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:	***2015.020a-aeB***	(to be completed by ICTV officers)

Short title: To amend the membership of the genus *T4likevirus*, and create six (6) new genera in the subfamily *Tevenvirinae*
(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 and Archaeal Virus Subcommittee

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

Please note that we have chosen to refer to this genus as *T4virus* rather than *T4likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" 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	***2015.020aB***	(assigned by ICTV officers)

To create 10 new species within:

Genus:	***T4likevirus*** (proposed name ***T4virus***)
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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 AR1	Escherichia phage AR1	AP011113
Escherichia virus Ime09	Escherichia phage ime09	JN202312
Escherichia virus E112	Escherichia phage vB_EcoM_112	KJ668714.2
Escherichia virus ECML134	Escherichia phage ECML-134	JX128259
Escherichia virus RB3	Escherichia phage RB3	KM606994
Escherichia virus C40	Escherichia phage vB_EcoM_ACG-C40	JN986846
Shigella virus Shfl2	Shigella phage Shfl2	HM035025
Shigella virus Pss1	Shigella phage pSs-1	KM501444
Yersinia virus PST	Yersinia phage PST	KF208315
Yersinia virus D1	Yersinia phage phiD1	HE956711

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

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	***2015.020bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020cB***	(assigned by ICTV officers)

To name the new genus: *Rb49virus*

Assigning the type species and other species to a new genus

Code	***2015.020dB***	(assigned by ICTV officers)

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

Escherichia phage RB49* (existing species)** to be renamed ***Escherichia virus RB49	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

This new genus will contain two species (*Escherichia virus RB49*, and *Escherichia virus phi1*) that were previously classified as t4likeviruses and are now moved into the new genus.
"Its [RB49] morphology is indistinguishable from the well-known T-even phage T4, but DNA hybridization indicated that it was phylogenetically distant from T4 and thus it was classified as a pseudo-T-even phage." (1). Phages of this group have 164.9 kb genomes with a mol%G+C of 40.5. They encode approximately 277 proteins and no tRNAs. Their DNA contains cytosine and not 5-hydroxymethylcytosine. They only share 41% protein homologs with *Escherichia* phage T4. Our phylogenetic analysis (Fig. 1) and BLASTN analysis (Table 1) indicate further that this group of phages is separate from t4viruses.

Origin of the new genus name:

Named after the first virus of its type to be sequenced - *Escherichia* phage RB49

Reasons to justify the choice of type species:

The first virus of its type to be sequenced - Escherichia phage RB49

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.

Please note that we have chosen to refer to this new genus as *Rb49virus* rather than *Rb49likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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	***2015.020eB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Rb69virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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 JS09	Escherichia phage vB_EcoM_JS09	KF582788
Escherichia virus HX01	Escherichia phage HX01	JX536493
Shigella virus UTAM	Shigella phage Shf125875	KM407600

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

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	***2015.020fB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020gB***	(assigned by ICTV officers)

To name the new genus: *Rb69virus*

Assigning the type species and other species to a new genus

Code	***2015.020hB***	(assigned by ICTV officers)

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

Escherichia virus RB69	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: 4**

4

Reasons to justify the creation of a new genus:

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

A long recognized member of a subgroup of T4-like phages (5) RB69 has been described as a "distant phylogenetic relative of T4" (6). Phages of this group have 168.7kb genomes with a mol%G+C of 37.6. They encode approximately 271 proteins and 2 tRNAs. They only share 74.7% protein homologs with *Escherichia* phage T4. Our phylogenetic analysis (Fig. 1) and BLASTN analysis (Table 1) indicate further that this group of phages is separate from *T4virus*.

Recently two *E.coli* O157 typing phages 3 (KP869101) & 6 (KP869104) have been characterized (11) and can be added to this genus.

Origin of the new genus name:

Named after the first virus of its type to be sequenced - *Escherichia* phage RB69

Reasons to justify the choice of type species:

The first virus of its type to be sequenced - *Escherichia* phage RB69

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.

