

vir.Acetyltransf_1.phy.HG1.seqs.iqtree.treefile
n=2539 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- Acetyltransf_1.HG2.17:NAA50 n = 43
- Acetyltransf_1.HG2.8:NAA60 n = 14
- Acetyltransf_1.HG4.1:SAT1/SAT2/SATL1 n = 6
- Acetyltransf_1.HG8.1:NAA20 n = 5
- Acetyltransf_1.HG1.14:NAA30 n = 3
- Acetyltransf_1.HG1.43:like:NAT14:likeclu:23 n = 3
- Acetyltransf_1.HG1.28:like:NAT14:likeclu:23 n = 2
- Acetyltransf_1.HG1.46:like:NAT14:likeclu:23 n = 2
- Acetyltransf_1.HG2.16:like:NAA50:likeclu:17 n = 2
- Acetyltransf_1.HG2.3:like:NAA50/NAA60:likeclu:8/17 n = 2
- Acetyltransf_1.HG6.0:like:NAA10/NAA11:likeclu:1 n = 2
- Acetyltransf_1.HG6.1:NAA10/NAA11 n = 2
- other n = 6

- Iridoviridae n = 1
- Mimiviridae n = 20
- Myoviridae n = 36
- NA n = 9
- Phycodnaviridae n = 3
- Podoviridae n = 6
- Siphoviridae n = 5

