Table S1. Features of LM12 predicted coding sequences (CDSs). For each CDS the transcription start and stop position, and the coding strand is given. At protein level the corresponding gene product size molecular weight and pI as well as the homolog predicted function, homology values and motifs are shown

DNA				Protein						
CDS	**Coordinates**	**Strand**	**Length**	**Mass**	**pI**	**aa residues**	**Function**	**Homolog**	**E-value**	**Motif**
1	156..473	+	318	12.70	9.99	105	HNH endonuclease	ORF085 [Staphylococcus virus G1]	6,00E-71	HNH_3 (PF13392) HNH endonuclease; HTH_23 (PF13384) Homeodomain-like domain
2	790..981	-	192	7.67	10.61	63	hypothetical protein	ORF221 [Staphylococcus virus G1]	6,00E-37	
3	1,031..1,318	-	288	11.06	6.52	95	TreK	hypothetical protein [Staphylococcus phage	1,00E-61	
4	1,524..1,832	-	309	11.80	4.57	102	TreJ	TreJ [Staphylococcus phage phiIPLA-RODI]	1,00E-69	
5	2,143..2,481	+	339	13.47	4.25	112	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	9,00E-72	
6	2,686..3,033	-	348	13.66	4.26	115	TreH	hypothetical protein [Staphylococcus phage	4,00E-77	
7	3,044..3,283	-	240	9.18	6.07	79	hypothetical protein	hypothetical protein CPT_phageK_gp007 [Staphylococcus virus K]	4,00E-50	
8	3,376..3,633	-	258	10.24	6.52	85	TreF	ORF175 [Staphylococcus virus G1]	5,00E-55	
9	3,637..3,93	-	294	11.59	4.09	97	TreE	TreE [Staphylococcus phage vB_Sau_CG]	7,00E-60	
10	3,93..4,217	-	288	10.90	7.85	95	TreD	ORF158 [Staphylococcus virus G1]	8,00E-61	
11	4,217..4,507	-	291	11.30	4.03	96	TreC	terminal repeat-encoded protein [Staphylococcus phage P108]	5,00E-60	
12	4,536..5,171	-	636	24.80	9.77	211	hypothetical protein	hypothetical protein [Staphylococcus phage SA3]	4,00E-66	
0012A	5,269..5,46	-	192	7.19	6.51	63	TreB	TreB [Staphylococcus phage vB_Sau_S24]	2,00E-26	
13	5,467..5,769	-	303	11.22	5.10	100	hypothetical protein	hypothetical protein vBSauClo6_132 [Staphylococcus phage vB_Sau_Clo6]	2,00E-61	
14	5,772..5,954	-	183	6.50	8.49	60	hypothetical membrane protein	hypothetical protein [Staphylococcus phage S25-	5,00E-15	
15	5,951..6,244	-	294	11.18	4.12	97	TreA	hypothetical protein [Staphylococcus phage MCE-2014]	3,00E-58	
16	6,26..6,43	-	171	6.27	4.26	56	hypothetical membrane protein	hypothetical protein P108_0115 [Staphylococcus phage P108]	3,00E-28	
17	7,061..7,174	-	114	4.27	3.86	37	hypothetical protein			

18	7,314..7,463	-	150	5.88	4.21	49	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-C1C]	2,00E-07	
19	7,463..7,798	-	336	12.88	4.84	111	hypothetical protein	ORF131 [Staphylococcus virus G1]	3,00E-72	
20	7,8..8,309	-	510	20.32	9.69	169	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	2,00E-116	
21	8,312..8,623	-	312	11.61	4.91	103	hypothetical protein	ORF142 [Staphylococcus virus G1]	1,00E-66	
22	8,689..8,886	-	198	7.86	4.11	65	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	2,00E-39	
23	8,888..9,28	-	393	15.44	4.79	130	hypothetical protein	ORF113 [Staphylococcus virus G1]	2,00E-87	
24	9,3..9,545	-	246	9.96	9.23	81	hypothetical protein	ORF178 [Staphylococcus virus G1]	4,00E-52	
25	9,624..11,093	-	1470	56.14	5.05	489	nicotinamide phosphoribosyl transferase	putative nicotinamide phosphoribosyl transferase [Staphylococcus phage GH15]	0,00E+00	NAPRTase (PF04095) Nicotinate phosphoribosyltransferase (NAPRTase) family
26	11,097..11,492	-	396	15.41	5.06	131	hypothetical protein			
27	11,507..12,415	-	909	35.02	4.74	302	phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase [Staphylococcus phage phiIPLA-RODI]	0,00E+00	
28	12,412..12,705	-	294	11.42	6.54	97	hypothetical protein	hypothetical protein GH15_201 [Staphylococcus phage GH15]	1,00E-64	
29	12,798..13,088	-	291	11.23	9.71	96	hypothetical membrane protein	putative membrane protein [Staphylococcus phage GH15]	1,00E-58	
30	13,089..13,289	-	201	7.60	4.88	66	hypothetical protein	ORF211 [Staphylococcus virus G1]	8,00E-42	
31	13,302..13,526	-	225	8.50	6.54	74	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	2,00E-45	
32	13,542..13,7	-	159	5.78	4.45	52	hypothetical membrane protein	hypothetical protein [Staphylococcus phage MCE-2014]	1,00E-21	
33	13,716..13,919	-	204	7.74	5.10	67	hypothetical protein	hypothetical protein GH15_196 [Staphylococcus phage GH15]	4,00E-38	
34	13,997..14,677	-	681	25.89	4.80	226	hypothetical protein	hypothetical protein [Staphylococcus phage	1,00E-109	
35	14,678..14,995	-	318	12.08	4.54	105	hypothetical protein	hypothetical protein GH15_194 [Staphylococcus phage GH15]	2,00E-65	
36	14,998..15,261	-	264	10.35	4.50	87	hypothetical protein	hypothetical protein GH15_193 [Staphylococcus phage GH15]	1,00E-51	
37	15,276..15,455	-	180	6.39	10.79	59	hypothetical membrane protein	hypothetical protein GH15_192 [Staphylococcus phage GH15]	1,00E-28	

