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:	***2015.019a-abB***	(to be completed by ICTV officers)

Short title: To amend the description of the genus *Tunalikevirus*; and, create four (4) new genera including 12 new species, within one (1) new subfamily, *Tunavirinae*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☒	**5** ☐
	6 ☐	**7** ☒	**8** ☒	**9** ☐	**10** ☒

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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)	Bacterial & Archaeal Virus Subcommittee

ICTV Study Group comments (if any) and response of the proposer:

Please note that the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

Date first submitted to ICTV: May 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2015.019aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Tunalikevirus*** (proposed name *T1virus**)
Subfamily:	***Tunavirinae*** **(new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus ADB2 *Shigella virus PSf2*	Escherichia phage ADB-2 Shigella phage pSf-2	JX912252 KP085586

*The new name, *T1virus*, is proposed in the accompanying proposal 2015.006aB.N.v1.Phage_Genera_ren

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

Please note that we have chosen to refer to this new genus as *T1virus* rather than *T1likevirus/Tunalikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

BLASTN, CoreGenes (1) (Table 1), progressiveMauve alignment (2) (Fig. 1) and phylogenetic analyses (3) (Fig. 2) all indicate that the proposed genus, *T1virus*, is cohesive and distinct from the other genera of viruses.

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	***2015.019bB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Tlsvirus* (new)**
Subfamily:	***Tunavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Salmonella virus SP126	Salmonella phage FSL SP-126	KC139513
Citrobacter virus Stevie	Citrobacter phage Stevie	KM236241

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

Please note that we have chosen to refer to this new genus as *Tlsvirus* rather than *Tlslikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.019cB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tunavirinae* (new)**
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	***2015.019dB***	(assigned by ICTV officers)

To name the new genus: *Tlsvirus*

Assigning the type species and other species to a new genus

Code	***2015.019eB***	(assigned by ICTV officers)

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

Escherichia phage Tls (proposed name ***Escherichia virus TLS***)

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

Phage TLS was sequenced at the same time as T1, but a specific manuscript was never published. The only published information on this virus can be obtained from (4). Two other phages belong to this genus *Salmonella* phage FSL SP-126 (5) and *Citrobacter* phage Stevie (6).

BLASTN, CoreGenes (1) (Table 2), progressiveMauve alignment (2) (Fig. 3) and phylogenetic analyses (Fig. 2 (3) (Fig. 2) all indicate that the proposed genus, *Tlsvirus*, is cohesive and distinct from the other genera of viruses.

The overall properties of their genomes are overall size: 50.3 kb (42.8 mol%G+C), encoding an average of 87 proteins and displaying >83% DNA sequence identity. The assignment of these three phages to this genus is in accord with the publication of Niu et al. (7). This group incorporated progressiveMauve analysis (1), Dot plot alignment of nucleotide using Gepard (8), and phylogenetic analysis of the large subunit of terminase, portal, tail fiber and major capsid proteins to assign 17 phages to a proposed subfamily the "Tunavirinae"; and in this specific case to a new genus, the "Tlslikevirus."

Origin of the new genus name:

Derived from name of first isolate: *E.coli* phage TLS

Reasons to justify the choice of type species:

First representative of this type of phage.

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 sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

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	***2015.019fB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Rtpvirus* (new)**
Subfamily:	***Tunavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus ACGM12	Escherichia phage vB_Eco_ACG-M12	JN986845

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

Please note that we have chosen to refer to this new genus as *Rtpvirus* rather than *Rtplikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.019gB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tunavirinae* (new)**
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	***2015.019hB***	(assigned by ICTV officers)

To name the new genus: *Rtpvirus*

Assigning the type species and other species to a new genus

Code	***2015.019iB***	(assigned by ICTV officers)

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

Escherichia phage Rtp (proposed name ***Escherichia virus Rtp***)

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:**

2

Reasons to justify the creation of a new genus:

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

"Electron microscopy revealed that phage Rtp has a morphologically unique tail tip consisting of four leaf-like structures arranged in a rosette, whereas phage T1 has thinner, flexible leaves that thicken toward the ends. In contrast to T1, Rtp did not require FhuA and TonB for infection (9)". "Phage ACG-M12 has an isometric head of about 157 nm in diameter between opposite apices and a relatively flexible tail of 172 × 7 nm, which terminate in 1–2 fibers of 12 nm in length (10)." *Escherichia* phage RES-2009a (GQ495225) is most probably a member of this genus, but the sequence is incomplete.