Please note that we have chosen to refer to this new genus as *Rb69virus* rather than *Rb69likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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	***2015.020iB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Js98virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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 IME08	Escherichia phage IME08	HM071924
Escherichia virus Bp7	Escherichia phage Bp7	HQ829472
Escherichia virus JS10	Escherichia phage JS10	EU863409
Escherichia virus VR5	Escherichia phage vb_EcoM-VR5	KP007359

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

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	***2015.020jB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020kB***	(assigned by ICTV officers)

To name the new genus: *Js98virus*

Assigning the type species and other species to a new genus

Code	***2015.020lB***	(assigned by ICTV officers)

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

Escherichia virus JS98	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: 5**

5

Reasons to justify the creation of a new genus:

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

Zuber et al. (5) stated "JS98 defines a new major subgroup of *E. coli* T4-like phages." Phages of this group possess 170.6 kb genomes (39.5 mol%G+C) and encode 262 proteins and usually 3 tRNAs. They only share 77.4% protein homologs with Escherichia phage T4. Our phylogenetic analysis (Fig. 1) and BLASTN analysis (Table 1) indicate further that this group of phages is separate from T4virus. A recent isolate, *Escherichia* virus RV5, is a member of this genus.

Origin of the new genus name:

Named after the first virus of its type to be sequenced - *Escherichia* phage JS98

Reasons to justify the choice of type species:

The first virus of its type to be sequenced - *Escherichia* phage JS98

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.

Please note that we have chosen to refer to this new genus as *Js98virus* rather than *Js98likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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	***2015.020mB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Sp18virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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)**
Shigella virus SP18	Shigella phage SP18	GQ981382
Escherichia virus VR7	Escherichia phage vB_EcoM_VR7	HM563683
Escherichia virus VR20	Escherichia phage vB_EcoM_VR20	KP007360
Escherichia virus VR25	Escherichia phage vB_EcoM_VR25	KP007361
Escherichia virus VR26	Escherichia phage vB_EcoM_VR26	KP007362

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

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	***2015.020nB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020oB***	(assigned by ICTV officers)

To name the new genus: *Sp18virus*

Assigning the type species and other species to a new genus

Code	***2015.020pB***	(assigned by ICTV officers)

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

Shigella virus SP18

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: 5**

5

Reasons to justify the creation of a new genus:

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

All VR phages fail to produce plaques at 37C, and that they are *E .coli* strain specific (VR7 and VR20 prefer BE strains while VR25 and VR26 form plaques on K12 strains only). Restriction enzymes that are known to recognize 5-hydroxymethylcytosine containing DNA (EcoRV, DraI, VspI, NdeI) cut the DNA suggesting to the authors that the DNA of phage VR7 has a similar modification to T4, yet the genomes failed to reveal alpha- or beta-glucosyltransferases or dCMP hydroxymethylase homologs (8). Phage SP18 was isolated from the Gap River in Korea (7) and lysed *Shigella sonnei*, but not *S. flexneri, S. boydii* or members of the genera *Escherichia* and *Salmonella*. Two common protein markers for these two phages are "hypothetical protein VR7_gp288"-"hypothetical protein SP18_gp282" and "hypothetical protein VR7_gp147"-"hypothetical protein SP18_gp148." Subsequent to our overall analysis three related phages were deposited by Kaliniene et al. - *Escherichia* phages vB_EcoM_VR20, vB_EcoM_VR25 and vB_EcoM_VR26.

These phages have genomes of approximately 170.0 kb with a GC content of 40.4%. They encode approximately 289 proteins and 2 tRNAs. Relative to coliphage T4 SP18 shares 71.8% proteins.

Origin of the new genus name:

Named after the first virus of its type to be sequenced - *Shigella* phage S18

Reasons to justify the choice of type species:

The first virus of its type to be sequenced - *Shigella* phage S18

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. Please note that we have chosen to refer to this new genus as *Sp18virus* rather than *Sp18likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating “like” and “Phi” from phage genus names.

