

**Table S1.** *S. aureus* phages.

(Pro)phage	Genome size (pb)	Morphological		Cluster (Class) <sup>g</sup>	Genome sequence	Reference
		sub-family	genus			
<b><i>Siphoviridae</i></b>						
phi187	39,620	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes	[1]
phi69	42,732	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes	[1]
phi53	43,883	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes	[1]
phi85	44,238	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes	[1]
phi2638A	41,318	lambda supergroup	Sfi21-like <sup>a</sup>	6(II)	yes	[1]
phi77	41,708	lambda supergroup	Sfi21-like <sup>a</sup>	6(II)	yes	[1]
phi42e	45,861	lambda supergroup	Sfi21-like <sup>a</sup>	4(II)	yes	[1]
phi3A	43,095	lambda supergroup	Sfi21-like <sup>a</sup>	4(II)	yes	[1]
phi47	44,777	lambda supergroup	Sfi21-like <sup>a</sup>	4(II)	yes	[1]
phi37	43,681	lambda supergroup	Sfi11-like <sup>a</sup>	3(II)	yes	[1]
phiEW	45,286	lambda supergroup	Sfi11-like <sup>a</sup>	3(II)	yes	[1]
phi96	43,576	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phiROSA	43,155	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi71	43,114	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi55	41,902	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi29	42,802	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi52A	41,690	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi88	43,231	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phiX2	43,440	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phi92	42,431	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[1]
phiPVL	41,401	lambda supergroup	Sfi21-like (gr1) <sup>b,c</sup>	5(II)	yes	[2, 3]
phiSLT	42,942	lambda supergroup	Sfi21-like (gr2) <sup>b,c</sup>	4(II)	yes	[3, 4]
phiPV83-pro	45,636	lambda supergroup	Sfi21-like (gr1) <sup>b,c</sup>	5(II)	yes	[3, 5]
phi108-PVL	44,107	lambda supergroup	Sfi21-like (gr1) <sup>b,c</sup>	5(II)	yes	[3, 6]
phiSa2mw	45,924	lambda supergroup	Sfi21-like (gr2) <sup>b,c</sup>	ND	yes	[6, 7]
phiSa2958	46,046	lambda supergroup	Sfi21-like (gr2) <sup>b,c</sup>	4(II)	yes	[3, 8]
phiSa2usa	43,062	lambda supergroup	Sfi21-like (gr2) <sup>b,c</sup>	ND	yes	[3, 9]
phi7247PVL	42,142	lambda supergroup	Sfi21-like (gr3) <sup>b,c</sup>	ND	yes	[3]
phi5967PVL	42,142	lambda supergroup	Sfi21-like (gr3) <sup>b,c</sup>	ND	yes	[3]
phiETA	43,081	lambda supergroup	Sfi11-like <sup>b</sup>	2(II)	yes	[10]
phiN315	44,257	lambda supergroup	Sfi21-like (gr3) <sup>b,c</sup>	6(II)	yes	[11, 12]

phiMu50A	43,053	lambda supergroup	Sfi21-like (gr3) <sup>b,c</sup>	ND	yes	[11, 12]
phiMu50B	44,391	lambda supergroup	Sfi11-like <sup>b</sup>	ND	yes	[11, 12]
phiSa3mw	ND	lambda supergroup	Sfi21-like (gr1) <sup>b,c</sup>	ND	yes (MW2 strain genome)	[7, 12]
phiSa3ms	42,612	lambda supergroup	Sfi21-like <sup>d</sup>	ND	yes	[13]
phiSa3	ND	lambda supergroup	Sfi21-like <sup>a</sup>	ND	yes (NCTC832 5 strain genome)	[14, 15]
phi11	43,658	lambda supergroup	Sfi11-like <sup>e</sup>	1(II)	yes	[16]
phi12	44,970	lambda supergroup	Sfi11-like <sup>e</sup>	4(II)	yes	[16]
phi13	42,774	lambda supergroup	Sfi21-like <sup>e</sup>	5(II)	yes	[16]
L54a <sup>f</sup>	ND	ND	ND	ND	No	[17]
phiNM1	43,128	lambda supergroup	ND	1(II)	yes	[18]
phiNM2	43,145	lambda supergroup	ND	ND	yes	[18]
phiNM3	44,061	lambda supergroup	ND	6(II)	yes	[18]
phiNM4	43,189	lambda supergroup	ND	2(II)	yes	[18]
phi80	42,140	lambda supergroup	Sfi11-like <sup>b</sup>	2(II)	yes	[19]
phi80alpha	43,864	lambda supergroup	Sfi11-like <sup>b</sup>	1(II)	yes	[19]
phiMR11	43,011	lambda supergroup	Sfi11-like <sup>a</sup>	2(II)	yes	[20]
phiMR25	44,342	lambda supergroup	Sfi11-like <sup>a</sup>	ND	yes	[21]
phiIPLA88	42,526	lambda supergroup	Sfi11-like <sup>b</sup>	1(II)	yes	[22]
phiIPLA35	45,344	lambda supergroup	Sfi21-like <sup>b</sup>	4(II)	yes	[22]
TEM126	33,540	ND	Sfi11-like <sup>b</sup>	ND	yes	[23]
SA11	136,326	ND	ND	ND	yes	[24]
<b><i>Podoviridae</i></b>						
66	18,199	<i>Picovirinae</i>	44AHJD-like	8(I)	yes	[1]
44AHJD	16,668	<i>Picovirinae</i>	44AHJD-like	8(I)	yes	[1, 25]
P68	18,221	<i>Picovirinae</i>	44AHJD-like	8(I)	yes	[1, 25]
SAP2	17,938	<i>Picovirinae</i>	44AHJD-like	8(I)	yes	[26]
<b><i>Myoviridae</i></b>						
K	127,395	Spounaviridae	Twort-like	7(III)	yes	[1, 27]
G1	138,715	Spounaviridae	Twort-like	7(III)	yes	[1]
Twort	130,706	Spounaviridae	Twort-like	7(III)	yes	[1]
SAP1	ND	ND	ND	ND	No	[28]
SAP3	ND	ND	ND	ND	No	[28]
MSA6	140,194	Spounaviridae	Twort-like	ND	yes	[29, 30]
phi812	146,500	ND	ND	ND	No	[31]