BLASTN, CoreGenes (1) (Table 3), progressiveMauve alignment (2) (Fig. 4) and phylogenetic analyses (3) (Fig. 2) all indicate that the proposed genus, *Rtpvirus*, is cohesive and distinct from the other genera of viruses.

The overall properties of their genomes are overall size: 46.2 kb (43.9mol%G+C), encoding an average of 76 proteins, one tRNA; and, displaying >63% DNA sequence identity.

The assignment of these phages to this genus is in accord with the publication of Niu et al. (7). This group incorporated progressiveMauve analysis (1), Dot plot alignment of nucleotide using Gepard (8), and phylogenetic analysis of the large subunit of terminase, portal, tail fiber and major

capsid proteins to assign 17 phages to a proposed subfamily the "Tunavirinae"; and in this specific case to a new genus, the "Rtplikevirus."

Origin of the new genus name:

Named after *E.coli* phage Rtp

Reasons to justify the choice of type species:

First representative of this type of phage.

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 sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

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	***2015.019jB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Kp36virus* (new)**
Subfamily:	***Tunavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Klebsiella virus KP36 *Klebsiella virus 1513*	Klebsiella phage KP36 Klebsiella phage 1513	JF501022 KP658157

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

Please note that we have chosen to refer to this new genus as *Kp36virus* rather than *Kp36likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.019kB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tunavirinae* (new)**
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	***2015.019lB***	(assigned by ICTV officers)

To name the new genus: *Kp36virus*

Assigning the type species and other species to a new genus

Code	***2015.019mB***	(assigned by ICTV officers)

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

Klebsiella virus KP36	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

Enterobacter aerogenes phage F20 has an isometric capsid of 50 nm in diameter and a tail of 15 nm in length (12). Phage KP36 is a lytic virus for *Klebsiella pneumoniae* strains (11).

BLASTN, CoreGenes (1) (Table 4), progressiveMauve alignment (2) (Fig. 5) and phylogenetic analyses (3) (Fig. 2) all indicate that the proposed genus, *Kp36virus*, is cohesive and distinct from the other genera of viruses.

The overall properties of their genomes are overall size: 50.3 kb (43.7 mol%G+C), encoding an average of 78 proteins, no tRNAs; and, displaying >71% DNA sequence identity.

The assignment of these phages to this genus is in accord with the publication of Niu et al. (7). This group incorporated progressiveMauve analysis (1), Dot plot alignment of nucleotide using Gepard (8), and phylogenetic analysis of the large subunit of terminase, portal, tail fiber and major capsid proteins to assign 17 phages to a proposed subfamily the "Tunavirinae"; and in this specific case to a new genus, the "Kp36likevirus."

Origin of the new genus name:

Derived from first isolate *Klebsiella* phage KP36

Reasons to justify the choice of type species:

First representative of this type of phage.

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 sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

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	***2015.019nB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Rogue1virus* (new)**
Subfamily:	***Tunavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus AHS24	Escherichia phage vB_EcoS_AHS24	KF771238
Escherichia virus KP26	Escherichia phage phiKP26	KC579452
Escherichia virus AHP42	Escherichia phage vB_EcoS_AHP42	KF771237
Escherichia virus AKS96	Escherichia phage vB_EcoS_AKS96	KF771239
Escherichia virus E41c	Escherichia phage e4/1c	KJ668713

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

Please note that we have chosen to refer to this new genus as *Rogue1virus* rather than *Rogueunalikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.019oB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tunavirinae* (new)**
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	***2015.019pB***	(assigned by ICTV officers)

To name the new genus: *Rogue1virus*

Assigning the type species and other species to a new genus

Code	***2015.019qB***	(assigned by ICTV officers)

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

Escherichia phage Rogue1 (proposed name ***Escherichia virus Rogue1***)	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:**

8

Reasons to justify the creation of a new genus:

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

Many of these phages were isolated from *E.coli* O157 super-shedder cattle in Alberta (7, 13). Rogue1 has the following dimensions - head: 53 nm; striated tail: 152x8 nm. Two other isolates of related phages have publications associated with their characterization (14, 15).

BLASTN, CoreGenes (1) (Table 5), progressiveMauve alignment (2) (Fig. 6) and phylogenetic analyses (3) (Fig. 2) all indicate that the proposed genus, *Kp36virus*, is cohesive and distinct from the other genera of viruses.

The overall properties of their genomes are overall size: 46.6 kb (44.0 mol%G+C), encoding an average of 76 proteins, one tRNAs; and, displaying >62% DNA sequence identity.