38	15,501..15,812	-	312	12.51	10.49	103	hypothetical protein	hypothetical protein P108_0092 [Staphylococcus phage P108]	2,00E-67	
39	15,793..16,32	-	528	20.62	6.87	175	metallophosphatase	hypothetical protein GH15_189 [Staphylococcus phage GH15]	4,00E-123	
40	16,317..16,553	-	237	9.16	8.39	78	hypothetical protein	hypothetical protein GH15_188 [Staphylococcus phage GH15]	7,00E-49	
41	16,558..16,962	-	405	15.24	9.63	134	hypothetical membrane protein	hypothetical protein [Staphylococcus phage	3,00E-73	
42	16,962..17,267	-	306	11.62	4.68	101	hypothetical protein	hypothetical protein [Staphylococcus phage pSco-	2,00E-56	
43	17,344..18,009	-	666	24.89	4.43	221	hypothetical protein	hypothetical protein vBSauCG_109 [Staphylococcus phage vB_Sau_CG]	7,00E-146	
44	18,025..18,297	-	273	10.54	10.65	90	hypothetical protein	hypothetical protein P108_0087 [Staphylococcus phage P108]	5,00E-53	
45	18,29..18,403	-	114	4.47	4.44	37	hypothetical protein	hypothetical protein GH15_184 [Staphylococcus phage GH15]	9,00E-15	bZIP_1 (PF00170) BZIP domain
46	18,414..18,641	-	228	8.26	4.83	75	hypothetical membrane protein	hypothetical protein [Staphylococcus phage pSco-	7,00E-44	
47	18,657..18,95	-	294	11.65	3.76	97	hypothetical protein	hypothetical protein [Staphylococcus phage	3,00E-62	
48	18,952..19,362	-	411	15.46	4.36	136	hypothetical membrane protein	membrane protein [Staphylococcus phage phiIPLA-RODI]	5,00E-90	
49	19,588..19,767	-	180	7.25	7.35	59	hypothetical protein	hypothetical protein GH15_180 [Staphylococcus phage GH15]	2,00E-35	
50	19,781..20,383	-	603	23.36	10.38	200	hypothetical protein	hypothetical protein GH15_179 [Staphylococcus phage GH15]	3,00E-145	
51	20,383..20,733	-	351	13.68	10.52	116	hypothetical protein	hypothetical protein GH15_178 [Staphylococcus phage GH15]	4,00E-77	
52	20,748..21,053	-	306	12.14	9.71	101	hypothetical protein	hypothetical protein GH15_177 [Staphylococcus phage GH15]	6,00E-68	
53	21,123..21,395	-	273	10.00	4.11	90	hypothetical membrane protein	membrane protein [Staphylococcus phage phiIPLA-RODI]	9,00E-55	
54	21,401..21,748	-	348	12.97	4.32	115	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	1,00E-77	
55	21,761..22,129	-	369	14.16	4.03	122	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	3,00E-83	
56	22,142..22,324	-	183	7.14	9.03	60	hypothetical membrane protein	hypothetical protein P108_0075 [Staphylococcus phage P108]	1,00E-33	
57	22,372..22,668	-	297	11.47	8.82	98	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	5,00E-64	

