SUPPLEMENTAL MATERIAL

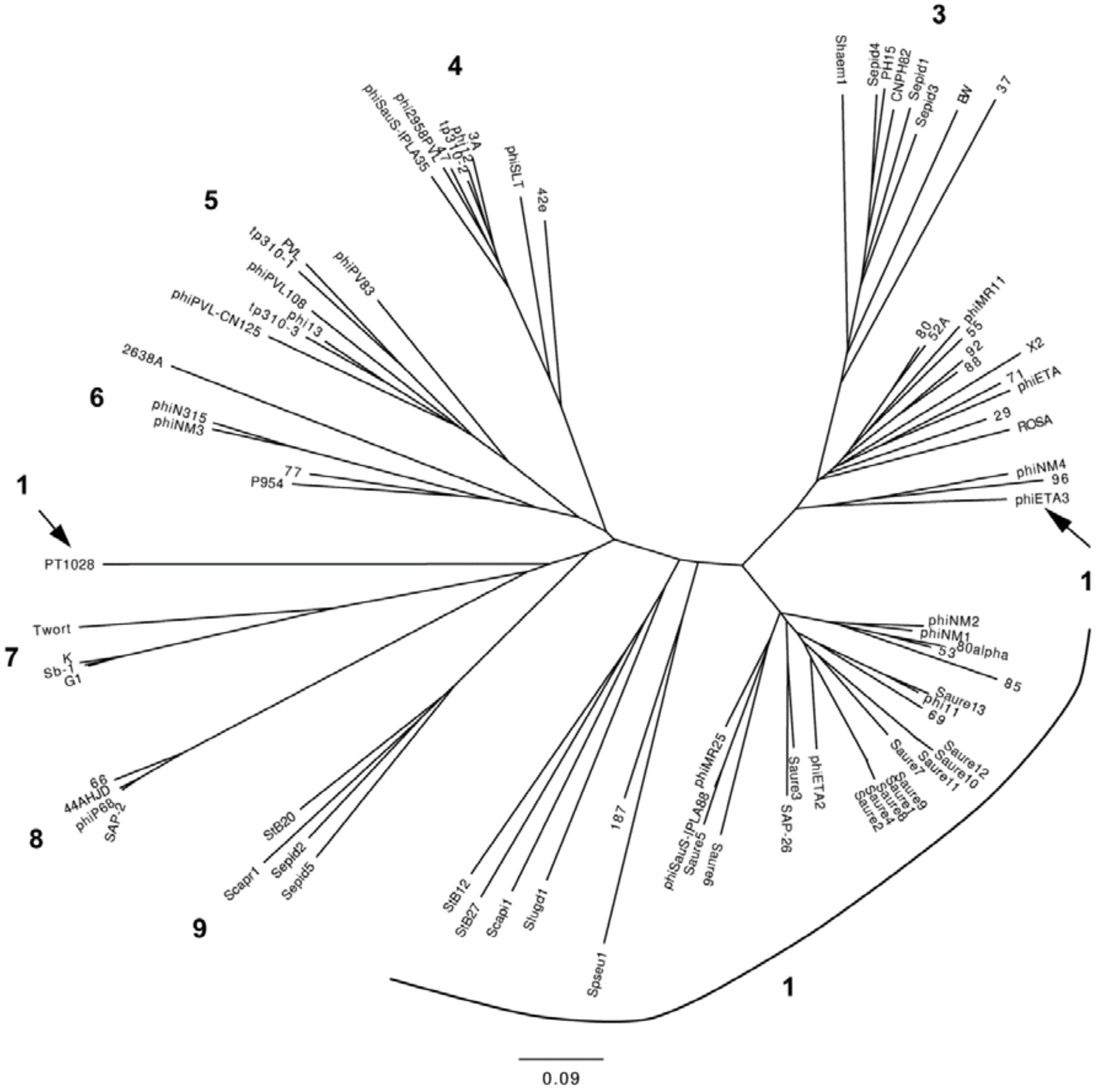

Figure S1: Neighbor Joinning tree of the 85 staphylococcal phages and prophages based on the protein content. Numbers refer to the different clusters defined by the clustering method (Figure 6). Globally, both classifications are similar, except for the *S. aureus* phages phiETA3 and PT1028, which were found included in cluster 1 in figure 6. The main characteristics of the phages and prophages included in the analysis are given in Data set 1.

Table S1: Primer sequences used for the determination of StB12, StB27 and StB20 integration sites in *S. hominis* T0C2HA1, T0C6HA2 and *S. capitis* R104 genomes, respectively

Primer	Sequence
HominisLocus1[1, 2]	TAACAAGTGATATTACACACGCAGGAG
StB12Int1[1]	GCTGAATTTATTCAAATGGCAATTAAG
StB12G61_1[1]	GGACTTCTAGCAAAATTATTTATTTAACC
HominisLocus2[1,2]	ATCTTTATTATTCCATGCTTCACGCCC
StB27Int1[2]	ATCGAATATGTATTAGGTAAGAACGAC
StB27Lys1[2]	GGAATAAGACAAATATCACCTACCCACAAGG
CapitisLocus1[3]	GAAGTATTCATTCCAAAACATTACATTACG
StB20Int2[3]	AAGATGGCCATTAAGTCTATCGAC
StB20Lys1[3]	AATACAGATAGTTTAGGTAAGTTGTGG
CapitisLocus2[3]	ACTTTAACATCTGATTTACCTAATTG

[1] primers used for StB12 integration site determination
[2] primers used for StB27 integration site determination
[3] primers used for StB20 integration site determination

Table S2: Genome annotation of StB12

ORF	Strand	Start..end	Size		Predicted function	NCBI best match (extent , % aa identity, total length aa)	Domain	Prot family Func Annot MgeId, MgeName, Hosts
			aa	**kDa**				
1	-	30..1415	461	54,8	integrase/serine site - specific recombinase	YP_254311, putative site-specific recombinase, *S. haemolyticus* JCSC1435 (347/461, 76%, 461)	PF00239: resolvase, N-terminal domain; PF07508: recombinase	family:vir_proph:25 no functions assigned mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
2	-	1462..2100	212	24,5	phage repressor	YP_873953, phage repressor protein, *Staphylococcus* phage phiNM (163/212, 77%, 212)	PF01381: HTH_3, Cro and CI family; PF00717:peptidase S24	family:vir_proph:2588 phi:0000044 - transcriptional-regulation of phage gene expression mge:2513, prophinder:44868, *S. aureus* subsp. *aureus* Newman
3	+	2292.2546	84	9,99	phage repressor	ZP_06930668.1, Gp5, *S. aureus* A8796 (50/81, 62%, 84)	PF01381: HTH_3, Cro and CI family	family:vir_proph:10057 no functions assigned mge:1662, phiNM, *S. aureus*
4	+	2686..3414	242	27,8		YP_004708098.1 hypothetical protein CXIVA_10290, *Clostridium* sp. SY8519 (36/102, 35%, 336) YP_302022.1, hypothetical protein SSP1932, *S. saprophyticus* subsp. *saprophyticus* ATCC 15305 (39/94,41%,86)	PF02195: ParBc, ParB like nuclease domain	family:vir_proph:595 go:0009008 - DNA-methyltransferase activity mge:2764, prophinder:46415, *Magnetococcus* sp. MC-1
5	+	3429..3647	72	8,2		no hits found		no hits found
6	+	3647..4411	255	29,1		YP_240190.1, ORF017, *Staphylococcus* phage EW (83/246, 34%, 256)	PF02195: ParBc, ParB like nuclease domain	family:vir_proph:2058 no functions assigned mge:1642, EW, *S. aureus*
7	+	4478..4555	25	2,9		no hits found		no hits found
8	-	5009..4548	154	17,8		ZP_07361801.1, conserved HP, *S. aureus* ATCC BAA-39 (51/147, 35%, 164)		family:vir_proph:1226 no functions assigned mge:2655, prophinder:43224, *Streptococcus pyogenes* MGAS6180
9	+	5066..5194	43	5,4		no hits found		no hits found
10	+	5172..5357	61	6,8		YP_253711.1, HP SH1796, *S. haemolyticus* JCSC1435 (23/56, 42%, 56)		family:vir_proph:6545 no functions assigned mge:2148,