The assignment of these phages to this genus is in accord with the publication of Niu et al. (7). This group incorporated progressiveMauve analysis (1), Dot plot alignment of nucleotide using Gepard (8), and phylogenetic analysis of the large subunit of terminase, portal, tail fiber and major capsid proteins to assign 17 phages to a proposed subfamily the "Tunavirinae"; and in this specific case to a new genus, the "Jk06likevirus." Because of the large number of frameshifts in the sequence of *Escherichia coli* phage JK06, we have chosen not to name this genus after it, but after the next isolate (Rogue1).

Origin of the new genus name:

Named after *E.coli* phage Rogue1

Reasons to justify the choice of type species:

Because of the large number of frameshifts in the sequence of *Escherichia coli* phage JK06, we have chosen not to name this genus after it, but after the next isolate (Rogue1).

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 sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2015.019rB***	(assigned by ICTV officers)

To create a new subfamily within:

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

If the family has yet to be created (in Module 5) please write "**(new)**" after the proposed name.

- If there is no Order, write "**unassigned**" here.

naming a new subfamily

Code	***2015.019sB***	(assigned by ICTV officers)

To name the new subfamily: *Tunavirinae*

genera and species assigned to the new subfamily

Code	***2015.019tB***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

Tunalikevirus (existing, proposed name ***T1virus***)

Rtpvirus – new

Tlsvirus – new

Kp36virus – new

Rogue1virus – new

The new subfamily 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 unassigned species that the subfamily will contain (those NOT within any of the genera listed above): *Cronobacter phage Esp2949-1* is unassigned**

1

Reasons to justify the creation of the new subfamily:

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

This is in accord with the suggestion of Niu et al. (7), and is the logical way of classifying these diverse T1-like phages.

Origin of the new subfamily name:

Derived from *Escherichia coli* phage T1

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.019uB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Tunalikevirus

The present taxonomic position of these taxon/taxa:

Genus:	-
Subfamily:	**unassigned**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

see 2015.019sB, above

Part (b) re-assign to a higher taxon

Code	***2015.019vB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

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

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

see 2015.019sB, above

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.019wB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Cronobacter phage Esp2949-1, Enterobacter phage F20, Escherichia phage Eb49, Escherichia phage Jk06, Escherichia phage Rogue1, Escherichia phage Rtp and *Escherichia phage Tls*

The present taxonomic position of these taxon/taxa:

Genus:	***Tunalikevirus*** (proposed name ***T1virus***)
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

The genus *Tunalikevirus* currently contains the following ICTV recognized species: *Cronobacter* phage Esp2949-1, *Enterobacter* phage F20, *Enterobacteria* phage T1, *Shigella* phage Shf11, and *Escherichia* phages Eb49, Jk06, Rogue1, Rtp and TLS. While these are undoubtedly T1-like phages they differ considerably in their overall DNA sequence identity.

Part (b) re-assign to a higher taxon

Code	***2015.019xB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Cronobacter phage Esp2949-1

Genus:	**unassigned**
Subfamily:	***Tunavirinae*** **(new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Part (b) re-assign to a higher taxon

Code	***2015.019yB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Escherichia phage Tls (proposed name *Escherichia virus TLS*)

Genus:	***Tlsvirus* (new)**
Subfamily:	***Tunavirinae* (new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Part (b) re-assign to a higher taxon

Code	***2015.019zB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Enterobacter phage F20 (proposed name *Enterobacter virus F20*)

Genus:	***Kp36virus* (new)**
Subfamily:	***Tunavirinae* (new)**
Family:	***Siphoviridae***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Part (b) re-assign to a higher taxon

Code	***2015.019aaB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Escherichia phage Rtp (proposed name *Escherichia virus Rtp*)

Genus:	***Rtpvirus* (new)**
Subfamily:	***Tunavirinae* (new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Part (b) re-assign to a higher taxon

Code	***2015.019abB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Escherichia virus Jk06, *Escherichia phage Rogue1* (proposed name *Escherichia virus Rogue1*) and *Escherichia phage Eb49* (proposed name *Escherichia virus EB49*)

