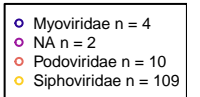
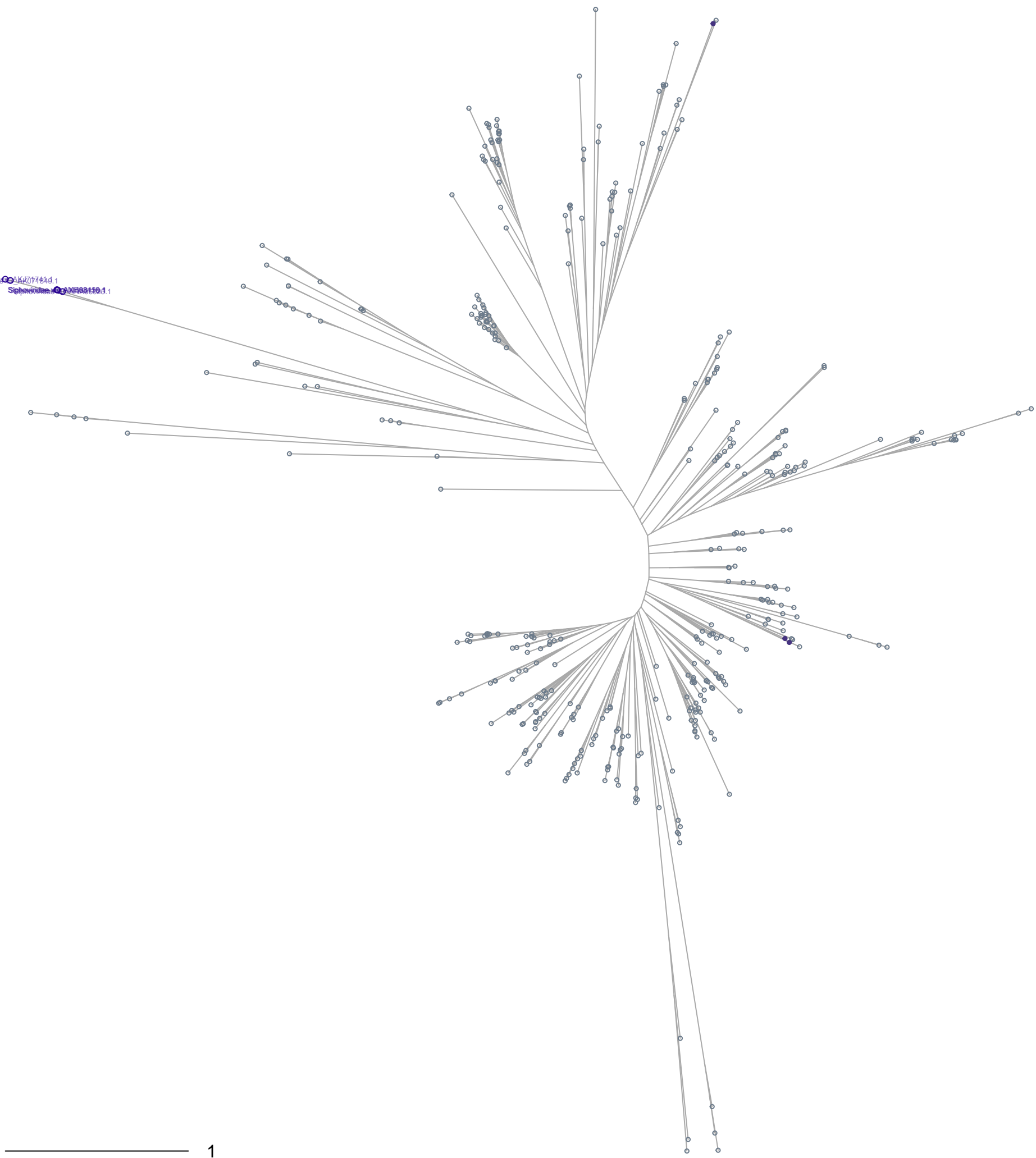


## SNF2\_N



## SNF2\_N

SNF2\_N



1

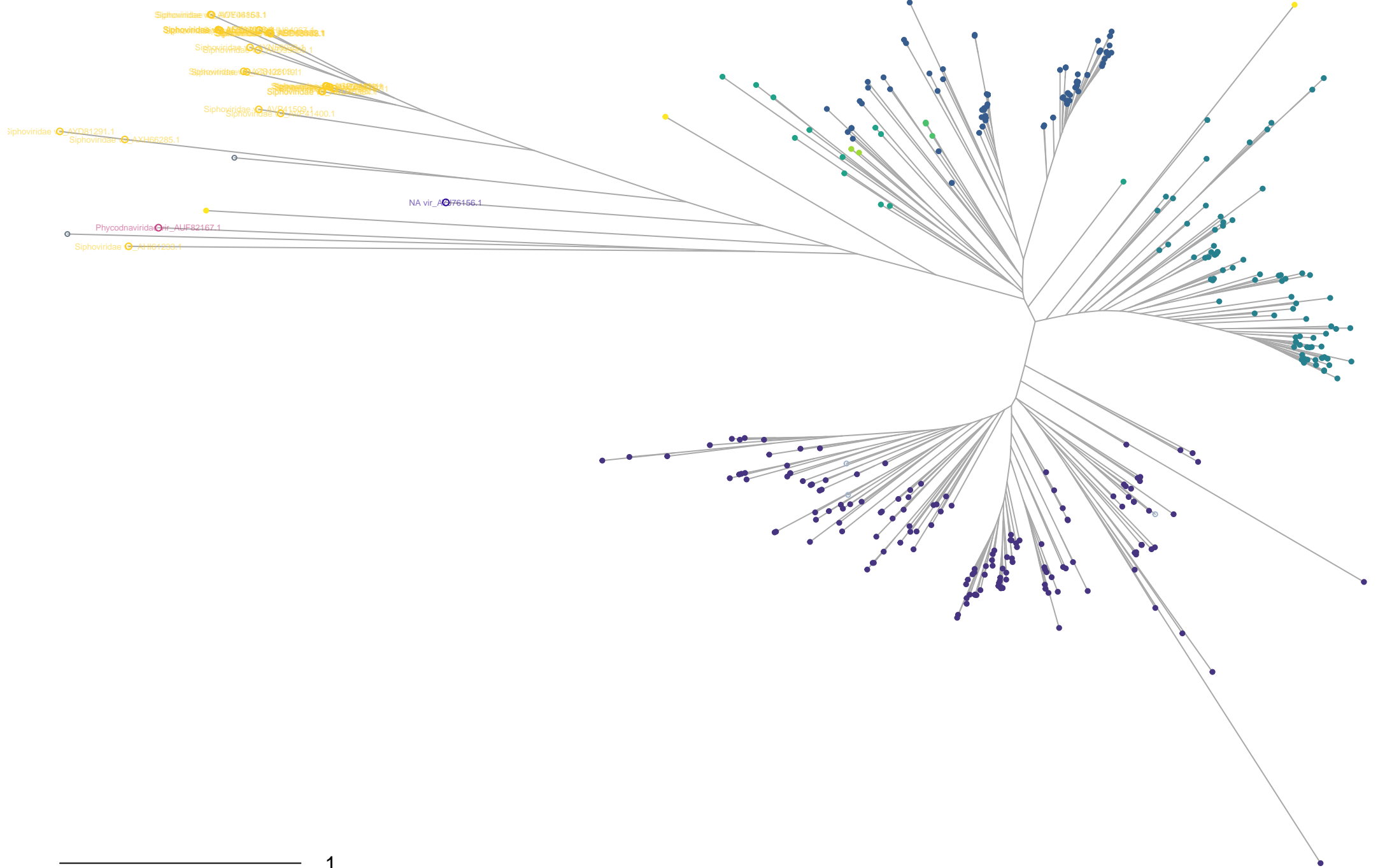
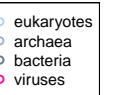
- SNF2\_N.HG11.1:BTA1 n = 3
- other n = 0