Acetyltransf_1
vir.Acetyltransf_1.phy.HG10.seqs.iqtree.treefile
n=194 sequences

- eukaryotes
- archaea
- bacteria
- viruses



2

- Mimiviridae n = 3
- Myoviridae n = 2
- NA n = 1
- Siphoviridae n = 1

Acetyltransf_1
vir.Acetyltransf_1.phy.HG11.seqs.iqtree.treefile
n=174 sequences

eukaryotes
archaea
bacteria
viruses

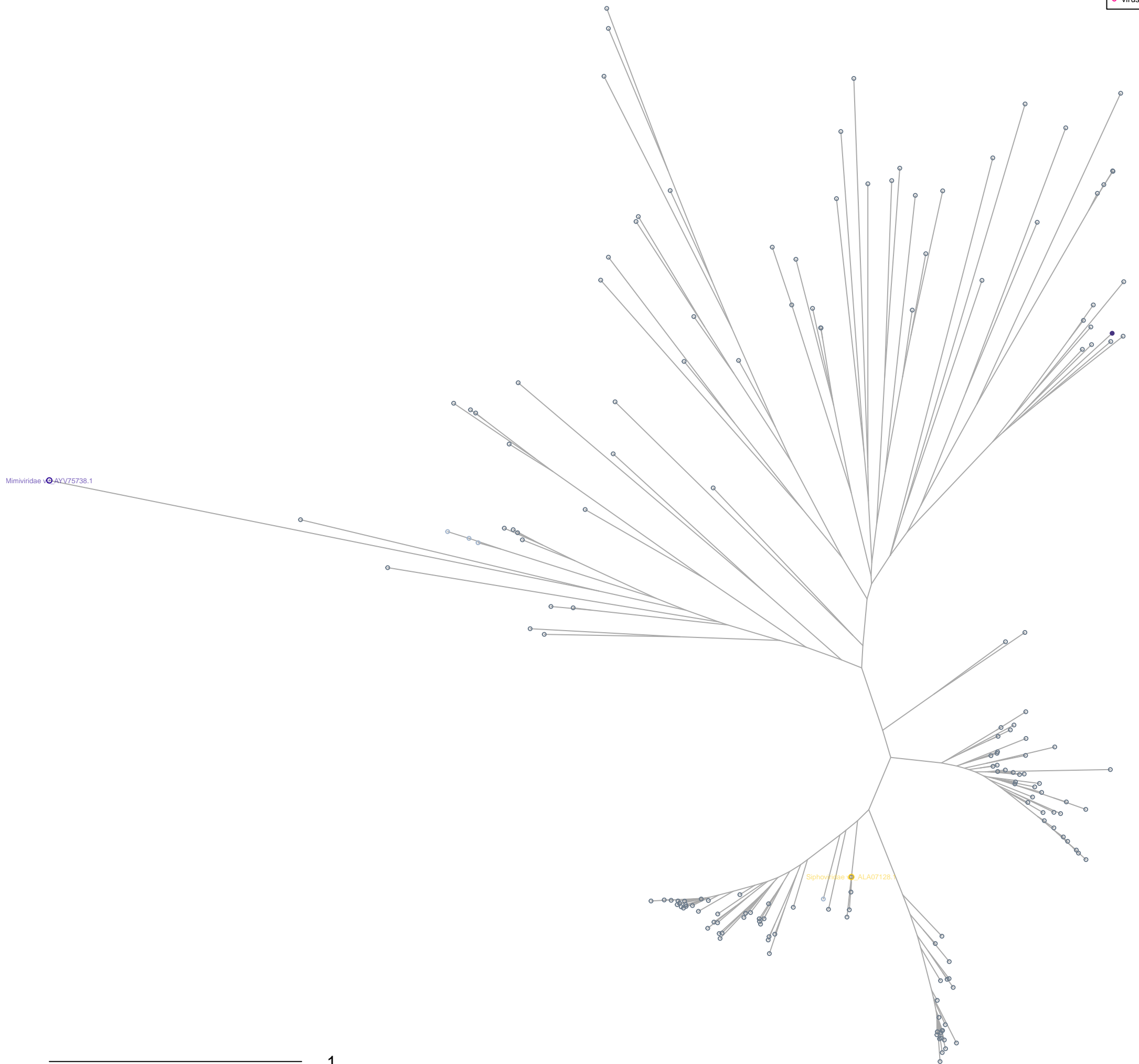
Mimiviridae AY75738.1

Siphoviridae ALA07128.1

1

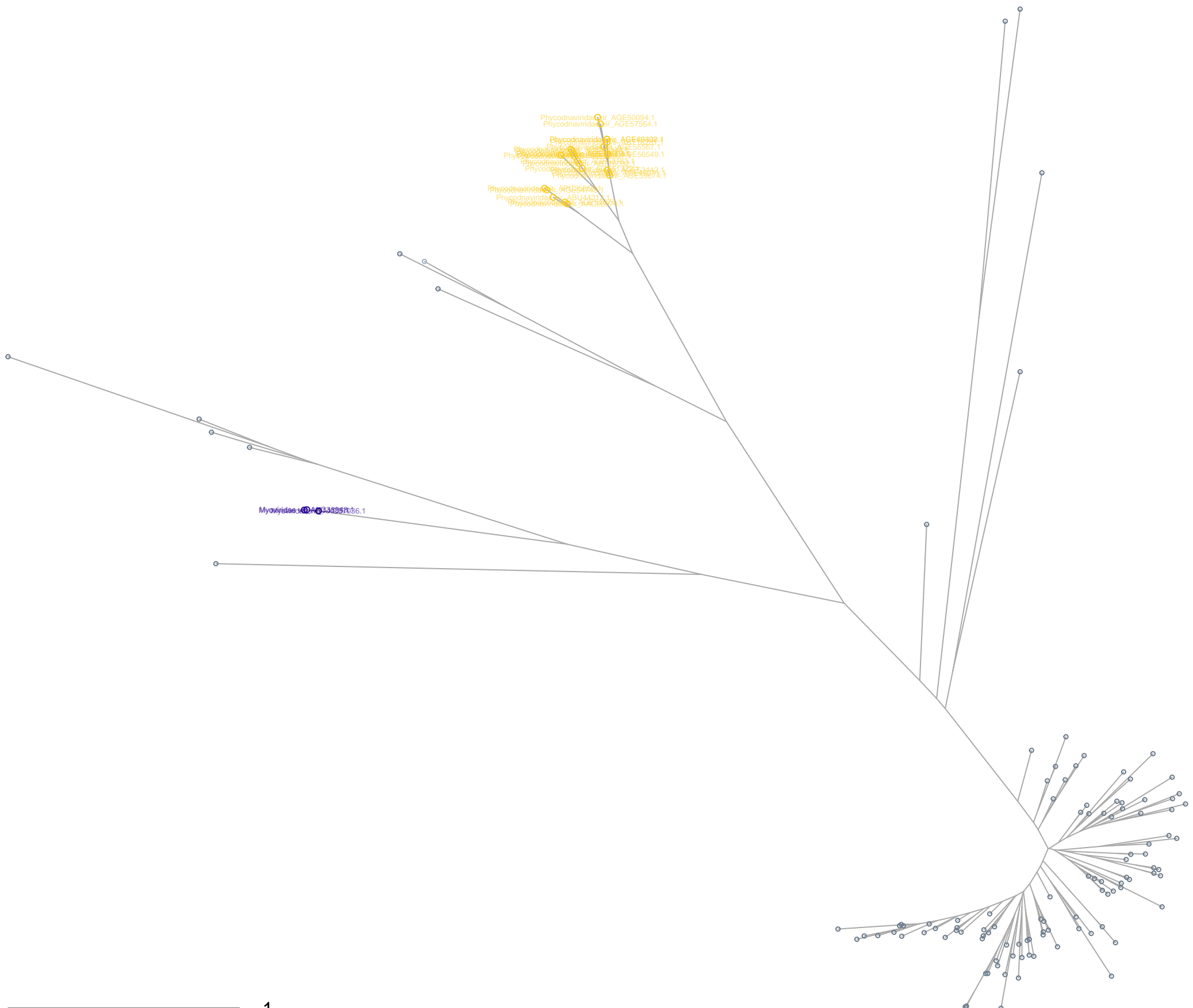
other n = 1

Mimiviridae n = 1
Siphoviridae n = 1



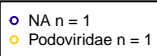
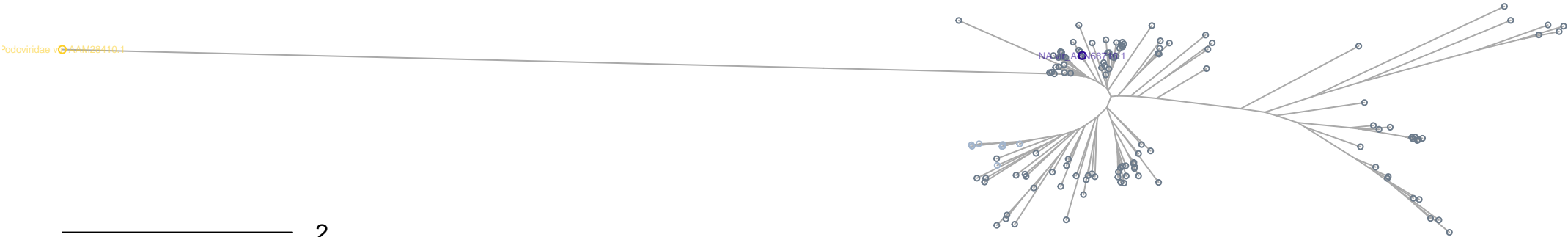
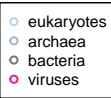
Acetyltransf_1
vir.Acetyltransf_1.phy.HG12.seqs.iqtree.treefile
n=142 sequences