58	22,661..22,837	-	177	7.01	10.67	58	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	2,00E-31
59	22,849..23,097	-	249	9.05	4.50	82	hypothetical membrane protein	hypothetical protein P108_0072 [Staphylococcus phage P108]	1,00E-45
60	23,113..23,757	-	645	25.10	6.06	214	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	6,00E-148
61	23,838..24,071	-	234	8.93	9.00	77	hypothetical protein	hypothetical protein P108_0070 [Staphylococcus phage P108]	5,00E-48
62	24,064..24,312	-	249	9.09	9.66	82	hypothetical membrane protein	hypothetical protein [Staphylococcus phage	1,00E-49
63	24,305..24,481	-	177	6.99	4.26	58	hypothetical protein	ORF240 [Staphylococcus virus G1]	4,00E-33
64	24,517..25,074	-	558	21.68	10.07	185	hypothetical membrane protein	membrane protein [Staphylococcus phage phiIPLA-RODI]	6,00E-132
65	25,079..25,321	-	243	9.39	9.94	80	hypothetical protein	ORF182 [Staphylococcus virus G1]	5,00E-49
66	25,468..25,866	-	399	15.45	9.53	132	hypothetical membrane protein	putative membrane protein [Staphylococcus phage GH15]	2,00E-90
67	25,929..26,633	-	705	27.46	4.33	234	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	4,00E-159
68	26,65..27,093	-	444	17.54	6.29	147	hypothetical protein	hypothetical protein GH15_162 [Staphylococcus phage GH15]	2,00E-99
69	27,158..27,616	-	459	17.85	4.58	152	hypothetical protein	hypothetical protein GH15_161 [Staphylococcus phage GH15]	2,00E-106
70	27,634..28,365	-	732	28.36	5.09	243	hypothetical protein	hypothetical protein qdsa002_176 [Staphylococcus phage qdsa002]	3,00E-173
71	28,737..29,6	-	864	32.33	5.47	287	hypothetical protein	ORF036 [Staphylococcus virus G1]	0,00E+00
72	29,6..30,046	-	447	17.34	10.90	148	hypothetical protein	ORF099 [Staphylococcus virus G1]	3,00E-104
73	30,024..30,791	-	768	30.05	10.00	255	hypothetical protein	hypothetical protein [Staphylococcus phage	0,00E+00
74	30,784..31,32	-	537	20.83	7.71	178	hypothetical protein	ORF075 [Staphylococcus virus G1]	4,00E-128
75	31,384..31,695	-	312	12.01	4.41	103	hypothetical protein	ORF143 [Staphylococcus virus G1]	7,00E-69
76	31,682..32,05	-	369	14.00	5.75	122	hypothetical membrane protein	ORF118 [Staphylococcus virus G1]	2,00E-81
77	32,064..33,314	-	1251	47.57	6.01	416	metallophosphoesterase	DNA polymerase [Staphylococcus phage phiIPLA-RODI]	0,00E+00
78	33,307..34,062	-	756	29.16	4.19	251	hypothetical protein	ORF046 [Staphylococcus virus G1]	0,00E+00
79	34,066..34,326	-	261	10.29	5.71	86	hypothetical protein	ORF174 [Staphylococcus virus G1]	2,00E-55
80	34,422..34,649	-	228	7.82	4.12	75	tai morphogenetic protein	ORF189 [Staphylococcus virus G1]	1,00E-45

81	34,664..35,176	-	513	17.85	4.09	170	tai morphogenetic protein	putative bacterial adhesin/Ig-like protein [Staphylococcus virus K]	6,00E-115	Big_2 (PF02368) Bacterial Ig-like domain (group 2)
82	35,199..35,831	-	633	23.20	4.44	210	putative Ig-like protein	ORF059 [Staphylococcus virus G1]	1,00E-150	
83	35,959..36,621	-	663	26.61	5.02	220	RNA polymerase sigma factor	ORF056 [Staphylococcus virus G1]	5,00E-157	
84	36,608..36,961	-	354	13.38	4.83	117	hypothetical protein	ORF121 [Staphylococcus virus G1]	6,00E-80	
85	36,965..38,221	-	1257	46.77	4.89	418	DNA repair recombinase	ORF021 [Staphylococcus virus G1]	0,00E+00	RecA (PF00154) recA bacterial DNA recombination protein; Rad51 (PF08423) Rad51; ATPase (PF06745) KaiC
86	38,281..39,552	-	1272	46.90	4.37	423	hypothetical protein	hypothetical protein [Staphylococcus phage S25-	0,00E+00	
87	39,639..40,121	-	483	18.95	5.32	160	hypothetical protein	ORF089 [Staphylococcus virus G1]	9,00E-116	
88	40,138..40,38	-	243	9.09	3.82	80	hypothetical protein	hypothetical protein GH15_142 [Staphylococcus phage GH15]	2,00E-50	
89	40,449..43,667	-	3219	124.62	5.11	1072	DNA polymerase A	DNA polymerase I [Staphylococcus phage phiSA12]	0,00E+00	DNA_pol_A (PF00476) DNA polymerase family A; DNA_pol_A_exo1 (PF01612) 3'-5' exonuclease
90	43,743..44,048	-	306	11.93	5.83	101	DNA binding protein	ORF147 [Staphylococcus virus G1]	5,00E-67	Bac_DNA_binding (PF00216) Bacterial DNA binding protein
91	44,058..44,618	-	561	22.11	6.36	186	hypothetical protein	hypothetical protein GH15_139 [Staphylococcus phage GH15]	8,00E-133	
92	44,861..45,181	-	321	12.05	4.54	106	thioredoxin-like protein	oxidoreductase [Staphylococcus phage MCE-2014]	1,00E-69	Thioredoxin (PF00085) Thioredoxin
93	45,165..45,494	-	330	12.46	4.36	109	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	2,00E-72	
94	45,512..46,561	-	1050	40.49	4.43	349	ribonucleotide reductase small subunit	ribonucleotide reductase small subunit [Staphylococcus phage phiIPLA-RODI]	0,00E+00	Ribonuc_red_sm (PF00268) Ribonucleotide reductase, small chain