- Siphoviridae n = 6

- eukaryotes
- archaea
- bacteria
- viruses

## SNF2\_N

SNF2\_N

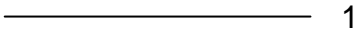


1

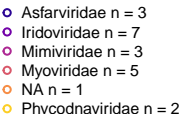
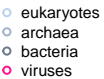
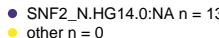
- SNF2\_N.HG8.1:CHD6/CHD7/CHD8/CHD9 n = 160
- SNF2\_N.HG4.0:AC006064.6/CHD3/CHD4/CHD5 n = 87
- SNF2\_N.HG4.6:CHD1/CHD2 n = 84
- SNF2\_N.HG4.4:like:CHD1/CHD2:likeclu:6 n = 12
- SNF2\_N.HG4.1:like:CHD1/CHD2:likeclu:6 n = 3
- SNF2\_N.HG4.3:like:CHD1/CHD2:likeclu:6 n = 2
- other n = 3

- NA n = 1
- Phycodnaviridae n = 1
- Siphoviridae n = 27

## SNF2\_N

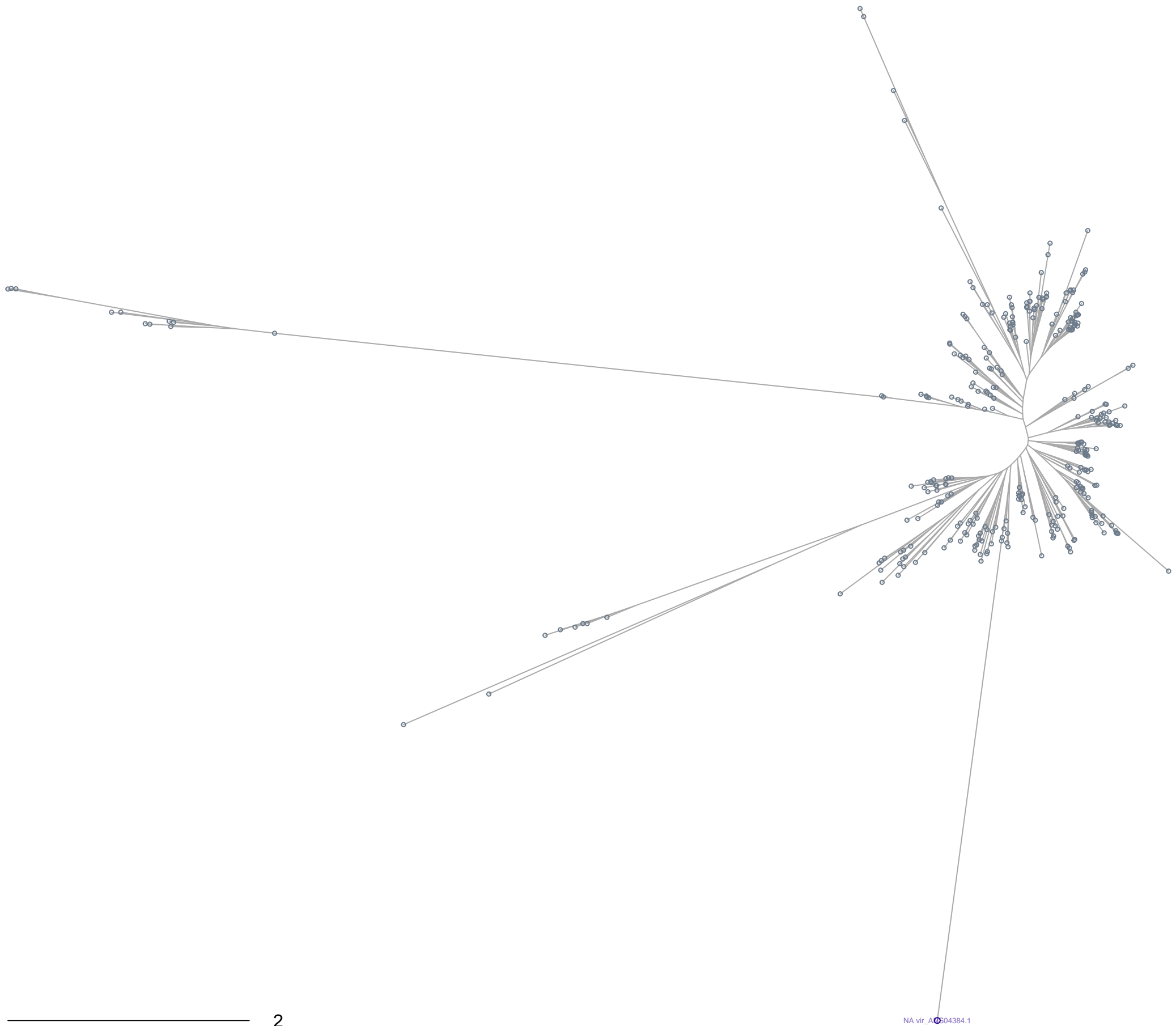


1



SNF2\_N  
vir.SNF2\_N.phy.HG13.seqs.iqtree.treefile  
n=330 sequences

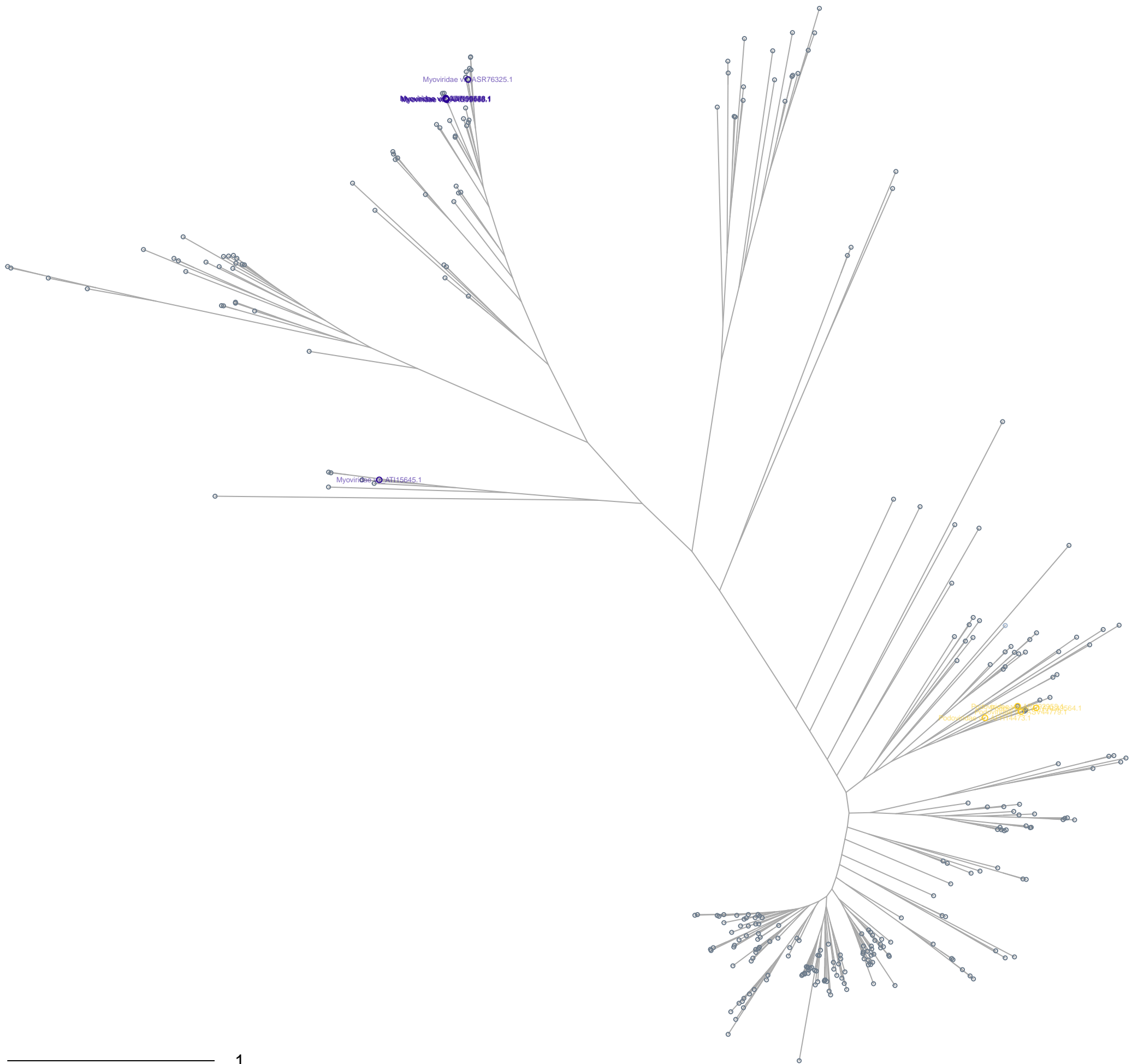
eukaryotes  
archaea  
bacteria  
viruses