								prophinder:46504, *S. haemolyticus* JCSC1435
11	+	5442..5642	66	7,5		YP_253710.1 ,HP SH1795, *S. haemolyticus* JCSC1435 (45/59, 77%, 91)		family:vir_proph:6544 no functions assigned mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
12	+	5690..6175	161	18,4		YP_003472493.1, HP SLGD_02278, *S. lugdunensis* HKU09-01 (142/161, 89%, 161)	PF05565: Sipho _Gp157	family:vir_proph:87 phi:0000326 - phage function unknown mge:2683, prophinder:43517,*Bacillus cereus* E33L
13	+	6176..6838	220	25,5	recombination protein, ERF-like recombinase*	YP_002633573.1, HP Sca_0474, *S. carnosus* (170/216, 79%, 223)	PF04404: ERF superfamily, DNA single-strand annealing proteins	family:vir_proph:1389 phi:0000326 - phage function unknown, 580 - ERF-like recombinase mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
14	+	6852..7271	139	15,6	recombination protein, DNA single-strand binding protein	ZP_06612891.1, single-strand binding protein, *S. epidermidis* M23864:W2(grey) (85/140, 61%, 140)	PF00436: SSB, single-strand binding protein family	family:vir_proph:30 go:000369 - single-stranded DNA binding mge:1679, PH15, *S. epidermidis*
15	+	7283..7588	101	11,6		no hits found		no hits found
16	+	7589..8266	225	26,0		YP_240873.1, ORF1, *Staphylococcus* phage X2 (178/222, 81%, 224)	PF06147: DUF968, unknown function	family:vir_proph:66 phi:0000326 - phage function unknown mge:2643, prophinder:45329, *S. aureus* subsp. *aureus* Mu3
17	+	8259..9053	264	31,0	replication initiation protein	YP_185233.1, HP SCOL0341, *S. aureus* subsp. *aureus* COL (154/216, 72%, 266)	PF09681: N-terminal phage replisome organiser	family:vir_proph:10 phi0000026 - phage DNA replication; go:0006270 - DNA replication initiation; go :0003677-DNA binding mge:2122, prophinder:45229, *S. aureus* subsp. *aureus* COL
18	+	9059..9415	118	14,2		ZP_06612896.1, conserved HP, *S.*		family:vir_proph:738

						epidermidis M23864:W2 (grey)(58/117, 50%, 117)		phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
19	+	9402..10649	416	47,7	helicase	YP_950645.1, putative DNA helicase, *Staphylococcal* phage CNPH82 (282/416, 68%, 416)	PF03796: DnaBC, DnaB like helicase C- term domain	family:vir_proph:24 phi:0000026 - phage DNA replication, go:0004386 - helicase activity mge:1571, CNPH82, *S. epidermidis*
20	+	10649..10831	60	7,2		YP_950714.1, HP ph52, *Staphylococcus* phage PH15 (22/47, 47%, 73)		family :vir_proph :737 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
21	+	10847..11071	74	8,8		YP_254291.1, HP SH2376, *S. haemolyticus* JCSC1435 (65/74, 88%)	PF11673: DUF3269, unknown function	family:vir_proph:185 phi:0000326 - phage function unknown mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
22	+	11082..11408	108	12,1		ZP_04679045.1, gp51, *S. warneri* L37603 (50/98, 52%, 103)	PF08774: VRR_NUC, restriction endonuclease-like domain	family:vir_proph:234 phi:0000326 - phage function unknown mge:1850, B025, *Listeria monocytogenes*
23	+	11395..11769	124	14,6		YP_254286, HP SH2371, *S. haemolyticus* JCSC1435 (71/131, 55%, 132)		family:vir_proph:29 phi:0000013 - phage release by lysis mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
24	+	11769..11951	60	6,8		YP_024543.1, ORF115, staphylococcal phage K (13/33, 40%, 117)		no hits found
25	+	11956..12159	67	8,0		YP_003472483.1, HP SLGD_02268, *S. lugdunensis* HKI09-01 (35/46, 77%, 104)		no hits found
26	+	12156..12617	154	18,0		YP_240214.1, ORF46, *Staphylococcus* phage EW (63/70, 90%, 102)	PF11753: DUF3310, unknown function	family:vir_proph:61 phi:0000326 - phage function unknown mge:1642, EW, *S. aureus*
27	+	12610..12912	100	12,1		YP_189126.1, HP SERP1561, *S. epidermidis* RP62A (53/92, 58%, 94)		family:vir_proph:7031 no functions assigned

								mge:2262 - prophinder:43410 *S. epidermidis* RP62A
28	+	12915..13628	238	28,4		ZP_04797554.1S, conserved HP, *S. epidermidis* W23144 (116/230, 51%, 243)	PF13392: HNH_3, HNH endonuclease	family:vir_proph:5009 no functions assigned MGE: mge:1571, CNPH82 *S. epidermidis*
29	+	13628..13813	61	7,1		ZP_04824904.1, conserved HP, *S. epidermidis* BCM-HMP0060(51/60, 85%, 65)		family:vir_proph:3305 no functions assigned mge:1571, CNPH82 *S. epidermidis*
30	+	13810..14217	135	15,7		YP_240139.1, ORF27 *Staphylococcus* phage 37(70/151, 47%, 154)	PF09643: YopX protein	family:vir_proph:29 phi:0000013- phage release by lysis mge:1602, 37, *S. aureus*
31	+	14218..14562	114	13,2	nuclease	ZP_04824908.1, nuclease, *S. epidermidis* BCM-HMP0060 (98/114, 86%, 114)	PF00565: staphylococcal nuclease homologue	family:vir_proph:158 go:0004530 - deoxyribonuclease I activity mge:1571, CNPH82, *S. epidermidis*
32	+	14567..14869	100	11,8		ZP_04824909.1, conserved HP, *S. epidermidis* BCM-HMP0060 (37/48, 78%, 50)		family:vir_proph:153 phi:0000326 - phage function unknown mge:2642, prophinder:45328, *S. aureus* subsp. *aureus* Mu3
33	+	14862..15107	81	9,4		no hits found		no hits found
34	+	15108..15653	181	20,9	dUTPase	ZP_05690702.1, conserved HP, *S aureus* A8115 (118/187, 64%, 179)	PF08761: dUTPase 2	family:vir_proph:144 phi:0000326 - phage function unknown mge:1607, 69, *S. aureus*
35	+	15693..15896	67	8,1		YP_253700.1 , HP SH1785, *S. haemolyticus* JCSC1435 (31/38, 82%, 74)	PF07129: DUF1381, unknown function	family:vir_proph:99 phi:0000326 - phage function unknown mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
36	+	15909..16187	92	10,4		no hits found		no hits found
37	+	16180..16347	55	6,5	RinB	YP_254279.1, HP SH2364, *S. haemolyticus* JCSC1435 (41/54, 76%, 52)	PF06116:transcriptional activator RinB	family:vir_proph:83 go:0016563 - transcription

								activator activity, phi:0000007 - phage lysogeny, phi:0000049 - positive transcriptional regulation of phage gene expression mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
38	+	16347..16790	147	17,4		ZP_06614644.1, conserved HP, *S. epidermidis* M23864:W2 (grey) (66/145, 46%, 140)		family:vir_proph:1192 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
39	+	16787..16864	25	3,0		no hits found		no hits found
40	+	16915..17316	133	15,6		NP_510932.1,ORF38, *Staphylococcus* phage phiETA (98/133, 74%, 133)		family:vir_proph:325 phi:0000326 - phage function unknown mge:1475, 55, *S. aureus*
41	+	17313..17528	71	8,5		no hits found		no hits found
42	+	17547..18038	164	18,6	TerS	YP_240669.1, orf28, *Staphylococcus* phage 88 (129/159,82%, 162)	PF03592: terminase 2,terminase small subunit	family:vir_proph:45 phi:0000074 - phage terminase small subunit, phi:0000019 - phage DNA maturation, go:0003677 - DNA binding (by ariane) mge:1676, 92, *S. aureus*
43	+	18022..19323	434	50,8	TerL	YP_417188.1, terminase large subunit, *S. aureus* RF122 (338/425,80% ,429)	PF04466: terminase 3,terminase large subunit	family:vir_proph:15 phi:0000019 - phage DNA maturation phi:0000073 - phage terminase large subunit mge:2670, prophinder:45952, *S. aureus* RF122
44	+	19340..20818	492	57,7	portal protein, SPP1 family*	ZP_03614346.1, phage portal protein, SPP1 family, *S. capitis* SK14 (431/473, 92%, 498)		family:vir_proph:52 phi:0000012 - phage head tail joining, phi:0000068 - phage portal protein (by ariane) mge:1662, phiNM, *S. aureus*