95	46,575..48,689	-	2115	80.32	5.41	704	ribonucleotide reductase large subunit	ribonucleotide reductase large subunit [Staphylococcus phage phiIPLA-RODI]	0,00E+00	Ribonuc_red_lgC (PF02867) Ribonucleotide reductase, barrel domain; RNR_N (PF08343) Ribonucleotide reductase N-terminal; Ribonuc_red_lgN (PF00317) Ribonucleotide reductase, all-alpha domain
96	48,704..49,096	-	393	14.75	10.45	130	ribonucleotide reductase stimulatory protein	putative NrdI protein [Staphylococcus phage GH15	6,00E-89	Flavodoxin_NdrI (PF07972) NrdI Flavodoxin like
97	49,114..49,722	-	609	23.62	5.15	202	resolvase	hypothetical protein P108_0033 [Staphylococcus phage P108]	2,00E-147	
98	49,709..50,161	-	453	17.05	4.52	150	hypothetical protein	hypothetical protein P108_0032 [Staphylococcus phage P108]	6,00E-101	
99	50,161..50,499	-	339	12.94	3.87	112	hypothetical protein	ORF127 [Staphylococcus virus G1]	1,00E-71	
100	50,565..51,632	-	1068	40.95	8.58	355	DNA primase	DNA primase [Staphylococcus phage JD007]	0,00E+00	zf-CHC2 (PF01807) CHC2 zinc finger
101	51,647..52,243	-	597	23.24	6.81	198	hypothetical protein	hypothetical protein P108_0028 [Staphylococcus phage P108]	3,00E-143	
102	52,243..54,162	-	1920	73.29	4.89	639	recombination exonuclease B	hypothetical protein P108_0027 [Staphylococcus phage P108]	0,00E+00	AAA_23 (PF13476) AAA domain; Rad50_zn_hook (PF04423) Rad50 zinc hook motif
103	54,162..54,539	-	378	15.17	5.32	125	hypothetical protein	hypothetical protein P108_0026 [Staphylococcus phage P108]	7,00E-86	
104	54,539..55,564	-	1026	39.38	4.78	341	recombination exonuclease A	hypothetical protein P108_0025 [Staphylococcus phage P108]	0,00E+00	Metallophos (PF00149) Calcineurin-like phosphoesterase; Metallophos_2 (PF12850) Calcineurin-like phosphoesterase superfamily domain
105	55,564..55,983	-	420	16.16	5.22	139	hypothetical protein	hypothetical protein [Staphylococcus phage SA3]	1,00E-97	

106	56,062..57,504	-	1443	54.57	5.56	480	DNA helicase	DNA helicase [Staphylococcus phage P108]	0,00E+00	DnaB_C (PF03796) DnaB-like helicase C terminal domain; AAA_25 (PF13481) AAA domain; ATPase (PF06745) KaiC
107	57,497..59,11	-	1614	63.14	8.38	537	Rep protein	putative Rep protein [Staphylococcus phage P108]	0,00E+00	
108	59,122..60,87	-	1749	67.28	5.87	582	DNA helicase A	DNA helicase [Staphylococcus phage SA3]	0,00E+00	Helicase_C (PF00271) Helicase conserved C-terminal domain; ResIII (PF04851) Type III restriction enzyme, res subunit
109	60,96..62,336	-	1377	50.64	6.41	458	tail fiber protein	putative tail fiber protein [Staphylococcus phage P108]	0,00E+00	
110	62,343..62,717	-	375	14.64	4.46	124	hypothetical protein	hypothetical protein P108_0018 [Staphylococcus phage P108]	5,00E-86	DUF2977 (PF11192) Protein of unknown function (DUF2977)
111	62,731..64,653	-	1923	72.60	6.95	640	hypothetical protein	hypothetical protein P108_0017 [Staphylococcus phage P108]	0,00E+00	CBM_4_9 (PF02018) Carbohydrate binding domain
112	64,654..64,812	-	159	6.31	9.01	52	hypothetical protein	hypothetical protein P108_0016 [Staphylococcus phage P108]	1,00E-27	
113	64,861..68,319	-	3459	129.23	4.80	1152	adsorption-associated tail protein	adsorption-associated tail protein [Staphylococcus phage P108]	0,00E+00	DUF4815 (PF16075) Domain of unknown function (DUF4815)
114	68,34..68,861	-	522	19.25	5.04	173	baseplate morphogenetic protein	hypothetical protein P108_0014 [Staphylococcus phage P108]	3,00E-123	
115	68,972..72,037	-	3066	116.40	4.64	1021	tail morphogenetic protein	hypothetical protein P108_0013 [Staphylococcus phage P108]	0,00E+00	
116	72,058..73,104	-	1047	39.21	4.48	348	baseplate morphogenetic protein	putative tail protein [Staphylococcus phage P108]	0,00E+00	Baseplate_J (PF04865) Baseplate J-like protein
117	73,119..73,823	-	705	26.59	4.38	234	baseplate wedge subunit	ORF052 [Staphylococcus virus G1]	3,00E-172	DUF2634 (PF10934) Protein of unknown function (DUF2634)
118	73,823..74,347	-	525	20.02	4.28	174	hypothetical protein	hypothetical protein [Staphylococcus phage SA3]	2,00E-122	

