59510	59944	435	144	16.71 (4.69)	Hypothetical protein	Hypothetical protein SEP1_058 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-94)	100% (100%)	AGR48185.1	PHA02277[PHA02277], Hypothetical protein (1.96e-08)
58	59937	60548	612	203	23.51 (4.81)	Resolvase	Hypothetical protein SEP1_059 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-146)	99% (99%)	YP_240945.1	COG1591[COG1591], Holliday junction resolvase - archaeal type [DNA replication, recombination, and repair] (7.68e-05)
59	60566	60964	399	132	15.02 (9.83)	Flavoprotein	FlavoproteinNrdI [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-90)	100% (100%)	AGR48187.1	Flavodoxin_NrdI[pfam07972], NrdI Flavodoxin like (1.86e-32)
60	60969	62123	1155	384	43.98 (5.13)	Ribonucleotide reductase large subunit	Ribonucleotide reductase large subunit [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48188.1	RNR_I[cd01679], Class I ribonucleotide reductase (2.84e-71) RNR_N[pfam08343], Ribonucleotide reductase N-terminal (6.97e-22)
61	62253	62837	585	194	22.36 (9.95)	Group I intron GIY-YIG homing endonuclease	Group I intron endonuclease [<i>Staphylococcus</i> phage vB_SepS_SEP9] (8e-22)	36% (53%)	AHG24002.1	GIY-YIG_SegABCDEF [cd10444], N-terminal catalytic GIY-YIG domain of bacteriophage T4 segABCDEF gene encoding proteins (1.05e-10)
62	63115	64038	924	307	34.73 (5.85)	Ribonucleotide reductase large subunit	Ribonucleotide reductase large subunit [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48188.1	RNR_I[cd01679], Class I ribonucleotide reductase (9.03e-72)
63	64053	65099	1047	348	40.76 (4.62)	Ribonucleotide reductase small subunit	Ribonucleotide reductase beta subunit [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48189.1	RNR2[cd01049], Ribonucleotide Reductase, R2/beta subunit, ferritin-like diiron-binding domain (2.18e-69)
64	65139	65450	312	103	12.11 (4.29)	Hypothetical protein	Hypothetical protein SEP1_063 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-66)	100% (100%)	AGR48190.1	
65	65453	65776	324	107	12.11 (4.08)	Thioredoxin-like	Thioredoxin-like protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-68)	100% (100%)	AGR48192.1	TRX_family[cd02947], TRX family (3.35e-07)
66	65842	66567	726	241	28.59 (9.06)	Hypothetical protein	Hypothetical protein SEP1_066 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-172)	100% (100%)	AGR48193.1	

67	66576	66875	300	99	11.85 (5.86)	DNA binding protein	DNA-binding protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-63)	100% (100%)	AGR48194.1	Bac_DNA_binding [pfam00216], Bacterial DNA-binding protein (1.40e-12)
68	66956	69187	2232	743	86.85 (6.10)	DNA polymerase	DNA polymerase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48195.1	DNA_polA_I_Ecoli_like_exo [cd06139] (4.46e-15) 35EXOc[smart00474], 3'-5' exonuclease (2.71e-07) UDG_F4_TTUDGA_like [cd10030] (1.17e-03)
69	69353	70162	810	269	31.39 (10.13)	Group I intron HNH homing endonuclease	HNH endonuclease [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48196.1	NUMOD4 [pfam07463], NUMOD4 motif (5.02e-08)
70	70429	71271	843	280	32.30 (5.32)	DNA polymerase	DNA polymerase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48195.1	DNA_pol_A_pol_I_C [cd08637] (4.07e-50)
71	71325	71807	483	160	18.75 (5.92)	Hypothetical protein	Hypothetical protein SEP1_071 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-112)	99% (100%)	AGR48197.1	
72	71898	73142	1245	414	47.22 (4.50)	Hypothetical protein	Hypothetical protein SEP1_072 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48198.1	
73	73200	73424	225	74	80.01 (8.66)	Recombination protein	Recombination protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-40)	100% (100%)	AGR48199.1	SSF52540 P-loop containing nucleoside triphosphate hydrolases (2.7e-07)
74	73769	74737	969	322	38.36 (9.53)	Intein DOD homing endonuclease	I-MsaII [<i>Staphylococcus</i> phage MSA6] (0.0)	98% (99%)	AFN38796.1	IPR004042 Intein DOD homing endonuclease (4.4e-07)
75	74885	75805	921	306	34.33 (5.20)	DNA repair protein	Recombination protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48199.1	recA[cd00983] (2.79e-18)
76	75802	76170	369	122	14.32 (6.37)	Hypothetical protein	Hypothetical protein SEP1_074 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-83)	100% (100%)	AGR48200.1	
77	76151	76807	657	218	26.09 (5.59)	Sigma factor	Putative sigma factor [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-150)	99% (99%)	AGR48201.1	
78	76883	77227	345	114	13.03 (10.19)	Holin	Holin [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-70)	100% (100%)	AGR48202.1	Holin_SPP1[TIGR01592], holin, SPP1 family (1.73e-06)
79	77244	77903	660	219	24.89 (4.40)	Hypothetical protein	Hypothetical protein SEP1_078 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-158)	100% (100%)	AGR48203.1	PHA02283[PHA02283], Hypothetical protein (2.59e-80)
80	78011	78271	261	86	10.13 (5.71)	Hypothetical protein	Hypothetical protein SEP1_079 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-54)	98% (100%)	AGR48204.1	
81	78274	79014	741	246	28.97 (5.63)	Hypothetical protein	Hypothetical protein SEP1_080 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-163)	93% (97%)	AGR48205.1	PHA02284[PHA02284], Hypothetical protein (1.81e-21)
82	79017	80282	1266	421	48.18 (5.71)	Mre11 nuclease	Putative metallophosphatase [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (100%)	AGR48206.1	MPP_Mre11_N[cd00840], Mre11 nuclease, N-terminal metallophosphatase domain (2.77e-05)
83	80295	80633	339	112	13.11 (9.37)	Hypothetical protein	Hypothetical protein SEP1_082 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-71)	99% (100%)	AGR48207.1	

