This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

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

MODULE 1: TITLE, AUTHORS, etc

Code assigned:	***2013.016aV***	(to be completed by ICTV officers)

Short title: To create 62 new species in the genus *L5likevirus*, within the family *Siphoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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

Evelien M Adriaenssens, evelien.adriaenssens@gmail.com
Andrew M Kropinski, kropinsk@queensu.ca
Rob Lavigne, rob.lavigne@biw.kuleuven.be
John Nash, john.nash@phac-aspc.gc.ca

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

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

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

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

MODULE 2: NEW SPECIES

creating and naming one or more new species.

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

Code	***2013.016aV***	(assigned by ICTV officers)

To create 62 new species within:

Genus:	***L5likevirus***
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

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

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Mycobacterium phage L5	Z18946
Mycobacterium phage SWU1	JF946695
Mycobacterium phage Che12	DQ398043
Mycobacterium phage D29	AF022214
Mycobacterium phage trixie	JN408461

Mycobacterium phage turbido	JN408460
Mycobacterium phage Ta17a	JN400277
Mycobacterium phage redrock	GU339467
Mycobacterium phage pukovnik	EU744250
Mycobacterium phage ericb	JN049605
Mycobacterium phage hammer	JF937094
Mycobacterium phage gladiator	JF704097
Mycobacterium phage jeffabunny	JN699019
Mycobacterium phage Bxb1	AF271693
Mycobacterium phage billknuckles	JN699000
Mycobacterium phage switzer	JF937108
Mycobacterium phage kssjeb	JF937110
Mycobacterium phage U2	AY500152
Mycobacterium phage mrgordo	JN020140
Mycobacterium phage museum	JF937103
Mycobacterium phage lesedi	JF937100
Mycobacterium phage solon	EU826470
Mycobacterium phage bethlehem	AY500153
Mycobacterium phage KBG	EU744248
Mycobacterium phage kugel	JN699016
Mycobacterium phage bruns	JN698998
Mycobacterium phage violet	JN687951
Mycobacterium phage euphoria	JN153086
Mycobacterium phage BBPiebs31	JF957057
Mycobacterium phage nepal	JQ698665
Mycobacterium phage doom	JN153085
Mycobacterium phage marcell	JX307705
Mycobacterium phage lockley	EU744249
Mycobacterium phage skipole	GU247132
Mycobacterium phage JC27	JF937099
Mycobacterium phage Jasper	EU744251
Mycobacterium phage Ridgecb	JN398369
Mycobacterium phage Perseus	JN572689
Mycobacterium phage Bxz2	AY129332
Mycobacterium phage JHC117	JF704098
Mycobacterium phage microwolf	JF704101
Mycobacterium phage wonder	HM755814
Mycobacterium phage heldan	JF957058
Mycobacterium phage rockstar	JF704111
Mycobacterium phage peaches	GQ303263
Mycobacterium phage arturo	JX307702
Mycobacterium phage LHTSCC	JN699015
Mycobacterium phage backyardigan	JF704093
Mycobacterium phage benedict	JN083852
Mycobacterium phage george	JF704107
Mycobacterium phage cuco	JN408459
Mycobacterium phage tiger	JQ684677
Mycobacterium phage timshel	JF957060
Mycobacterium phage saintus	JN831654
Mycobacterium phage astro	JX015524
Mycobacterium phage packman	JF704110

Mycobacterium phage alma	JN699005
Mycobacterium phage rebeuca	JX411619
Mycobacterium phage goose	JX307704
Mycobacterium phage twister	JQ512844
Rhodococcus phage RGL3	JN116826
Rhodococcus phage RER2	JN116827

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

This genus was originally recognized by the Mycobacteriophage group (www.phagesdb.org) as belonging to cluster A. Phages belonging to this genus share a comparable genome size (49 – 53 kb), a comparable GC content (60 – 65%), and comparable defined genome ends. Members of this genus also have a comparable morphology, with an isometric head and a long, non-contractile tail (Figure 1).

A ClustalW analysis of the complete genomes of this genus with all other *Mycobacterium* phages belonging to the *Siphoviridae* reveals that this genus is a clearly separate group (Figures 2 and 3).