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	***2015.020qB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***S16virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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 STML198 *Salmonella virus S16*	Salmonella phage STML-198 Salmonella phage vB_SenM-S16	JX181825 HQ331142

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

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. Under these conditions, *Salmonella* phage STP4-a is considered a strain.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.020rB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020sB***	(assigned by ICTV officers)

To name the new genus: *S16virus*

Assigning the type species and other species to a new genus

Code	***2015.020tB***	(assigned by ICTV officers)

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

Salmonella virus S16

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**

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

Virulent phage S16 is the second T-even-like phage specific for Salmonella. "It can infect a larger variety of *Salmonella* strains than Felix-O1" (9). Its physical dimensions are: head, 117 by 91; and, a contractile tail 120 nm in length. It can infect LPS 'Re' mutants and binds to OmpC. The "presence of DNA modification functions (dCMP hydroxymethylase, β-glucosyltransferase and β-glucosyl-HMC-α-glucosyl-transferase)" leads to resistance to most restriction endonucleases. There is no manuscript associated with *Salmonella* phage STML-198. The genomes of this genus are characterized by an average size of 159.2 kb (36.9 mol%G+C), encoding 262 proteins and 3 tRNAs. Using CoreGenes S16 shares 62.3% homologs with T4.

Origin of the new genus name:

Named after the *Salmonella* phage S16

Reasons to justify the choice of type species:

This is the only phage of the pair which has been fully described (9).

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.

Please note that we have chosen to refer to this new genus as *S16virus* rather than *S16likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "like" and "Phi" from phage genus names.

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	***2015.020uB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Cc31virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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)**
Enterobacter virus CC31 *Enterobacter virus PG7*	Enterobacter phage CC31 Enterobacter phage PG7	*GU323318* *KJ101592*

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

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	***2015.020vB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020wB***	(assigned by ICTV officers)

To name the new genus: *Cc31virus*

Assigning the type species and other species to a new genus

Code	***2015.020xB***	(assigned by ICTV officers)

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

Enterobacter virus CC31

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**

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

The two members of the Cc31virus genus are lytic for *Enterobacter* species and are characterized by possessing genomes with the following average properties – size: 169.4 kb; mol%G+C: 39.9; number of proteins encoded: 287; number of tRNAs: 14. Percentage of CC31 proteins which find homologs in T4: 57.0.

Origin of the new genus name:

Enterobacter phage CC31

Reasons to justify the choice of type species:

The first virus of its type to be sequenced

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.

Please note that we have chosen to refer to this new genus as *Cc31virus* rather than *Cc31likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating “like” and “Phi” from phage genus names.

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	***2015.020yB***	(assigned by ICTV officers)

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

Aeromonas phage 25
Aeromonas phage 31
Aeromonas phage 44RR2.8t
Enterobacteria phage SV14
Escherichia phage JS98
Escherichia phage phi1
Escherichia phage RB16
Escherichia phage RB32
Escherichia phage RB43
Escherichia phage RB49
Escherichia phage RB69
Pseudomonas phage 42

The present taxonomic position of these taxon/taxa:

Genus:	***T4likevirus***
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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

Based predominantly on the sequence of the major capsid protein (gp23) the T4-related phages were assigned to five groups: T-evens (T4, RB69), pseudoT-evens (AR1, RB49, RB42, RB43), schizoT-evens (nt-1, KVP20, 65, and Aeh1), JS98 and the exoT-even phages (cyanomyoviruses) [1-4]. Petrov et al. [5], re-examined the T4-related bacteriophages which they state contain genomes ranging from approximately 157-255 kb, and sharing a "core genome" of approximately 40 genes involved in nucleotide metabolism, DNA replication, repair, recombination and packaging, transcriptional regulation and morphogenesis. Their analysis indicates that this assemblage includes not only well-characterized coliphages but also viruses infecting *Acinetobacter* (e.g. 133), *Aeromonas* (44RR2.8t), *Campylobacter* (CP220), *Delftia* (φW-14), *Klebsiella* (KP15), *Prochlorococcus* (P-SSM2), *Salmonella* (ViI), *Shigella* (φSboM-AG3), *Synechococcus* (Syn9), and *Vibrio* (KVP40). The diversity displayed by these viruses is equivalent to that of the *Herpesvirales*. Previous ICTV proposals have identified a new genus *Viunalikevirus* and a subfamily the *Eucampyvirinae* (*Cp220likevirus*, *Cp8unalikevirus*) which, at some taxonomic level, fall within the "T4 superfamily."