45	+	20815..22317	501	58,5	minor head protein*	ZP_3614353.1, phage head morphogenesis protein, SPP1 family, *S. capitis* SK14 (137/314, 44%, 316)	PF04233 :Phage Mu F, putative minor head protein	family:vir_proph:50 phi:0000185 - phage head/capsid minor protein mge:1557, 187, *S. aureus*
46	+	22321..22473	50	5,8		YP_001850461.1, HP, *S. capitis* SK14 (25/43, 59%, 181)		no hits found
47	+	22466..22615	49	5,7		ZP_3614379, HP STACA0001_2036, *S. capitis* SK14 (25/39, 65%, 47)		no hits found
48	+	22860..23381	174	20,3	scaffold protein	ZP_03614352.1, putative scaffold protein, *S. capitis* SK14 (80/166,49%, 204)		family:vir_proph:103 phi:0000017 - phage prohead/capsid assembly, phi:0000065 - phage scaffolding protein mge:1510, phiJL-1, *Lactobacillus plantarum*
49	+	23486..24463	326	36,9	major head protein*	YP_873992.1, head protein, *Staphylococcus* phage phiNM (222/322, 69%, 324)	PF05065: phage capsid family	family:vir_proph:110 phi:0000066 - phage head/capsid major protein mge:2670, prophinder:45952, *S. aureus* RF122
50	+	24489..24758	89	10,2		ZP_03614372.1, conserved HP, *S. capitis* SK14 (78/89, 88%, 89)		family:vir_proph:107 phi:0000326 - phage function unknown mge:2430, prophinder:45292, *S. aureus* subsp. *aureus* JH1
51	+	24760..25086	109	12,5	DNA packaging, minor head protein	ZP_03614383.1, conserved HP, *S. capitis* SK14 (100/109, 92%, 109)	PF05135: phage QLRG family, putative DNA packaging	family:vir_proph:160 phi:0000186 - minor capsid structural protein mge:2670, prophinder:45952, *S.aureus* RF122
52	+	25086..25388	100	11,8	minor head protein	ZP_03614351.1, conserved HP, *S. capitis* SK14 (88/93, 95%, 93)		family:vir_proph:277 phi:0000186 - minor capsid structural protein mge:1662, phiNM, *S.aureus*
53	+	25388..25753	121	14,0		ZP_03614378.1, HK97 gp10 family, *S. capitis* SK14 (75/113, 67%, 119)	PF04883 : DUF646, possible tail component	family:vir_proph:76 phi:0000326 - phage function unknown mge:2643, prophinder:45329, *S.aureus*

								subsp. *aureus* Mu3
54	+	25754..26143	129	14,8	head structural protein	ZP_03614357.1, HP, *S. capitis* SK14 (98/129, 76%, 129)		family:vir_proph:215 phi:0000173 - major capsid structural protein mge:2670, prophinder:45952, *S. aureus* RF122
55	+	26190..26735	181	20,3	major tail protein*	ZP_03614344.1, phage major tail protein, *S. capitis* SK14 (150/180, 84%,184)	PF06199 : phage tail2	family:vir_proph:196 phi:0000082 - phage major tail protein mge:1557, 187, *S. aureus*
56	+	26801..27166	121	13,6	tail assembly protein	YP_003472460.1, HP, *S. lugdunensis* HKU09-01 (66/111, 60%, 121)	PF12363 : phage protein	family:vir_proph:209 phi:0000015 - phage tail assembly mge:1613, 53, *S. aureus*
57	+	27208..27555	115	13,6		ZP_03614371.1, conserved HP, *S. capitis* SK14 (82/113, 72%, 114)		family:vir_proph:210 phi:0000326 - phage function unknown mge:1607, 69, *S. aureus*
58	+	27568..31065	1165	86,6	tail tape measure protein	ZP_0361436.01, phage tail tape measure protein, *S. capitis* SK14 (509/774, 66%, 1320)	PF01576: myosine tail contractile prot/SMC_prokA/COG5412 (phage related protein, unknown function)	family:vir_proph:1 phi:0000086 - phage tail tape measure protein mge:2149, prophinder : 46506, *S. haemolyticus* JCSC1435
59	+	31078..32034	318	37,3	minor tail protein*	ZP_03614373.1,conserved HP, *S. capitis* SK14 (215/317, 68%, 318)	PF05709: sipho tail, phage tail protein	family:vir_proph:190 phi:0000178 - phage minor tail protein mge:1654, 85, *S. aureus*
60	+	32044..33291	416	47,0	tail protein, endopeptidase*	ZP_03614382.1, conserved phage protein, *S. capitis* SK14 (221/378, 59%, 486)	PF06605.6: prophage endopeptidase tail	family:vir_proph:35 phi:0000178 - phage minor tail protein, go:0016298-lipase activity mge:2430, prophinder:45258, *S. aureus* subsp. *aureus* JH1
61	+	33305..35239	645	74,2	tail protein, Zn carboxypeptidase*	ZP_03614336.1, zinc carboxypeptidase family, *S capitis* SK14 (428/601, 72%, 628)	PF00246: peptidase_M14, Zn carboxypeptidase	family:vir_proph:458 phi:0000178 - phage minor tail protein mge:1602, 37, *S. aureus*
62	+	35427..36384	318	36,0	tail protein, likely tail fiber*	ZP_03614350.1, conserved HP, *S. capitis* SK14 (171/307, 56%, 395)	PF10651: DUF2479, unknown function	family:vir_proph:69 phi:0000178 - phage minor

								tail protein mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
63	+	36405..36896	163	18,4	holin	YP_0025600381.1, holin, *Macrococcus caseolyticus* JCSC5402 (82/152, 54%, 170)	PF05105: phage holin 4	family:vir_proph:42 phi:0000088 - phage base plate protein, go:0034290- holin activity mge:1669, 66, *S. aureus*
64	+	36946..37065	39	4,2	peptidoglycan hydrolase, tail associated protein*	ZP_03614366.1, mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase, *S. capitis* SK14		family:vir_proph:6 phi:0000013 - phage release by lysis, phi:0000340- phage cell wall amidase activity mge:1602, 37, *S. aureus*
65	+	37304..37543	79	9,1	peptidoglycan hydrolase, tail associated protein*	ZP_03614366.1, mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase, *S. capitis* SK14	PF05257: CHAP domain	family:vir_proph:6 phi:0000013 - phage release by lysis, phi:0000340- phage cell wall amidase activity mge:2670, prophinder:45952, *S. aureus* RF122
66	+	37916..39436	506	57,2	peptidoglycan hydrolase, tail associated protein*	ZP_03614366.1, mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase, *S. capitis* SK14 (288/501, 58%, 626)	PF01832: glucosaminidase	family:vir_proph:6 phi:0000013 - phage release by lysis, phi:0000340- phage cell wall amidase activity mge:1613, 53, *S. aureus*
67	+	39489..40533	348	38,4	tail protein, likely tail fiber*	ZP_06612939.1, tail fiber protein, *S epidermidis* M23864:W2(grey) (160/396, 41%, 384)	PF10651: DUF2479, unknown function; PF01391: collagen triple helix repeat	family:vir_proph:199 phi:0000178 - phage minor tail protein mge:1571, CNPH82, *S. epidermidis*
68	+	40549..40893	114	13,2		ZP_06614673.1, conserved HP, *S epidermidis* M23864:W2(grey) (86/114, 76%, 114)		family:vir_proph:1391 phi:0000326 - phage function unknown mge:1571, CNPH82 *S. epidermidis*
69	+	40886..41029	47	5,8		ZP_06614674.1,conserved HP, *S. epidermidis* M23864:W2(grey) (37/42, 89%, 48)	PF09693: phage XkdX uncharacterized protein	family:vir_proph:1045 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
70	+	41088..41708	206	23,3		ZP_06612936.1,conserved HP, *S.*	PF05908: DUF867,	family:vir_proph:1435