Genus:	***Rogue1virus* (new)**
Subfamily:	***Tunavirinae* (new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.
2. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140.
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Genomic characterization provides new insight into *Salmonella* phage diversity. BMC Genomics. 2013;14:481. [SP-126]
6. Shaw JP, Aviles Medina CA, Chen Y, Luna AJ, Hernandez AC, Kuty Everett GF.
Complete Genome of *Citrobacter freundii* Siphophage Stevie. Genome Announc. 2015;3(1). pii: e01434-14.
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12. Mishra CK, Choi TJ, Kang SC. Isolation and characterization of a bacteriophage F20 virulent to *Enterobacter aerogenes*. J Gen Virol. 2012;93(Pt 10):2310-4.
13. Kropinski AM, Lingohr EJ, Moyles DM, Ojha S, Mazzocco A, She YM, Bach SJ,
Rozema EA, Stanford K, McAllister TA, Johnson RP. Endemic bacteriophages: a cautionary tale for evaluation of bacteriophage therapy and other interventions for infection control in animals. Virol J. 2012;9:207. [Rogue1]
14. Battaglioli EJ, Baisa GA, Weeks AE, Schroll RA, Hryckowian AJ, Welch RA. Isolation of generalized transducing bacteriophages for uropathogenic strains of *Escherichia coli*. Appl Environ Microbiol. 2011;77(18):6630-5. [PhiEB49]
15. Amarillas L, Cháidez-Quiroz C, Sañudo-Barajas A, León-Félix J. Complete genome
sequence of a polyvalent bacteriophage, phiKP26, active on *Salmonella* and *Escherichia* coli. Arch Virol. 2013;158(11):2395-8.

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.

Table 1. Properties of the four phages belonging to the genus *T1virus*, and type species of their closest relative.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**
T1	AY216660	48.8	45.6	78	100	100
Shfl1	HM035024	50.7	45.4	80	80	84.6
ADB-2	JX912252	50.6	45.6	78	86	78.2
pSf-2	KP085586	50.1	45.4	83	82	88.5
TLS	AY308796				29	

* Determined using BLASTN; ** Determined using CoreGenes (2);

Table 2. Properties of the three phages belonging to the genus *Tlsvirus*, and type species of their closest relative.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
TLS	AY308796	49.9	42.7	87	0	100	100
FSL SP-126	KC139513	51.1	42.9	83	0	83	82.8
Stevie	KM236241	49.8	42.8	90	0	86	90.8
T1	AY216660					28	

* Determined using BLASTN; ** Determined using CoreGenes (2);

Table 3. Properties of the two phages belonging to the genus *Rtpvirus*, and type species of their closest relative.

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Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
Rtp	AM156909	46.2	44.3	75	1***	100	100
vB_EcoS_ACG-M12	JN986845	46.1	43.5	78	1	63	77.3
Rogue1	KC333879					38	

* Determined using BLASTN; ** Determined using CoreGenes (2); *** Not indicated in GenBank file. *Escherichia* phage RES-2009a (GQ495225) is most probably a member of this genus, but the sequence is incomplete.

Table 4. Properties of the three phages belonging to the genus *Kp36virus*, and type species of their closest relative.

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Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
KP36	JF501022	49.8	50.7	79	0	100	100
1513	KP658157	49.5	50.6	72	0	85	86.1
F20***	JN672684	51.5	47.9	83	0	71	86.1
T1	AY216660					20	

* Determined using BLASTN; ** Determined using CoreGenes (2);*** described in GenBank is being partial

Table 5. Properties of the nine phages belonging to the genus *Rogue1virus*, and their closest relative.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
vB_EcoS_Rogue1	JQ182736	45.8	44.2	74	1	100	100
vB_EcoS_AHS24§	KF771238	46.4	43.8	81	1	89	91.9
phiKP26§§	KC579452	47.3	44.3	78	1	91	87.8
phiEB49	JF770475	47.2	44.0	74	2	62	77.0
JK06	DQ121662	46.1	44.0	82	1♥	93	62.2#
vB_EcoS_AKS96	KF771239	45.8	43.9	74	1	89	87.8
vB_EcoS_AHP42	KF771237	46.9	44.0	76	1	91	87.8
e4/1c	KJ668713	47.1	44.1	72	1♥	84	81.1
RTP	AM156909					40	

* Determined using BLASTN; ** Determined using CoreGenes (2);*** #, this genome has numerous frameshift errors; § phage vB_EcoS_AHP24 (KF771236) is a strain; §§, phage phiJLA23 (KC333879) is a strain, and sequence contains 230 ambiguous bases; ♥, not indicated in GenBank file. §§This sequence contains 149 ambiguous bases.

Fig. 1. progressiveMauve alignment of the annotated genomes of the new members of the *T1virus* genus – from top to bottom: T1, ADB-2 and pSf-2 (1). 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 (Aaron Darling, personal communication).