NA n = 1

SNF2\_N  
vir.SNF2\_N.phy.HG14.seqs.iqtree.treefile  
n=299 sequences

- eukaryotes
- archaea
- bacteria
- viruses

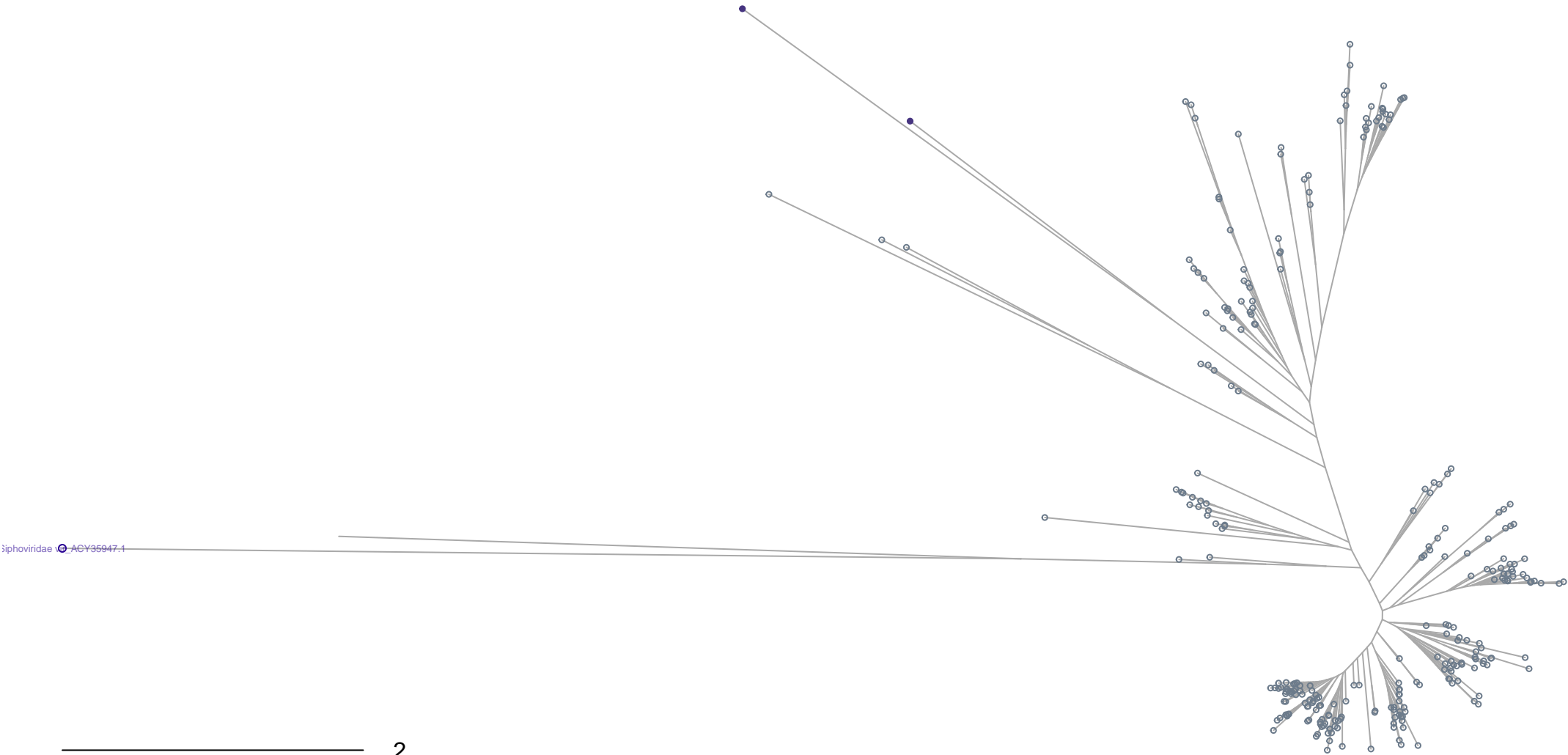


1

- Myoviridae n = 8
- Podoviridae n = 4

SNF2\_N  
vir.SNF2\_N.phy.HG15.seqs.iqtree.treefile  
n=286 sequences

eukaryotes  
archaea  
bacteria  
viruses

