This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2013.042a-lB***	(to be completed by ICTV officers)

Short title: To create three new genera, *3alikevirus*, *77likevirus* and *Phietalikevirus* in the family *Siphoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	June 2013
Date of this revision (if different to above):	July 2014

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.042aB***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***3alikevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Staphylococcus phage 3a	AY954956
Staphylococcus phage 42e	AY954955
Staphylococcus phage 47	AY954957
Staphylococcus phage Ipla35	EU861005
Staphylococcus phage Slt	AB045978
Staphylococcus phage Phi12	AF424782

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Blastn analysis revealed that these phages were related and distinct from other groups. We have 95% DNA identity as species demarcation criterium.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.042bB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***77likevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.

Order:	***Caudovirales***	• If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Staphylococcus phage 77 *Staphylococcus phage 13* *Staphylococcus phage Pvl108*	AY508486 AF424783 AB243556

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Blastn analysis revealed that these phages were related and distinct from other groups. We have 95% DNA identity as species demarcation criterium.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.042cB***	(assigned by ICTV officers)

To create 31 new species within:

Genus:	***Phietalikevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**

Staphylococcus phage 11	AF424781
Staphylococcus phage 187	AY954950
Staphylococcus phage 29	AY954964
Staphylococcus phage 37	AY954958
Staphylococcus phage 52a	AY954965
Staphylococcus phage 53	AY954952
Staphylococcus phage 55	AY954963
Staphylococcus phage 69	AY954951
Staphylococcus phage 71	AY954962
Staphylococcus phage 80	DQ908929
Staphylococcus phage 80alpha	DQ517338
Staphylococcus phage 85	AY954953
Staphylococcus phage 88	AY954966
Staphylococcus phage 92	AY954967
Staphylococcus phage 96	AY954960
Staphylococcus phage Cnph82	DQ831957
Staphylococcus phage Ew	AY954959
Staphylococcus phage Ph15	DQ834250
Staphylococcus phage Phieta	AP001553
Staphylococcus phage Phieta2	AP008953
Staphylococcus phage Phieta3	AP008954
Staphylococcus phage phimr11	AB370268
Staphylococcus phage phimr25	AB370205
Staphylococcus phage Ipla88	EU861004
Staphylococcus phage Sap26	GU477322
Staphylococcus phage X2	AY954968
Staphylococcus phage phinm1	DQ530359
Staphylococcus phage phinm4	DQ530362
Staphylococcus phage Ipla5	JN192400
Staphylococcus phage Ipla7	JN192401
Staphylococcus phage phinm2	DQ530360

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Blastn analysis revealed that these phages were related and distinct from other groups. We have 95% DNA identity as species demarcation criterium.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.042dB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.042eB***	(assigned by ICTV officers)

To name the new genus: *3alikevirus*

Assigning the type species and other species to a new genus

Code	***2013.042fB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Staphylococcus phage 3a

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

6

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The *3alikevirus* genus includes six of the staphylococcal phages. All these viruses were reported to possess a prolate capsid (siphovirus B2 morphotype), 100 nm long and 50 nm wide, and a tail of 300-400 nm (for references see Table 1). These phages all share over 40% proteins with each other as calculated with CoreGenes 3.0 [1].

Comparative proteomic analyses using CoreGenes 3.0 and BLASTP indicates the presence of several group-specific proteins. Among the replication associated proteins there are a helicase-like protein and an A-type DNA polymerase. At the morphogenesis module, a unique capsid protein containing a pfam05065 motif (Phage capsid family) and a major_cap_HK97 (TIGR01554; phage major capsid protein, HK97 family) motif can be distinguished. The tail module contains two specific proteins, the first shows a Sipho_tail (pfam05709) motif, while the latter, corresponds to a predicted prophage endopeptidase tail motif (pfam06605). Other protein exclusive of these phages is RinA, whereas the RinB homolog can be found in other phages.

Comparative analysis of DNA sequences using progressive-MAUVE alignments also indicates a particularly high degree of conservation in a region spanning the DNA packaging proteins (small and large terminase subunits, portal and scaffolding proteins) (Figure 1). In addition, all phages

belonging to the genus *3alikevirus*, share a region encoding a putative nuclease (HNH superfamily).

Origin of the new genus name:

Staphylococcus phage 3a

Reasons to justify the choice of type species:

One of the original isolates of this group.