119	74,347..75,138	-	792	29.33	8.64	263	hypothetical protein	hypothetical protein P108_0008 [Staphylococcus phage P108]	0,00E+00	
120	75,245..77,791	-	2547	96.05	4.57	848	glycerophosphoryl diester phosphodiesterase	putative glycerophosphoryl diester phosphodiesterase [Staphylococcus phage P108]	0,00E+00	GDPD (PF03009) Glycerophosphoryl diester phosphodiesterase family
121	77,791..78,678	-	888	34.53	4.17	295	peptidoglycan hydrolase	hypothetical protein P108_0006 [Staphylococcus phage P108]	0,00E+00	
122	78,692..81,118	-	2427	91.31	6.40	808	tail murein hydrolase	N-acetylmuramoyl-L-alanine amidase [Staphylococcus phage SA3]	0,00E+00	CHAP (PF05257) CHAP domain
123	81,196..85,254	-	4059	143.86	9.72	1352	tail tape measure	hypothetical protein [Staphylococcus phage SA3]	0,00E+00	
124	85,307..85,843	-	537	20.98	4.02	178	tail morphogenetic protein	tail morphogenetic protein [Staphylococcus phage P108]	4,00E-127	
125	85,887..86,345	-	459	18.11	4.42	152	hypothetical protein	hypothetical protein GH15_105 [Staphylococcus phage GH15]	3,00E-106	
126	86,477..86,788	-	312	12.24	5.94	103	hypothetical protein	hypothetical protein GH15_104 [Staphylococcus phage GH15]	7,00E-67	
127	86,859..87,053	-	195	7.34	10.21	64	hypothetical membrane protein	hypothetical protein P108_0223 [Staphylococcus phage P108]	7,00E-34	
128	87,066..87,518	-	453	17.81	10.29	150	hypothetical protein	hypothetical protein GH15_103 [Staphylococcus phage GH15]	2,00E-105	
129	87,561..87,701	-	141	5.44	11.42	46	hypothetical protein	hypothetical protein [Staphylococcus phage	2,00E-23	
130	87,691..87,849	-	159	6.47	10.63	52	hypothetical protein	hypothetical protein GH15_101 [Staphylococcus phage GH15]	4,00E-29	
131	87,939..88,367	-	429	15.93	5.25	142	tail tube protein	ORF105 [Staphylococcus virus G1]	9,00E-101	
132	88,44..90,203	-	1764	64.47	4.59	587	major tail sheath protein	putative major tail sheath protein [Staphylococcus phage P108]	0,00E+00	
133	90,23..90,445	-	216	8.28	8.91	71	hypothetical protein	ORF202 [Staphylococcus virus G1]	4,00E-46	
134	90,447..91,283	-	837	31.76	4.41	278	hypothetical protein	hypothetical protein GH15_097 [Staphylococcus phage GH15]	0,00E+00	
135	91,302..91,922	-	621	23.75	11.09	206	hypothetical protein	hypothetical protein GH15_096 [Staphylococcus phage GH15]	2,00E-149	
136	91,922..92,8	-	879	33.71	5.52	292	capsid protein	capsid protein [Staphylococcus phage JD007]	0,00E+00	
137	92,814..93,722	-	909	34.17	4.89	302	hypothetical protein	ORF030 [Staphylococcus virus G1]	0,00E+00	
138	93,735..94,031	-	297	11.23	10.12	98	hypothetical protein	hypothetical protein GH15_093 [Staphylococcus phage GH15]	7,00E-61	

139	94,123..95,514	-	1392	51.22	4.80	463	major capsid protein	putative capsid protein [Staphylococcus phage GH15]	0,00E+00	
140	95,63..96,589	-	960	36.17	4.07	319	hypothetical protein	hypothetical protein qdsa002_106 [Staphylococcus phage qdsa002]	0,00E+00	
141	96,608..97,381	-	774	28.65	4.64	257	prohead protease	ORF048 [Staphylococcus virus G1]	0,00E+00	Peptidase_S78 (PF04586) Caudovirus prohead serine protease Peptidase_S78 (PF04586)
142	97,574..99,265	-	1692	64.10	6.56	563	portal protein	putative portal protein [Staphylococcus phage GH15]	0,00E+00	Phage_portal (PF04860) Phage portal protein
143	99,269..99,64	-	372	14.51	5.78	123	hypothetical protein	ORF115 [Staphylococcus virus G1]	2,00E-83	
144	99,659..99,847	-	189	7.17	9.66	62	hypothetical membrane protein	putative membrane protein [Staphylococcus phage GH15]	2,00E-36	
145	100,085..101,236	-	1152	42.05	3.83	383	hypothetical protein	putative membrane protein [Staphylococcus phage phiSA12]	0,00E+00	
146	101,329..101,808	-	480	18.53	4.53	159	hypothetical protein	ORF091 [Staphylococcus virus G1]	2,00E-110	
147	101,805..101,978	-	174	6.69	9.93	57	hypothetical membrane protein	hypothetical protein [Staphylococcus phage	2,00E-30	
148	101,965..102,765	-	801	29.87	5.03	266	hypothetical protein	hypothetical protein 812_087 [Staphylococcus phage 812]	0,00E+00	
149	102,779..104,596	-	1818	70.25	6.87	605	terminase large subunit	ORF010 [Staphylococcus virus G1]	0,00E+00	Terminase_GpA (PF05876) Phage terminase large subunit (GpA)
150	104,611..105,021	-	411	15.65	4.11	136	hypothetical protein	ORF133 [Staphylococcus virus G1]	2,00E-92	
151	105,018..105,296	-	279	10.58	10.23	92	hypothetical protein	ORF161 [Staphylococcus virus G1]	2,00E-61	
152	105,274..105,54	-	267	10.34	8.85	88	hypothetical protein	ORF168 [Staphylococcus virus G1]	7,00E-55	
0152A	105,801..106,067	+	267	10.12	9.71	88	hypothetical membrane protein	ORF169 [Staphylococcus virus G1]	7,00E-51	
153	106,1..106,426	+	327	13.08	5.67	108	hypothetical membrane protein	putative membrane protein [Staphylococcus phage GH15]	8,00E-72	
154	106,439..106,771	+	333	12.50	4.99	110	hypothetical protein	hypothetical protein [Staphylococcus phage	4,00E-70	
155	106,784..106,993	+	210	8.02	5.78	69	hypothetical protein	ORF207 [Staphylococcus virus G1]	4,00E-43	
156	107,484..107,702	+	219	8.68	9.38	72	Iro	ORF200 [Staphylococcus virus G1]	6,00E-46	
157	109,248..109,433	+	186	7.07	4.72	61	hypothetical protein	ORF233 [Staphylococcus virus G1]	2,00E-34	
158	109,518..110,021	+	504	18.10	3.85	167	holin	phage philc3 family protein [Staphylococcus phage JD007]	3,00E-117	Phage_holin_1 (PF04531) Bacteriophage holin