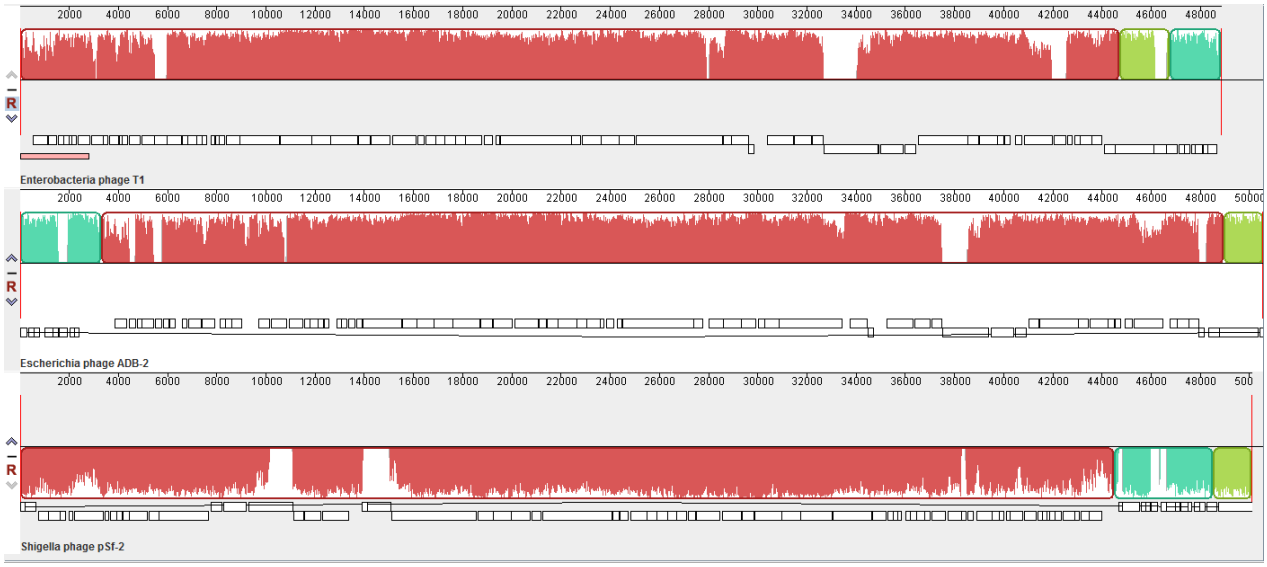

Fig. 2. Phylogenetic analysis of A. large subunit terminase protein and B. major capsid protein of members of the subfamily *Tunavirinae* and two outliers (*Xanthomonas* and *Erwinia* phages) constructed using "one click" at phylogeny.fr (3). "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details." Boxes: blac = *Rogue1virus*; red = *Rtpvirus*; green = *T1virus*; blue = *Tlsvirus*; purple = *Kp36virus*