84	80698	81237	540	179	20.64 (8.74)	Hypothetical protein	Hypothetical protein SEP1_083 [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-125)	100% (100%)	AGR48208.1	
85	81227	81976	750	249	29.45 (9.81)	Hypothetical protein	Hypothetical protein SEP1_084 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48209.1	
86	81969	82382	414	137	16.08 (10.81)	Hypothetical protein	Hypothetical protein SEP1_085 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-93)	99% (100%)	AGR48210.1	
87	82382	83227	846	281	32.40 (5.49)	Hypothetical protein	Hypothetical protein SEP1_086 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48211.1	
88	83311	83811	501	166	18.97 (4.16)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-109)	98% (98%)	AGR48212.1	
89	84149	84874	726	241	28.15 (5.15)	Hypothetical protein	Hypothetical protein SEP1_088 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-167)	98% (98%)	AGR48213.1	
90	84899	85387	489	162	19.04 (4.56)	Hypothetical protein	Hypothetical protein SEP1_089 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-111)	100% (100%)	AGR48214.1	
91	85430	85870	441	146	17.33 (9.28)	Hypothetical protein	Hypothetical protein SEP1_090 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-98)	100% (100%)	AGR48215.1	IPR009057 Homeodomain-like(1e-05)
92	85903	86604	702	233	26.97 (4.48)	Hypothetical protein	Hypothetical protein SEP1_091 [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-165)	99% (100%)	AGR48216.1	PHA02290[PHA02290], Hypothetical protein (1.56e-17)
93	86669	87052	384	127	14.63 (9.93)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-69)	90% (98%)	AGR48217.1	PHA02291[PHA02291], Hypothetical protein (1.03e-11)
94	87189	87371	183	60	7.32 (10.34)	Hypothetical protein	Hypothetical protein SEP1_093 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-31)	93%(95%)	AGR48218.1	
95	87364	87645	282	93	10.95 (6.13)	Hypothetical protein	Hypothetical protein SEP1_094 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-58)	96% (100%)	AGR48219.1	
96	87642	87995	354	117	13.95 (10.08)	Hypothetical protein	Hypothetical protein SEP1_096 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-28)	96% (100%)	AGR48221.1	
97	87995	88495	501	166	19.42 (5.64)	Hypothetical protein	Hypothetical protein SEP1_097 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-113)	100% (100%)	AGR48222.1	
98	88499	88822	324	107	12.20 (4.52)	Hypothetical protein	Hypothetical protein SEP1_098 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-63)	95% (96%)	AGR48223.1	
99	88915	89475	561	186	22.05 (9.82)	Hypothetical protein	Hypothetical protein SEP1_099 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-123)	96% (97%)	AGR48224.1	
100	89529	89876	348	115	13.20 (10.06)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage	71% (80%)	AGR48225.1	

							phiIBB-SEP1] (4e-48)			
101	89890	90117	228	75	8.69 (4.43)	Hypothetical protein	Hypothetical protein SEP1_101 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-46)	100% (100%)	AGR48226.1	
102	90135	92471	2337	778	92.03 (6.24)	RNA ligase	Hypothetical protein SEP1_102 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48227.1	RNA_lig_T4_1[pfam09511], RNA ligase (2.26e-38) MPP_PPP_family[cd00144], phosphoprotein phosphatases of the metallophosphatase superfamily (5.91e-15) AAA_33[pfam13671], AAA domain (1.49e-23)
103	92669	92812	144	47	5.49 (4.71)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-10)	96% (95%)	AGR48228.1	
104	92815	93621	807	268	29.79 (9.08)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	100% (100%)	AGR48229.1	Band_7[pfam01145], SPFH domain / Band 7 family (1.80e-26)
105	93740	93928	189	62	6.76 (4.65)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-29)	100% (100%)	AGR48230.1	
106	93943	94119	177	58	6.89 (4.83)	Hypothetical protein	Hypothetical protein SEP1_106 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-30)	98% (98%)	AGR48231.1	
107	94135	94644	510	169	19.96 (9.90)	Hypothetical protein	Hypothetical protein SEP1_107 [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-116)	98% (99%)	AGR48232.1	
108	94698	95807	1110	369	43.41 (7.99)	Hypothetical protein				
109	95883	96077	195	64	7.78 (10.02)	Hypothetical protein	Hypothetical protein PhageK_209 [<i>Staphylococcus</i> phage K] (0.38)	50% (78%)	AHB80124.1	
110	96110	96619	510	169	20.24 (5.16)	Hypothetical protein				
111	96649	96816	168	55	6.14 (4.43)	Hypothetical protein				
112	96951	97259	309	102	11.85 (5.51)	Hypothetical protein				
113	97286	97447	162	53	6.32 (5.02)	Hypothetical protein	Hypothetical protein PhageK_209 [<i>Staphylococcus</i> phage K] (4e-06)	46% (72%)	AHB80124.1	UPF0182[pfam03699], Uncharacterized protein family (UPF0182) (6.06e-03)
114	97463	97969	507	168	19.72 (4.44)	Hypothetical protein	Hypothetical protein [<i>Paenibacilluspolymyxa</i>] (1e-11)	28% (53%)	WP_019687640.1	
115	97996	98232	237	78	9.16 (4.65)	Hypothetical protein	Hypothetical protein IPLA7_0054 [<i>Staphylococcus</i> phage vB_SepiS-phiIPLA7] (1e-44)	91% (93%)	YP_006561216.1	
116	98256	98666	411	136	15.76 (8.46)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage vB_SepS_SEP9] (9e-52)	89% (90%)	YP_009007710.1	
117	98672	99208	537	178	21.08 (4.92)	Hypothetical protein	Hypothetical protein SEP1_108 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-109)	87% (94%)	AGR48234.1	
118	99224	99424	201	66	7.82 (5.14)	Hypothetical protein	Hypothetical protein SEP1_109 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-39)	100% (100%)	AGR48235.1	
119	99450	99707	258	85	9.89 (5.53)	Hypothetical protein	Hypothetical protein SEP1_110	99% (100%)	AGR48236.1	