We propose a shared protein content of at least 40% with the type phage, *Mycobacterium phage L5*. Based on the recognizable groups in Figure 2 within this genus, we performed a CoreGenes 3.5 analysis [1–3] with selected phages from each group against L5 as the reference phage (Table 1). An exception on the 40% rule is made for the *Rhodococcus* phages RGL3 and RER2, which both have 38.8 % shared proteins with L5, due to their small number of CDS annotated. Figure 3 shows the clear relatedness at the protein level between RGL3 and L5.

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 EMBOSS Stretcher algorithm.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

1. Mahadevan P, King JF, Seto (2009) 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 2: 100–114.

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

3. Zafar N, Mazumder R, Seto D (2002) CoreGenes: A computational tool for identifying and cataloging “core” genes in a set of small genomes. BMC Bioinformatics 3: 12. doi:10.1186/1471-2105-3-12.

4. Hatfull GF, Sarkis GJ (1993) DNA sequence, structure and gene expression of mycobacteriophage L5: a phage system for mycobacterial genetics. Molecular microbiology 7: 395–405.

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.

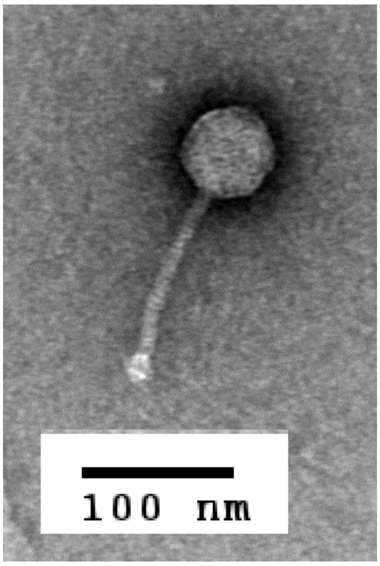

Figure 1: EM picture of *Mycobacterium phage L5* (http://phagesdb.org/media/emPics/L5.tif)