159	110,021..111,511	+	1491	54.74	10.08	496	endolysin	endolysin [Staphylococcus phage phiIPLA-RODI]	0,00E+00	SH3_5 (PF08460) Bacterial SH3 domain; CHAP (PF05257) CHAP domain; Amidase_2 (PF01510) N-acetylmuramoyl-L-alanine amidase
160	111,574..112,194	+	621	24.61	9.52	206	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	4,00E-146	
161	112,308..112,616	+	309	12.21	9.73	102	hypothetical membrane protein	hypothetical protein vBSauCG_215 [Staphylococcus phage vB_Sau_CG]	8,00E-55	
162	112,616..113,407	+	792	29.37	9.40	263	hypothetical membrane protein	ORF044 [Staphylococcus virus G1]	0,00E+00	Band_7 (PF01145) PFH domain / Band 7 family
163	113,474..114,109	+	636	24.83	9.439	211	hypothetical protein	ORF058 [Staphylococcus virus G1]	1,00E-152	
164	114,296..114,988	+	693	24.88	4.77	230	transglycosylase	putative transglycosylase [Staphylococcus phage phiSA12]	2,00E-166	
165	115,097..115,324	+	228	9.23	10.61	75	hypothetical protein	ORF190 [Staphylococcus virus G1]	1,00E-45	
166	115,327..115,557	+	231	8.83	9.79	76	transcriptional regulator	transcriptional regulator [Staphylococcus phage JD007]	2,00E-47	HTH_3 (PF01381) Helix-turn-helix
167	115,547..116,188	+	642	24.59	3.81	213	hypothetical protein	ORF057 [Staphylococcus virus G1]	2,00E-144	
168	116,211..116,402	+	192	7.47	5.79	63	hypothetical protein	ORF222 [Staphylococcus virus G1]	6,00E-38	
169	116,392..116,817	+	426	15.81	7.40	141	ribonuclease H	ORF096 [Staphylococcus virus G1]	2,00E-95	RNase_H (PF00075) Rnase H; RVT_3 (PF13456) - transcriptase-like
170	116,833..117,447	+	615	23.02	3.82	204	hypothetical protein	ORF063 [Staphylococcus virus G1]	4,00E-145	
171	117,499..118,239	+	741	28.59	4.93	246	PhoH-related protein	ORF049 [Staphylococcus virus G1]	0,00E+00	PhoH (PF02562) PhoH-like protein
172	118,308..118,532	+	225	8.17	9.10	74	hypothetical membrane protein	hypothetical protein [Staphylococcus phage	1,00E-40	
173	118,532..119,428	+	897	35.03	5.25	298	DNA ligase	DNA ligase [Staphylococcus phage JD007]	0,00E+00	RNA_ligase (PF09414) RNA ligase
174	119,421..120,014	+	594	22.26	4.56	197	nucleoside 2-deoxyribosyltransferase	hypothetical protein [Staphylococcus phage MCE-2014]	8,00E-144	
175	120,007..120,585	+	579	21.38	8.58	192	hypothetical membrane protein	hypothetical protein [Staphylococcus phage MCE-2014]	5,00E-131	
176	120,592..120,765	+	174	6.69	7.35	57	hypothetical protein	hypothetical protein [Staphylococcus phage JD007]	2,00E-32	LysM (PF01476) LysM domain