According to the latest ICTV taxonomy report the subfamily *Tevenvirinae* contains only two genera – *Schizot4likevirus* (one species, Vibrio phage nt-1) and the *T4likevirus* of which the following phages are members: *Aeromonas* phages 25, 31 and 44RR2.8t, *Escherichia* phages T4, JS98, phi1, RB14, RB16, RB32, RB43, RB49, RB69 and SV14; and, *Pseudomonas* phage 42. The question here is not the total diversity of the T4-like phages but what viruses actually constitute the *T4likevirus*. In the past the Bacterial and Archaeal Virus Subcommittee has relied on percent homologous proteins to group phages, but with increasing deposits of complete phage genomes to public databases we are seeing that this results in "lumping" of species which can be clearly distinguished on the basis of numerous criteria, including DNA sequence identity – the gold standard to bacterial classification. Using the latter parameter as the primary taxonomic tool we have seen the suggestion made that the *Tunalikevirus* [7] and the *N4likevirus* (J. Whitman, submitted manuscript) are not monophyletic. With many more T4-like phages sequenced we have reassessed their taxonomy. This has been accomplished through BLASTN analysis in which we calculated the total sequence identity by multiplying the % coverage by the % identity; total proteome by TBLASTX comparisons and CoreGenes3.0 [8]; and a phylogenetic analysis of the large subunit terminase protein using phylogeny.fr [9]. It is clear that many of the phages listed as members of the T4likevirus are sufficiently different to warrant reclassification.

1. Zuber S, Ngom-Bru C, Barretto C, Bruttin A, Brüssow H, Denou E: Genome analysis of phage JS98 defines a fourth major subgroup of T4-like phages in *Escherichia coli*. Journal of Bacteriology 2007, 189:8206-8214.
2. Tétart F, Desplats C, Kutateladze M, Monod C, Ackermann H-W, Krisch HM: Phylogeny of the major head and tail genes of the wide-ranging T4-type bacteriophages. Journal of Bacteriology 2001, 183:358-366.
3. Desplats C, Krisch HM: The diversity and evolution of the T4-type bacteriophages. Res Microbiol 2003, 154:259-267.
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5. Petrov VM, Ratnayaka S, Nolan JM, Miller ES, Karam JD: Genomes of the T4-related bacteriophages as windows on microbial genome evolution. Virology Journal 2010, 7:292.
6. Petrov VM, Nolan JM, Bertrand C, Levy D, Desplats C, Krisch HM, Karam JD: Plasticity of the gene functions for DNA replication in the T4-like phages. Journal of Molecular Biology 2006, 361:46-68.
7. Niu YD, McAllister TA, Nash JH, Kropinski AM, Stanford K: Four *Escherichia coli* O157:H7 phages: a new bacteriophage genus and taxonomic classification of T1-like phages. PLoS ONE 2014, 9:e100426.
8. Mahadevan P, King JF, Seto D: Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and in silico proteomes. International Journal of Computational Biology and Drug Design 2009, 2:100-114.
9. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O: Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research 2008, 36:W465-W469.
10. Lavigne R, Darius P, Summer EJ, Seto D, Mahadevan P, Nilsson AS, Ackermann H-W, Kropinski AM: Classification of *Myoviridae* bacteriophages using protein sequence similarity. BMC Microbiology 2009, 9:224.