A. Terminase, large subunit

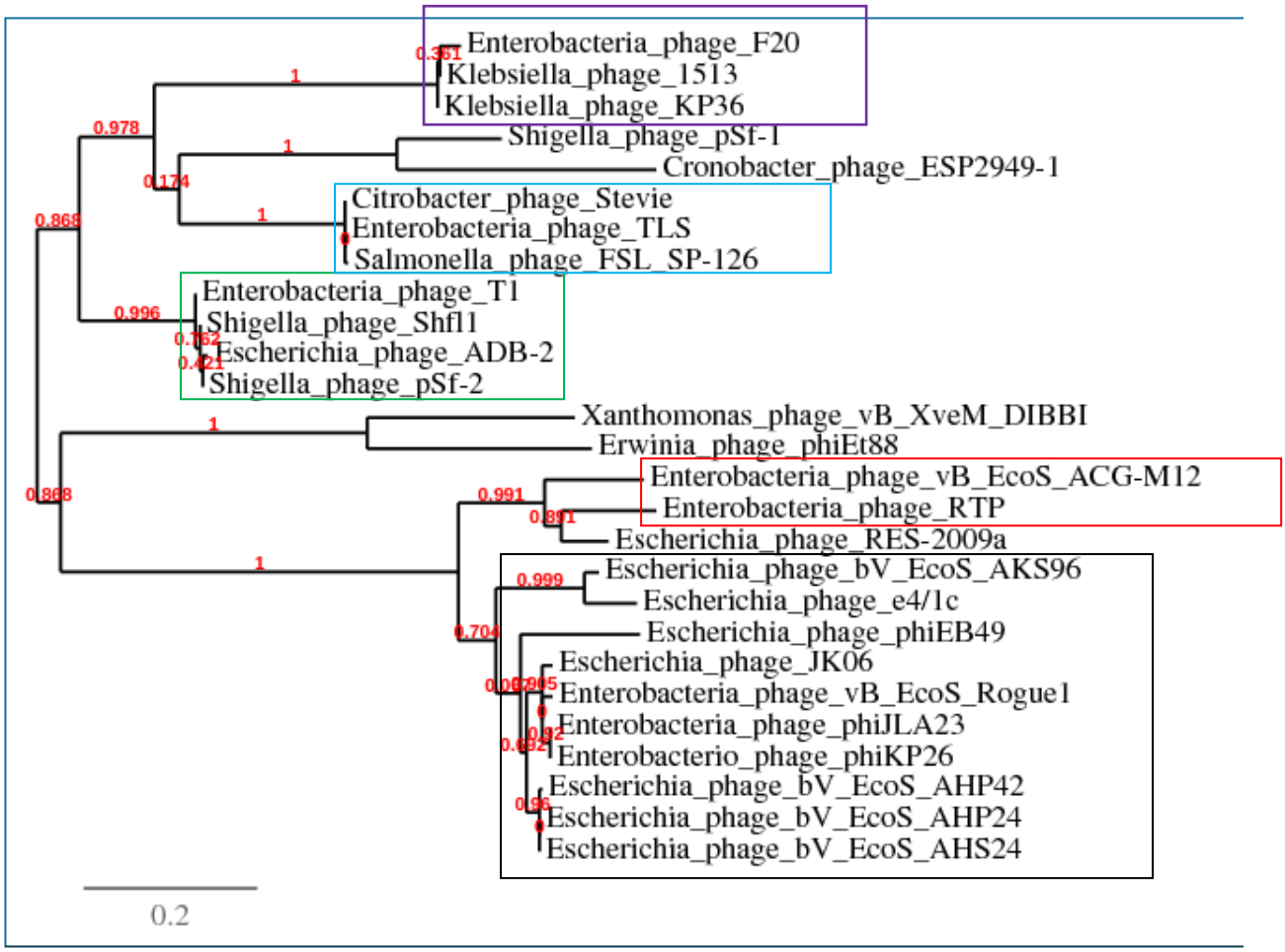

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

B. Major capsid protein

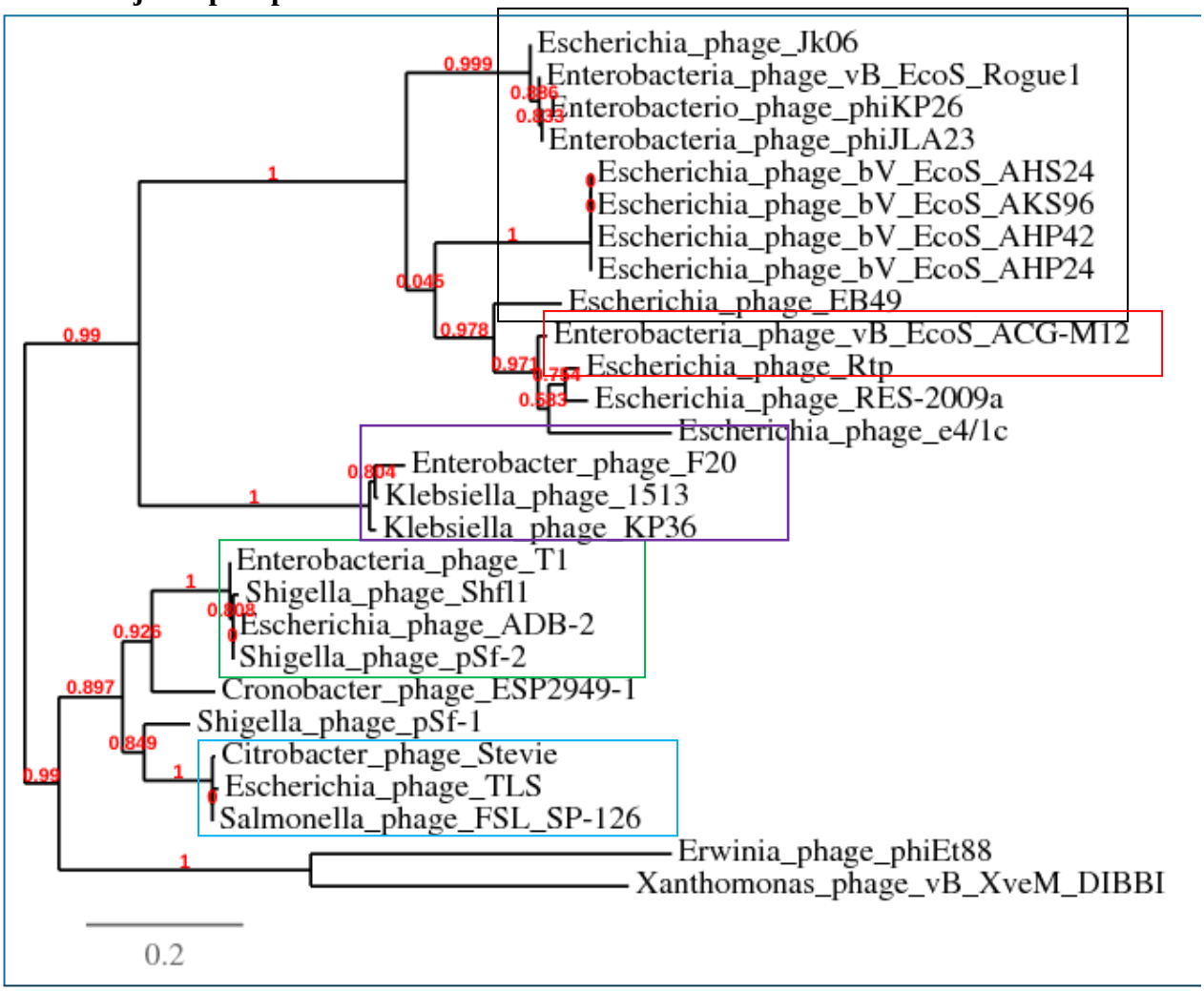

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

Fig. 3. progressiveMauve alignment of the annotated genomes of the new members of the *Tlsvirus* genus – from top to bottom: TLS, Stevie and SP-126 (1). 