177	120,782..121,045	+	264	10.23	4.89	87	hypothetical protein	hypothetical protein P108_0172 [Staphylococcus phage P108]	3,00E-55	
178	121,124..123,172	+	2049	79.71	6.65	682	hypothetical protein	hypothetical protein phi_676Z_ORF036 [Staphylococcus phage 676Z]	0,00E+00	PcfJ (PF14284) PcfJ-like protein
179	123,172..123,333	+	162	6.37	4.35	53	hypothetical protein	ORF259 [Staphylococcus virus G1]	7,00E-30	
180	123,377..123,565	+	189	7.30	4.03	62	hypothetical protein	hypothetical protein phi_A3R_ORF034 [Staphylococcus phage A3R]	8,00E-35	
181	123,565..123,867	+	303	11.31	4.53	100	hypothetical protein	ORF149 [Staphylococcus virus G1]	7,00E-65	MazG (PF03819) MazG nucleotide pyrophosphohydrolase domain
182	124,001..124,417	+	417	15.98	4.84	138	hypothetical protein	ORF106 [Staphylococcus virus G1]	6,00E-96	DUF3310 (PF11753) Protein of unknwon function (DUF3310)
183	124,41..124,736	+	327	12.98	4.41	108	hypothetical protein	ORF134 [Staphylococcus virus G1]	3,00E-73	
184	124,888..126,006	+	1119	42.22	4.47	372	AAA family ATPase	ORF024 [Staphylococcus virus G1]	0,00E+00	AAA_5 (PF07728) AAA domain (dynein-related subfamily)
185	126,018..126,863	+	846	31.77	9.64	281	hypothetical protein	ORF038 [Staphylococcus virus G1]	0,00E+00	
186	126,863..127,138	+	276	10.86	4.68	91	hypothetical membrane protein	ORF163 [Staphylococcus virus G1]	9,00E-54	MFS_Mycoplasma (PF07672) Mycoplasma MFS transporter
187	127,141..127,305	+	165	6.26	10.22	54	hypothetical membrane protein	ORF256 [Staphylococcus virus G1]	2,00E-29	
188	127,308..127,841	+	534	20.81	4.11	177	hypothetical protein	ORF077 [Staphylococcus virus G1]	1,00E-122	
189	127,841..128,383	+	543	20.34	4.57	180	hypothetical protein	ORF072 [Staphylococcus virus G1]	3,00E-122	
190	128,433..128,915	+	483	18.84	4.26	160	hypothetical protein	ORF090 [Staphylococcus virus G1]	8,00E-111	
191	128,956..129,129	+	174	6.81	4.92	57	hypothetical protein	ORF245 [Staphylococcus virus G1]	8,00E-35	
192	129,228..129,617	+	390	15.15	4.63	129	hypothetical protein	ORF114 [Staphylococcus virus G1]	4,00E-89	
193	129,619..129,858	+	240	9.35	4.39	79	hypothetical protein	gpORF020 [Staphylococcus phage A5W]	3,00E-51	
0193A	129,87..129,974	+	105	4.11	4.45	34	hypothetical protein	ORF437 [Staphylococcus virus G1]	1,00E-14	
194	130,037..130,774	+	738	28.67	6.54	245	hypothetical protein	ORF050 [Staphylococcus virus G1]	3,00E-175	
195	130,764..130,958	+	195	7.64	4.32	64	hypothetical protein	ORF218 [Staphylococcus virus G1]	2,00E-38	
196	130,959..131,177	+	219	8.43	4.14	72	hypothetical protein	ORF201 [Staphylococcus virus G1]	9,00E-44	

197	131,181..131,729	+	549	21.95	4.18	182	hypothetical protein	ORF071 [Staphylococcus virus G1]	9,00E-125	
0197A	131,945..132,145	+	201	7.27	10.24	66	hypothetical protein	hypothetical protein qdsa002_45 [Staphylococcus phage qdsa002]	8,00E-41	
198	132,715..133,032	+	318	11.84	6.87	105	hypothetical protein	ORF138 [Staphylococcus virus G1]	6,00E-68	
199	133,048..133,602	+	555	21.22	4.29	184	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	9,00E-131	
200	133,702..134,409	+	708	27.63	4.85	235	serine/threonine protein phosphatase	phosphatase [Staphylococcus phage phiIPLA-RODI]	5,00E-172	Metallophos (PF00149) Calcineurin-like phosphoesterase; Metallophos_2 (PF12850) Calcineurin-like phosphoesterase superfamily domain
201	134,406..134,804	+	399	16.11	9.35	132	hypothetical protein	hypothetical protein [Staphylococcus phage S25-	7,00E-89	
202	134,817..135,305	+	489	19.53	10.07	162	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	2,00E-117	DUF1768 (PF08719) Domain of unknown function (DUF1768)
203	135,317..135,859	+	543	21.56	9.85	180	nucleotidyl transferase	nucleotidyl transferase [Staphylococcus phage phiIPLA-RODI]	1,00E-125	
204	135,873..136,304	+	432	16.75	3.93	143	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	1,00E-98	
205	136,297..136,782	+	486	18.36	9.85	161	hypothetical membrane protein	membrane protein [Staphylococcus phage phiIPLA-RODI]	3,00E-109	
0205A	136,779..136,97	+	192	7.88	10.37	63	hypothetical membrane protein	hypothetical protein [Staphylococcus phage	7,00E-37	
206	136,973..137,404	+	432	17.25	4.23	143	UboA	UboA [Staphylococcus phage phiIPLA-RODI]	6,00E-96	
207	137,404..137,811	+	408	16.47	5.03	135	hypothetical protein	ORF109 [Staphylococcus virus G1]	3,00E-94	
208	137,824..138,309	+	486	19.12	5.51	161	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	2,00E-108	
209	138,311..138,547	+	237	9.56	4.52	78	BofL	hypothetical protein CPT_phageK_gp022 [Staphylococcus virus K]	5,00E-50	
210	138,651..138,941	+	291	11.60	4.23	96	hypothetical protein	hypothetical protein [Staphylococcus phage phiIPLA-RODI]	5,00E-64	
0210A	139,094..139,195	-	102	3.82	8.91	33	hypothetical protein	ORF450 [Staphylococcus virus G1]	6,00E-14	
211	139,269..139,49	-	222	8.70	4.56	73	TreU	hypothetical protein CPT_phageK_gp021 [Staphylococcus virus K]	7,00E-43	