						epidermidis M23864:W2(grey) (106/203, 53%, 211)	unknown function	phi:0000326 - phage function unknown mge:125, SPP1, *Bacillus subtilis*
71	+	41762..42056	97	10,9	holin	YP_415770.1, phage related holin, *S. aureus* RF122 (68/95, 72%, 100)	PF04688: phage holin	family:vir_proph:23 phi:0000013 - phage release by lysis, go:0034290 - holin activity mge:2669, prophinder:45944, *S. aureus* RF122
72	+	42066..43518	483	54,4	lysin	YP_040898.1, amidase, *S. aureus* MRSA252 (338/485, 70%, 484)	PF05257: CHAP domain; PF01520: amidase_3 domain, N-acetylmuramoyl-L-alanine amidase; PF08460:SH3 domain	family:vir_proph:6 phi:0000013 - phage release by lysis, phi:0000340 - phage cell wall amidase activity mge:2273, prophinder:43713, *S. aureus* subsp. *aureus* MRSA252
73	+	43788..44190	133	15,3		YP_239892, ORF031, *Staphylococcus* phage 42E (44/137, 33%, 141)		family:vir_proph:3349 no functions assigned mge:1643, 42e, *S. aureus*
74	+	44192..44597	134	15,8		ZP_04824950, HP, *S. epidermidis* BCM-HMP0060 (31/83, 38%, 111)		family:vir_proph:3348 no functions assigned mge:1588,71, *S. aureus*

*Proteins identified in proteomic analysis

Table S3: Genome annotation of StB27

ORF	Strand	Start..end	Size		Predicted function	NCBI best match (extent , % aa identity, total length aa)	Domain	Prot family Func Annot MgeId, MgeName, Hosts
			aa	kDa				
1	-	30..1415	461	54,8	integrase	YP_254311.1, putative site-specific recombinase, *S. haemolyticus* JCSC1435 (346/461, 75%, 461)	PF00239: Resolvase; PF07508: Recombinase	family:vir_proph:25 phi:0000330 - site-specific DNA inversion; phi:0000056 - prophage DNA integration; phi:0000144 - serine-based site-specific recombinase activity mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
2	-	1610..2353	281	29,1		YP_001247418.1, hypothetical protein SaurJH9_2059, *S. aureus* subsp. *aureus* JH9 (118/232, 51%, 245)	PF02452: PemK	family:vir_proph:449 phi:0000326 - phage function unknown mge:2334, prophinder:45294, *S. aureus* subsp. aureus JH9
3	-	2476..3558	360	39,1	*	YP_240704.1, ORF012, *Staphylococcus* phage 88 (124/218, 57%, 309)		family:vir_proph:227 phi:0000326 - phage function unknown mge:1508, 88, *S. aureus*
4	-	3581..4039	152	17,8		YP_002633564.1, hypothetical protein Sca_0465, *S. carnosus* subsp. *carnosus* TM300 (83/150, 55%, 154)	DUF955 : domain of unknown function (HEXXH domain)	family:vir_proph:149 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
5	-	4044..4316	104	12,3	transcriptional regulator	NP_371375.1, hypothetical protein SAV0851, *S. aureus* subsp. *aureus* Mu50 (49/65, 75%, 109)	PF01381:HTH3, Cro and CI family	family:vir_proph:12 phi:0000057 - maintenance of prophage immunity; go:0016564 - transcription repressor activity mge:2493, prophinder:43758, *S. aureus* subsp. *aureus* MSSA476
6	+	4537..4728	66	7,1	transcriptional regulator	YP_043025.1, putative phage regulatory protein, *S. aureus* subsp. *aureus* MSSA476 (43/63, 65%, 66)	PF01381:HTH3, Cro and CI family	family:vir_proph:749 go:0016564 - transcription repressor activity mge:2684, prophinder:45205, *S. aureus* subsp. *aureus* USA300
7	+	4780..5499	239	27,7	transcriptional regulator	YP_240864.1, ORF016, *Staphylococcus* phage X2 (158/237, 67%, 235)	PF02498: Bro-N, Bro family, N-terminal domain; PF10552: ORF6C domain	family:vir_proph:3 go:0016564 - transcription repressor activity mge:1549, X2, *S. aureus*
8	+	5500..5631	43	5,4		no hits found		no hits found

9	+	5621..5839	72	8,7		no hits found		no hits found
10	+	5852..6022	56	6,3		YP_253711.1, hypothetical protein SH1796, *S. haemolyticus* JCSC1435 (23/56, 41%, 56)		family:vir_proph:6545 no functions assigned mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
11	+	6025..6312	95	11,4	transcriptional regulator	ZP_01795715.1, hypothetical protein CGSHiII_00287, *Haemophilus influenzae* PittII (83/95, 87%, 95)	PF01381: HTH3, Cro and CI family	family:vir_proph:4463 no functions assigned mge:2670, prophinder:45952, *S. aureus* RF122
12	+	6395..6625	76	9,1		ZP_07841349.1, conserved hypothetical protein, *S. caprae* C87 (58/68, 85%, 70)		family:vir_proph:6544 no functions assigned mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
13	+	6625..8574	649	75,1	recombination protein, exonuclease*	ZP_06336108.1, conserved hypothetical protein, *S. aureus* A9765 (439/647, 68%, 647)		family:vir_proph:108 phi:0000129 - DNA recombination; go:0004530 - deoxyribonuclease I activity mge:2274, prophinder:43714, *S. aureus* subsp. *aureus* MRSA252
14	+	8608..9498	296	33,7	recombination protein, DNA single-strand binding protein*	CBI49855.1, RecT family phage protein, *S. aureus* subsp. *aureus* TW20 (244/296, 82%, 306)	PF03837 : RecT family, DNA single-strand annealing proteins	family:vir_proph:71 go:0000739 - DNA strand annealing activity; phi:0000130 - homologous DNA recombination; RedB-like recombinase mge:2256, prophinder:42793, *S. aureus* subsp. *aureus* N315
15	+	9710..10201	163	18,5		NP_646739.1, hypothetical protein MW1922, *S. aureus* subsp. *aureus* MW2 (129/160, 81%, 161)		family:vir_proph:347 phi:0000326 - phage function unknown mge:2144, prophinder:45312, *S. aureus* subsp. *aureus* MW2
16	+	10198..10791	197	22,6		YP_001429787.1, hypothetical protein 0305phi8-36p061, *Bacillus* phage 0305phi8-36 (24/75, 32%, 248)		family:vir_proph:1076 phi:0000326 - phage function unknown mge:1892, *Geobacillus* virus E2, *Geobacillus*
17	+	10803..11267	154	17,2	DNA single-strand binding protein	ZP_06930763.1 single-stranded DNA-binding protein, *S. aureus* A8796 (114/158, 72%, 156)	PF00436 : SSB	family:vir_proph:30 go:0003697 - single-stranded DNA binding mge:2274, prophinder:43714, *S. aureus* subsp. *aureus* MRSA252
18	+	11282..11485	67	7,7		YP_240206.1, ORF084 , *Staphylococcus* phage EW (38/65, 58%, 68)	PF01381: HTH3	family:vir_proph:1191 phi:0000044 - transcriptional-regulation of phage gene expression mge:1642, EW, *S. aureus*