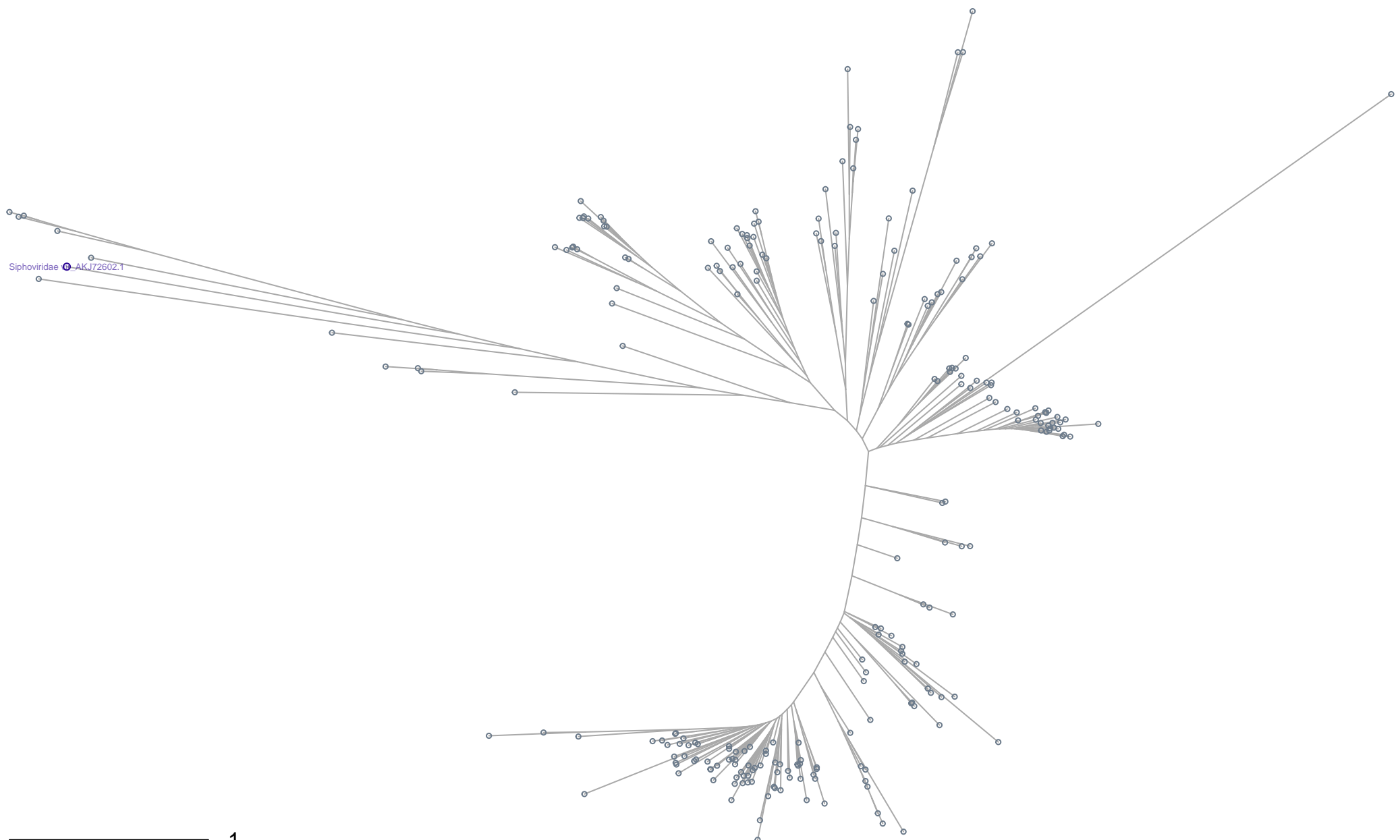


other n = 2

Siphoviridae n = 1

SNF2\_N  
vir.SNF2\_N.phy.HG16.seqs.iqtree.treefile  
n=240 sequences

- eukaryotes
- archaea
- bacteria
- viruses

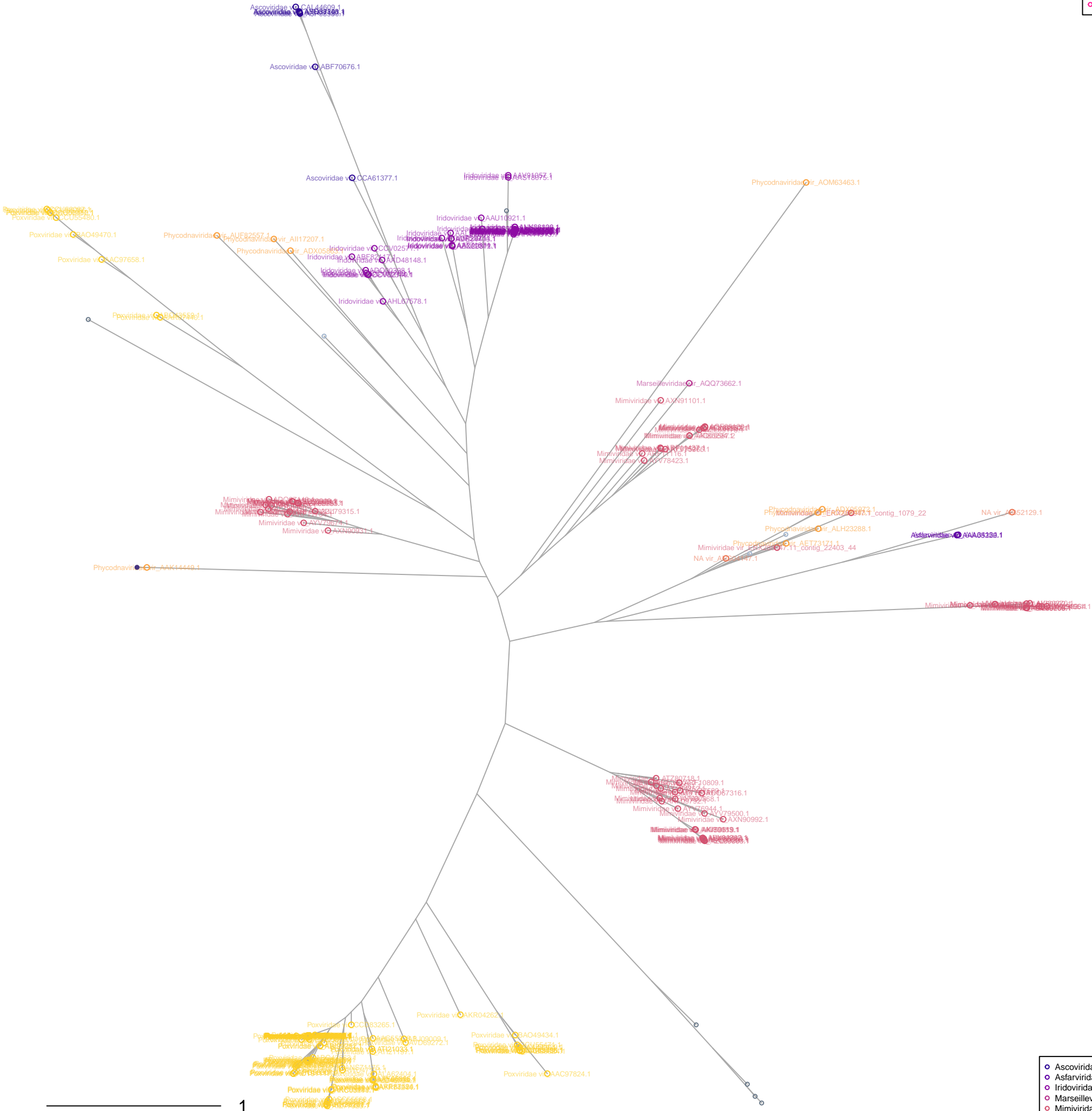


Siphoviridae n = 1



vir.SNF2\_N.phy.HG17.seqs.iqtree.treefile  
n=230 sequences

- eukaryotes
- archaea
- bacteria