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 (Aaron Darling, personal communication). N.B. The genomes are not collinear.

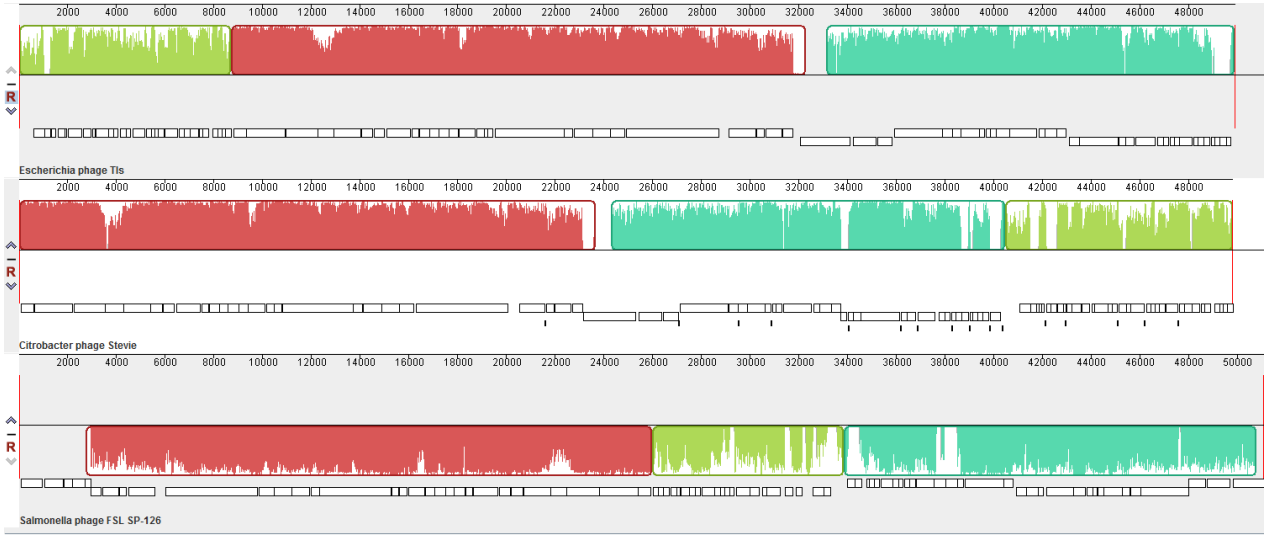

Fig. 4. progressiveMauve alignment of the annotated genomes of the new members of the *Rtpvirus* genus – from top to bottom: RTP and vB_EcoS_ACG-M12 (1). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).