Species demarcation criteria in the new genus:
If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

We have chosen 95% DNA identity as species demarcation criterium.

MODULE 3: **NEW GENUS**

creating a new genus
Ideally, a genus should be placed within a higher taxon.

Code	***2013.042gB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.042hB***	(assigned by ICTV officers)

To name the new genus: *77likevirus*

Assigning the type species and other species to a new genus

Code	***2013.042iB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Staphylococcus phage 77

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

3

Reasons to justify the creation of a new genus:
Additional material in support of this proposal may be presented in the Appendix, Module 9

The *77likevirus* genus includes three *S. aureus* phages with a similar genome size and morphology (B1 morphotype). No data on the size of the viral particles are available. CoreGenes analysis

revealed that these phages share more than 40% protein content (Table 1) and progressiveMauve alignment showed their relatedness (Figure 2).
These phages shared characteristics with the other genera (*3alikevirus* and *Phietalikevirus*), such as the presence of nucleases in phages 77 and Φ13, similar to those from the *3alikevirus* genus , and a common morphotype with *Phietalikevirus*.

Origin of the new genus name:

Staphylococcus phage 77

Reasons to justify the choice of type species:

The oldest well-described member of this genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

We have chosen 95% DNA identity as species demarcation criterium.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.042jB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.042kB***	(assigned by ICTV officers)

To name the new genus: *Phietalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.042lB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Staphylococcus phage Phieta

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

31

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The *Phietalikevirus* genus includes 31 staphylococcal phages with very similar genome sizes, sharing over 40% proteins (Table 1, Figures 3-5). Virion morphology is nearly identical, with isometric heads of about 50 nm in diameter, and a tail of 175 nm long. All phages belonging to this genus show a B1 morphotype, with the exception of phage EW, which was described to have an A morphotype [2]. Due its high homology with B1-bacteriophages we might conclude that this could be a misinterpretation.

It is remarkable that most of the phages belonging to the genus *Phietalikevirus* share similar genes and DNA homology in a sequence of proteins in the tail morphogenesis module (data not shown). Five arrangements with small differences were observed. In most of the phages from subgroup 1 and subgroup 2 (ΦETA, 52A, 80, 29, 71, 55, ΦMR11, ΦETA3, 88, 92, X2, ΦNM4, 96, ΦETA2, Φ11, 53, 69, 80α, 85, ΦMR25, ΦNM1, ΦNM2, and phiIPLA88) this region is composed of a protein belonging to the SGNH hydrolase superfamily, a hypothetical protein, a tail protein, a virion-associated peptidoglycan hydrolase and a tail fiber protein. For most phages belonging to subgroup 3 (37, CNPH82, PH15, phiIPLA5 and phiIPLA7) a pectin lyase encoding gene can be observed downstream of the SGNH protein. In all these phages, with the exception of phages

phiIPLA7 and PH15, a tail protein is also present. Remarkable differences can be seen on the makeup of this region for phages 187 and EW, which lacks the pectin lyase protein. No tail protein could be identified on 187. The SGNH hydrolases containing lipase and esterase domains are present in all phages within the genus, including phage 187 which has a truncated protein. Moreover, peptidoglycan hydrolytic activities are present in all phages as virion-associated proteins containing two catalytic domains: a CHAP domain and a glucosaminidase domain. All phages, except phiIPLA7, PH15 and phage 187, encode tail fiber proteins with a collagen helix domain downstream from the peptidoglycan hydrolases. This domain consists of a triple helix formed by repetitions of the amino acid sequence glycine-X-Y. A shorter sequence of this protein is also observed for phages phiIPLA5 and CNPH82. The members of the subgroup 3, with the exception of phage 187, have a pre-neck appendage protein between the SGNH hydrolase and the tail protein endowed with a pectin lyase and a peptidase domain.

Origin of the new genus name:

Staphylococcus phage ΦETA

Reasons to justify the choice of type species:

Oldest well-characterized isolate of this genus

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

We have chosen 95% DNA identity as species demarcation criterium.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Mahadevan P, King JF, Seto D (2009) CGUG: in silico proteome and genome parsing tool for the determination of "core" and unique genes in the analysis of genomes up to ca. 1.9 Mb. BMC Res Notes 2: 168. doi:10.1186/1756-0500-2-168.