- viruses

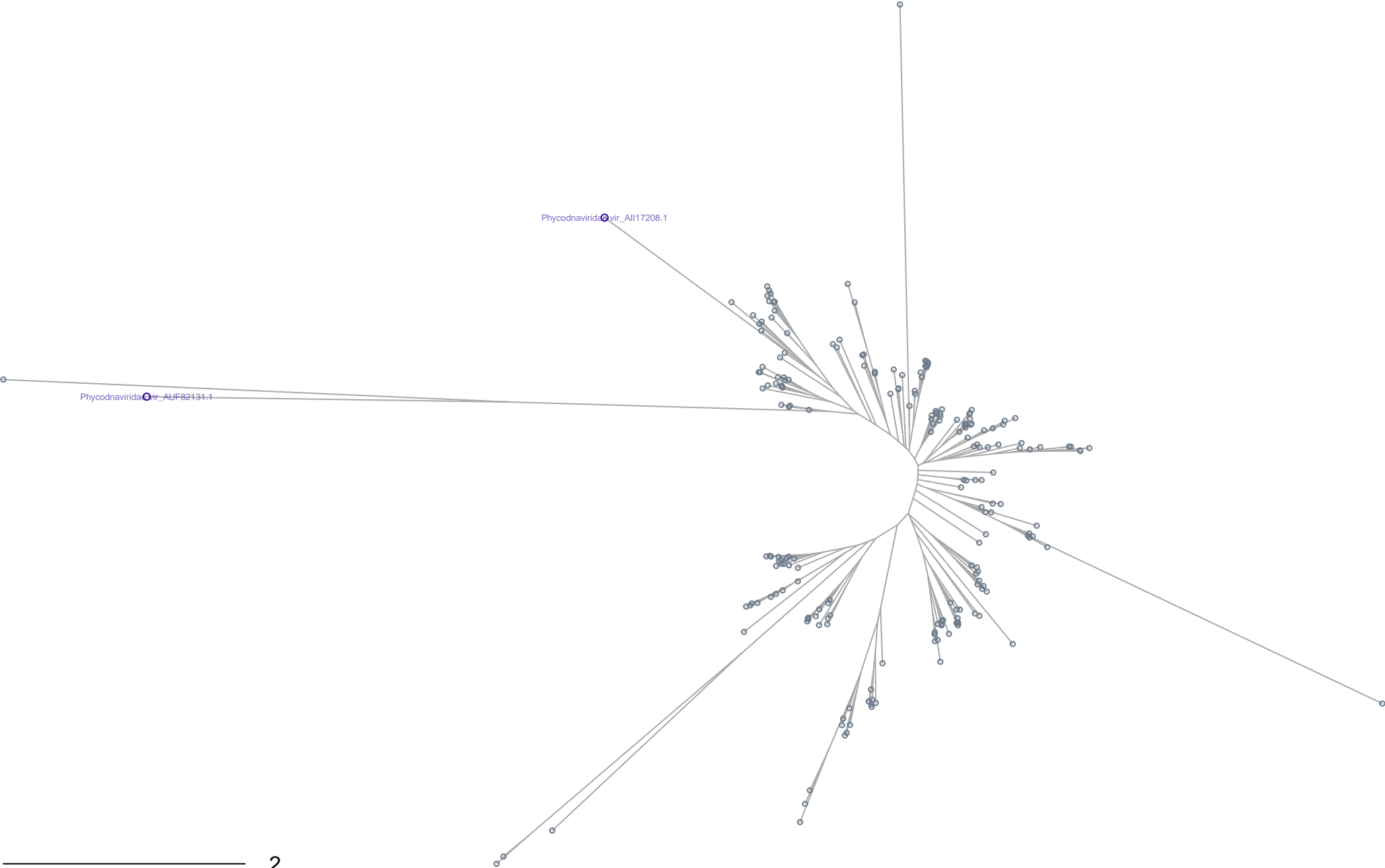


other n = 1

- Ascoviridae n = 7
- Asfarviridae n = 3
- Iridoviridae n = 40
- Marseilleviridae n = 1
- Mimiviridae n = 65
- NA n = 2
- Phycodnaviridae n = 9
- Poxviridae n = 91

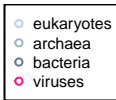
SNF2\_N  
vir.SNF2\_N.phy.HG18.seqs.iqtree.treefile  
n=213 sequences