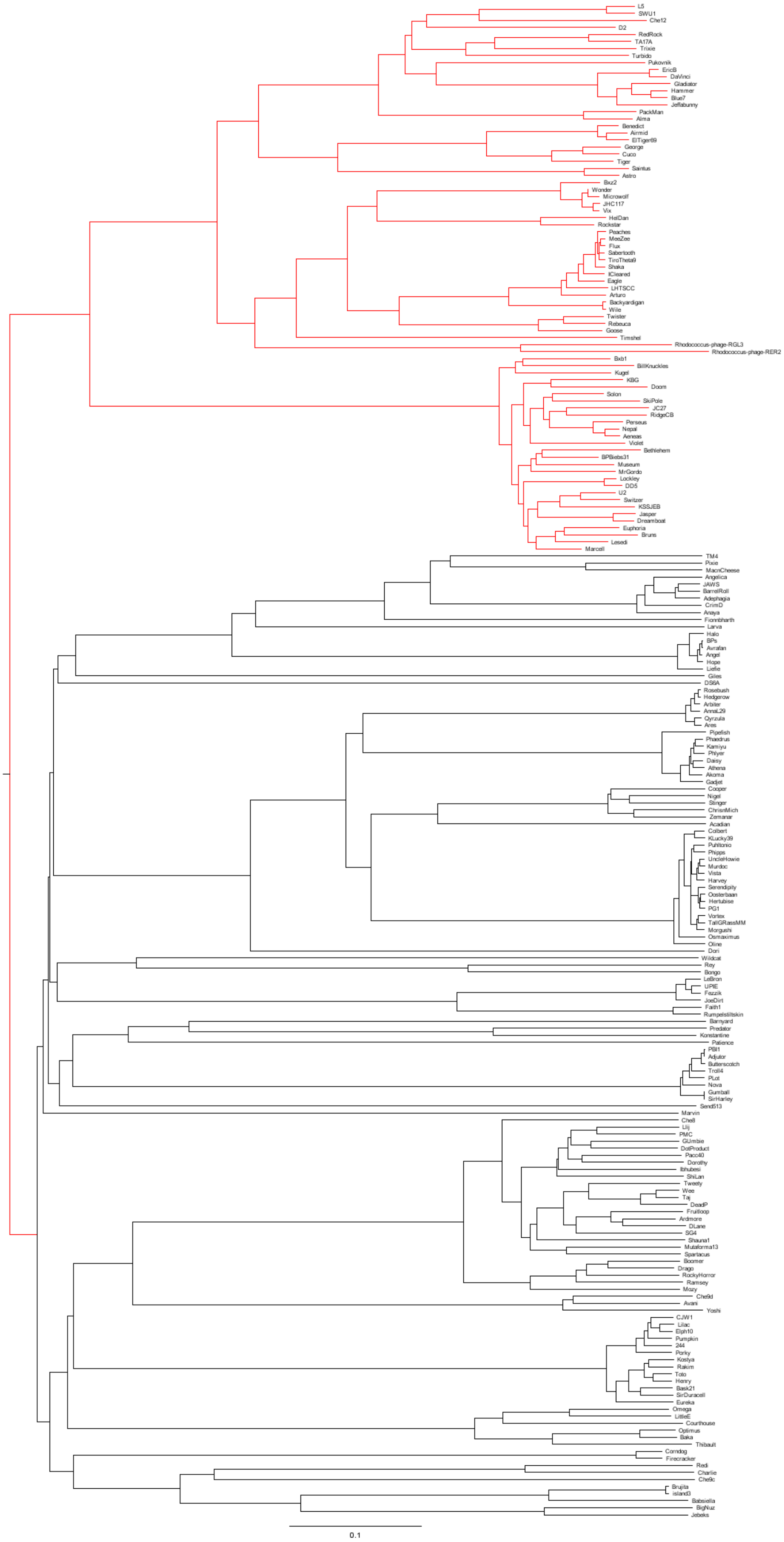
L5
SWU1
Che12
D2
RedRock
TA17A
Trixie
Turbido
Pukovnik
EricB
DaVinci
Gladiator
Hammer
Blue7
Jeffabunny
PackMan
Alma
Benedict
Airmid
ElTiger69
George
Cuco
Tiger
Saintus
Astro
Bxz2
Wonder
Microwolf
JHC117
Vix
HelDan
Rockstar
Peaches
MeeZee
Flux
Sabertooth
TiroTheta9
Shaka
ICleared
Eagle
LHTSCC
Arturo
Backyardigan
Wile
Twister
Rebeuca
Goose
Timshel
Rhodococcus-phage-RGL3
Rhodococcus-phage-RER2
Bxb1
BillKnuckles
Kugel
KBG
Doom
Solon
SkiPole
JC27
RidgeCB
Perseus
Nepal
Aeneas
Violet
Bethlehem
BPBiebs31
Museum
MrGordo
Lockley
DD5
U2
Switzer
KSSJEB
Jasper
Dreamboat
Euphoria
Bruns
Lesedi
Marcell
TM4
Pixie
MacnCheese
Angelica
JAWS
BarrelRoll
Adephagia
CrimD
Anaya
Fionnbharth
Larva
Halo
BPs
Avrafan
Angel
Hope
Liefie
Giles
DS6A
Rosebush
Hedgerow
Arbiter
AnnaL29
Qyrzula
Ares
Pipefish
Phaedrus
Kamiyu
Phlyer
Daisy
Athena
Akoma
Gadjet
Cooper
Nigel
Stinger
ChrisnMich
Zemanar
Acadian
Colbert
KLucky39
Puhltonio
Phipps
UncleHowie
Murdoc
Vista
Harvey
Serendipity
Oosterbaan
Hertubise
PG1
Vortex
TallGRassMM
Morgushi
Osmaximus
Oline
Dori
Wildcat
Rey
Bongo
LeBron
UPIE
Fezzik
JoeDirt
Faith1
Rumpelstiltskin
Barnyard
Predator
Konstantine
Patience
PBI1
Adjutor
Butterscotch
Troll4
PLot
Nova
Gumball
SirHarley
Send513
Marvin
Che8
Llij
PMC
GUmbie
DotProduct
Pacc40
Dorothy
Ibhubesi
ShiLan
Tweety
Wee
Taj
DeadP
Fruitloop
Ardmore
DLane
SG4
Shauna1
Mutaforma13
Spartacus
Boomer
Drago
RockyHorror
Ramsey
Mozy
Che9d
Avani
Yoshi
CJW1
Lilac
Elph10
Pumpkin
244
Porky
Kostya
Rakim
Toto
Henry
Bask21
SirDuracell
Eureka
Omega
LittleE
Courthouse
Optimus
Baka
Thibault
Corndog
Firecracker
Redi
Charlie
Che9c
Brujita
island3
Babsiella
BigNuz
Jebeks
0.1

Figure 2: ClustalW phylogenetic tree (NJ) of complete genomes of all *Mycobacterium* siphoviruses in the NCBI database in November 2012. The genus *L5likevirus* with its newly proposed members is in red.