2. Kwan T, Liu J, DuBow M, Gros P, Pelletier J (2005) The complete genomes and proteomes of 27 *Staphylococcus aureus* bacteriophages. Proc Natl Acad Sci U S A 102: 5174–5179. doi:10.1073/pnas.0501140102.

3. García P, Martínez B, Obeso JM, Lavigne R, Lurz R, et al. (2009) Functional genomic analysis of two *Staphylococcus aureus* phages isolated from the dairy environment. Appl Environ Microbiol 75: 7663–7673. doi:10.1128/AEM.01864-09.

4. Narita S, Kaneko J, Chiba J, Piémont Y, Jarraud S, et al. (2001) Phage conversion of Panton-Valentine leukocidin in *Staphylococcus aureus*: molecular analysis of a PVL-converting phage, φSLT. Gene 268: 195–206. doi:10.1016/S0378-1119(01)00390-0.

5. Iandolo JJ, Worrell V, Groicher KH, Qian Y, Tian R, et al. (2002) Comparative analysis of the genomes of the temperate bacteriophages φ11, φ12 and φ13 of *Staphylococcus aureus* 8325. Gene 289: 109–118. doi:10.1016/S0378-1119(02)00481-X.

6. Ma XX, Ito T, Chongtrakool P, Hiramatsu K (2006) Predominance of clones carrying Panton-Valentine leukocidin genes among methicillin-resistant *Staphylococcus aureus* strains isolated in Japanese hospitals from 1979 to 1985. J Clin Microbiol 44: 4515–4127. doi:10.1128/JCM.00985-06.

7. Yamaguchi T, Hayashi T, Takami H, Nakasone K, Ohnishi M, et al. (2000) Phage conversion of exfoliative toxin A production in *Staphylococcus aureus*. Mol Microbiol 38: 694–705. doi:10.1046/j.1365-2958.2000.02169.x.

8. Christie GE, Matthews AM, King DG, Lane KD, Olivarez NP, et al. (2010) The complete genomes of *Staphylococcus aureus bacteriophages* 80 and 80α--implications for the specificity of SaPI mobilization. Virology 407: 381–390. doi:10.1016/j.virol.2010.08.036.

9. Matsuzaki S, Yasuda M, Nishikawa H, Kuroda M, Ujihara T, et al. (2003) Experimental protection of mice against lethal *Staphylococcus aureus* infection by novel bacteriophage phi MR11. J Infect Dis 187: 613–624. doi:10.1086/374001.

10. Bae T, Baba T, Hiramatsu K, Schneewind O (2006) Prophages of *Staphylococcus aureus* Newman and their contribution to virulence. Mol Microbiol 62: 1035–1047. doi:10.1111/j.1365-2958.2006.05441.x.

11. Hoshiba H, Uchiyama J, Kato S, Ujihara T, Muraoka A, et al. (2010) Isolation and characterization of a novel *Staphylococcus aureus* bacteriophage, phiMR25, and its

References:

therapeutic potential. Arch Virol 155: 545–552. doi:10.1007/s00705-010-0623-2.

12. Swanson MM, Reavy B, Makarova KS, Cock PJ, Hopkins DW, et al. (2012) Novel bacteriophages containing a genome of another bacteriophage within their genomes. PLoS One 7: e40683. doi:10.1371/journal.pone.0040683.

13. Gutiérrez D, Martínez B, Rodríguez A, García P (2012) Genomic characterization of two *Staphylococcus epidermidis* bacteriophages with anti-biofilm potential. BMC Genomics 13: 228. doi:10.1186/1471-2164-13-228.

14. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147. doi:10.1371/journal.pone.0011147.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

The taxonomy proposals described here are based on the paper in submission with Archives of Virology: Three proposed new bacteriophage genera of staphylococcal phages: “3alikevirus”, “77likevirus” and “Phietalikevirus” by Diana Gutiérrez, Evelien M. Adriaenssens, Beatriz Martínez, Ana Rodríguez, Rob Lavigne, Andrew M. Kropinski and Pilar García

Table 1: Phages belonging to the genera *3alikevirus, 77likevirus* and *Phietalikevirus*.