- eukaryotes
- archaea
- bacteria
- viruses



Phycodnaviridae n = 2

SNF2\_N



- Myoviridae n = 6
- Podoviridae n = 1

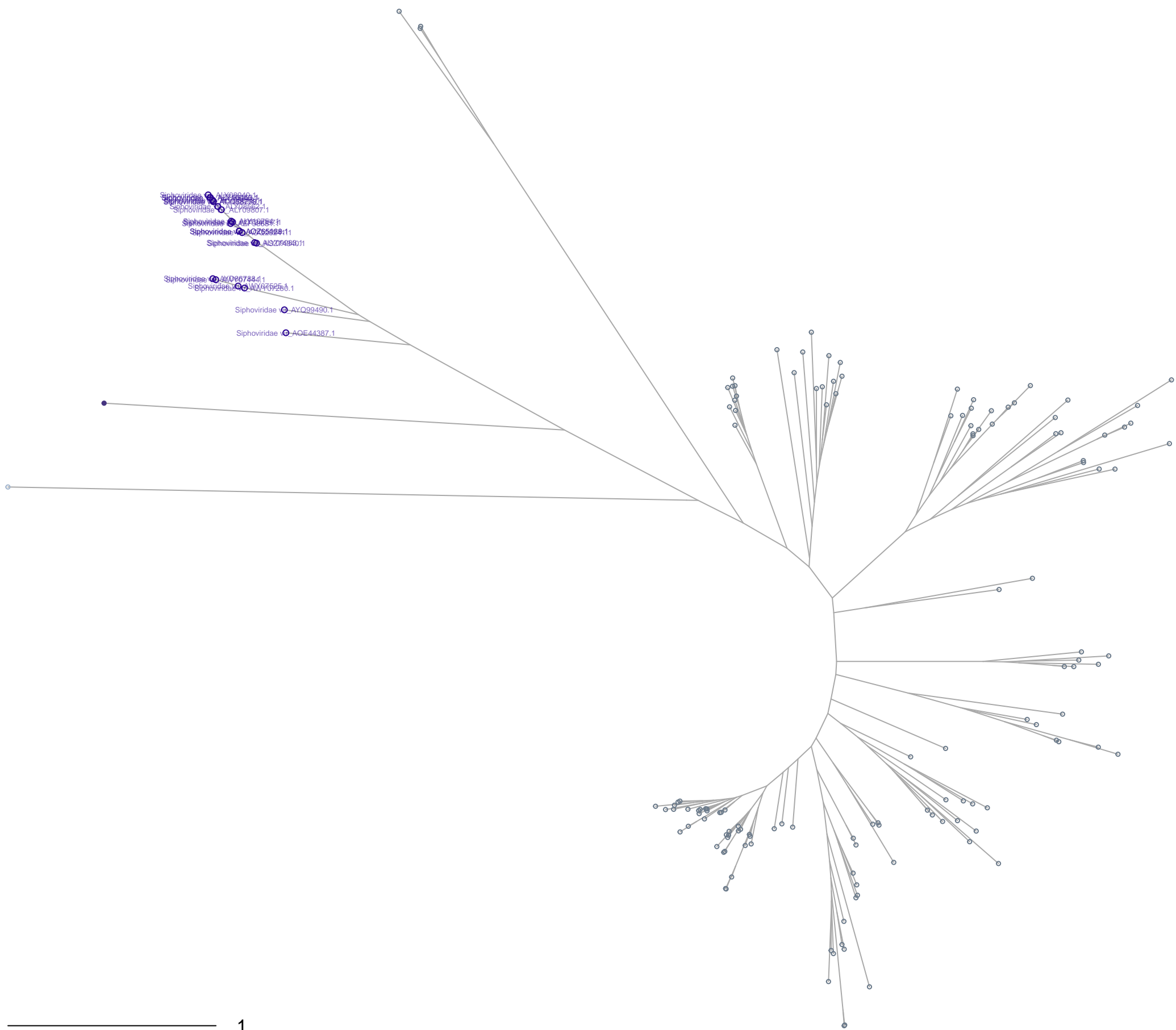
## SNF2\_N



- Mimiviridae n = 1
- NA n = 1
- Siphoviridae n = 9

SNF2\_N  
vir.SNF2\_N.phy.HG20.seqs.iqtree.treefile  
n=162 sequences