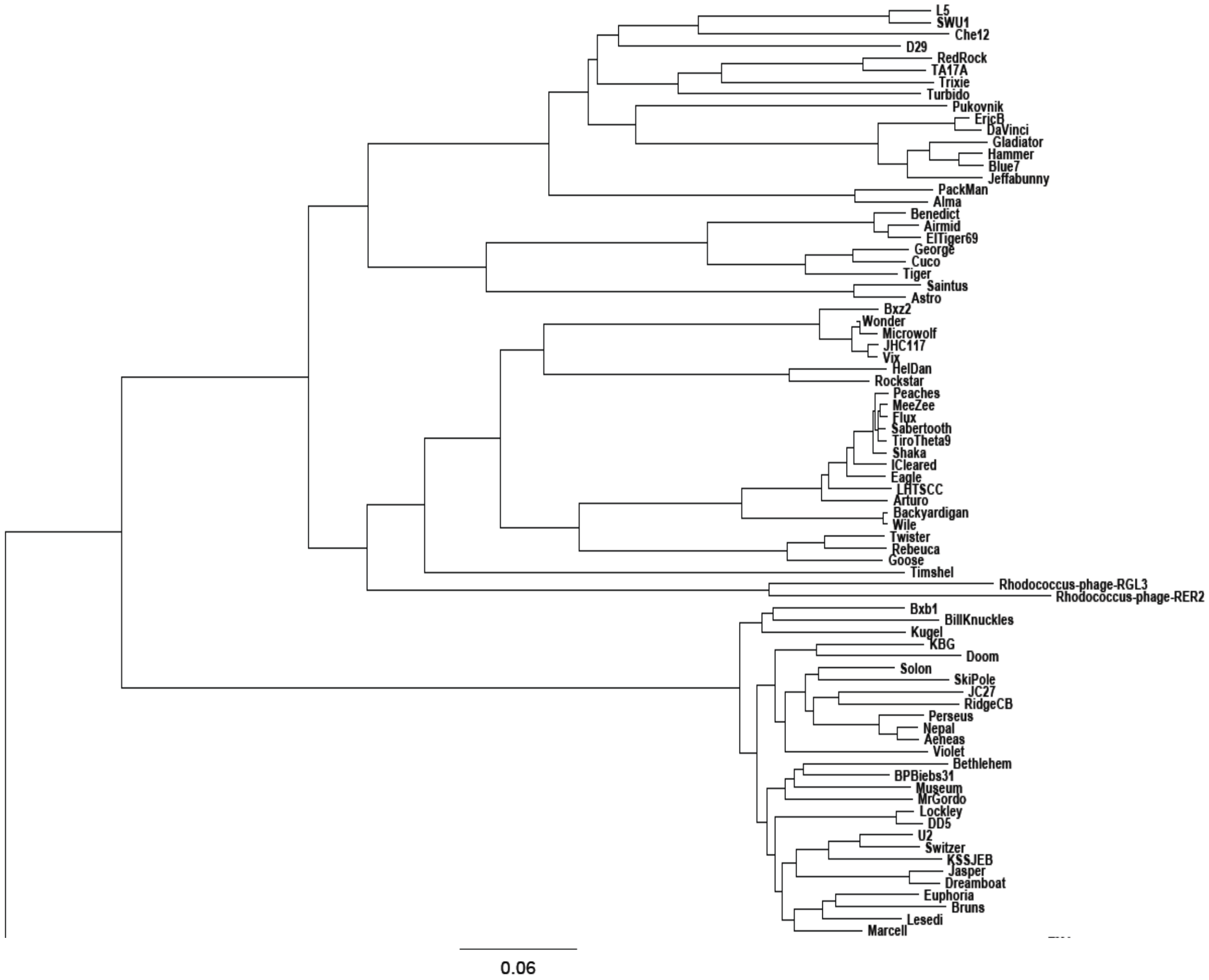

Figure 3: ClustalW phylogenetic tree of complete genomes of the members of the genus *L5likevirus*, excerpt of Figure 2.