- eukaryotes
- archaea
- bacteria
- viruses



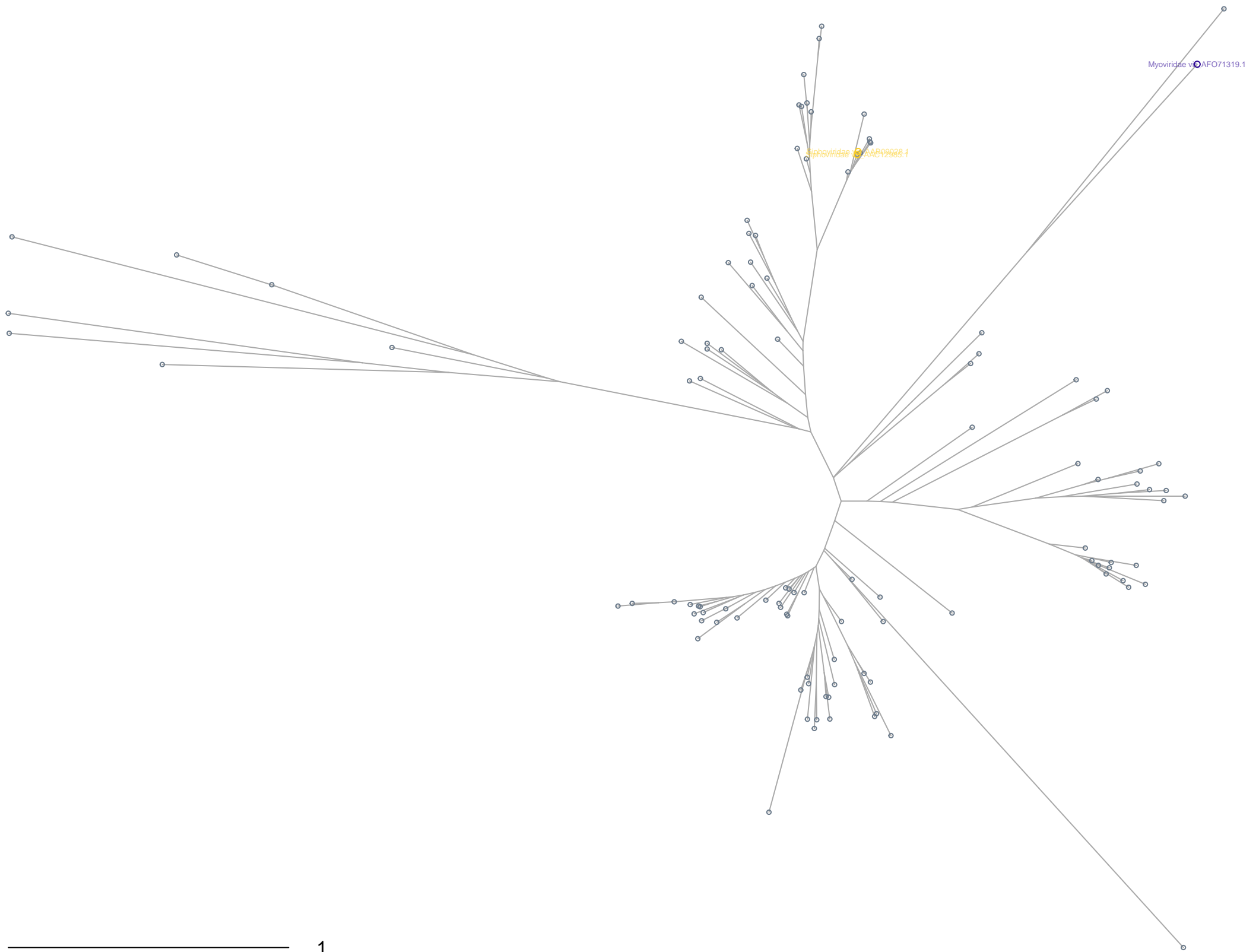
1

- Myoviridae n = 3
- Phycodnaviridae n = 24

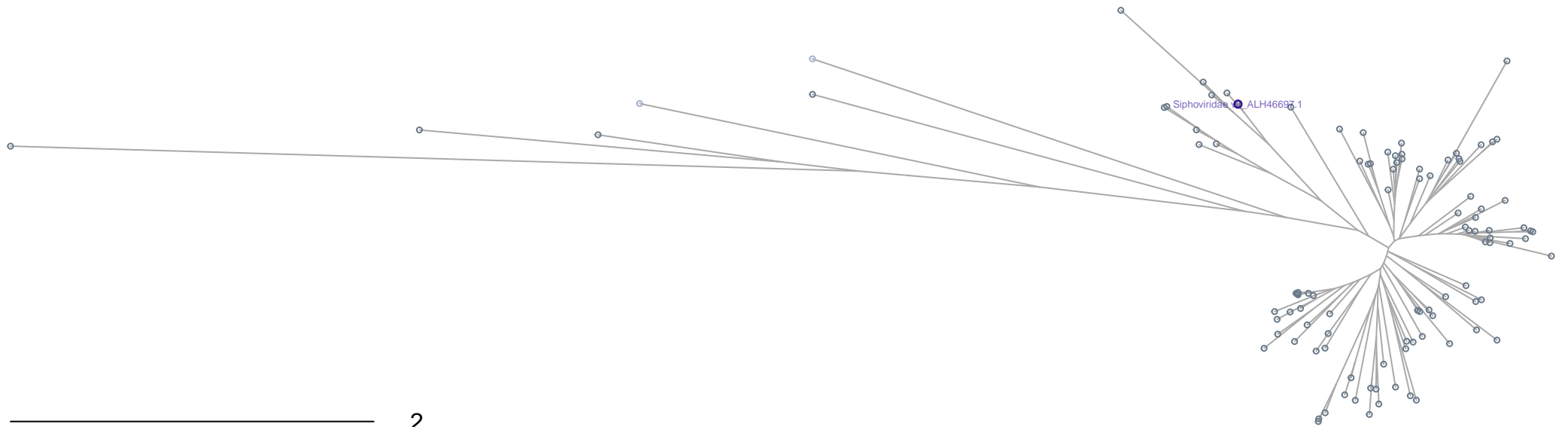


Acetyltransf_1
vir.Acetyltransf_1.phy.HG14.seqs.iqtree.treefile
n=113 sequences

- eukaryotes
- archaea
- bacteria
- viruses

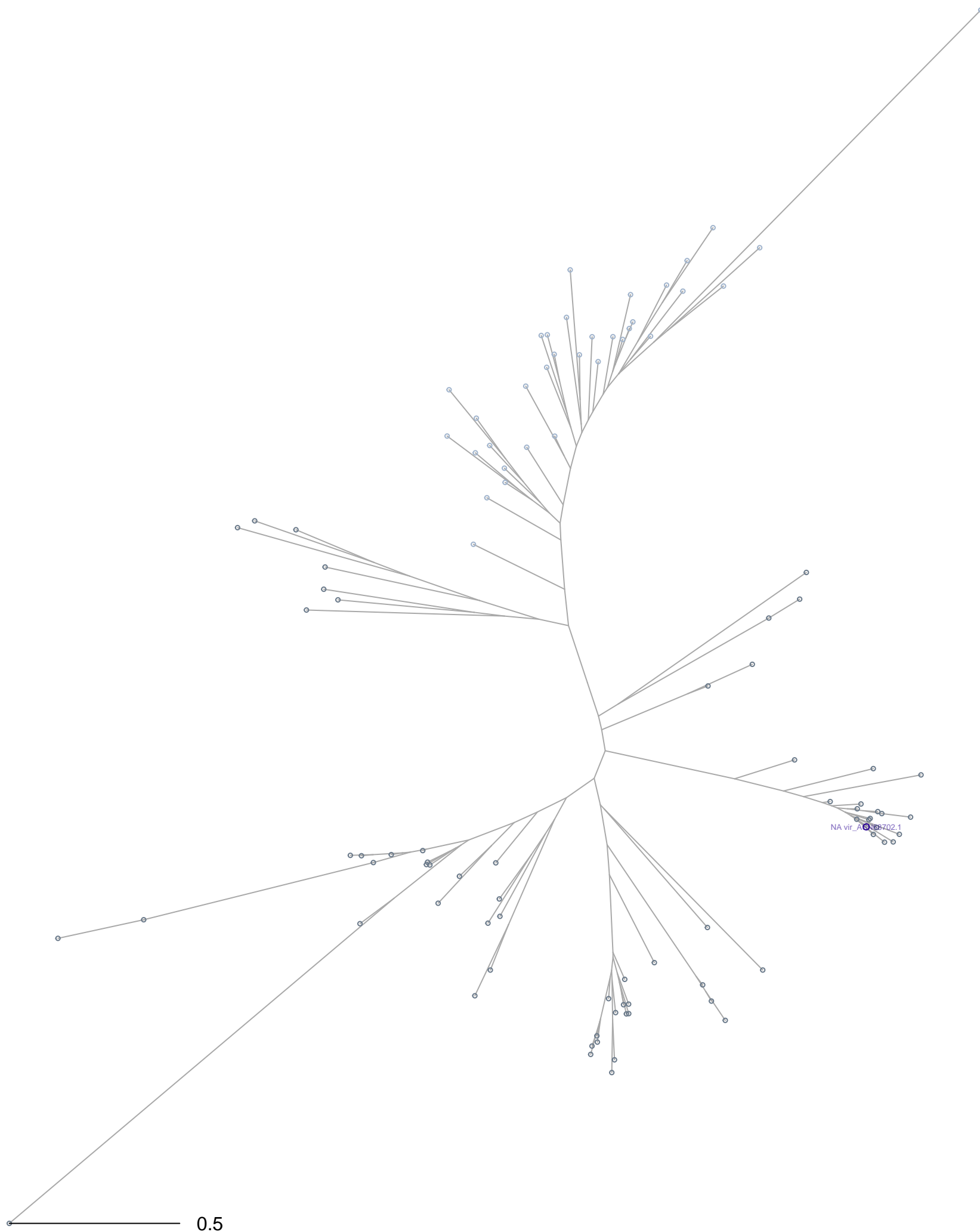