Part (b) re-assign to a higher taxon

Code	***2015.020zB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:
Escherichia phage RB49 (proposed name *Escherichia virus RB49*)
Escherichia phage phi1 (proposed name *Escherichia virus phi1*)

Genus:	***Rb49virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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.

Code	***2015.020aaB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:
Escherichia phage RB69 (proposed name *Escherichia virus RB69*)

Genus:	***Rb69virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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.

Code	***2015.020abB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:
Escherichia phage JS98 (proposed name *Escherichia virus JS98*)

Genus:	***Js98virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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.

Code	***2015.020acB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:
Enterobacteria phage SV14 (proposed name *Enterobacteria virus SV14*)
Escherichia phage RB16 (proposed name *Escherichia virus RB16*)
Escherichia phage RB32 (proposed name *Escherichia virus RB32*)
Escherichia phage RB43 (proposed name *Escherichia virus RB43*)
Pseudomonas phage 42 (proposed name *Pseudomonas phage 42*)

Genus:	***Unassigned***
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2015.020adB***	(assigned by ICTV officers)

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

Aeromonas phage 25 (proposed name *Aeromonas virus 25*)

Aeromonas phage 31 (proposed name *Aeromonas virus 31*)

Genus:	***Secunda5virus* (new)**
Subfamily:	
Family:	***Myoviridae***
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	***2015.020aeB***	(assigned by ICTV officers)

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

Aeromonas phage 44RR2.8t (proposed name *Aeromonas virus 44RR2*)

Genus:	***Biquartavirus* (new)**
Subfamily:	
Family:	***Myoviridae***
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 above

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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6. Yeh LS, Hsu T, Karam JD. Divergence of a DNA replication gene cluster in the T4-related bacteriophage RB69. J Bacteriol. 1998; 180(8):2005-13.
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11. Cowley LA, Beckett SJ, Chase-Topping M, Perry N, Dallman TJ, Gally DL, Jenkins C. Analysis of whole genome sequencing for the *Escherichia coli* O157:H7 typing phages. BMC Genomics. 2015;16(1):271.

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.

Fig. 1. Phylogenetic analysis of the large subunit terminase proteins.