Phage name	Host	Shared protein content with phage type (%)[a]	Shared DNA identity with type phage (%)[b]	Reference	Accession number
3a-likevirus					
3A	*S. aureus*	100	100	[2]	NC_007053
phiIPLA35	*S. aureus*	68.7	86.4	[3]	NC_011612
ΦSLT	*S. aureus*	56.7	77.1	[4]	NC_002661
47	*S. aureus*	77.6	85.4	[2]	NC_007054
Φ12	*S. aureus*	65.7	88.6	[5]	NC_004616
42e	*S. aureus*	61.2	74.7	[2]	NC_007052
77-likevirus					
77	*S. aureus*	100	100	[2]	NC_005356
PVL108	*S. aureus*	52.2	60.5	[6]	NC_008689
Φ13	*S. aureus*	46.4	61.4	[5]	NC_004617
Phietalikevirus					
ΦETA	*S. aureus*	100	100	[7]	NC_003288

52A	*S. aureus*	65.2	74.2	[2]	NC_007062
80	*S. aureus*	66.7	76.3	[8]	DQ908929
29	*S. aureus*	66.7	76.3	[2]	NC_007061
71	*S. aureus*	80.3	78.5	[2]	NC_007059
55	*S. aureus*	80.3	79.8	[2]	NC_007060
ΦMR11	*S. aureus*	66.7	75.3	[9]	NC_010147
ΦETA3	*S. aureus*	63.6	72.6	[7]	NC_008799
88	*S. aureus*	69.7	74.8	[2]	NC_007063
92	*S. aureus*	68.2	73.9	[2]	NC_007064
X2	*S. aureus*	66.7	70.8	[2]	NC_007065
ΦNM4	*S. aureus*	74.2	68.6	[10]	DQ530362
96	*S. aureus*	68.2	66.8	[2]	NC_007057
ΦETA2	*S. aureus*	60.6	67.5	[7]	NC_008798
11	*S. aureus*	50.0	60.4	[5]	NC_004615
53	*S. aureus*	53	60.5	[2]	NC_007049
69	*S. aureus*	56.1	62.5	[2]	NC_007048
80α	*S. aureus*	56.1	60.8	[8]	NC_009526
85	*S. aureus*	48.5	60.1	[2]	NC_007050
ΦMR25	*S. aureus*	57.6	61.0	[11]	NC_010808
ΦNM1	*S. aureus*	60.6	63.7	[10]	NC_008583
ΦNM2	*S. aureus*	53.0	60.9	[10]	DQ530360
phiIPLA88	*S. aureus*	51.5	57.6	[3]	NC_011614
187	*S. aureus*	45.5	53.3	[2]	NC_007047
SAP-26	*S. aureus*	53.1	62.6	Rahman et al.,unpublished	NC_014460
37	*S. aureus*	42.4	53.5	[2]	NC_007055
EW	*S. aureus*	45.5	54.5	[2]	NC_007056
CNPH82	*S. epidermidis*	51.5	55.5	[12]	NC_008722
PH15	*S. epidermidis*	47.0	54.7	[12]	NC_008723
phiIPLA5	*S. epidermidis*	47.0	55	[13]	NC_018281
phiIPLA7	*S. epidermidis*	43.9	56.2	[13]	NC_018284

Figure 1: progressiveMauve alignment of the phage genomes belonging to the proposed genus *3alikevirus* [14]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.**