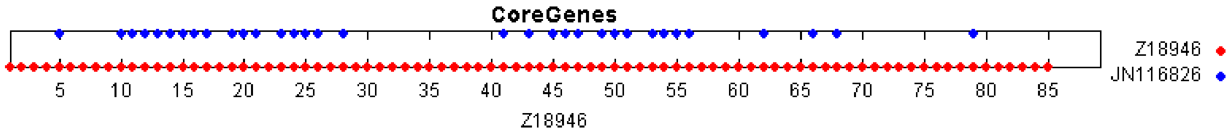

Figure 4: CoreGenes 3.5 comparison of *Mycobacterium phage L5* (GenBank accession number Z18946) and *Rhodococcus phage Rgl3* (GenBank accession number JN116826).

Table 1: CoreGenes 3.5 analysis of selected phages with the type phage of the genus, *Mycobacterium phage L5*.

Phage Name	% proteins in common with L5	Isolates belonging to the same species
Mycobacterium phage SWU1	95.3	
Mycobacterium phage Che12	82.4	
Mycobacterium phage trixie	72.9	
Mycobacterium phage turbido	70.6	
Mycobacterium phage Ta17a	68.2	
Mycobacterium phage redrock	69.4	
Mycobacterium phage pukovnik	68.2	
Mycobacterium phage ericb	67.1	EricB, DaVinci
Mycobacterium phage hammer	68.2	Hammer, Blue
Mycobacterium phage gladiator	65.9	
Mycobacterium phage jeffabunny	60.0	
*Mycobacterium phage Bxb1**	43.5	
Mycobacterium phage billknuckles	42.4	
Mycobacterium phage switzer	43.5	
Mycobacterium phage kssjeb	43.5	
Mycobacterium phage U2	42.4	
Mycobacterium phage mrgordo	43.5	
Mycobacterium phage museum	43.5	
Mycobacterium phage lesedi	44.7	
Mycobacterium phage solon	43.5	
Mycobacterium phage bethlehem	44.7	
Mycobacterium phage KBG	42.4	
Mycobacterium phage kugel	43.5	
Mycobacterium phage bruns	43.5	
Mycobacterium phage violet	43.5	
Mycobacterium phage euphoria	44.7	
Mycobacterium phage BPBiebs31	43.5	
Mycobacterium phage nepal	42.4	Nepal, Aeneas
Mycobacterium phage doom	44.7	
Mycobacterium phage marcell	43.5	
Mycobacterium phage lockley	42.4	Lockley, DD5
Mycobacterium phage skipole	44.7	
Mycobacterium phage JC27	44.7	
Mycobacterium phage jasper	44.7	Jasper, Dreamboat
Mycobacterium phage ridgecb	43.5	
Mycobacterium phage perseus	43.5	
Mycobacterium phage Bxz2	61.2	
Mycobacterium phage JHC117	61.2	
Mycobacterium phage microwolf	62.4	
Mycobacterium phage wonder	34.1	
Mycobacterium phage heldan	60.0	
Mycobacterium phage rockstar	56.5	
Mycobacterium phage peaches	56.5	Peaches, TiroTheta9, Flux, Sabertooth, MeeZee, Shaka, ICleared, Eagle
Mycobacterium phage arturo	57.7	
Mycobacterium phage LHTSCC	58.8	

Mycobacterium phage backyardigan	55.3	Backyardigan, Wile
Mycobacterium phage benedict	49.4	
Mycobacterium phage george	48.2	
Mycobacterium phage cuco	51.8	
Mycobacterium phage tger	49.4	
Mycobacterium phage timshel	57.7	
Mycobacterium phage saintus	50.6	
Mycobacterium phage astro	52.9	
Mycobacterium phage packman	68.2	
Mycobacterium phage alma	69.4	
Mycobacterium phage rebeuca	55.3	
Mycobacterium phage goose	57.7	
Mycobacterium phage twister	56.5	
Rhodococcus phage RGL3	38.8	
Rhodococcus phage RER2	38.8	