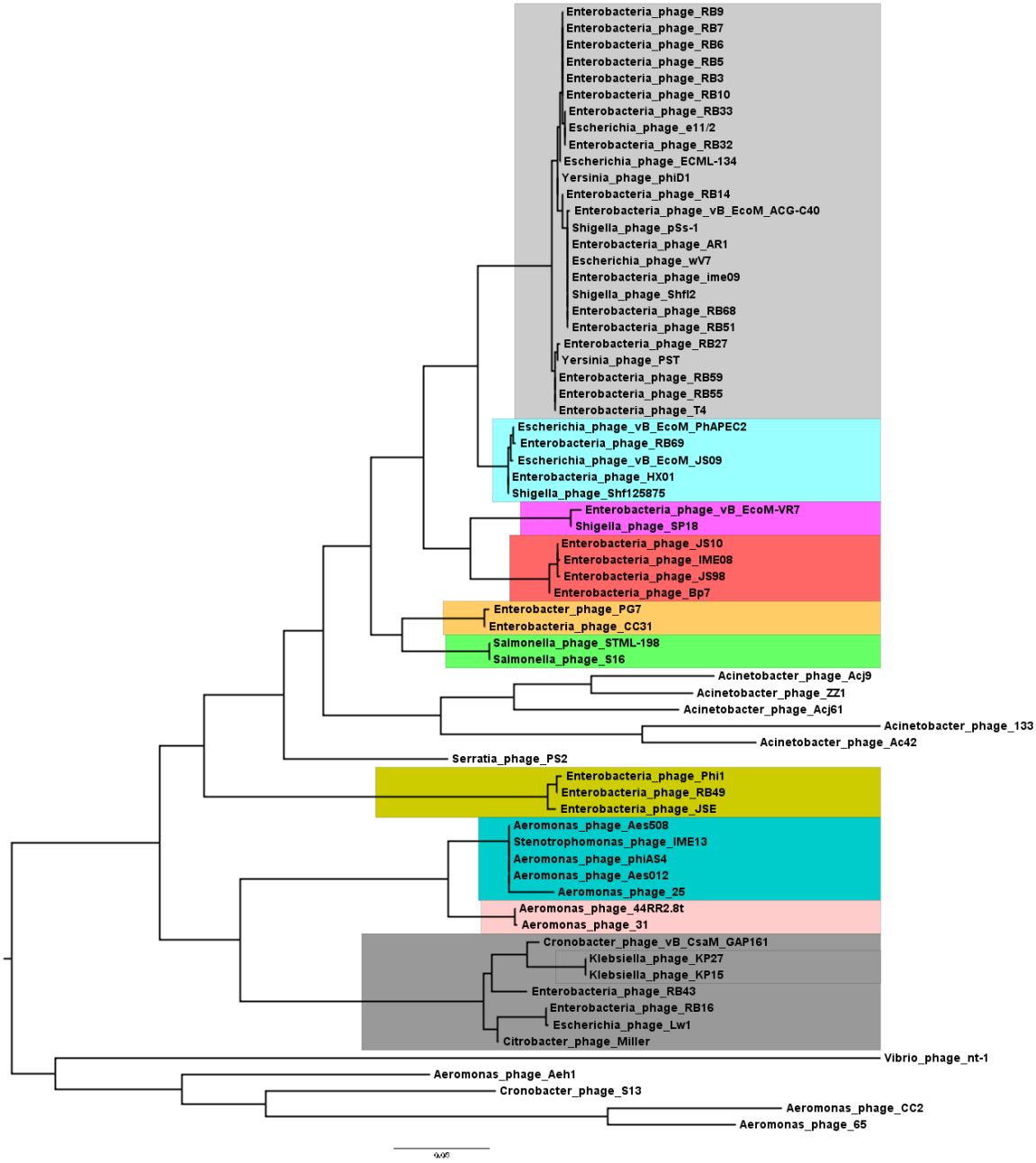

Table 1. BLASTN analyses

	T4	PST	Shfl2	e11/2	phiD1	ECML-134	RB3	RB14	AR1	ime09	RB32	ACG-C40	pSs-1
T4	100	87	87	86	87	86	87	86	85	85	84	82	81
PST	87	100	89	84	89	91	86	93	88	89	91	83	86
Shfl2	86	88	100	86	91	89	89	90	91	94	89	84	91
e11/2	86	84	87	100	87	87	87	88	90	86	89	87	90
phiD1	86	88	92	86	100	86	89	90	90	91	90	85	89
ECML-134	86	91	90	86	86	100	90	92	89	86	92	89	89
RB3	86	86	90	87	90	91	100	93	88	88	91	88	88
RB14	84	91	90	87	89	91	91	100	90	89	92	88	90
AR1	84	87	92	89	91	89	87	91	100	87	89	86	93
ime09	84	89	94	85	91	86	97	90	86	100	89	82	92
RB32	82	90	89	87	89	91	89	92	88	88	100	88	89
vB_EcoM_ACG-C40	81	83	85	87	85	89	88	89	86	83	89	100	87
pSs-1	79	85	90	87	88	87	86	90	91	91	89	86	100
vB_EcoM_JS09	57	53	58	55	60	53	53	58	57	59	57	56	54
HX01	56	55	56	53	62	53	53	55	65	56	54	56	55
Shf125875	54	53	56	56	58	54	53	58	58	56	58	57	56
RB69	54	53	56	56	57	53	53	58	57	56	57	56	56
vB_EcoM_PhAPEC2	53	54	57	56	57	54	53	58	58	57	58	57	56
IME08	45	44	46	43	44	43	44	45	44	47	45	44	45
JS98	43	44	45	41	45	43	43	45	45	45	44	44	46
Bp7	43	43	43	49	47	42	42	43	43	43	43	43	45
JS10	43	43	44	40	44	43	42	43	44	43	43	43	45
SP18	42	42	52	42	54	52	41	52	53	53	52	41	54
vB_EcoM-VR7	41	41	41	41	41	41	41	42	41	43	41	41	42
S16	40	40	39	39	39	39	39	41	39	41	39	40	41
STML-198	40	40	39	38	39	39	39	42	39	42	39	41	41
PG7	38	39	40	37	40	40	41	39	39	40	39	39	41
CC31	37	38	39	38	39	38	39	39	39	40	39	38	41
JSE	14	14	15	14	13	14	14	13	13	13	14	13	13
RB49	14	14	14	14	13	14	14	14	13	14	14	14	12
Phi1	12	14	14	13	15	14	14	14	15	14	14	14	14