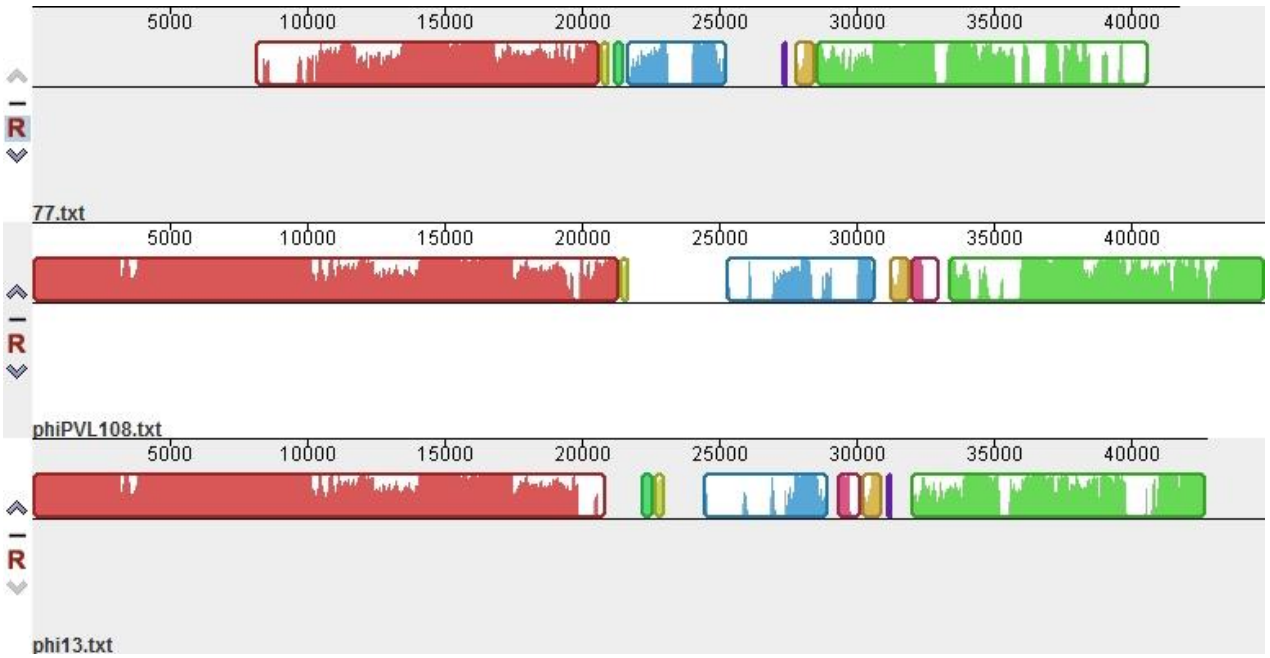

Figure 2: progressiveMauve alignment of the phage genomes belonging to the proposed genus *77likevirus* [14]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different**

random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

Figure 3: progressiveMauve alignment of a selection of the phage genomes belonging to the proposed genus *Phietalikevirus* [14]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.**