							[<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-53)			
120	99709	100209	501	166	19.28 (5.92)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-106)	97% (98%)	AGR48237.1	
121	100220	100609	390	129	14.38 (5.51)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage vB_SepS_SEP9] (3e-53)	73% (87%)	YP_009007709.1	
122	100699	101094	396	131	15.57 (4.47)	YopX	Phage conserved Hypothetical protein TIGR01671 [<i>Staphylococcus epidermidis</i>] (5e-44)	64% (72%)	WP_002504181.1	YopX [pfam09643], YopXprotein (4.94e-24)
123	101095	101412	318	105	12.29 (5.03)	Hypothetical protein	Hypothetical protein, partial [<i>Staphylococcus aureus</i>] (1e-23)	54% (73%)	WP_000193480.1	
124	101502	101795	294	97	11.31 (5.02)	Hypothetical protein	Hypothetical protein SEP1_112 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-62)	98% (97%)	AGR48238.1	
125	101816	102034	219	72	8.61 (4.28)	Hypothetical protein	Hypothetical protein SEP1_113 [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-40)	96% (97%)	AGR48239.1	
126	102038	102253	216	71	8.35 (4.42)	Hypothetical protein	Hypothetical protein SEP1_114 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-43)	100% (100%)	AGR48240.1	
127	102297	102650	354	117	13.28 (4.85)	Hypothetical protein	Hypothetical protein SEP1_115 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-80)	99% (100%)	AGR48241.1	
128	102679	103077	399	132	15.19 (4.88)	Hypothetical protein	Hypothetical protein SEP1_116 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-91)	99% (99%)	AGR48242.1	
129	103131	103334	204	67	8.10 (9.83)	Hypothetical protein	Hypothetical protein [<i>Staphylococcus epidermidis</i>] (2e-39)	99% (100%)	WP_002469455.1	
130	103346	103615	270	89	10.61 (5.73)	Hypothetical protein	Hypothetical protein SEP9_088 [<i>Staphylococcus</i> phage vB_SepS_SEP9] (4e-49)	91% (95%)	YP_009007756.1	
131	103627	104040	414	137	16.00 (4.65)	Hypothetical protein	Hypothetical protein SEP1_120 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-77)	85% (94%)	AGR48246.1	
132	104272	104673	402	133	16.02 (9.87)	Hypothetical protein				
133	104686	104886	201	66	7.63 (9.20)	Hypothetical protein	Hypothetical protein SEP9_038 [<i>Staphylococcus</i> phage vB_SepS_SEP9] (2e-34)	92% (98%)	YP_009007708.1	
134	104918	105334	417	138	16.42 (4.50)	Hypothetical protein	Hypothetical protein SEP1_122 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-90)	97% (98%)	AGR48248.1	
135	105337	105573	237	78	9.31 (4.19)	Hypothetical protein	Hypothetical protein SEP1_123 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-47)	99% (100%)	AGR48249.1	
136	105589	106032	444	147	17.63 (9.81)	Hypothetical protein	Hypothetical protein SEP1_124	88% (93%)	AGR48250.1	

							[<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-87)			
137	106051	106389	339	112	13.04 (4.58)	Hypothetical protein				
138	106410	106853	444	147	17.46 (5.39)	Hypothetical protein	Hypothetical protein SEP1_126 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-88)	90% (94%)	AGR48252.1	
139	106867	107259	393	130	15.53 (7.32)	Hypothetical protein				
140	108656	108390	267	88	10.26 (4.14)	Hypothetical protein	Hypothetical protein SEP1_131 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-52)	98%/98%	AGR48257.1	
141	108935	108675	261	86	9.87 (4.09)	Hypothetical protein	Hypothetical protein SEP1_132 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-52)	100% (100%)	AGR48258.1	
142	109349	109011	339	112	13.50 (4.21)	Hypothetical protein	Hypothetical protein SEP1_133 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-54)	84% (84%)	AGR48259.1	
143	109491	110165	675	224	25.45 (4.54)	Pentapeptide repeat protein	Pentapeptide repeat protein [Staphylococcus phage phiIBB-SEP1] (3e-140)	92% (92%)	AGR48263.1	IPR001646 Pentapeptide repeat (3.3e-08)
144	110252	110596	345	114	13.53 (5.08)	Hypothetical protein	Hypothetical protein SEP1_137 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-71)	98% (100%)	AGR48264.1	
145	110738	111073	336	111	13.30 (8.88)	Hypothetical protein	Hypothetical protein SEP1_138 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-69)	100% (100%)	AGR48265.1	
146	111098	111298	201	66	7.84 (4.51)	Hypothetical protein	Hypothetical protein SEP1_139 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-35)	100% (100%)	AGR48266.1	
147	112349	112149	201	66	7.83 (10.58)	Hypothetical protein	Hypothetical protein SEP1_142 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-32)	98% (100%)	AGR48269.1	
148	112603	112382	222	73	8.62 (5.04)	Hypothetical protein	Hypothetical protein SEP1_143 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-47)	100% (100%)	AGR48270.1	
149	113189	113497	309	102	11.71 (5.08)	Hypothetical protein	Hypothetical protein SEP1_144 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-67)	100% (100%)	AGR48271.1	
150	113700	113981	282	93	10.92 (5.73)	TreK	Hypothetical protein SEP1_145 [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-51)	90% (91%)	AGR48272.1	
151	114031	114303	273	90	10.47 (4.35)	Hypothetical protein				
152	114979	115110	132	43	5.09 (10.36)	TreO	Hypothetical protein SEP1_146 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-20)	98% (100%)	AGR48273.1	
153	115176	115316	141	46	5.61 (4.53)	Hypothetical protein	Hypothetical protein SEP1_147 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-	100% (100%)	AGR48274.1	

							19)				
154	115396	115635	240	79	9.13 (7.96)	Hypothetical protein	Hypothetical protein SEP1_148 [<i>Staphylococcus</i> phage phiIBB-SEP1 (2e-49)]	100% (100%)	AGR48275.1		
155	115639	115785	147	48	5.42 (9.61)	TreN	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-23)	100% (100%)	AGR48276.1		
156	115953	116282	330	109	13.11 (3.70)	Hypothetical protein	Hypothetical protein SEP1_151 [<i>Staphylococcus</i> phage phiIBB-SEP1 (7e-66)]	96% (97%)	AGR48278.1		
157	116456	116719	264	87	10.46 (4.12)	Tre protein	Hypothetical protein SEP1_152 [<i>Staphylococcus</i> phage phiIBB-SEP1 (1e-52)]	100% (100%)	AGR48279.1		
158	116791	117264	474	157	18.53 (3.60)	Hypothetical protein	Hypothetical protein SEP1_153 [<i>Staphylococcus</i> phage phiIBB-SEP1 (2e-102)]	99% (98%)	AGR48280		
159	117376	117645	270	89	10.44 (4.94)	Hypothetical protein					
160	117704	117841	138	45	5.18 (4.32)	Hypothetical protein	Hypothetical protein SEP1_154 [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-19)	91% (95%)	AGR48281.1		
161	117911	118189	279	92	11.18 (3.87)	Hypothetical protein	Hypothetical protein SEP1_155 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-31)	93% (96%)	AGR48282.1		
162	118527	119954	1428	475	56.41 (9.26)	Hypothetical protein	Hypothetical protein SEP1_156 [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	98% (98%)	YP_007005520.1		
163	120441	120013	429	142	16.49 (4.18)	Hypothetical protein	ORF062 [<i>Staphylococcus</i> phage Twort] (4e-11)	31% (56%)	YP_238669.1		
164	121022	120516	507	168	20.44 (4.76)	Hypothetical protein	Hypothetical protein SEP1_157 [<i>Staphylococcus</i> phage phiIBB-SEP1 (5e-103)]	99% (100%)	AGR48284.1		
165	121335	121081	255	84	10.34 (4.59)	BofL	Hypothetical protein SEP1_158 [<i>Staphylococcus</i> phage phiIBB-SEP1 (1e-51)]	99% (98%)	AGR48285.1		
166	121922	121338	585	194	23.29 (4.81)	Hypothetical protein	Hypothetical protein SEP1_159 [<i>Staphylococcus</i> phage phiIBB-SEP1 (1e-129)]	98% (98%)	AGR48286.1		
167	122270	121962	309	102	12.19 (8.65)	Hypothetical protein	Hypothetical protein SEP1_161 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-66)]	97% (98%)	AGR48288.1		
168	122721	122359	363	120	14.19 (5.06)	Staphylococcal nuclease	Nuclease [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-81)]	100% (100%)	AGR48289.1	Staphylococcal nuclease homologues (1.40e-16)	
169	123080	122802	279	92	9.67 (4.03)	Tail protein	Hypothetical protein SEP1_163 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-57)]	100% (100%)	AGR48290.1		
170	124126	123548	579	192	22.38 (4.63)	Hypothetical protein	Hypothetical protein SEP1_164 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-	100% (100%)	AGR48291.1		