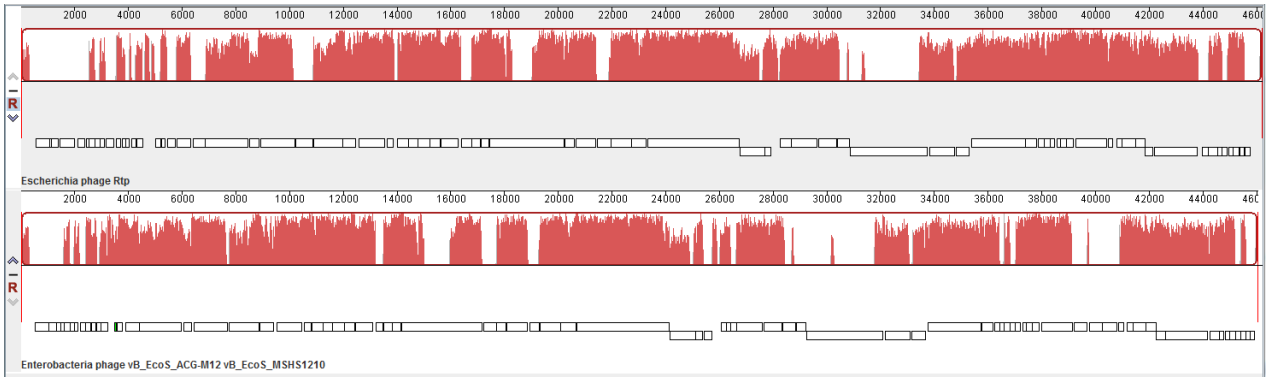

Fig. 5. progressiveMauve alignment of the annotated genomes of the new members of the *Kp36virus* genus – from top to bottom: KP36, 1513 and F20 (1). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication). N.B. The genomes are not collinear.

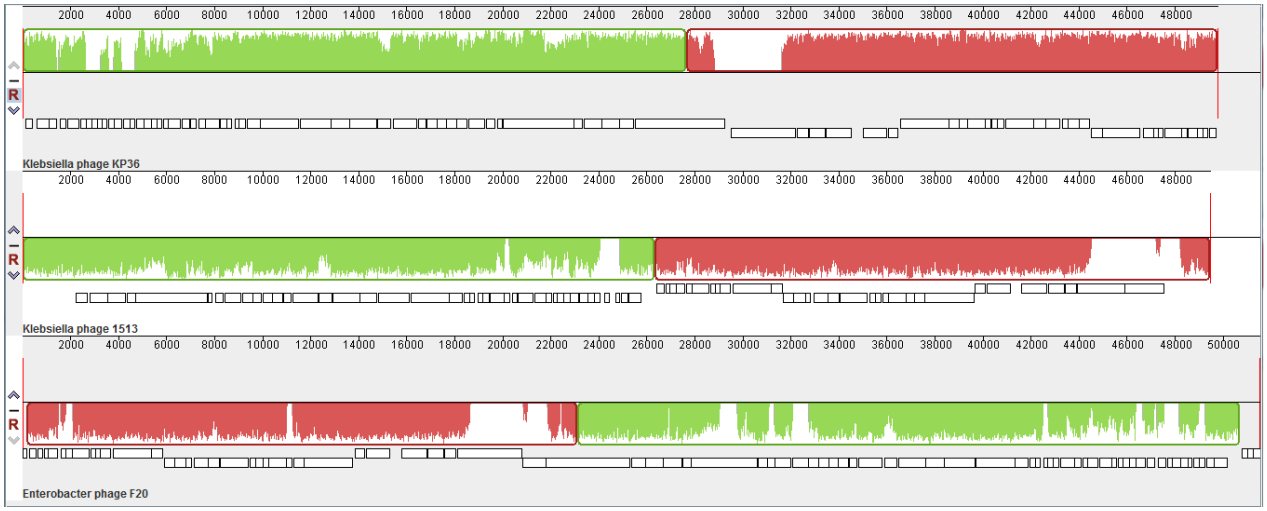

Fig. 6. progressiveMauve alignment of the some genomes of the new members of the *Rogue1virus* genus – from top to bottom: Rogue1, phiKP26, AHS24, e4/1c and EB49 (1). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of 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 (Aaron Darling, personal communication).