19	+	11482..11679	65	7,5	transcriptional regulator	ZP_06612894.1, DNA-binding protein, *S. epidermidis* M23864:W2(grey) (39/64, 61%, 73)	PF01381:HTH3	family:vir_proph:1191 phi:0000044 - transcriptional-regulation of phage gene expression mge:1642, EW, *S. aureus*
20	+	11714..12601	295	35,5	DNA replication protein	YP_002560316.1, hypothetical protein MCCL_0913, *Macrococcus caseolyticus* JCSC5402 (174/297, 59%,296)	PF07261: DnaB2	family:vir_proph:10 go:0006270 - DNA replication initiation; phi:0000026 - phage DNA replication; go:0003677 - DNA binding mge:2144, prophinder:45312, *S. aureus* subsp. *aureus* MW2
21	+	12594..12818	74	8,2		no hits found		no hits found
22	+	12964..13209	81	9,4		AAC28960.2, orf10 pathogenicity island protein, *S. aureus*, (36/71, 51%, 97)		family:vir_proph:6426 no functions assigned mge:2121, prophinder:45224, *S. aureus* subsp. *aureus* COL
23	+	13206..13493	95	10,7		no hits found		no hits found
24	+	13486..13653	55	6,3	RinB	YP_240450.1, ORF144 , *Staphylococcus* phage 71 (35/50, 70%, 57)	PF06116 : RinB	family:vir_proph:83 phi:0000049 - positive transcriptional regulation of phage gene expression mge:1588, 71, *S. aureus*
25	+	13650..14096	148	17,5		ZP_06614644.1, conserved hypothetical protein, *S. epidermidis* M23864:W2(grey) (68/145, 47%, 140)		family:vir_proph:1192 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
26	+	14167..14664	165	19,1	Holliday junction-specific endonuclease RecU	BAH18242.1, conserved hypothetical protein, *M. caseolyticus* JCSC5402 (72/160, 45%, 170)	PF03838: RecU	family:vir_proph:1313 go:0008821 - crossover junction endodeoxyribonuclease activity mge:1567, GBSV1, *Geobacillus* sp. 6k51
27	+	14664..15071	135	16,3		YP_240149.1 ORF044, *Staphylococcus* phage 37 (70/134, 52%, 134)		family:vir_proph:1230 phi:0000326 - phage function unknown mge:1602, 37, *S. aureus*
28	+	15331..15792	153	17,8		no hits found		no hits found
29	+	15903..16328	141	16	TerS	ZP_07844472.1, prophage LambdaCh01, terminase, small subunit, *S. hominis* subsp. *hominis* C80 (95/139,68%,142)	PF03592:Terminase2, terminase small subunit	family:vir_proph:45 phi:0000074 - phage terminase small subunit; phi:0000019 - phage DNA maturation; go:0003677 - DNA binding mge:2655, prophinder:43224,

								Streptococcus pyogenes MGAS6180
30	+	16482..17621	379	44,3	TerL	YP_004148742.1, Phage terminase, large subunit, *S. pseudintermedius* HKU10-03 (318/376, 85%, 424)	PF04466 : Terminase3	family:vir_proph:15 phi:0000019 - phage DNA maturation; phi:0000073 - phage terminase large subunit mge:2670, prophinder:45952, *S. aureus* RF122
31	+	17622..19073	483	55,8	portal protein*	YP_004148743.1, Phage portal protein, *S. pseudintermedius* HKU10-03(345/469 , 74%, 481)	PF05133: phage prot Gp6 (portal protein SPP1 Gp6-like)	family:vir_proph:52 phi:0000012 - phage head tail joining; phi:0000068 - phage portal protein mge:1557, 187, *S. aureus*
32	+	19057..20094	348	39,6	minor head protein	YP_239491.1, ORF009 , *Staphylococcus* phage 187 (214/340,63%,322)	PF04233:phage Mu F protein, possible minor head proteins	family:vir_proph:50 phi:0000185 - phage head/capsid minor protein mge:1557, 187, *S. aureus*
33	+	20330..20935	201	22,7	scaffold protein	YP_003472468.1, hypothetical protein SLGD_02253, *S. lugdunensis* HKU09-01 (120/197, 61%, 196)		family:vir_proph:103 phi:0000017 - phage prohead/capsid assembly; phi:0000065 - capsid scaffolding protein mge:1557, 187, *S. aureus*
34	+	20951..21862	303	33	major head protein*	YP_003472467.1, Phage major capsid protein Fam0118, *S. lugdunensis* HKU09-01 (214/298, 72%, 301)		family:vir_proph:527 phi:0000326 - phage function unknown mge:1557, 187, *S. aureus*
35	+	21890..22225	111	12,9	DNA packaging , minor head protein	YP_239495.1, ORF042, *Staphylococcus* phage 187 (69/111, 62%, 128)	PF05135:Phage QLRG putative DNA packaging	family:vir_proph:160 phi:0000186 - minor capsid structural protein mge:1557, 187, *S. aureus*
36	+	22222..22536	104	12,3	minor head protein	YP_239496.1, ORF107, *Staphylococcus* phage 187 (49/102, 48%, 104)		family:vir_proph:277 phi:0000186 - minor capsid structural protein mge:1557, 187, *S. aureus*
37	+	22526..22876	116	13,7		YP_239497.1, ORF049, *Staphylococcus* phage 187 (78/115, 68%, 115)	PF04883:DUF646, possible tail component	family:vir_proph:76 phi:0000326 - phage function unknown mge:1557, 187, *S. aureus*
38	+	22884..23282	132	14,9	head structural protein	YP_239498.1 , ORF039, *Staphylococcus* phage 187 (54/131, 41%, 131)		family:vir_proph:215 phi:0000173 - major capsid structural protein mge:1557, 187, *S. aureus*
39	+	23297..23896	199	22,2	major tail protein*	YP_417178,1, phage-like protein, *S. aureus* RF122 (119/184, 65%, 193)	PF06199: phage tail 2, major tail proteins	family:vir_proph:196 phi:0000082 - phage major tail protein mge:2670, prophinder:45952, *S. aureus*

								RF122
40	+	23965..24336	123	13,5	tail assembly protein	YP_239500.1, ORF043, *Staphylococcus* phage 187 (61/114, 54%, 126)	PF12363 : phage protein	family:vir_proph:209 phi:0000015 - phage tail assembly mge:1557, 187, *S. aureus*
41	+	24366..24731	121	14,4		YP_004148754.1, hypothetical protein SPSINT_0589, *S. pseudintermedius* HKU10-03 (72/116, 62%, 116)		family:vir_proph:210 phi:0000326 - phage function unknown mge:1557, 187, *S. aureus*
42	+	24731..28123	1130	121,2	tail tape measure protein*	YP_254260.1 hypothetical protein SH2345, *S. haemolyticus* JCSC1435 (482/1027, 47%, 1070)		family:vir_proph:1 phi:0000086 - phage tail tape measure protein mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
43	+	28136..29092	318	37,4	tail protein*	ZP_03614373.1, conserved hypothetical protein, *S. capitis* SK14 (205/317, 65%, 318)	PF05709: Sipho tail, phage tail protein	family:vir_proph:190 phi:0000178 - phage minor tail protein mge:1654, 85, *S. aureus*
44	+	29102..30352	416	47	tail protein, endopeptidase*	ZP_03614382.1, conserved phage protein, *S. capitis* SK14 (222/383, 58%, 486)	PF06605: prophage endopeptidase tail	family:vir_proph:35 phi:0000178 - phage minor tail protein; go:0016298 - lipase activity mge:2332, prophinder:45292, *S. aureus* subsp. *aureus* JH9
45	+	30363..32237	624	71,5	tail protein, Zn carboxypeptidase*	ZP_03614336.1, zinc carboxypeptidase family, *S. capitis* SK14 (434/614, 71%, 628)	PF00246: peptidase M14	family:vir_proph:458 phi:0000178 - phage minor tail protein mge:1602, 37, *S. aureus*
46	+	32250..33446	398	45,3	tail protein, likely tal fiber*	ZP_03614350.1, conserved hypothetical protein, *S. capitis* SK14 (237/391, 61%, 395)	PF10651 : DUF2479, unknown function	family:vir_proph:69 phi:0000178 - phage minor tail protein mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
47	+	33468..33959	163	18,4	holin	YP_002560381.1, holin, *M. caseolyticus* JCSC5402 (81/152, 53%, 170)	PF05105: phage holin 4	family:vir_proph:42 phi:0000088 - phage base plate protein; go:0034290 - holin activity mge:169, 44AHJD, *S. aureus*
48	+	34009..35946	645	72,8	peptidoglycan hydrolase, tail associated protein*	ZP_03614366.1, mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase, *S. capitis* SK14 (389/644, 60%, 626)	PF05257: CHAP domain PF01832: glucosaminidase	family:vir_proph:6 phi:0000013 - phage release by lysis; phi:0000340 - phage cell wall amidase activity mge:2670, prophinder:45952, *S. aureus* RF122
49	+	35999..37345	448	49,6	tail protein, likely tail fiber*	ZP_03614374.1, tail fiber protein, *S. capitis* SK14 (144/258, 56%, 552)	PF10651: DUF2479, unknown function; PF01391: collagen triple helix repeat	family:vir_proph:199 phi:0000178 - phage minor tail protein mge:1602, 37, *S. aureus*