							136)			
171	124487	124146	342	113	26.48 (10.25)	Tail protein	Hypothetical protein SEP1_165 [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-74)	100% (100%)	AGR48292.1	
172	125186	124503	684	227	15.62 (10.16)	GIY-YIG homing endonuclease	Intron-associated endonuclease [<i>Staphylococcus</i> phage vB_SepS_SEP9] (2e-22)	41% (61%)	YP_009007670.1	SSF82771 GIY-YIG endonuclease (1.5e-11)
173	125347	125186	162	53	6.39 (10.63)	Resolvase	Resolvase [<i>Lactobacillusequi</i>] (3e-15)	66% (86%)	WP_023859949.1	IPR000551 MerR-type HTH domain (1.3e-10)
174	126136	125474	663	220	23.67 (6.27)	Transglycosylase	Transglycosylase-like domain protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-155)	97% (98%)	AGR48293.1	IPR008258 Lytic transglycosylase-like SLT domain (1.1e-07)
175	126411	126259	153	50	5.86 (5.76)	RinB	Transcriptional activator RinB [<i>Staphylococcus</i> phage phiIBB-SEP1] (9e-22)	90% (94%)	AGR48294.1	
176	126732	126415	318	105	12.50 (5.69)	Hypothetical protein	Hypothetical protein SEP1_168 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-63)	93% (97%)	AGR48295.1	
177	127141	126725	417	138	16.24 (5.13)	Hypothetical protein	Hypothetical protein SEP1_169 [<i>Staphylococcus</i> phage phiIBB-SEP1] (4e-91)	99% (100%)	AGR48296.1	IPR021739 Bacteriophage T7, Gp1.7 (1.8e-08)
178	127566	127264	303	100	10.99 (4.68)	NTP pyrophosphohydrolase	Pyrophosphatase [<i>Solibacillus silvestris</i> StLB046] (8e-39)	67% (82%)	YP_006461979.1	IPR004518 NTP pyrophosphohydrolase MazG, putative catalytic core (1.5e-07)
179	127780	127613	168	55	6.57 (4.99)	Hypothetical protein	Hypothetical protein SEP1_172 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-29)	96% (100%)	AGR48299.1	
180	128169	127903	267	88	9.95 (5.13)	Hypothetical protein	Hypothetical protein SEP1_173 [<i>Staphylococcus</i> phage phiIBB-SEP1] (6e-41)	94% (98%)	AGR48300.1	
181	128785	128150	636	211	23.63 (9.63)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-138)	97% (99%)	AGR48301.1	
182	129158	128856	303	100	11.25 (9.15)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-59)	93% (97%)	AGR48302.1	
183	129777	129160	618	205	23.37 (4.21)	Nucleoside-2-deoxyribosyltransferase	nucleoside 2-deoxyribosyltransferase [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-80)	63% (74%)	AGR48303.1	IPR007710 Nucleoside 2-deoxyribosyltransferase (2.8e-16)
184	130051	129791	261	86	9.84 (10.13)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (7e-34)	69% (79%)	AGR48305.1	
185	130308	130066	243	80	9.73 (6.74)	Hypothetical protein	Hypothetical protein SEP9_060 [<i>Staphylococcus</i> phage vB_SepS_SEP9] (6e-47)	98% (100%)	YP_009007729.1	
186	131139	130363	777	258	31.03 (9.86)	HNH homing endonuclease	HNH endonuclease [<i>Staphylococcus</i> phage vB_SepS_SEP9] (3e-179)	97% (98%)	YP_009007730.1	HNH_3[pfam13392], HNH endonuclease (7.35e-03)
187	131879	131151	729	242	27.83 (5.29)	PhoH-related protein	PhoH-related protein [<i>Staphylococcus</i> phage vB_SepS_SEP9] (1e-169)	94% (97%)	YP_009007731.1	IPR003714 PhoH-like protein (2.3e-25)