	JS09	HX01	Shf125875	RB69	PhAPEC2	IME08	JS98	Bp7	JS10	SP18	VR7
T4	58	57	54	54	54	45	43	44	42	42	42
PST	53	54	53	53	54	43	44	43	43	41	41
Shfl2	57	55	55	56	56	45	44	43	43	52	41
e11/2	56	53	56	56	56	43	41	50	40	42	41
phiD1	59	62	57	57	57	44	44	47	43	53	41
ECML-134	53	53	53	53	54	43	43	42	42	51	41
RB3	53	53	53	53	53	43	43	43	42	41	41
RB14	57	54	58	58	58	44	44	43	43	52	41
AR1	57	65	57	57	58	43	45	44	44	52	41
ime09	58	56	56	55	57	46	44	43	43	52	42
RB32	56	53	57	56	57	44	43	43	43	51	41
vB_EcoM_ACG-C40	55	55	57	56	57	43	44	43	43	41	40
pSs-1	53	53	55	55	55	43	46	44	43	53	41
vB_EcoM_JS09	100	94	91	91	92	48	48	47	46	55	43
HX01	94	100	90	90	91	51	50	44	49	54	39
Shf125875	91	89	100	94	94	47	50	49	47	50	41
RB69	90	89	93	100	95	46	49	48	47	51	40
vB_EcoM_PhAPEC2	92	90	94	95	100	47	50	49	47	51	41
IME08	48	51	47	47	47	100	78	84	78	62	57
JS98	48	50	49	50	50	77	100	98	93	59	62
Bp7	46	43	48	48	48	82	83	100	83	58	59
JS10	47	49	47	47	47	78	94	85	100	59	60
SP18	55	55	51	52	52	62	60	59	59	100	94
vB_EcoM-VR7	42	39	41	41	41	55	62	59	59	84	100
S16	36	36	36	36	36	33	31	34	33	31	32
STML-198	36	36	35	36	36	32	33	33	33	31	33
PG7	37	37	37	37	37	35	35	34	35	31	32
CC31	37	37	37	37	37	34	35	34	34	32	31
JSE	13	12	12	13	13	11	11	12	11	12	11
RB49	13	13	14	14	13	11	12	11	11	12	11
Phi1	13	12	13	13	13	12	11	11	11	12	11