50	+	37406..37702	98	11,2		ZP_06614673.1, conserved hypothetical protein, S. *epidermidis* M23864:W2(grey) (69/98, 70%, 114)		family:vir_proph:1391 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
51	+	37695..37838	47	57,5		ZP_06614674.1, conserved hypothetical protein, S. *epidermidis* M23864:W2(grey) (37/42, 88%, 48)	PF09693: phage XkdX	family:vir_proph:1045 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
52	+	37894..38181	95	10,4	holin	ZP_04824946.1, possible holin, *S. epidermidis* BCM-HMP0060 (52/95, 55%, 95)	PF04531: phage holin 1	family:vir_proph:34 go:0034290 - holin activity; phi:0000013 - phage release by lysis mge:1859, A006, *Listeria monocytogenes*
53	+	38194..39930	578	66,2	lysin	ZP_04824947.1, possible N-acetylmuramoyl-L-alanine amidase, *S. epidermidis* BCM-HMP0060 (428/578, 74%, 574)	PF01510: Amidase 2, N-acetylmuramoyl-L-alanine amidase PF05257: CHAP	family:vir_proph:6 phi:0000013 - phage release by lysis; phi:0000340 - phage cell wall amidase activity mge:2256, prophinder:42793, *S. aureus* subsp. *aureus* N315

*Proteins indentified in proteomic analysis

Table S4: Genome annotation of StB20

ORF	Strand	Start..end	Size		predicted function	NCBI best match (extent , % aa identity, total length aa)	Domain	Prot family Func Annot MgeId, MgeName, Hosts
			aa	kDa				
1	-	97..1401	434	51,2	integrase	YP_950630.1, putative site-specifc recombinase, *Staphylococcus* phage CNPH82 (380/407, 93%, 458)	PF00239: resolvase, N-terminal domain; PF07508: recombinase	family:vir_proph:67 phi:0000330 - site-specific DNA inversion, phi:0000056 - prophage DNA integration, phi:0000144 - serine-based site-specific recombinase activity mge:1571, CNPH82, *S. epidermidis*
2	-	1470..2393	307	34,2		EGG74041.1, putative lipoprotein, *S. epidermidis* VCU028 (238/291, 82%, 314)		family:vir_proph:22 phi:0000326 - phage function unknown mge:1508, 88, *S. aureus*
3	-	2445..2585	46	5,8		YP_254310.1, hypothetical protein SH2395, *S. haemolyticus* JCSC1435 (34/41, 83%, 45)		family:vir_proph:6557 no functions assigned mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
4	-	2597..3313	238	27,1	transcription repressor	EGA99200.1, hypothetical protein SAO46_2483, *S. aureus* O46 (176/238, 74%, 237)	PF01381:HTH_3, Cro and CI family; PF00717:peptidase S24	family:vir_proph:378 go:0016564 - transcription repressor activity mge:2685, prophinder:45206, *S. aureus* subsp. *aureus* USA300
5	+	3450..3719	89	10,5	transcription repressor	EGA99199.1, putative phage transcriptional regulator, *S. aureus* O46 (85/89, 96%, 89)	PF01381: HTH_, Cro and CI family	family:vir_proph:378 go:0016564 - transcription repressor activity mge:2685, prophinder:45206, *S. aureus* subsp. *aureus* USA300
6	+	3733..4452	239	27,3	transcription antirepressor	ADI97590.1, prophage, antirepressor, putative, *S. aureus* subsp. *aureus* ED133 (188/238, 79%, 237)	PF10552:BRO family, N-terminal domain PF02498.10: ORF6C domain	family:vir_proph:3 phi:0000048 - negative transcriptional regulation of phage gene expression, go:0016564 - transcription repressor activity mge:1676, 92, *S. aureus*
7	+	4478..4642	54	6,1		ZP_07841352.1, hypothetical protein HMPREF0786_00897, *S. caprae* C87 (51/53, 96%, 54)		no hits found
8	+	4639..4743	34	4,1		ZP_06284324.1, conserved domain protein, *S. epidermidis* SK135 (31/34, 91%, 56)		family:vir_proph:1390 phi:0000326 - phage function unknown mge:1679, PH15, *S. epidermidis*

9	+	4740..4916	58	6,7		YP_950705.1, hypothetical protein ph43, *Staphylococcus* phage PH15 (54/58, 93%, 58)		family:vir_proph:10541 no functions assigned mge:1679, PH15, *S. epidermidis*
10	+	4971..5246	91	11		YP_950638.1, hypothetical protein cn40, *Staphylococcus* phage CNPH82 (86/91, 95%, 91)		family:vir_proph:5007 no functions assigned mge:1571, CNPH82, *S. epidermidis*
11	+	5218..5445	75	8,5		EGG72642.1 hypothetical protein SEVCU028_0999, *S. epidermidis* VCU028 (64/75, 85%, 75)	PF10656: DUF2483, domain of unknown function	family:vir_proph:259 phi:0000326 - phage function unknown mge:1607, 69, *S. aureus*
12	+	5438..6082	214	24,6	recombination protein, ERF-like recombinase	ZP_04824890.1, conserved hypothetical protein *S. epidermidis* BCM-HMP0060 (204/214, 95%, 214)	PF04404: ERF superfamily	family:vir_proph:1389 phi:0000326 - phage function unknown, 580 - ERF-like recombinase mge:1602, 37, *S. aureus*
13	+	6082..6492	136	15	recombination protein, single-strand DNA binding protein	ZP_06612891.1, single-strand binding protein *S. epidermidis* M23864:W2(grey) (131/140, 94%, 140)	PF00436: SSB, single-strand binding protein family	family:vir_proph:30 go:0003697 - single-stranded DNA binding mge:1571, CNPH82, *S. epidermidis*
14	+	6596..7057	153	17,8	HNH endonuclease	YP_002633575.1 putative HNH family endonuclease, phage associated, *S. carnosus* subsp. *carnosus* TM300 (109/151, 72%, 183)	PF13392: HNH_3, HNH endonuclease	family:vir_proph:27 go:0004530 - deoxyribonuclease I activity mge:1508, 88, *S. aureus*
15	+	7058..7732	224	26,1		EGG69330.1, hypothetical protein SEVCU028_0950, *S. epidermidis* VCU028 (198/224, 88%, 229)	PF06147:DUF968, domain of unknown function	family:vir_proph:66 phi:0000326 - phage function unknown mge:1679, PH15, *S. epidermidis*
16	+	7725..8525	266	31,1	replication initiation protein	EGS74699.1, phage replisome organizer N-terminal domain protein, *S. epidermidis* VCU107 (259/266, 97%, 266)	PF09681: N-terminal phage replisome organizer; PF07261: DnaB_2, replication, initiation and membrane attachment	family:vir_proph:10 go:0006270 - DNA replication initiation, phi:0000026 - phage DNA replication, go:0003677 - DNA binding mge:1679, PH15, *S. epidermidis*
17	+	8525..8884	119	14,2		YP_950712.1, YP_950712.1 conserved phage protein S*taphylococcus* phage PH15 (118/119, 99%, 119)		family:vir_proph:738 phi:0000326 - phage function unknown mge:1679, PH15, *S. epidermidis*
18	+	8877..10112	411	47,3	helicase	EGS74699.1, phage replisome organizer N-terminal domain protein, *S. epidermidis* VCU107 (259/266, 97%, 266)	PF03796: DnaB_C, DnaB-like helicase C terminal domain	family:vir_proph:24 phi:0000026 - phage DNA replication, go:0004386 - helicase activity mge:1679, PH15, *S. epidermidis*
19	+	10109..10330	73	8,7		YP_950714.1, hypothetical protein ph52 *Staphylococcus* phage PH15 (71/73, 97%, 73)		family:vir_proph:737 phi:0000326 phage function unknown mge:1679, PH15, *S. epidermidis*