SK311	141,100	ND	ND	ND	No	[31]
Stau2	134,500	ND	ND	ND	No	[32]
phiSA012	ND	ND	ND	ND	No	[31]
phiSA039	ND	ND	ND	ND	No	[31]
GH15	139,806	ND	ND	ND	yes	[33]
A5W	137,087	Spounaviridae	Twort-like	ND	yes	[30]
Staph1N	137,192	Spounaviridae	Twort-like	ND	yes	[30]
Fi200W	140,079	Spounaviridae	Twort-like	ND	yes	[30]
P4W	139,173	Spounaviridae	Twort-like	ND	yes	[30]
676Z	140,115	Spounaviridae	Twort-like	ND	yes	[30]
A3R	132,712	Spounaviridae	Twort-like	ND	yes	[30]
ISP	138,339	Spounaviridae	Twort-like	ND	yes	[30, 34]
Sb-1	127,188	Spounaviridae	Twort-like	7(III)	yes	[30, 35]
<b>Unclassified</b>						
PT1028	15,603	ND	ND	ND	yes	[1]

Prophages identified by genome strain sequencing and not further characterized are not indicated.

- (a) Based on the presence of a putative prohead protease encoded within the DNA packaging and head morphogenesis module, not experimentally tested. Determined in this study
- (b) Based on Authors information, experimentally tested or determined on the basis of head genes pattern
- (c) Groups 1-3 within Sfi21-like genus determined on the basis of sequences comparison
- (d) Determined in this study, based on the presence of a putative prohead protease encoded within the DNA packaging and head morphogenesis module, not experimentally tested. The phiSa3ms phage was indicated as a Sfi11-like *pac*-type phage by the Authors [13]
- (e) Experimentally shown as Sfi11-like *pac*-type phage, although a gene encoding a putative prohead protease was annotated, which indicates Sfi21-like *cos*-type phage
- (f) The L54a phage is likely a *Siphoviridae* phage since L54a and phi11 were shown to be closely related phages [16]
- (g) Following the classification proposed by [40]

ND: not determined; the table is likely not exhaustive.

**Table S2.** *Staphylococci* phages from non-*S. aureus* species

(Pro)phage	Genome size (pb)	Morphological			Cluster (Class) <sup>c</sup>	Genome sequence	Host	Ref
		family	sub-family	genus				
CNPH82	43,420	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	3(II)	Yes (phage)	<i>S. epidermidis</i>	[36]
PH15	44,047	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	3(II)	Yes (phage)	<i>S. epidermidis</i>	[36]
phi909	30,124	<i>Sipho</i>	lambda supergroup	Sfi21-like <sup>b</sup>	ND	Yes (prophage)	<i>S. epidermidis</i> <i>FRI909</i>	[37]
vB_SepiS-phiIPLA5	43,581	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	ND	Yes (phage)	<i>S. epidermidis</i>	[38]
vB_SepiS-phiIPLA7	42,123	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	ND	Yes (phage)	<i>S. epidermidis</i>	[38]
phiTM300	45,700	<i>Sipho</i>	lambda supergroup	Sfi21-like <sup>b</sup>	ND	yes (prophage)	<i>S. carnosus</i> <i>TM300</i>	[39]
StB12	44,714	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes (phage)	<i>S. hominis</i>	[40]
StB27	40,071	<i>Sipho</i>	lambda supergroup	Sfi11-like <sup>a</sup>	1(II)	yes (phage)	<i>S. hominis</i>	[40]
StB20	40,917	<i>Sipho</i>	lambda supergroup	Sfi21-like <sup>a</sup>	9(II)	yes (phage)	<i>S. capitis</i>	[40]

Prophages identified by genome strain sequencing and not further characterized are not indicated. (a) Based on Authors information, experimentally tested or determined on the basis of head genes pattern. (b) Determined on the basis of DNA packaging and head morphogenesis gene annotations during this analysis. (c) Following the classification proposed by [40].

*Sipho*: *Siphoviridae*; Ref, reference; ND, not determined.

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