- eukaryotes
- archaea
- bacteria
- viruses



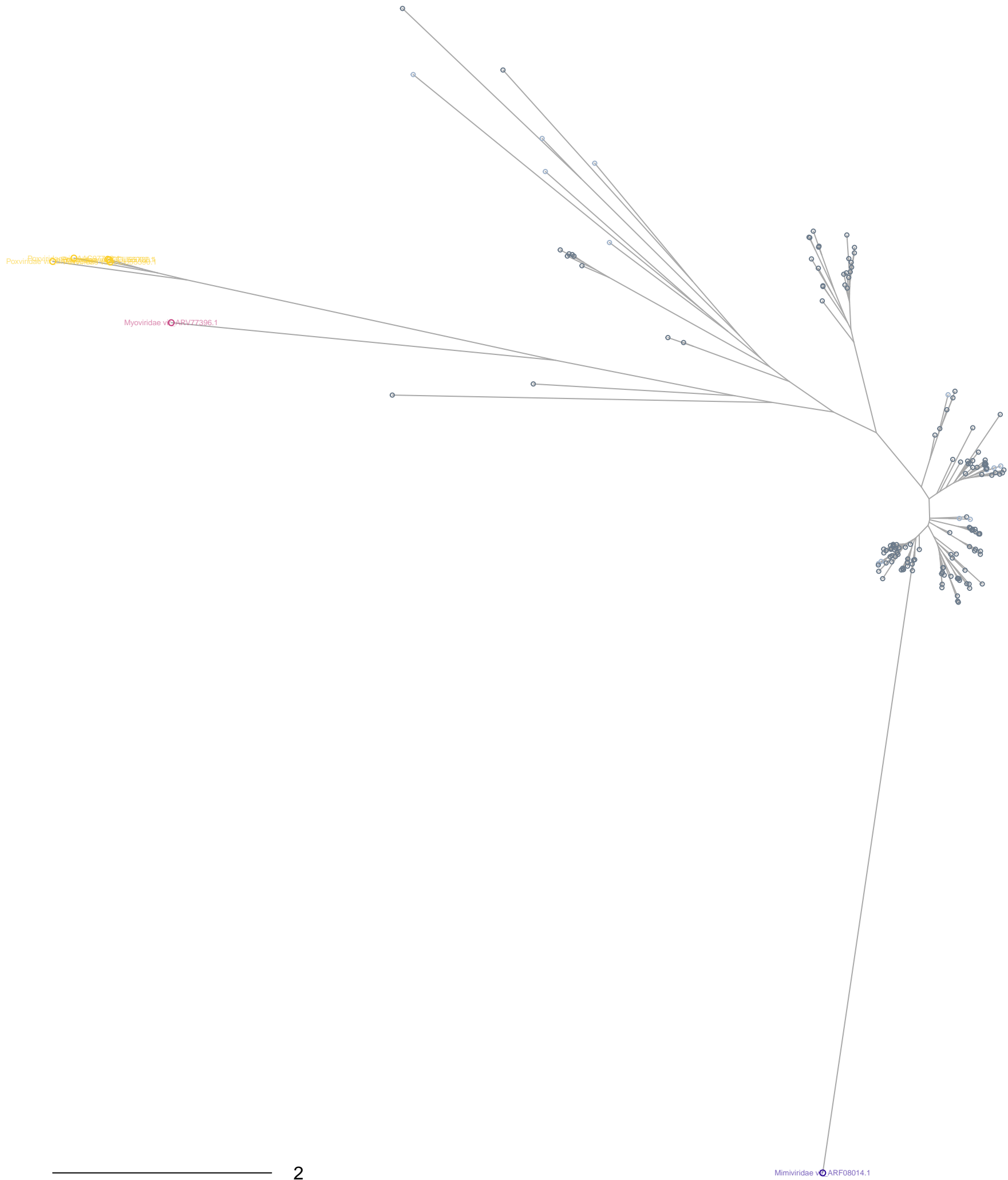
1

other n = 1

Siphoviridae n = 22

SNF2\_N  
vir.SNF2\_N.phy.HG21.seqs.iqtree.treefile  
n=161 sequences

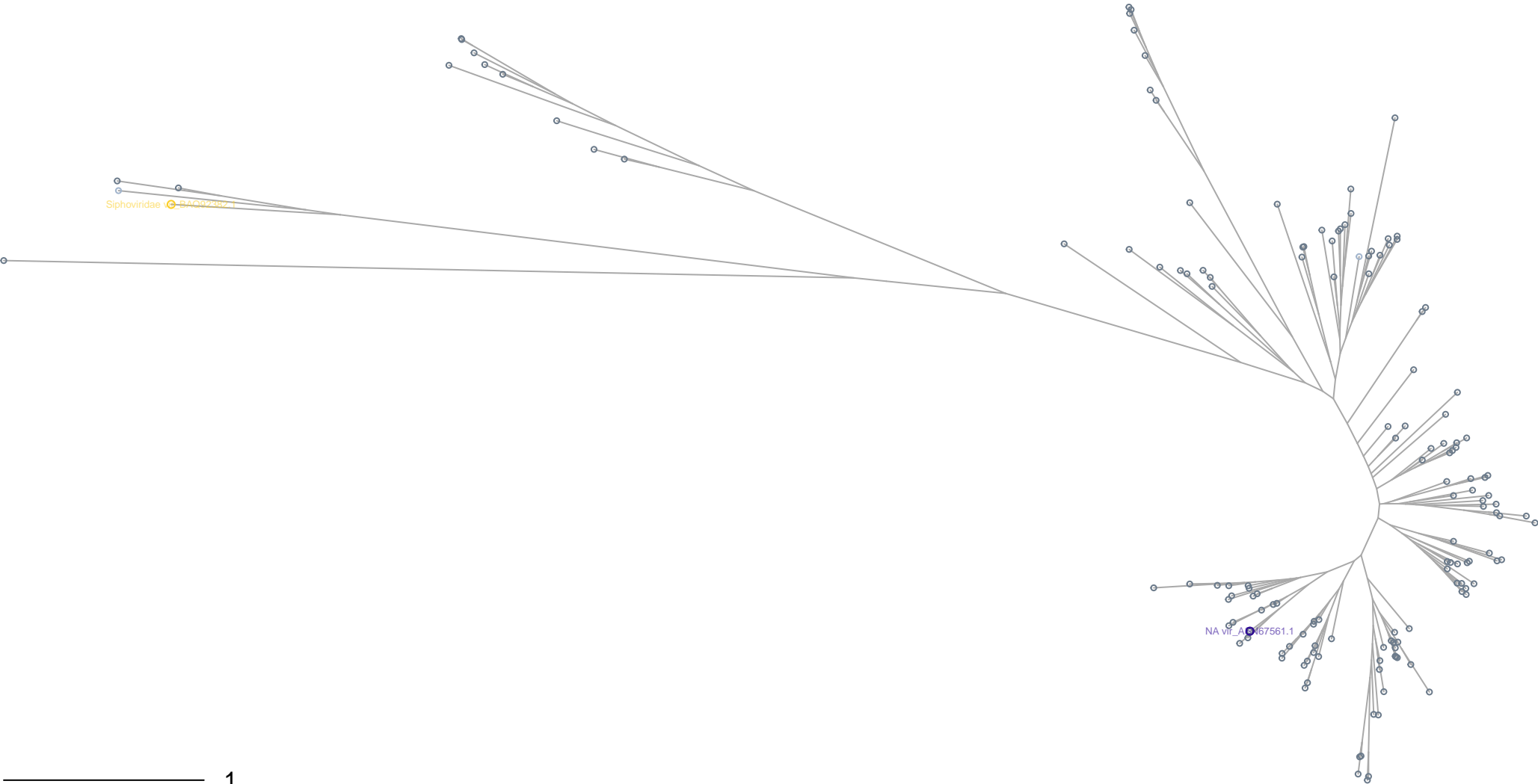
- eukaryotes
- archaea
- bacteria
- viruses