20	+	10308..10553	81	9,7		EGS38355.1, hypothetical protein SEVCU116_0394 *S. epidermidis* VCU116 (75/81, 93%, 81)	PF11673: DUF3269, unknown function	family:vir_proph:5008 no functions assigned mge:1679 - PH15, *S. epidermidis*
21	+	10562..10969	135	16,3		EGS38373.1, hypothetical protein SEVCU116_0393 *S. epidermidis* VCU116 (120/123, 98%, 136)	PF06356: DUF1064, domain of unknown function	family:vir_proph:97 phi:0000326 - phage function unknown mge:102, phiPV83, *S.* aureus
22	+	10962..11156	64	7,5		ZP_04818984.1, conserved hypothetical protein *S. epidermidis* M23864:W1 (59/64, 92%, 64)		family:vir_proph:11021 no functions assigned mge:1571, CNPH82, *S. epidermidis*
23	+	11157..11522	121	14,7		EGS38387.1, PVL ORF-50-like family protein, *S. epidermidis* VCU116 (110/121, 91%, 121)	PF07768: PVL_ORF50, PVL ORF-50-like family	family:vir_proph:73 phi:0000326 - phage function unknown mge:1679, PH15, *S. epidermidis*
24	+	11523..11720	65	7,7		EGS40333.1, hypothetical protein SEVCU116_1798, *S. epidermidis* VCU116 (59/65, 91%, 65)		no hits found
25	+	11723..12202	159	18,4		EGS40327.1, hypothetical protein SEVCU116_1797, *S. epidermidis* VCU116 (147/158, 93%, 159)	PF05014: Nuc_deoxyrib_tr, nucleoside deoxyribosyltransferase (pyrimidine metabolism)	family:vir_proph:1693 phi:0000326, phage function unknown mge:1577, G1, *S. aureus*
26	+	12199..12384	61	7,2		YP_950654.1, hypothetical protein cn56 *Staphylococcus* phage CNPH82 (53/61, 87%, 61)		family:vir_proph:3305 no functions assigned mge:1571, CNPH82, *S. epidermidis*
27	+	12381..12641	86	9,9		ZP_04824909.1, hypothetical protein HMPREF0789_0717, *S. epidermidis* BCM-HMP0060 (36/46, 78%, 50)		family:vir_proph:153 phi:0000326, phage function unknown mge:2642, prophinder:45328, *S. aureus* subsp. aureus Mu3
28	+	12625..12804	59	7,2		no hits found		no hits found
29	+	12806..13231	141	15,6	dUTPase	ZP_03614365.1, deoxyuridine 5'-triphosphate nucleotidohydrolase (dutpase) (dutp pyrophosphatase) (ppar-interacting protein 4) (Pip4), *S. capitis* SK14 (134/141, 95%, 141)	PF00692:dUTPase	
30	+	13280..13462	60	7,4	RinB	ZP_06612912.1, regulator RinB, *S. epidermidis* M23864:W2(grey) (55/60, 92%, 59)	PF06116: RinB, transcriptional activator	family:vir_proph:83 phi:0000007 - phage lysogeny, go:0016563 - transcription activator activity, phi:0000049 - positive transcriptional regulation of phage gene expression mge:1679, PH15, *S. epidermidis*

31	+	13463..13612	49	5,8		ZP_06612913.1, hypothetical protein HMPREF0794_0195, *S. epidermidis* M23864:W2(grey) (49/49, 100%, 49)	PF07438: DUF1514, domain of unknown function	no hits found
32	+	13629..14075	148	17,6		ZP_07841334.1, hypothetical protein HMPREF0786_00879, *S. caprae* C87 (145/148, 98%, 148)		family:vir_proph:63 phi:0000007 - phage lysogeny, go:0016563 - transcription activator activity, phi:0000049 - positive transcriptional regulation of phage gene expression mge:1476, 77, *S. aureus*
33	+	14677..15054	125	15,2	HNH endonuclease	ZP_07841333.1, prophage L54a, HNH endonuclease family protein *S. caprae* C87 (116/124, 94%, 125)	PF01844:HNH endonuclease	family:vir_proph:9 go:0004530 - deoxyribonuclease I activity mge:57, phiSLT, *S. aureus*
34	+	15083..15220	45	5		no hits found		no hits found
35	+	15199..15669	156	18	TerS	EGG63311.1, phage terminase, small subunit, P27 family *S. epidermidis* VCU144] (155/156, 99%, 156)	PF05119: Terminase_4, phage terminase, small subunit	family:vir_proph:44 phi:0000074 - phage terminase small subunit, go:0003677 - DNA binding mge:2140, prophinder:45399, *S. saprophyticus* subsp. *saprophyticus* ATCC 15305
36	+	15656..17413	585	67,9	TerL	EGG63322.1, putative phage terminase, large subunit *S. epidermidis* VCU144 (596/583, 98%, 583)	PF03354: Terminase_1, phage terminase, large subunit	family:vir_proph:8 phi:0000019 - phage DNA maturation, phi:0000073 - phage terminase large subunit, mge:2556, prophinder:46163, *Streptococcus pyogenes* SSI-1
37	+	17427..17621	64	7		EGG63233.1, hypothetical protein SEVCU144_2382 *S. epidermidis* VCU144 (60/64, 94%, 65)		no hits found
38	+	17624..18856	410	46,5	portal HK97 family*	ZP_06612919.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (402/410, 988%, 410)	PF04860: phage portal protein	family:vir_proph:7 phi:0000012 - phage head tail joining, phi:0000068 - phage portal protein mge:1875, tp310-3, *S.* aureus410
39	+	18846..19403	185	20,9	prohead protease	ZP_07841328.1, phage prohead protease, HK97 family, *S. caprae* C87 (179/185, 97%, 188)	PF04586.10: peptidase U35, caudovirus prohead protease	family:vir_proph:21 phi:0000017 - phage prohead/capsid assembly , phi:0000123 - prohead protease activity mge:2494, prophinder:43759, *S.* aureus subsp. aureus MSSA476
40	+	19445..20803	452	50,4	major head protein*	ZP_06612921.1, prophage pi2 protein 33 *S. epidermidis* M23864:W2(grey) (408/452, 90%, 451)	PF05065: phage capside proteins (HK97, phi-105, P27,	family:proph:20 phi:0000066 - phage head/capsid major protein