	SP18	VR7	S16	STML-198	PG7	CC31	JSE	RB49	Phi1
T4	42	42	42	42	37	38	15	14	13
PST	41	41	42	42	38	38	14	14	14
Shfl2	52	41	41	41	39	39	15	14	14
e11/2	42	41	41	41	37	39	13	14	14
phiD1	53	41	41	41	39	39	13	14	15
ECML-134	51	41	41	41	38	38	14	14	14
RB3	41	41	42	41	39	40	15	14	14
RB14	52	41	42	44	38	39	13	14	14
AR1	52	41	41	41	38	39	13	13	15
ime09	52	42	42	44	39	40	13	14	14
RB32	51	41	41	41	38	39	14	14	14
vB_EcoM_ACG-C40	41	40	42	44	38	39	13	14	14
pSs-1	53	41	42	44	39	41	13	13	14
vB_EcoM_JS09	55	43	39	39	36	37	13	13	13
HX01	54	39	39	39	36	37	12	14	13
Shf125875	50	41	38	38	37	37	13	14	13
RB69	51	40	38	38	33	37	13	14	13
vB_EcoM_PhAPEC2	51	41	39	38	35	37	13	13	13
IME08	62	57	35	35	34	35	12	12	12
JS98	59	62	34	36	33	35	11	12	11
Bp7	58	59	35	35	33	34	12	11	11
JS10	59	60	35	36	33	35	11	12	11
SP18	100	94	33	34	31	33	12	12	12
vB_EcoM-VR7	84	100	33	36	31	31	11	12	11
S16	31	32	100	92	44	45	12	13	13
STML-198	31	33	91	100	43	45	12	13	13
PG7	31	32	48	47	100	87	13	14	14
CC31	32	31	47	48	84	100	13	14	14
JSE	12	11	12	13	13	13	100	94	91
RB49	12	11	13	13	14	14	92	100	94
Phi1	12	11	13	14	13	14	90	94	100

Table 2. T4-related phage genera and species

Genus	Species	Host	Accession No.	Related strains
T4virus	T4	*Escherichia*	AF158101.6	T4T; T4 strain wild; T4 strain GT7; T4 strain 147; RB55(KM607002); RB59 (KM607003)
	AR1	*Escherichia*	AP011113	RB51 (FJ839693); RB68 (KM607004); wV7 (HM997020); RB27 (KM607000)
	RB32	*Escherichia*	DQ904452	RB33(KM607001)
	RB14	*Escherichia*	FJ839692	
	ime09	*Escherichia*	JN202312	
	e11/2 (vB_EcoM_ 112)	*Escherichia*	KJ668714.2	
	ECML-134	*Escherichia*	JX128259	
	RB3	*Escherichia*	KM606994	RB5 (KM606995);

				RB6 (KM606996); RB7 (KM606997); RB9 (KM606998); RB10 (KM606999)
	vB_EcoM_ACG-C40	*Escherichia*	JN986846	
	Shfl2	*Shigella*	HM035025	
	pSs-1	*Shigella*	KM501444	
	PST	*Yersinia*	KF208315	
	phiD1	*Yersinia*	HE956711	
Rb69virus	RB69	*Escherichia*	AY303349	vB_EcoM_PhAPEC2 (KF562341)
	vB_EcoM_JS09	*Escherichia*	KF582788	O157 typing phages 3 (KP869101) & 6 (KP869104)
	HX01	*Escherichia*	JX536493	
	Shf125875	*Shigella*	KM407600	
Rb49virus	RB49	*Escherichia*	AY343333	GEC-3S (HE978309)
	Phi1	*Escherichia*	EF437941	
Js98virus	JS98	*Escherichia*	EF469154	
	IME08	*Escherichia*	HM071924	
	Bp7	*Escherichia*	HQ829472	
	JS10	*Escherichia*	EU863409	
	vB_EcoM_VR5	*Escherichia*	KP007359	
S16virus	STML-198	*Salmonella*	JX181825	
	S16	*Salmonella*	HQ331142	STP4-a (KJ000058)
Sp18virus	SP18	*Shigella*	GQ981382	
	vB_EcoM-VR7	*Escherichia*	HM563683	
	vB_EcoM-VR20	*Escherichia*	KP007360	
	vB_EcoM-VR25	*Escherichia*	KP007361	
	vB_EcoM-VR26	*Escherichia*	KP007362	
Cc31virus	CC31	*Enterobacter*	GU323318	
	PG7	*Enterobacter*	KJ101592	

Table 3. Average properties of each genus

Phage genus	Size (kb)	GC%	No. of Proteins	No. of tRNAs
T4virus	166.9	35.4	274	9

Rb69virus	168.7	37.6	271	2
Rb49virus	164.9	40.5	277	0
Js98virus	170.6	39.5	262	2
S16virus	159.2	36.9	262	3
Sp18virus	170.0	40.4	289	2
Cc31virus	169.4	39.9	287	14