188	132419	131907	513	170	19.55 (4.63)	Hypothetical protein	Hypothetical protein SEP1_181 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-114)	99% (99%)	AGR48308.1	
189	132850	132434	417	138	15.81 (8.99)	Ribonuclease H	Ribonuclease H [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-94)	100% (100%)	AGR48309.1	RNase_HI_bacteria_HBD[cd09277], Bacterial RNase HI containing a hybrid binding domain (HBD) at the N-terminus (2.36e-41)
190	133028	132840	189	62	7.33 (9.16)	Hypothetical protein	Hypothetical protein SEP1_183 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-35)	100% (100%)	AGR48310.1	
191	133647	133051	597	198	22.72 (4.11)	Hypothetical protein	Hypothetical protein SEP1_184 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-129)	99% (98%)	AGR48311.1	
192	133861	133640	222	73	8.70 (5.38)	Transcriptional regulator	Putative transcriptional regulator [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-41)	99% (98%)	AGR48312.1	IPR001387 Cro/C1-type helix-turn-helix domain (3.8e-13)
193	134092	133871	222	73	8.80 (10.41)	Hypothetical protein	Hypothetical protein SEP1_186 [<i>Staphylococcus</i> phage phiIBB-SEP1] (5e-33)	97% (100%)	AGR48313.1	
194	135717	134263	1455	484	55.01 (9.78)	Endolysin	Endolysin [<i>Staphylococcus</i> phage phiIBB-SEP1] (0.0)	99% (99%)	AGR48314.1	Amidase_2[pfam01510], N-acetylmuramoyl-L-alanineamidase (1.68e-14) CHAP[pfam05257], CHAP domain (2.70e-24) H3_5[pfam08460], Bacterial SH3 domain (1.01e-10)
195	136280	135720	561	186	20.03 (4.27)	Holin	Holin [<i>Staphylococcus</i> phage phiIBB-SEP1] (8e-128)	99% (100%)	AGR48316	Phage_holin_1[pfam04531], Bacteriophage holin (1.18e-19)
196	136958	136593	366	121	14.08 (9.98)	Hypothetical protein	Hypothetical protein SEP9_085 [<i>Staphylococcus</i> phage vB_SepS_SEP9] (3e-59)	77% (89%)	YP_009007753.1	
197	138169	137948	222	73	9.02 (10.09)	Hypothetical protein	Hypothetical protein SEP1_194 [<i>Staphylococcus</i> phage phiIBB-SEP1] (1e-45)	99% (100%)	AGR48320.1	
198	138833	138624	210	69	78.97 (7.74)	Hypothetical protein	Hypothetical protein SEP1_196 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-41)	100% (100%)	AGR48322.1	
199	139176	138844	333	110	12.82 (4.73)	Hypothetical protein	Hypothetical protein SEP1_197 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-67)	99% (100%)	AGR48323.1	
200	139513	139187	327	108	12.72 (6.51)	Hypothetical protein	Hypothetical protein SEP1_198 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-67)	98% (99%)	AGR48324.1	
201	139924	140283	360	119	13.97 (5.42)	Membrane protein	Membrane protein [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-75)	99% (100%)	AGR48326.1	

202	140264	140527	264	87	10.01 (10.19)	Membrane protein	Hypothetical protein SEP1_200 [<i>Staphylococcus</i> phage phiIBB-SEP1] (2e-55)	99% (100%)	AGR48327.1	
203	140532	140951	420	139	15.67 (4.08)	Hypothetical protein	Hypothetical protein SEP1_201 [<i>Staphylococcus</i> phage phiIBB-SEP1] (3e-92)	99% (100%)	AGR48328.1	

Table S2: Features of bacteriophage phiIPLA-C1C *orfs*, gene products (gp) and functional assignments.

Promoter	Strand	Sequence	Nt position	Spacer	TG	Gene
phiIPLA-RODI						
P1	-	<u>TTGACATTCTAATTAATATCCTTTATACT</u>	1964-1992	17	-	Orf5
P2	-	<u>TTGACTTTTTTTACTAAGTATGGTAAGAT</u>	6909-6937	17	+	Orf16
P3	-	<u>TTGACAAAATAGAAAAAGTAGGTATAGT</u>	11380-11408	17	+	Orf25
P4	-	<u>TTGACAAATGAAAATACTTGTATTATAAT</u>	15732-15760	17	-	Orf33
P5	-	<u>TTGACAAATATGACTTACTATGATATGAT</u>	19495-19523	17	+	Orf39
P6	-	<u>TTGACAAACCTCCTTAGTTATGGTATACT</u>	22318-22346	17	+	Orf45
P7	-	<u>TTGACTTCATAAGTTAACTATGCTATAAT</u>	25531-25559	17	+	Orf52
P8	-	<u>TTGACAAAATTAATACATAGTGTATAGT</u>	27631-27659	17	+	Orf55
P9	-	<u>TTGACTTATTTATCAATATAGTATATAGT</u>	32469-32497	17	-	Orf60
P10*	+	<u>TTGACCTATTATTTCTAGAAGCTTTTAGATT</u>	34122-34151	18	-	Orf64
P11	+	<u>TTGACAAATTAATAACTAATAAATTATAAT</u>	55708-55736	17	-	Orf91
P12	+	<u>TTGACAGAAAGTTAATAATATGGTATACT</u>	73596-73624	17	+	Orf103
P13	+	<u>TTGACTTAGGGAGCATTATGTGGTATACT</u>	81631-81659	17	+	Orf109
P14	+	<u>TTGACATTTTATATGTTAGGTGGTATAAT</u>	86518-86546	17	+	Orf112
P15	+	<u>TTGACAAGATTTAAAATATATGGTATAGT</u>	98834-98862	17	+	Orf128
P16	+	<u>TTGACAATATGTTTAACTTATGTTATACT</u>	102120-102148	17	+	Orf129
P17	+	<u>TTGACAAATATAAAAACTATGTTATAAT</u>	102944-102972	17	+	Orf131
P18	+	<u>TTGACAAGAACAATAAGTGTAGTATAGT</u>	118027-118055	17	-	Orf154
P19	+	<u>TTGACAAATCATTTTATATAGTGTATAGT</u>	118747-118775	17	-	Orf157
P20	+	<u>TTGACACTTCTAAACTTTTGTATTATACT</u>	121451-121479	17	-	Orf165
P21	+	<u>TTGACAAATGAGTGTGCATAGGTTATACT</u>	122469-122497	17	-	Orf168
P22	+	<u>TTGACAAAGGGAGTTTTTTATTTGATAGT</u>	126557-126585	17	+	Orf175
P23	+	<u>TTTACATTTAGTAAGTAATATGGTAATATT</u>	127212-127241	18	-	Orf177
P24	+	<u>TTGACAACGAAGGAAACATGTAGTATAGT</u>	128429-128457	17	-	Orf181
P25	+	<u>TTGACAACAAATAAACCATGTAGTATAAT</u>	129202-129230	17	-	Orf183
P26	+	<u>TTGACAATAGTAAAGTAATAGGTTATAAT</u>	130829-130857	17	-	Orf187
P27	+	<u>TTGACATGGATAGAGTTTTACTATATACT</u>	131544-131572	17	-	Orf188
P28	+	<u>TTGACAATCATGAAGCGGTATGTTATAAT</u>	133272-133300	17	+	Orf192
P29*	-	<u>TTGACTTCTGAATAACTATACTGTAATAT</u>	137054-137082	17	-	Orf202
P30	+	<u>TTGACTTTATTATCATATGGTAGTAATAT</u>	137177-137205	17	-	Orf203
P31	+	<u>TTGACACCTTACAAGATACATGTTATTAT</u>	137687-137715	17	+	Orf204
P32	-	<u>TTGACATTAAGACCGAATTATTATATAAT</u>	139360-139388	17	-	Orf206
P33	+	<u>TTGACTTATGTTTATTTCTATAGTAATAT</u>	139434-139362	17	-	Orf207
P34	+	<u>TTGACAACCTATAAACAACGTGTTAATAT</u>	139655-139683	17	+	Orf208
P35	+	<u>TTGACAGTCACTTGAAACCATGATATTAT</u>	139969-139997	17	+	Orf209
P36	+	<u>TTGACTTCCAAGCCCTAGCATGTTATTAT</u>	140373-140401	17	+	Orf210
P37	+	<u>TTGACAACCTTCCAACATCATGTTATTAT</u>	141244-141272	17	+	Orf211
P38	+	<u>TTGACAAACTAACCCTTCATGATAATAT</u>	141728-141756	17	+	Orf212
P39	+	<u>TTGACATTTAGCCCCTTAGATGTTATTAT</u>	141972-142000	17	+	Orf213
P40	+	<u>TTGACATCCTAGCAAATAGATGGTAATAT</u>	142290-142318	17	+	Orf1
phiIPLA-C1C						
P1*	+	<u>TTGACAAAATAATAATATATGATATAAT</u>	372-399	16	+	Orf2
P2	+	<u>TTGACAACCATCAAGGGTTAAATTATAAT</u>	17452-17480	17	-	Orf21
P3	+	<u>TTGACAAACTAATAAAGAGAAGATATAAT</u>	18306-18334	17	-	Orf24
P4	+	<u>TTGACTTATTAAGGTTAAGTGGTATAAT</u>	53130-53158	17	+	Orf49
P5	+	<u>TTGACTTATCAAAAGTTAAGTGGTATAAT</u>	55110-55138	17	+	Orf52
P6*	+	<u>TTGACAAACTATATCTATTTATGATATAGT</u>	71274-71303	18	+	Orf71
P7*	+	<u>TTGACAAATATATACATATATGTTATAGT</u>	77949-77975	17	+	Orf80
P8*	+	<u>TTGACAAAAAGTTATTATAGTTTATAGT</u>	89480-89508	17	-	Orf100
P9	+	<u>TTGACAGGGGTCTTTTTTTTATGTTATAGT</u>	93681-93710	18	+	Orf105