- Myoviridae n = 1
- Siphoviridae n = 2

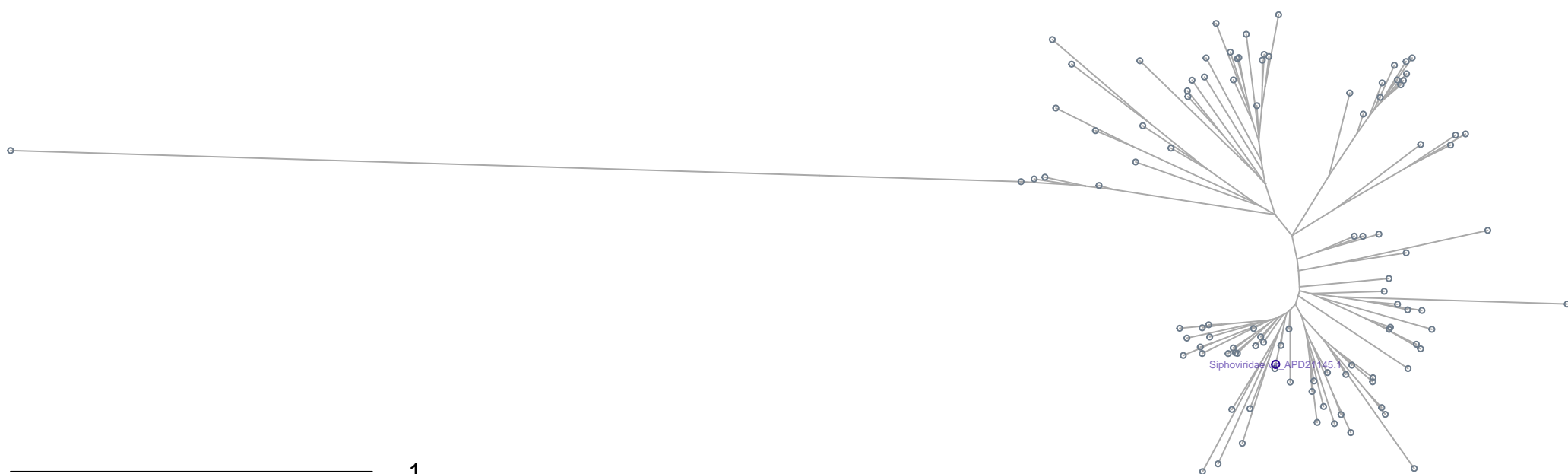


Acetyltransf_1
vir.Acetyltransf_1.phy.HG16.seqs.iqtree.treefile
n=103 sequences

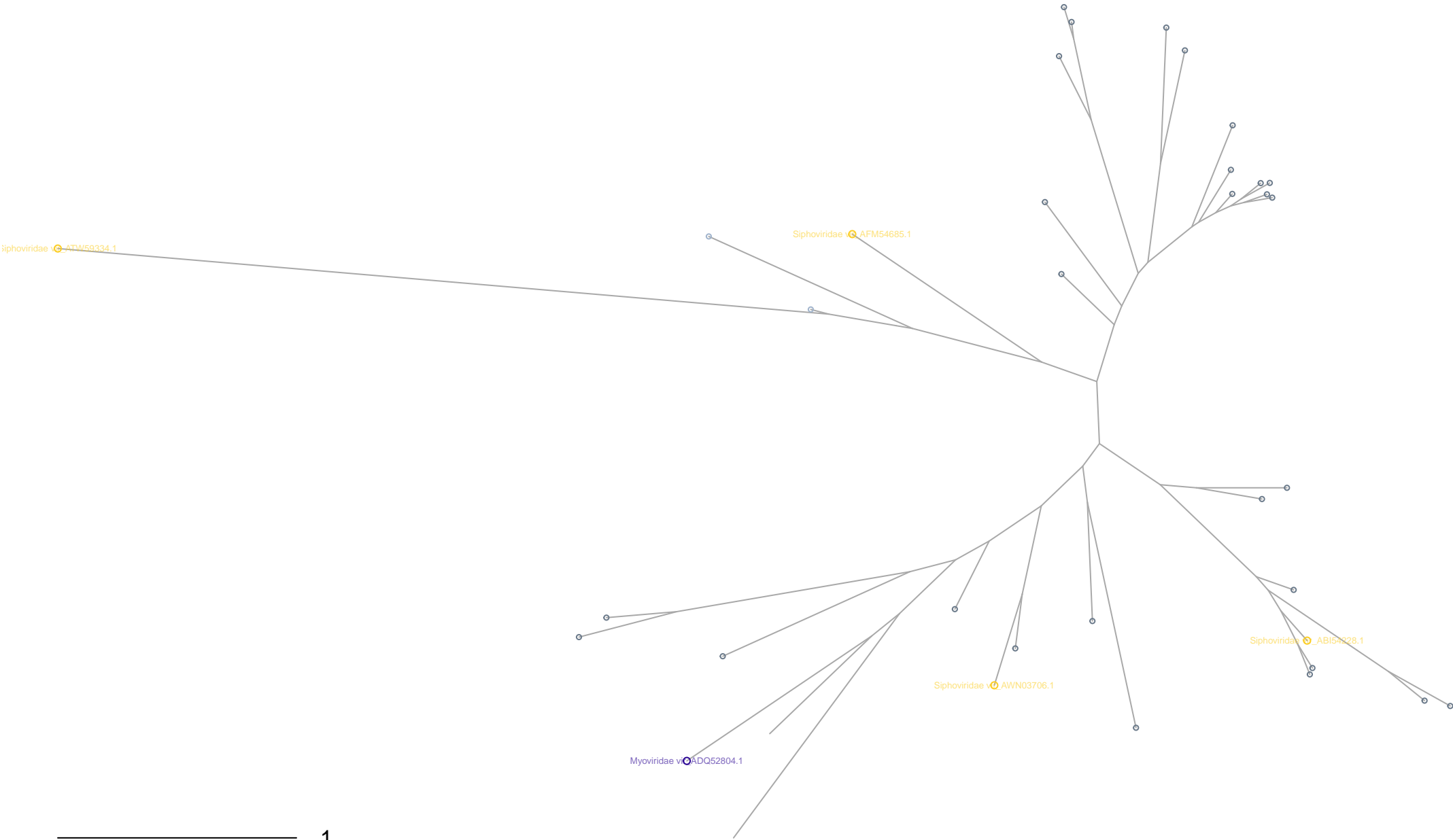
eukaryotes
archaea
bacteria
viruses



NA n = 1



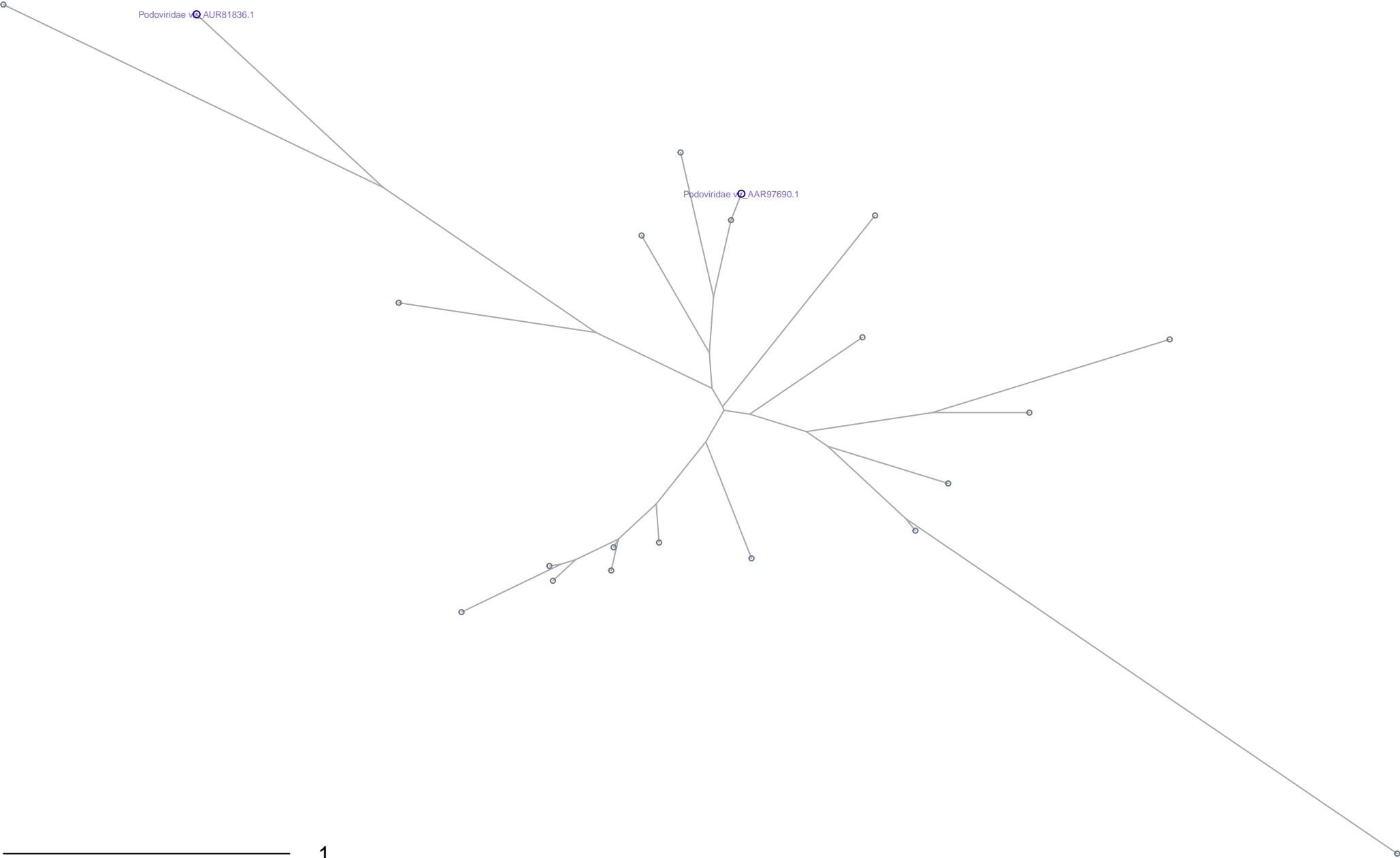
- eukaryotes
- archaea
- bacteria
- viruses