212	139,575..139,844	-	270	10.24	6.80	89	TreT	ORF166 [Staphylococcus virus G1]	4,00E-57
213	139,844..140,017	-	174	6.66	4.69	57	TreS	ORF234 [Staphylococcus virus G1]	5,00E-31
214	140,076..140,546	-	471	17.92	3.52	156	hypothetical protein	ORF092 [Staphylococcus virus G1]	6,00E-104
215	140,626..140,862	-	237	9.08	3.98	78	hypothetical protein	hypothetical protein CPT_phageK_gp017 [Staphylococcus virus K]	5,00E-47
216	140,953..141,117	-	165	6.38	4.39	54	hypothetical protein	hypothetical protein [Staphylococcus phage	2,00E-28
217	141,188..141,325	-	138	5.45	4.13	45	hypothetical protein	hypothetical protein [Staphylococcus phage	8,00E-25
218	141,406..141,627	-	222	8.47	3.91	73	hypothetical protein	hypothetical protein GH15_008 [Staphylococcus phage GH15]	1,00E-45
219	142,122..142,523	-	402	15.48	4.18	133	hypothetical protein	hypothetical protein [Staphylococcus phage MCE-2014]	5,00E-92
220	142,623..142,946	-	324	12.44	4.90	107	TreP	hypothetical protein CPT_phageK_gp016 [Staphylococcus virus K]	1,00E-69
221	143,114..143,245	-	132	5.15	10.67	43	TreO	ORF297 [Staphylococcus virus G1]	2,00E-21

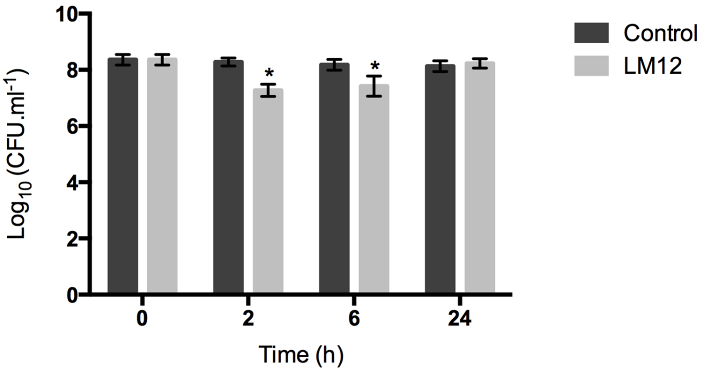

Figure S1: *Phage LM12 infection on 24 h S. aureus biofilms, using a MOI 1.* Data was assessed by colony forming units (CFU) counting and the values represent the mean plus and minus of three independent experiments performed in duplicate. Statistical differences ($p < 0.01$) between control biofilms and LM12-treated biofilms (*) were determined by two-way repeated-measures analysis of variance (ANOVA) with Sidak post test.

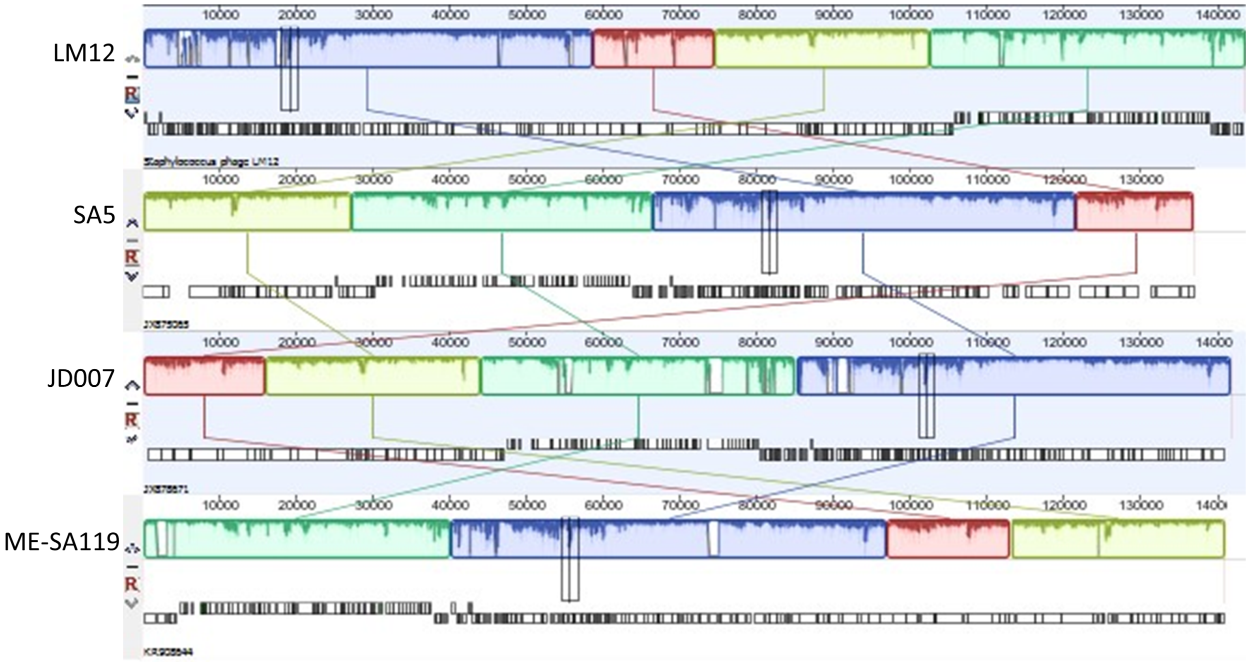

Figure S2*: Multiple genome alignment of Staphylococcus phage LM12 with closest homologs.* The figure was performed using Geneious 9.1.4.