P10	+	<u>TTGACACTGGGTGTTTTTGTATATACT</u>	95823-95851	17	-	Orf109
P11	+	<u>TTGACA</u> ACTGTATAAAATATAGTGTATATT	104207-104235	17	-	Orf132
P12	-	<u>TTGACAGGAGGTCTTTTCTATGATATACT</u>	108967-108995	17	+	Orf141
P13	-	<u>TTGACA</u> ACTAATATTACTTATGCTATAAT	109378-109406	17	+	Orf142
P14*	-	<u>TTGACTATTGCTTTTTAATGCAGATTAATAT</u>	112897-112927	19	-	Orf148
P15	+	<u>TTGACACCTTATAAGAAACATGTTAATAT</u>	113600-113628	17	+	Orf150
P16	+	<u>TTGACA</u> ATATTATATTTAAAAATGCTATAAT	114425-114454	18	+	Orf152
P17	+	<u>TTGACA</u> ACTTAAACACAACATGTTATTAT	115114-115142	17	+	Orf153
P18	+	<u>TTGACA</u> ATCAACCCCTACACATGTTATTAT	115333-115362	18	+	Orf154
P19	+	<u>TTGACA</u> ATCTCTTCACTATTTGATATTAT	115788-115816	17	+	Orf156
P20	+	<u>TTGACAGTAATTTGAAACTATGATAATAT</u>	116298-116326	17	+	Orf157
P21	+	<u>TTGACA</u> ACGTAAC TAGAACATGATATTAT	116730-116758	17	+	Orf158
P22	+	<u>TTGACAGTTTCTATGTTATAATGTTATAAT</u>	117850-117879	18	+	Orf161
P23	-	<u>TTGACAGATAAAAGTTATCTATGGTATACT</u>	122302-122330	17	+	Orf167
P24	-	<u>TTGACA</u> AAAAATGAATAGCTATGGTATACT	127601-127629	17	+	Orf178
P25	-	<u>TTGACA</u> ACTTAAAGTAGTAAATGTTATAAT	127855-127883	17	+	Orf179
P26	-	<u>TTGACTTTTAAGTTTATATGTGTTATAAT</u>	134125-134153	17	+	Orf193
P27	-	<u>TTGACATTTATCAAAAATAAGATTATAAT</u>	138211-138239	17	+	Orf197

Table S3: Putative promoters of phages phiIPLA-RODI and phiIPLA-C1C. -10 and -35 boxes are underlined. Nucleotide positions and presence of the TG dinucleotide were also indicated. * Promoters without AT-rich upstream sequences.