- Myoviridae n = 1
- Siphoviridae n = 4

Acetyltransf_1
vir.Acetyltransf_1.phy.HG19.seqs.iqtree.treefile
n=21 sequences

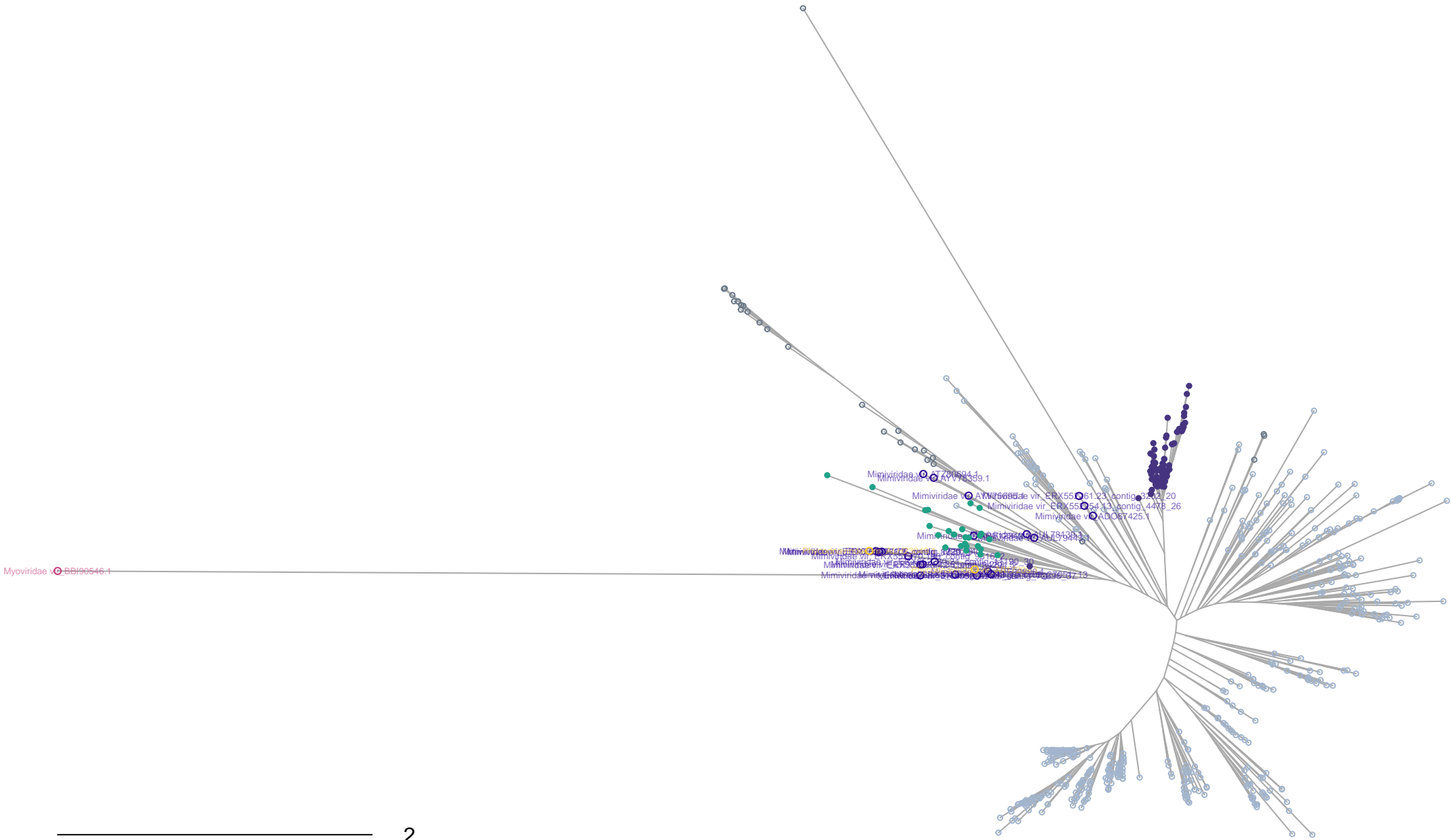
- eukaryotes
- archaea
- bacteria
- viruses



Podoviridae n = 2

Acetyltransf_1
vir.Acetyltransf_1.phy.HG2.seqs.iqtree.treefile
n=614 sequences

- eukaryotes
- archaea
- bacteria
- viruses

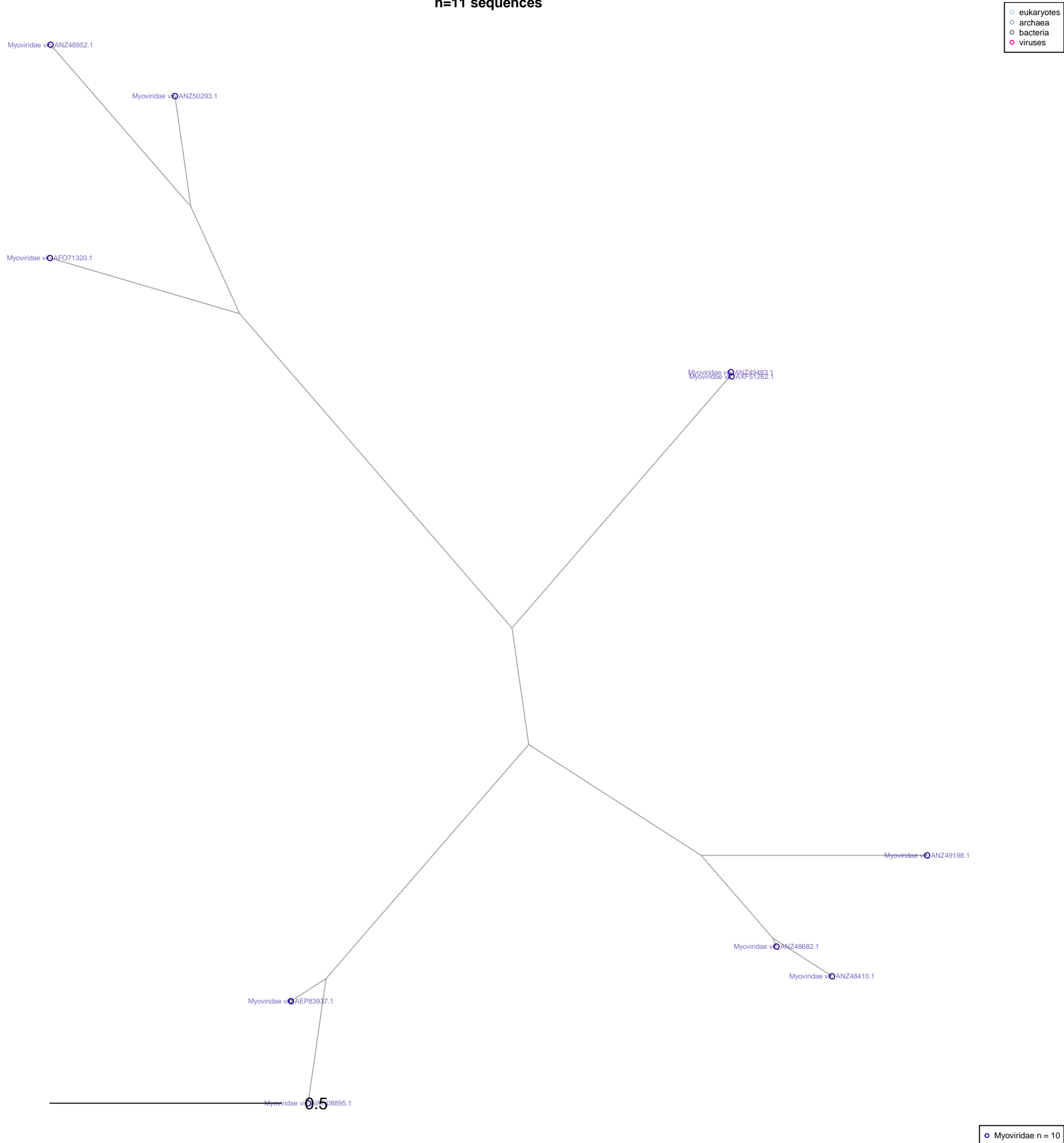


2

- Acetyltransf_1.HG9.1:ELP3 n = 78
- Acetyltransf_1.HG9.0:like:ELP3:likeclu:1 n = 25
- other n = 0