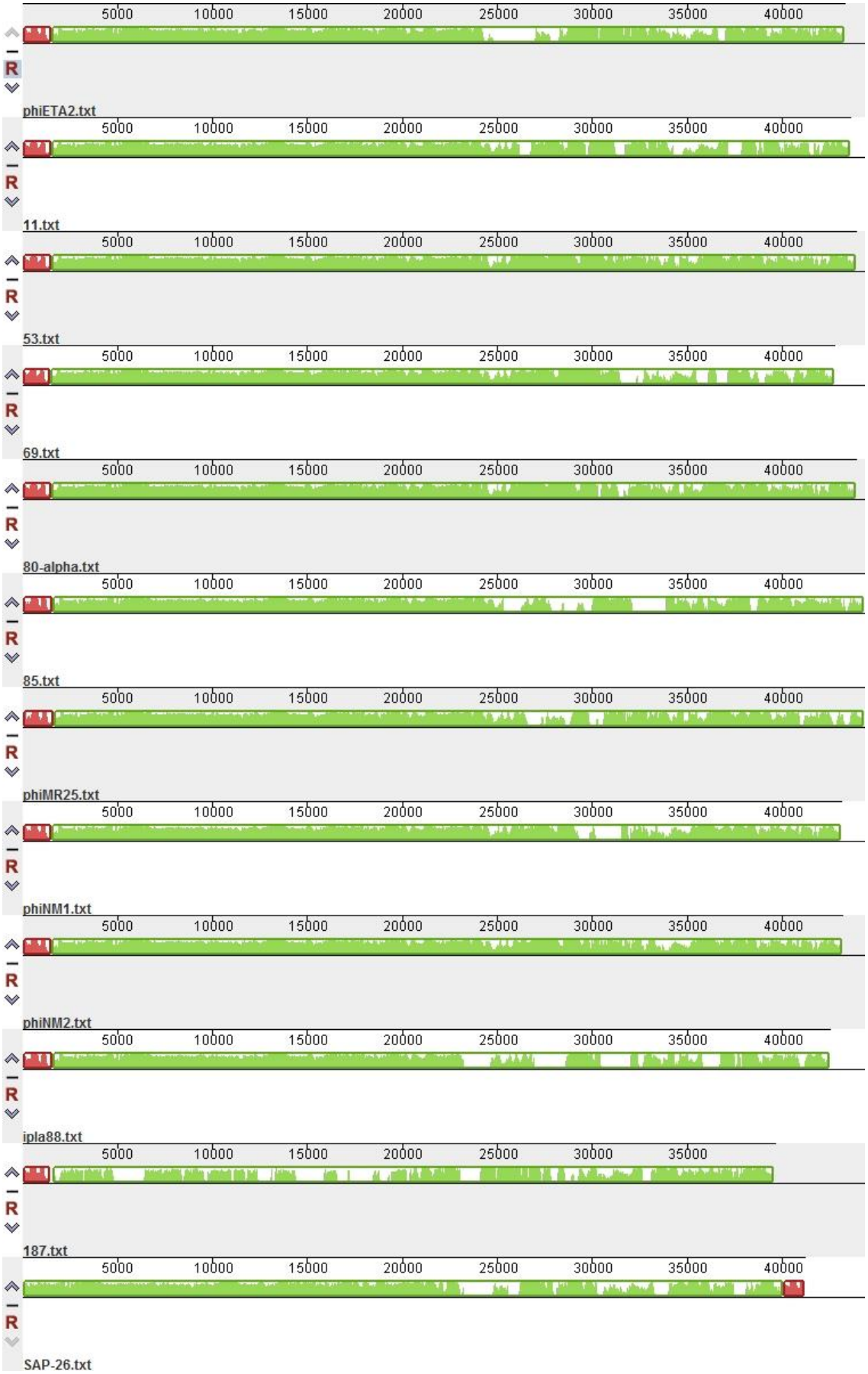

Figure 4: progressiveMauve alignment of a selection of the phage genomes belonging to the proposed genus *Phietalikevirus* [14]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement**

breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

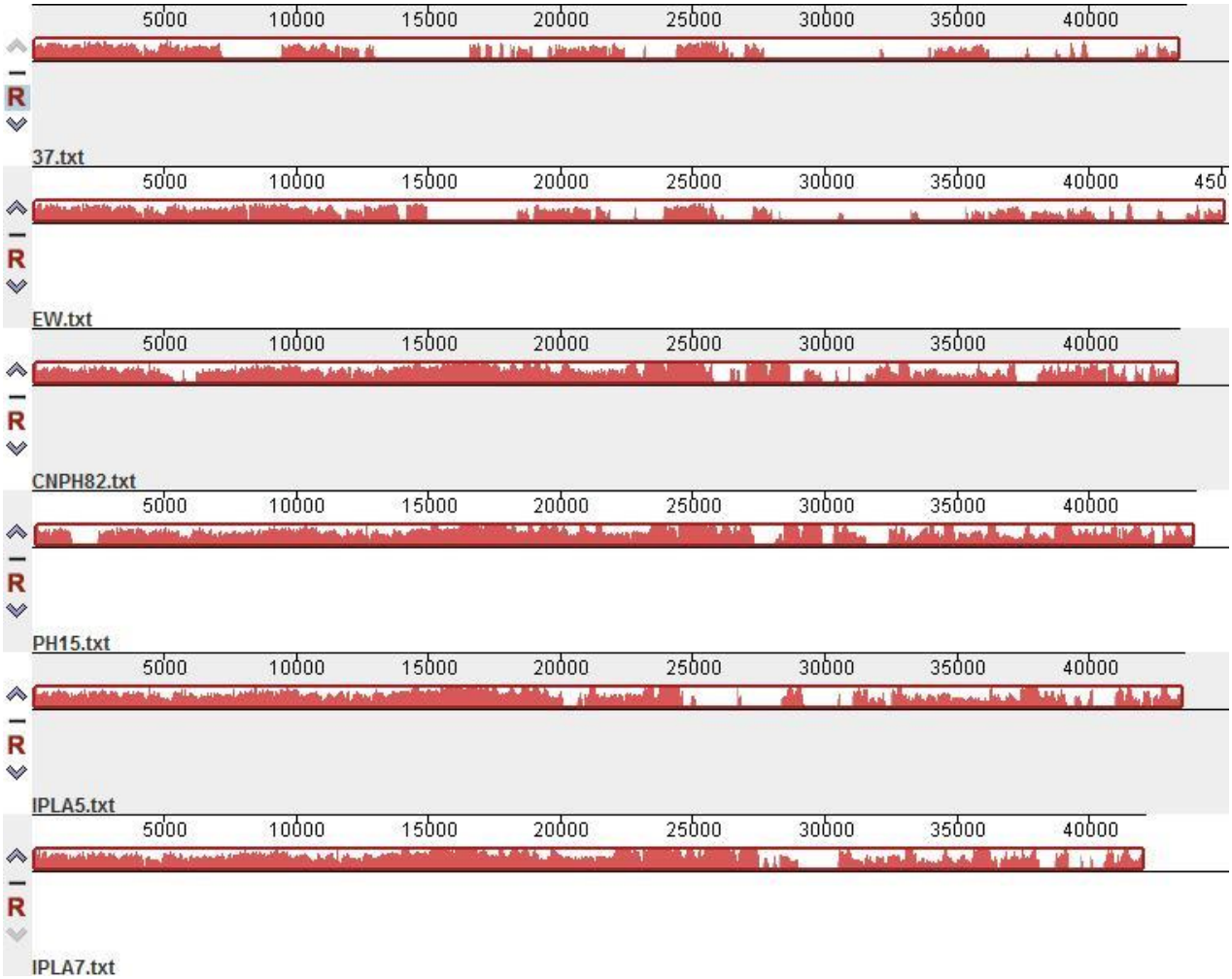

Figure 5: progressiveMauve alignment of a selection of the phage genomes belonging to the proposed genus *Phietalikevirus* [14]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide**

identity.

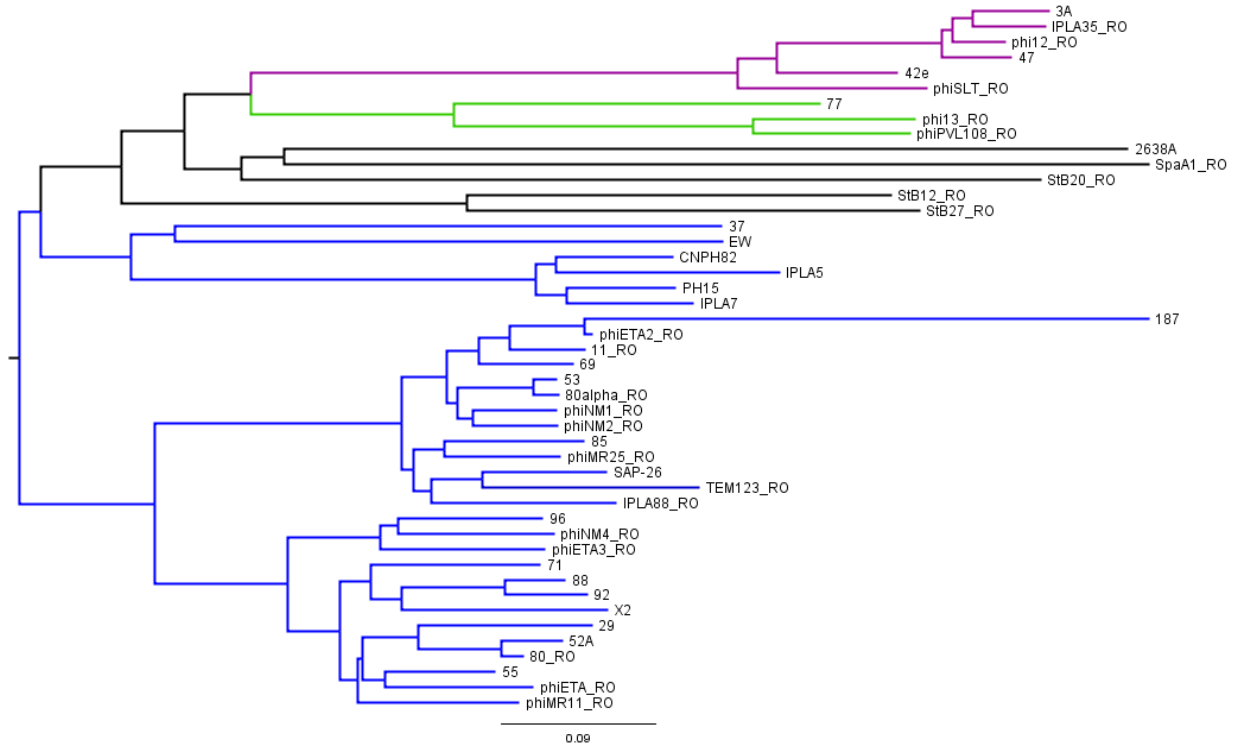

Figure 6: ClustalW phylogenetic tree (NJ) of complete genomes of the *Staphylococcus* phages described in the proposal (*3alikevirus* in purple, *77likevirus* in green, *Phietalikevirus* in blue), including orphan phages (black).