Terminator	Strand	Sequence (5'-3')	Nt position	Stem length	ΔG	After gene
phiPLA-RODI						
T1	+	GUUUAGACUAAGAGGGAAUAAAAUCCCUCUUUUUAUUUUUAU	1304-1344	18	-9.8	Orf4
T2	-	UGAACUAGUUGGAGGGGAGUUAACUCCUCUCUUUUUUUUUU	1608-1649	19	-8.4	Orf5
T3	-	UUAAAUGAUAAACACCUAUUAAAUUAAUAGGUGUUUUUUUAUUGACU	6932-6978	23	-8.6	Orf17
T4	-	AUUAAUUCUUAGGCUACUUUAAUUAGUAGCCUUUUUUUGUUGA	11405-11447	20	-11.2	Orf26
T5	-	UAGGUACAGAAGCAGACUUUAAUAAGUCUGCUUUUCUCUUAUUAU	12171-12215	21	-11.8	Orf28
T6	-	CUUUCUUUUUCACCUUGCUUGUAUCCAAGCAGGGUGUUUUUUUAUUA	16604-16652	26	-11.7	Orf36
T7	-	AUAUUGACAAAACCUCUUAGUUAUGGUAUACUUAUUAAUAACUAAGGAGGaUUUUUUUAUGAAU	22282-22349	43	-10.6	Orf46
T8	-	UAAUAUAUUAAGACUAAGAUAUUUUCUUAGUCUUUUUUGUAUAU	25564-25609	22	-10.5	Orf53
T9	-	AAUAAUAAAUUAGAGAGGUUAAUACCUCUCUUUUUUUUGUCUUUA	26457-26501	20	-11.6	Orf54
T10	-	AAUAGUAAUUUAGACGGAUUUUAAAUCCGUCUaUUUUUUUGCAA	27666-27711	21	-11	Orf56
T11	+	AUAAAACUGAAGAGGAGUAUUACUCCUCUUUUUUUGUUUGC	40917-40957	18	-10.8	Orf72
T12	+	AUUAAUAAUAAGCCUAGAUAUAAUCUAGGCUUUGUUUAUUUUUU	43443-43487	21	-11.3	Orf75
T13	+	ACAAGAGAAUAGGGAUAAACUUAGGGUUUAUCCCUUUUUUAUUAAAA	46911-46957	23	-10.2	Orf78
T14	+	UUUCUUAUUAAGACCUAACAUAUAAAAGUUAGGUCUUUUUUUAUUGA	53676-53721	23	-11.4	Orf86
T15	+	GUUAUUGUAAAGGGUGGUAGGGUAUACUACCAUCCUUAUUUUUUUA	57242-57288	24	-12.1	Orf93
T16	+	UUUAAUAUUAAGACCUAUUAAUUUAGGUCUUUUUUUAGUUGUA	67310-67353	20	-9	Orf97
T17	+	UGAAUAAACUAGAGGGGUUGAUUGACCCUCUUUAUUUAUAA	77692-77734	20	-14.4	Orf104
T18	+	AAUUGCCAUAAGACUAGGAAACUUAUCCUAGUCUUUUUUUCUUGA	81590-81634	22	-12.1	Orf108
T19	+	GACUAAUGAAGAAGAGAAUAAUUCUCUUCUUUUUUUAUUGACA	98795-98839	20	-9.3	Orf127
T20	+	UAUAAGAUAUAGAGUGCCUUAAGAGCACUCUUUUUAUUUGAGA	104276-104316	18	-9.2	Orf131
T21	+	GUAAAAGAAUCUUUGGGGAAUGCAAUUCUCAGAUUGUUCUCCUU	105633-105679	24	-8.2	Orf132
T22	+	AUAAUAAUUAAGACCAACUAAAAAGUUGGUCUUUUUUUAUUGA	108136-108178	20	-11.5	Orf137
T23	+	GAUUUCUUUAUAGAGUCAAGUCUUUACUUGACUCUUUUUACUAUAU	111166-111210	22	-12.1	Orf142
T24	+	GAACAGUGAUUGAGUCAAGUUAUUCUUGACUCUCUUUUUGUUUU	117159-117203	22	-11.5	Orf151
T25	+	AUAAAUCUUAACUCCCUAUUGACAAGGGAGUUUUUUUAUUGUAUA	126538-126583	22	-10.2	Orf174
T26	+	AAAAACUUUGACUCUAUCUAUUGACAUGGAUAGAGUUUUACUAUAUA	131524-131570	24	-9.5	Orf187
T27	+	AAAAUAAAUACACUAGGAUAUUUUAUCCUAGUGUAUUUAUAAAU	136582-136626	22	-12.3	Orf201
T28	-	AAUUAUAUAAUACACUAGGAUAAUAUCCUAGUGUaUUUAUUUUUGCGG	136578-136626	24	-12.2	Orf202
T29	+	AAUUAUACAAUCCCUAGGAUUAUUUCCUAGGGAUUUUUAUUUGUU	138352-138398	24	-14.6	Orf205
T30	-	ACAAAUAAAAUCCCUAGGAUUUUUUAUCCUAGGGAaUUGUAUAAUUUU	138349-138397	24	-14.9	Orf206
T31	+	AAAAUUAAAAUAGGGGUUGACAUUUAGCCCUUaUGUUAUUUAUUA	141954-142003	25	-11.5	Orf213
T32	+	AUAAAUCUUAACUCCCUAUUGACAAGGGAGUUUUUUUAUUGUAUA	126538-126583	22	-10.2	Orf174

T33	+	AAAAACUUUGACUCUAUCUAUUGACAUGGAUAGAGUUUUACUAUAUA	131524-131570	24	-9.5	Orf187
T34	+	AAAAAUAAAUACACUAGGAUAUUU <u>UCCUAGUGUAUUUAUAAUU</u>	136582-136626	22	-12.3	Orf201
T35	-	AAUUAUAUUAAUACACUAGGAAUAAU <u>UCCUAGUGUaUUUAUUUUUGCGG</u>	136578-136626	24	-12.2	Orf202
T36	+	AAUUAUACA <u>AUCCCUAGGAUUAAUCCUAGGGAUUUUUAUUUGUU</u>	138352-138398	24	-14.6	Orf205
T37	-	ACAAAUAAAAUCCCUAGGAAUUU <u>AAUCCUAGGGAaUUGUAUAAUUUUU</u>	138349-138397	24	-14.9	Orf206
T38	+	AAAAAUUAAAAUAAGGGGUUGACA <u>UUUAGCCCCUUAgaUGUUAUUAAUUAA</u>	141954-142003	25	-11.5	Orf213
T39	+	AUAAAUCUUA <u>AAACUCCCUAUUGACA</u> AAAGGGAGUUUUUAUUGUAUA	126538-126583	22	-10.2	Orf174
T40	+	AAAAACUUUGACUCUAUCUAUUGACAUGGAUAGAGUUUUACUAUAUA	131524-131570	24	-9.5	Orf187
T41	+	AAAAAUAAAUACACUAGGAUAUUU <u>UCCUAGUGUAUUUAUAAUU</u>	136582-136626	22	-12.3	Orf201
T42	-	AAUUAUAUUAAUACACUAGGAAUAAU <u>UCCUAGUGUaUUUAUUUUUGCGG</u>	136578-136626	24	-12.2	Orf202
T43	+	AAUUAUACA <u>AUCCCUAGGAUUAAUCCUAGGGAUUUUUAUUUGUU</u>	138352-138398	24	-14.6	Orf205
T44	-	ACAAAUAAAAUCCCUAGGAAUUU <u>AAUCCUAGGGAaUUGUAUAAUUUUU</u>	138349-138397	24	-14.9	Orf206
T45	+	AAAAAUUAAAAUAAGGGGUUGACA <u>UUUAGCCCCUUAgaUGUUAUUAAUUAA</u>	141954-142003	25	-11.5	Orf213
T46	+	AUAAAUCUUA <u>AAACUCCCUAUUGACA</u> AAAGGGAGUUUUUAUUGUAUA	126538-126583	22	-10.2	Orf174
T47	+	AAAAACUUUGACUCUAUCUAUUGACAUGGAUAGAGUUUUACUAUAUA	131524-131570	24	-9.5	Orf187
T48	+	AAAAAUAAAUACACUAGGAUAUUU <u>UCCUAGUGUAUUUAUAAUU</u>	136582-136626	22	-12.3	Orf201
T49	-	AAUUAUAUUAAUACACUAGGAAUAAU <u>UCCUAGUGUaUUUAUUUUUGCGG</u>	136578-136626	24	-12.2	Orf202
T50	+	AAUUAUACA <u>AUCCCUAGGAUUAAUCCUAGGGAUUUUUAUUUGUU</u>	138352-138398	24	-14.6	Orf205
T51	-	ACAAAUAAAAUCCCUAGGAAUUU <u>AAUCCUAGGGAaUUGUAUAAUUUUU</u>	138349-138397	24	-14.9	Orf206
T52	+	AAAAAUUAAAAUAAGGGGUUGACA <u>UUUAGCCCCUUAgaUGUUAUUAAUUAA</u>	141954-142003	25	-11.5	Orf213
phiPLA-C1C						
T1	+	UAAGUAAUUUAAGGGUAGAU <u>AUACUACCCUUUUUUUGCAUGUUAU</u>	3632-3676	21	-10.6	Orf5
T2	+	AAAAUUUUUAUAGAGGGUAAAC <u>UUUGUUUAUCCUCUUUUUUUAUUAU</u>	9623-9668	23	-8.7	Orf11
T3	+	UUCUAAGUAAAUAGACCAGGAUUAAU <u>UCUUGGUCUAUUUAACUUGACA</u>	16407-16455	26	-9	Orf19
T4	+	UUAAUACAAAACCUAUACUAUCUGUUAAU <u>AAUUAUGAAUAAUAAAUAGUAUAGGUUUUUUUACGUU</u>	18696-18765	46	-7.31	Orf24
T5	+	UAUUAUGUAGGGUGGUAGGAUGUUACUACC <u>CCUUUUUUUAAGU</u>	19728-19773	23	-14.2	Orf26
T6	+	GAGUUUAAUAAGGUGGUUUAA <u>AAACCACCUUUUAUACAUAU</u>	25289-25329	18	-10.1	Orf30
T7	+	UUAAUUUAUAGGCGGUUUUAUACCGUC <u>UUUUUUUAUUAG</u>	31717-31756	17	-8.5	Orf33
T8	+	UAUCUAUUUAAGACUAAGUUAAAACU <u>UAGUCUUUUUUUAUUUGCA</u>	455639-45684	21	-9.3	Orf44
T9	+	AAAGACUUAGAGAGACAGAU <u>UUAAAAUUUGUCUCUUUUUUUAUUGA</u>	66853-66899	24	-9.2	Orf67
T10	+	AUUUAAUAAUAGAGUGCU <u>UAAGCACUCUUUUUAUUUGAUU</u>	73137-73174	16	-9.7	Orf72
T11	+	ACCGCUUUUUAGACUAGGAUUAAU <u>UCCUAGUCUUUUUUUAUUUG</u>	77907-77951	22	-12.9	Orf79
T12	+	AUUAAAGAAAAGUAGAGGCAU <u>UUUGCUUCUACUUUAUUUAUUG</u>	80619-80663	22	-11.9	Orf83
T13	+	CUUUUUUAAGCAGUCGAUAC <u>UAAAAAGUAUUGACUGUUUUUUGCUUUU</u>	87110-87158	26	-7.4	Orf94
T14	+	AAUUUUUUACUGACCCCUA <u>UUGACAGGGGUCUUUUUUUUUAUGU</u>	93662-93704	20	-12.7	Orf104