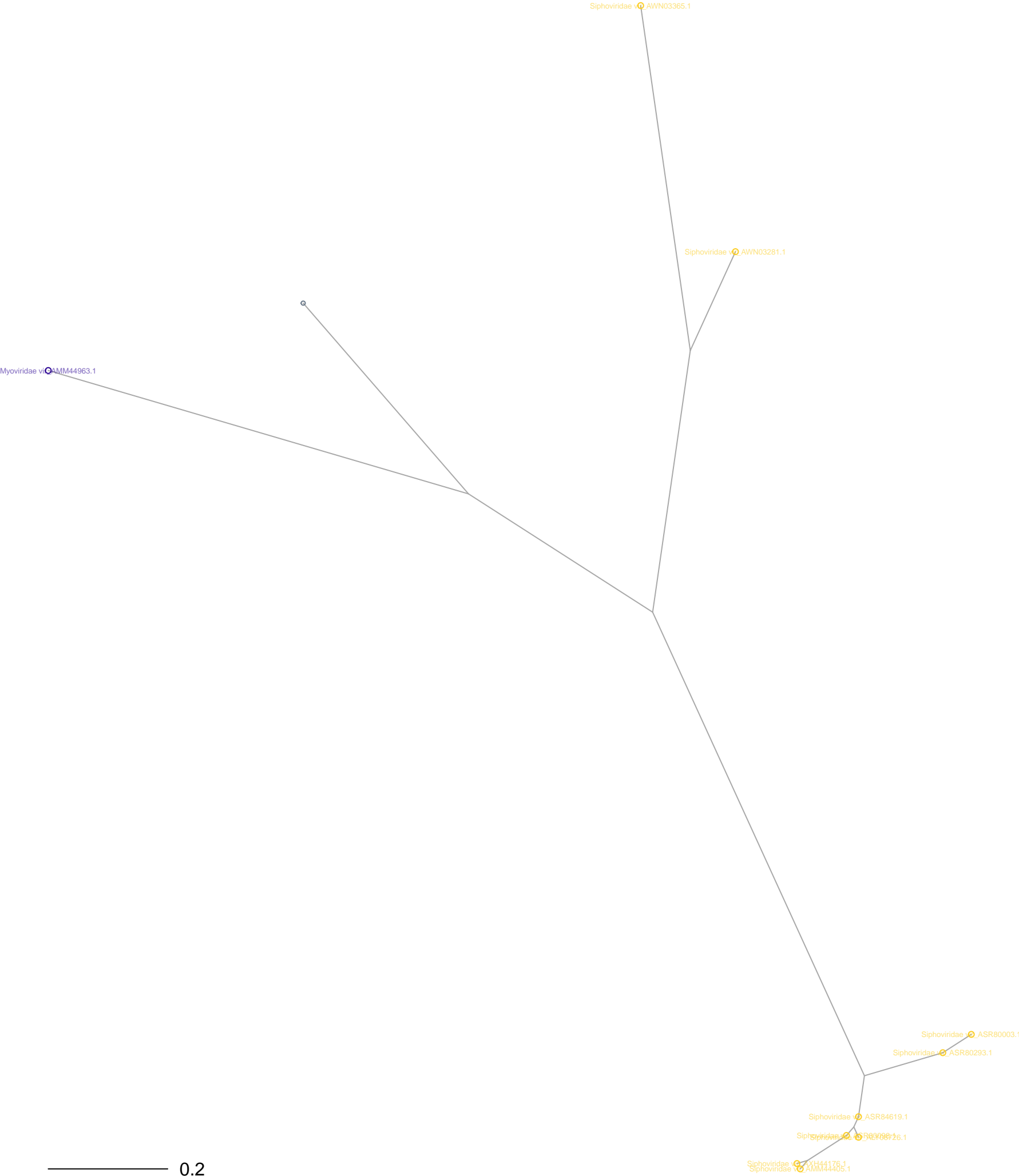
- Mimiviridae n = 21
- Myoviridae n = 1
- Phycodnaviridae n = 2

Acetyltransf_1
vir.Acetyltransf_1.phy.HG20.seqs.iqtree.treefile
n=11 sequences



Acetyltransf_1
vir.Acetyltransf_1.phy.HG21.seqs.iqtree.treefile
n=11 sequences

- eukaryotes
- archaea
- bacteria
- viruses



0.2

- Myoviridae n = 1
- Siphoviridae n = 9

vir.Acetyltransf_1.phy.HG22.seqs.iqtree.treefile
n=7 sequences

- eukaryotes
- archaea
- bacteria
- viruses

Mimiviridae vir_ERX5520.108_contig_13617_24

Mimiviridae vir_ERX5520.54.32_contig_2861_16

Phycodnaviridae vir_AFK65923.1

Phycodnaviridae vir_68Y29674.1

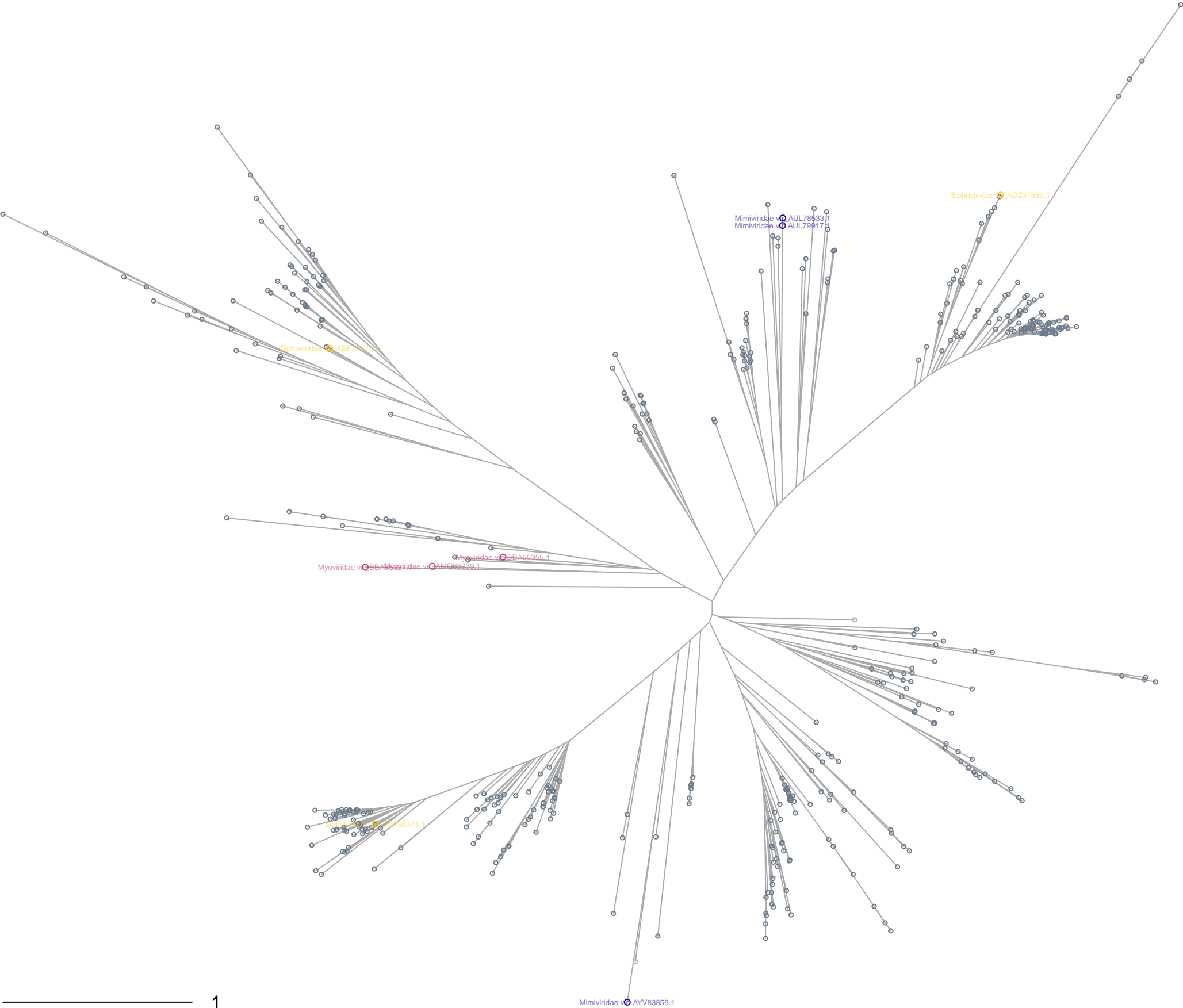
Phycodnaviridae vir_AET84509.1

—0.1

- Mimiviridae n = 2
- Phycodnaviridae n = 4

Acetyltransf_1
vir.Acetyltransf_1.phy.HG3.seqs.iqtree.treefile
n=462 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- Mimiviridae n = 3
- Myoviridae n = 3
- Siphoviridae n = 3

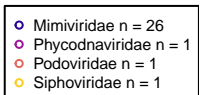
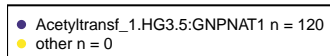
vir.Acetyltransf_1.phy.HG4.seqs.iqtree.treefile
n=360 sequences