							and related phage)	mge:2187, prophinder:46329, *Listeria innocua* Clip11262
41	+	20822..21163	113	13	DNA packaging protein	EGG63250.1, DNA packaging protein, QLRG family *S. epidermidis* VCU144 (107/113, 95%, 113)	PF05135: Phage_connect_1, phage gp6-like head-tail connector protein	family:vir_proph:152 phi:0000326 - phage function unknown mge:2568, prophinder:42609, *Rhodobacter sphaeroides* 2.4.1
42	+	21153..21482	109	12,2	phage head-tail joining protein	ZP_07841325.1, hypothetical protein HMPREF0786_00870, *S. caprae* C87 (109/109, 100%, 109)	PF05521: Phage_H_T_join, phage head-tail joining protein	family:vir_proph:111 phi:0000326 - phage function unknown mge:2431, prophinder:45259, *S. aureus* subsp. *aureus* JH1
43	+	21617..21883	88	10,4		ZP_07841324.1, hypothetical protein HMPREF0786_00869, *S. caprae* C87 (88/88, 100%, 88)		family:vir_proph:220 phi:0000326 - phage function unknown mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
44	+	21903..22292	129	15,4		EGG63239.1, hypothetical protein SEVCU144_2375 *S. epidermidis* VCU144 (126/129, 98%, 134)		family:vir_proph:219 phi:0000326 - phage function unknown mge:1476 , 77, *S.* aureus
45	+	22305..22934	209	22,8	major tail protein*	EGG63212.1, phage major tail protein, phi13 family *S. epidermidis* VCU144 (208/209, 99%, 209)	PF04630: phage_tail, phage major tail protein	family:vir_proph:39 phi:0000082 - phage major tail protein mge:2494, prophinder:43759, *S. aureus* subsp. *aureus* MSSA476
46	+	22953..23138	61	7,1		EGG63234.1, hypothetical protein SEVCU144_2373 *S. epidermidis* VCU144 (61/61, 100%, 61)		family:vir_proph:107 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*
47	+	23202..23564	120	13,7		ZP_07841320.1, hypothetical protein HMPREF0786_00865, *S. caprae* C87 (116/120, 97%, 120)		family:vir_proph:574 phi:0000326 - phage function unknown mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
48	+	23597..23749	50	5,8		ZP_06612929.1, hypothetical protein HMPREF0794_0211, *S. epidermidis* M23864:W2(grey) (50/50, 100%, 50)		no hits found
49	+	23778..25574	598	63,5	tail tape measure protein*	ZP_06612930.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (567/585, 97%, 1586)	PF10145: phage_min_tail, phage-related minor tail protein	family:vir_proph:1 phi:0000086 - phage tail tape measure protein mge:2494, prophinder:43759, *S. aureus* subsp. aureus MSSA476
50	+	25549..27282	577	62,7	tail tape measure protein*	ZP_07841318.1, phage tail tape measure protein, TP901 family, core region domain protein, *S. caprae* C87 (428/544, 79%, 1611)		family:vir_proph:1 phi:0000086 - phage tail tape measure protein mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435

51	+	27234..28670	478	51,1	tail tape measure protein	EGS40310.1, peptidase, M23 family *S. epidermidis* VCU116 401/446, 90%,1906)	PF015551: Peptidase_M23, zinc metallopeptidase; PF01464: transglycosylase SLT domain	family:vir_proph:1 phi:0000086 - phage tail tape measure protein mge:2148, prophinder:46504, *S. haemolyticus* JCSC1435
52	+	28672..29505	277	32,5	tail protein*	EGG63317.1, hypothetical protein SEVCU144_2369, *S. epidermidis* VCU144, (275/277, 99%, 277)	PF05709: sipho_tail, phage tail protein	family:vir_proph:202 phi:0000174 - phage tail mge:1485 - 3A, *S. aureus*
53	+	29506..31074	522	60,5	tail protein, endopeptidase*	ZP_06612932.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (513/522, 98%, 522)	PF06605:prophage_tail, endopeptidase tail	family:vir_proph:236 phi:0000174 - phage tail protein mge:1855, tp310-2, *S.* aureus
54	+	31067..31240	57	6,7		ZP_07841315.1, hypothetical protein HMPREF0786_00860, *S. caprae* C87 (56/57, 98%, 57)		no hits found
55	+	31256..33118	620	71,4	tail protein, Zn carboxypeptidase*	ZP_07841314.1, zinc carboxypeptidase superfamily *S. caprae* C87 (612/620, 99%, 620)	PF00246: Peptidase_M14,Zn carboxypeptidase	family:vir_proph:123 phi:0000178 - phage minor tail protein mge:1531, 29, *S.* aureus
56	+	33118..34332	404	46,1	tail protein, likely tail fiber*	EGG63243.1, hypothetical protein SEVCU144_2365 *S. epidermidis* VCU144 (394/404, 98%, 404)	PF10651: DUF2479, unknown function	family:vir_proph:69 phi:0000178 - phage minor tail protein mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
57	+	34334..34960	208	23,8		ZP_06612936.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (206/208, 99%, 211)	PF05908: DUF867, unknown function	family:vir_proph:1435 phi:0000326 - phage function unknown mge:13, SPBc2, *Bacillus subtilis*
58	+	34957..35382	141	15,7		EGG63280.1, conserved domain protein, *S. epidermidis* VCU144 (141/141, 100%, 141)		family:vir_proph:929 phi:0000326 - phage function unknown mge:1602, 37, *S. aureus*
59	+	35369..35776	135	15,7		ZP_07841310.1, conserved hypothetical protein *S. caprae* C87 (130/135, 96%, 146)		family:vir_proph:199 phi:0000178 - phage minor tail protein mge:1602, 37, *S. aureus*
60	+	35877..37259	460	51,8	tail protein, likely tail fiber*	ZP_07841309.1, putative phage tail fiber protein, *S. caprae* C87 (240/375, 64%, 543)	PF10651:DUF2479, domain of unknown function; PF01391: collagen, collagen helix	family:vir_proph:199 phi:0000178 - phage minor tail protein mge:1642, EW, *S.* aureus
61	+	37271..37630	119	13,9		ZP_06614673.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (52/91, 57%, 114)		family:vir_proph:1391 phi:0000326 - phage function unknown mge:1602, 37, *S.* aureus
62	+	37623..37769	48	5,7		ZP_06614674.1, conserved hypothetical protein *S. epidermidis* M23864:W2(grey) (43/48, 90%, 48)	PF09693: Phage_XkdX, phage uncharacterized	family:vir_proph:1045 phi:0000326 - phage function unknown mge:1571, CNPH82, *S. epidermidis*

							protein	
63	+	37833..38243	136	14,7	holin	ZP_07841307.1, holing, *S. caprae* C87 (125/136, 92%, 136)	PF04531: phage holin1	family:vir_proph:34 go:0034290 - holin activity phi:0000013 - phage release by lysis mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
64	+	38218..38847	209	24	lysin	ZP_07841306.1, autolysin (N-acetylmuramoyl-L-alanine amidase) *S. caprae* C87 (201/209, 96%, 487)	PF05257: CHAP domain	family:vir_proph:6 phi:0000013 - phage release by lysis, phi:0000340 - phage cell wall amidase activity mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435
65	+	38909..39454	181	21,2	homing HNH endonuclease	YP_240848.1, ORF027, *S.* phage X2 (133/181, 73%, 181)	PF07463: NUMOD4, putative DNA-binding motif in homing endonucleases; PF01844: HNH endonuclease	family:vir_proph:27 go:0004530 - deoxyribonuclease I activity mge:1549, X2, *S. aureus*
66	+	39802..40614	270	30,8	lysin	ZP_03614343.1, autolysin (N-acetylmuramoyl-L-alanine amidase), *S.* capitis SK14 (259/270, 96%, 487)	PF01510: amidase2, N-acetylmuramoyl-L-alanine amidase; PF08460: SH3_5, bacterial SH3 domain	family:vir_proph:6 phi:0000013 - phage release by lysis phi:0000340 - phage cell wall amidase activity mge:2149, prophinder:46506, *S. haemolyticus* JCSC1435

*Proteins identified in proteomic analysis