T15	+	UAAAUUAUAAAAACACCCU <u>UGACAC</u> UGGGUGUUUUUUUGUUAUAUAC	95805-95849	22	-10.3	Orf108
T16	+	GAUGAAAUGGGGGAGUAGGGAAACUACUCCUUUUUUUAUUUA	101395-101437	20	-15	Orf123
T17	-	AAUAGUUGAGUACCGCUUCAGUAAU <u>AUAGA</u> AGCGGU _a UUUUUUUUUGUUU	108276-108325	25	-12.2	Orf140
T18	-	AAUAAUUACUAGACCUCU <u>UGAC</u> AGGAGGUCUUUUUCUAUGAUAU	108970-109012	19	-10.3	Orf142
T19	+	UAUAAUAAACAAACCGCUUCAGAUUAA <u>UUUC</u> CGAAGCGGU _c UUAUUUUUUUAGG	111294-111347	29	-11.3	Orf146
T20	-	AUAUCAAUUAGACUAGGGUUU <u>UCCCU</u> AGUCUUUUUAUGUUCUA	112122-112165	20	-14	Orf147
T21	+	UAAUUUAAAAUUAGGGGUUGCAAUC <u>AAAACCCCU</u> AUUUGCUAUAUA	113490-113536	24	-12.5	Orf149
T22	+	AAUAAUAAUAAAGCCUAGGAUUAA <u>AUCCU</u> AGGUUUUUUUUUUUUUUU	114326-114371	22	-12.6	Orf151
T23	+	GUAAGAGAGUACA <u>AAAGGGGAA</u> UAAUCCCUUUGUAUUUUUUUGUU	118166-118210	22	-10.1	Orf161
T24	+	AUAUUUUAAAAAGCAAGAGAU <u>AAAAAC</u> UCUUGCUUUUAUUUAUAUAGA	119932-119979	23	-10.2	Orf162
T25	-	AAAGAUUUAAAAGACUAGUUACA <u>AAACU</u> AGUCUUUUUUUAUUUAUA	122332-122376	21	-9	Orf168
T26	-	AAUAAUUACUAGGACUAGGAUUAA <u>AUCCU</u> AGUCCUUAUUUUUUUAGG	122731-122777	23	-14.3	Orf169
T27	-	AUUAGUAAUAAACAAGGGAUAA <u>AAACCCU</u> UGUUUAUUUUUUUUAC	125421-125464	20	-9.5	Orf174
T28	-	UCUUCCUUUUCCCUUAUUACUUU <u>UGU</u> AGUAAGGGUUUUUAUUUAUA	127155-127201	24	-8.5	Orf178
T29	-	ACUAAUACUACAGAAGAACUUU <u>AAAAAG</u> UUCUUCUUUUUUUUUAUUGACA	127878-127926	24	-9	Orf180
T30	-	AUUUAUUUUUAGACUAGGAUUAA <u>AUCCU</u> AGUCUUUUUUUAUUGA	134211-134255	22	-12.9	Orf194
T31	-	AUAUAGAAUAACCACCUAUUU <u>AUGU</u> AGGGUUUUUCUUAUAUU	136347-136389	20	-12	Orf196
T33	-	GAAUUAUUAAAGGCUAACU <u>UAUG</u> UUAGUCUUUUUUUAUAUA	138593-138633	18	-8.3	Orf198

Table S4: Putative terminators of phages phiIPLA-RODI and phiIPLA-C1C. The underline sequence corresponds to the terminator stem.

Lowercase letter in RNA motifs indicates the spacer element between the stem-loop and T-rich region.