- eukaryotes
- archaea
- bacteria
- viruses



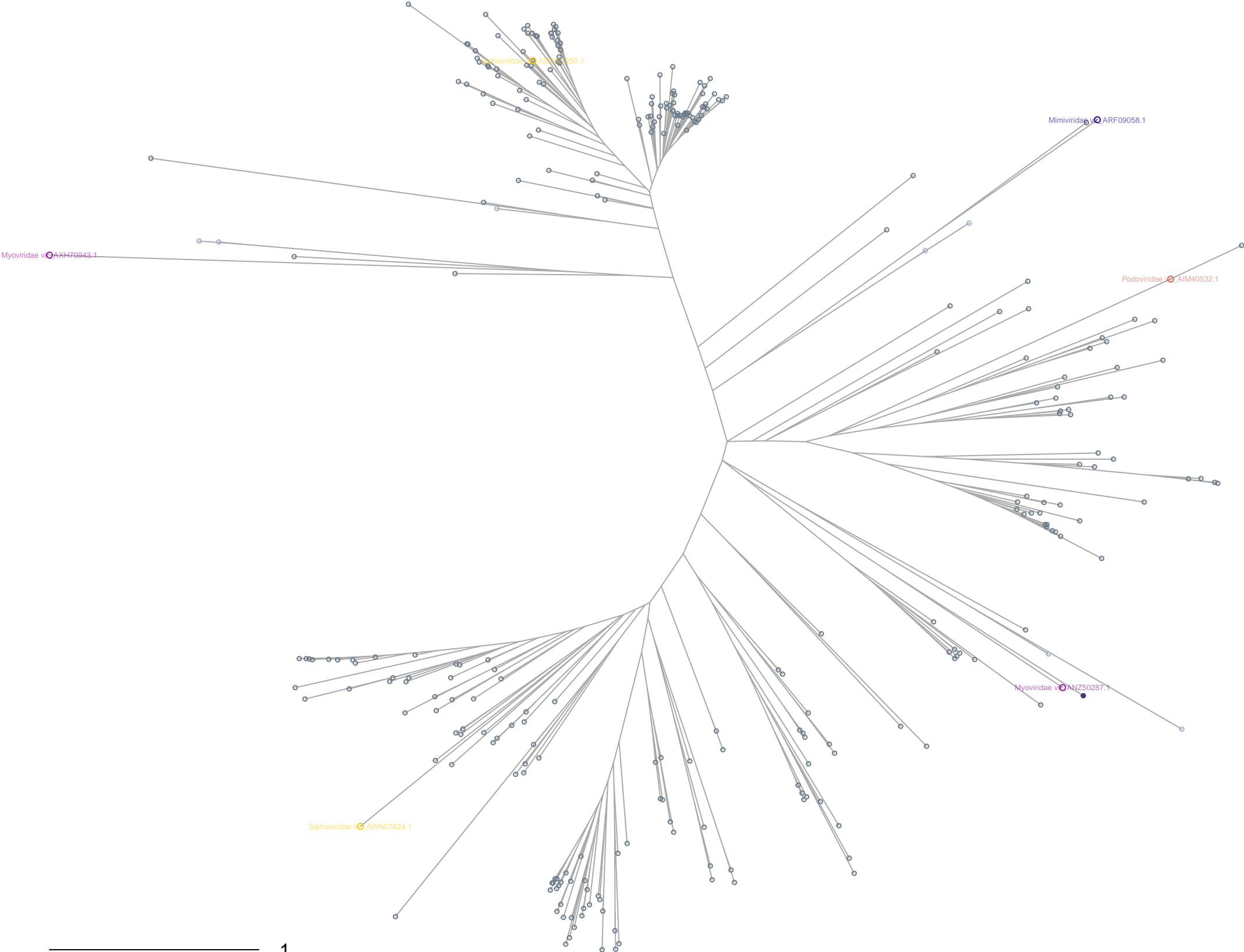
- Iridoviridae n = 1
- Myoviridae n = 6
- Siphoviridae n = 6

sf_1.phy.HG5.seqs
n=341 sequences



Acetyltransf_1
vir.Acetyltransf_1.phy.HG6.seqs.iqtree.treefile
n=299 sequences

- eukaryotes
- archaea
- bacteria
- viruses

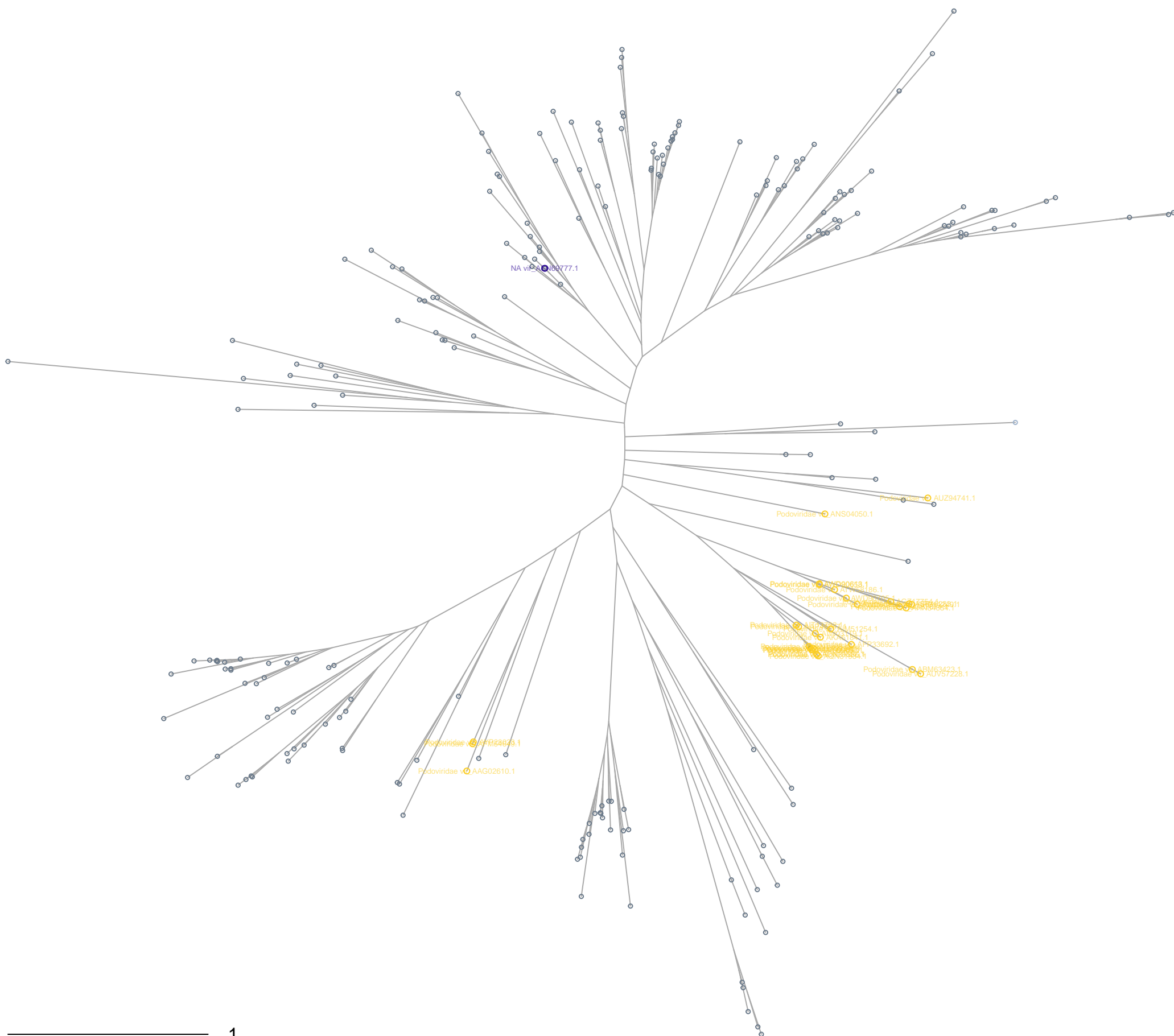


other n = 1

- Mimiviridae n = 1
- Myoviridae n = 2
- Podoviridae n = 1
- Siphoviridae n = 2

Acetyltransf_1
vir.Acetyltransf_1.phy.HG7.seqs.iqtree.treefile
n=244 sequences

- eukaryotes
- archaea
- bacteria
- viruses

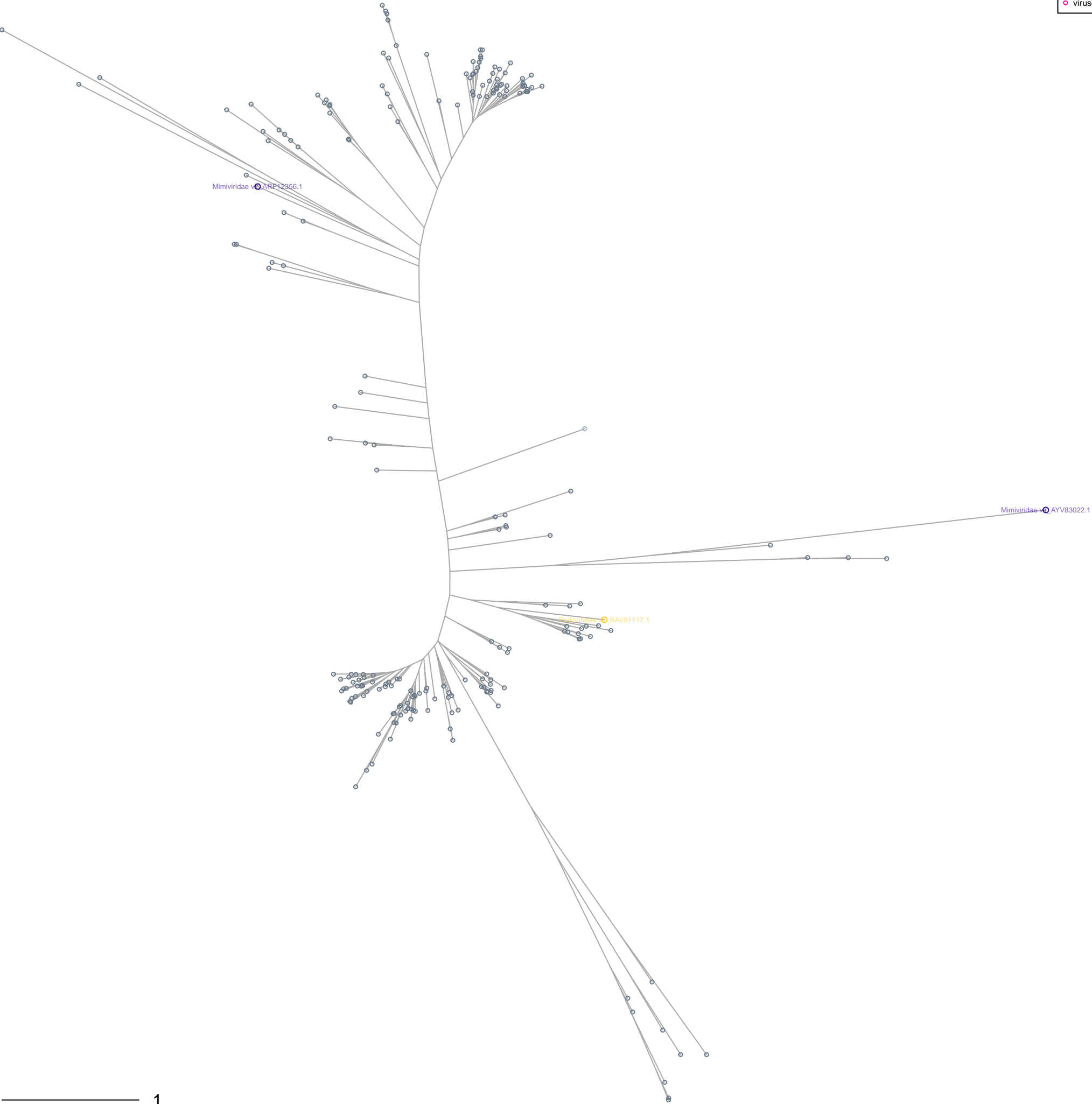


1

- NA n = 1
- Podoviridae n = 32

Acetyltransf_1
vir.Acetyltransf_1.phy.HG8.seqs.iqtree.treefile
n=219 sequences

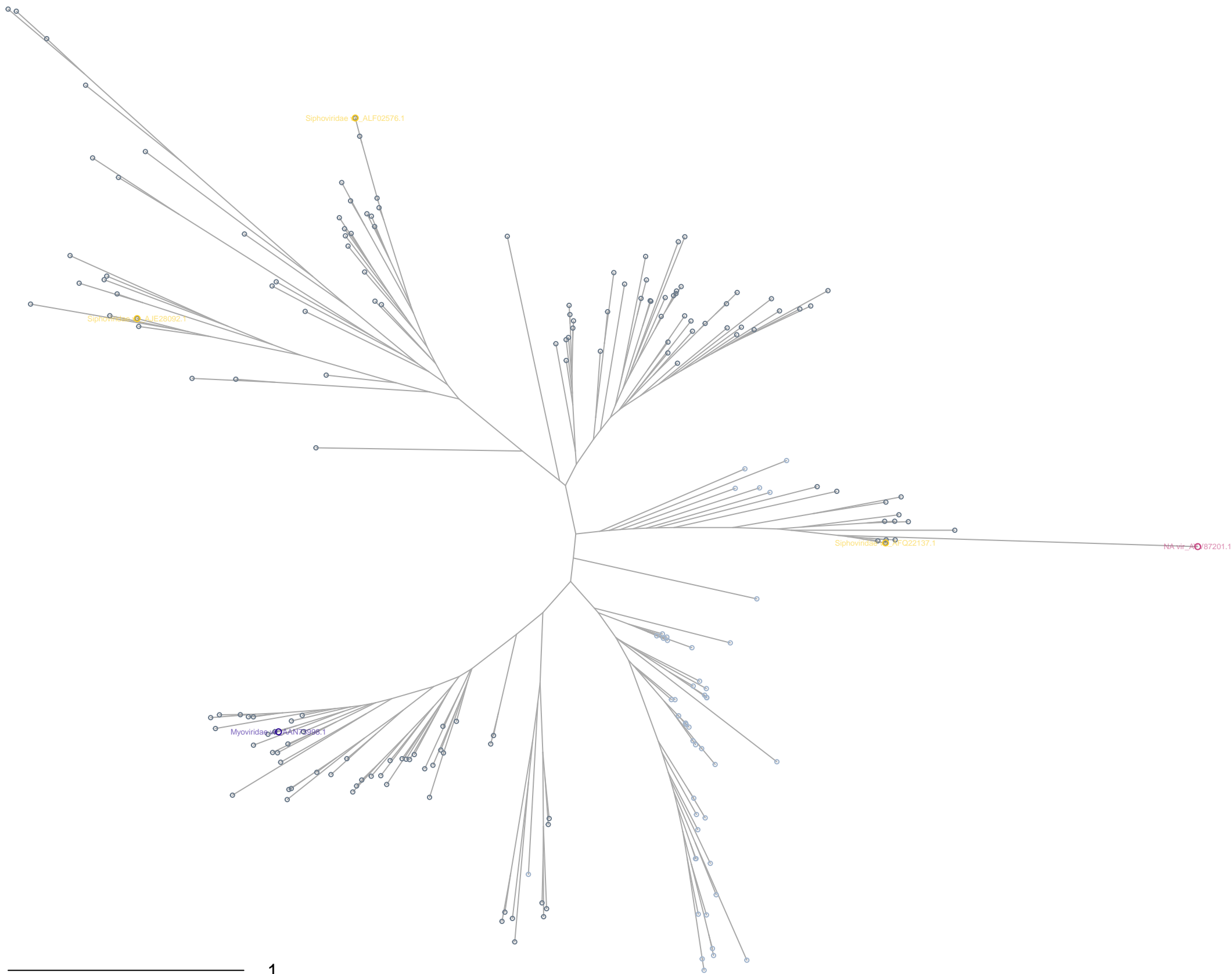
- eukaryotes
- archaea
- bacteria
- viruses



- Mimiviridae n = 2
- Podoviridae n = 1

Acetyltransf_1
vir.Acetyltransf_1.phy.HG9.seqs.iqtree.treefile
n=201 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- Myoviridae n = 1
- NA n = 1
- Siphoviridae n = 3