- Mimiviridae n = 1
- Myoviridae n = 1
- Poxviridae n = 5

SNF2\_N  
vir.SNF2\_N.phy.HG22.seqs.iqtree.treefile  
n=154 sequences

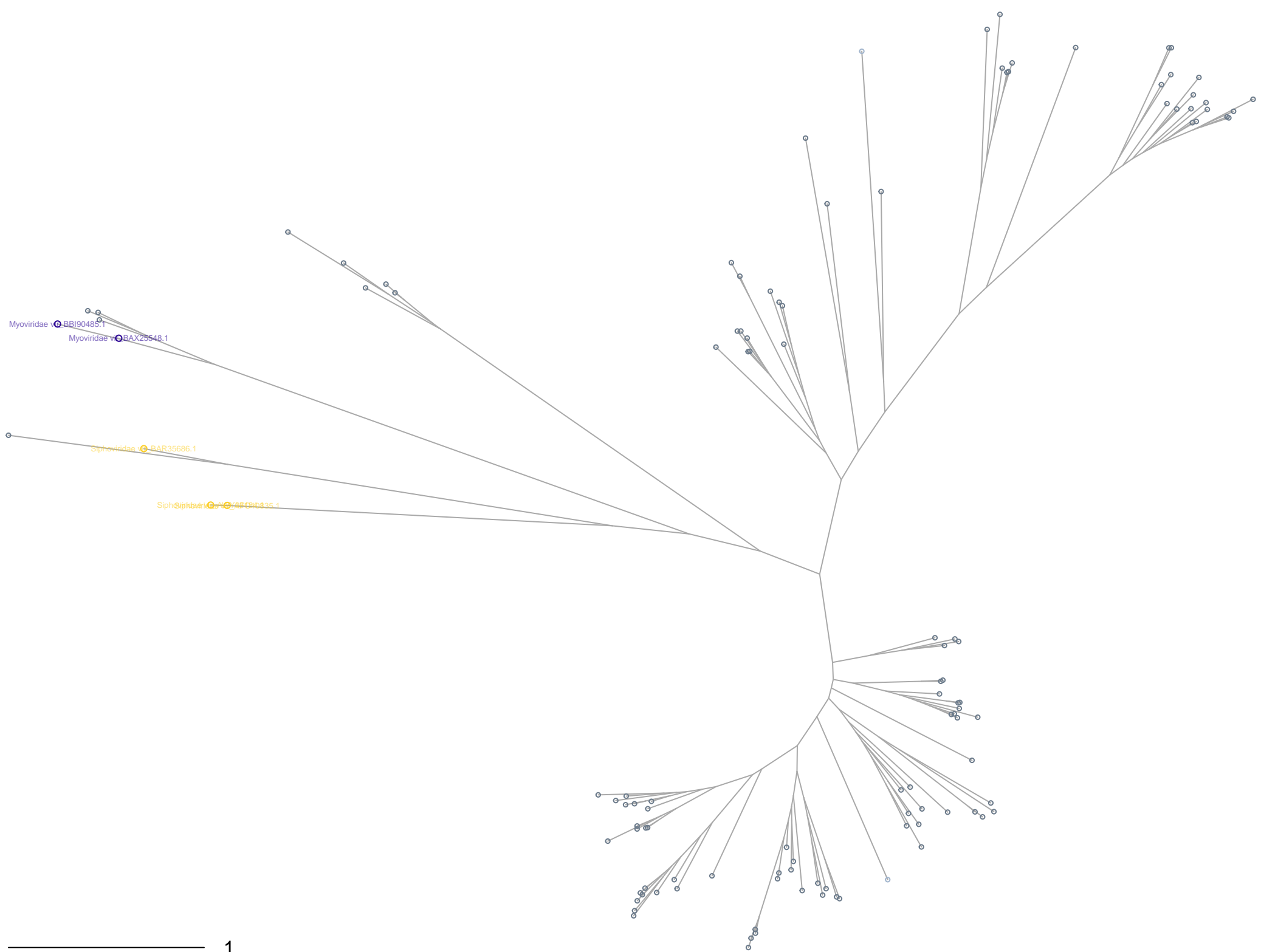
- eukaryotes
- archaea
- bacteria
- viruses



- NA n = 1
- Siphoviridae n = 1

SNF2\_N  
vir.SNF2\_N.phy.HG23.seqs.iqtree.treefile  
n=119 sequences

- eukaryotes
- archaea
- bacteria
- viruses

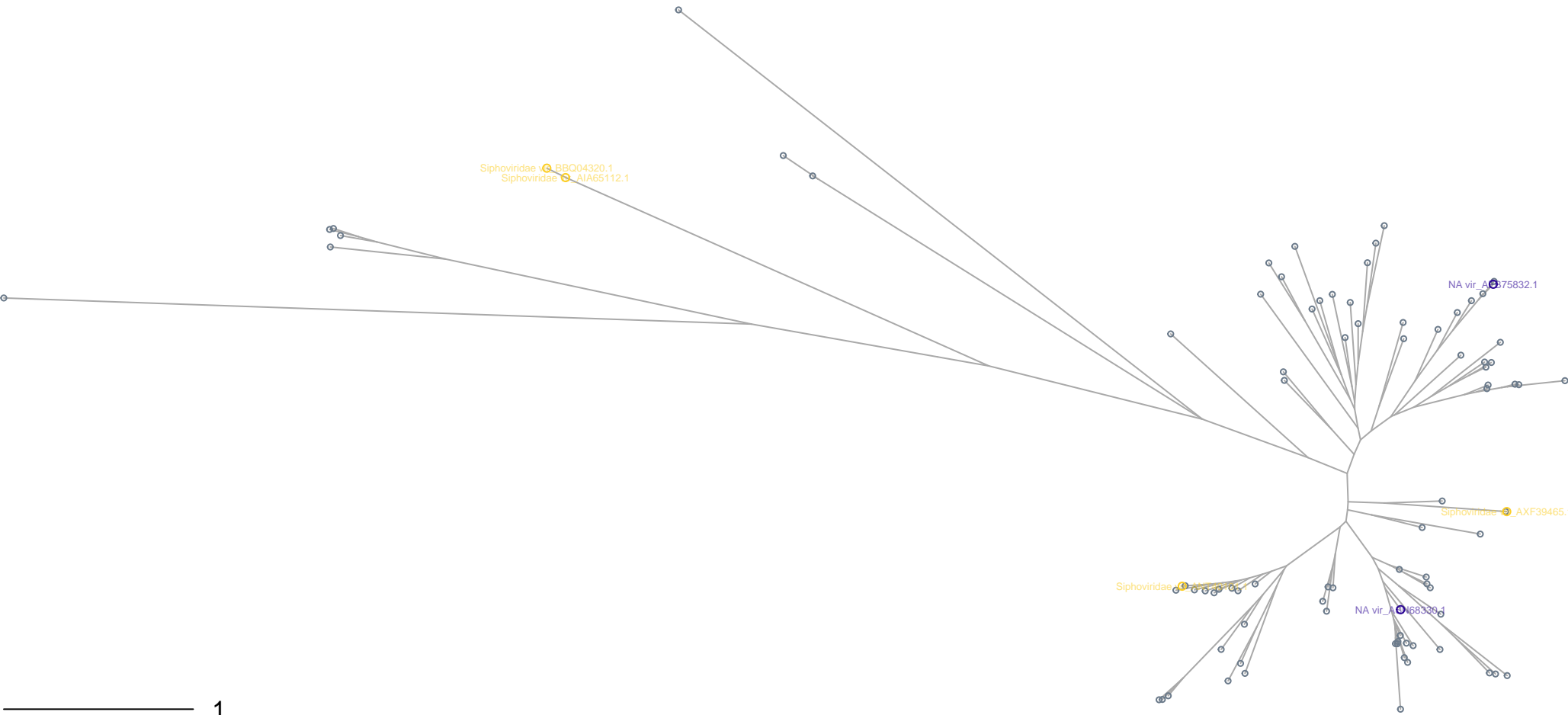


- Myoviridae n = 2
- Siphoviridae n = 3



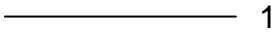
SNF2\_N  
vir.SNF2\_N.phy.HG24.seqs.iqtree.treefile  
n=90 sequences

- eukaryotes
- archaea
- bacteria
- viruses



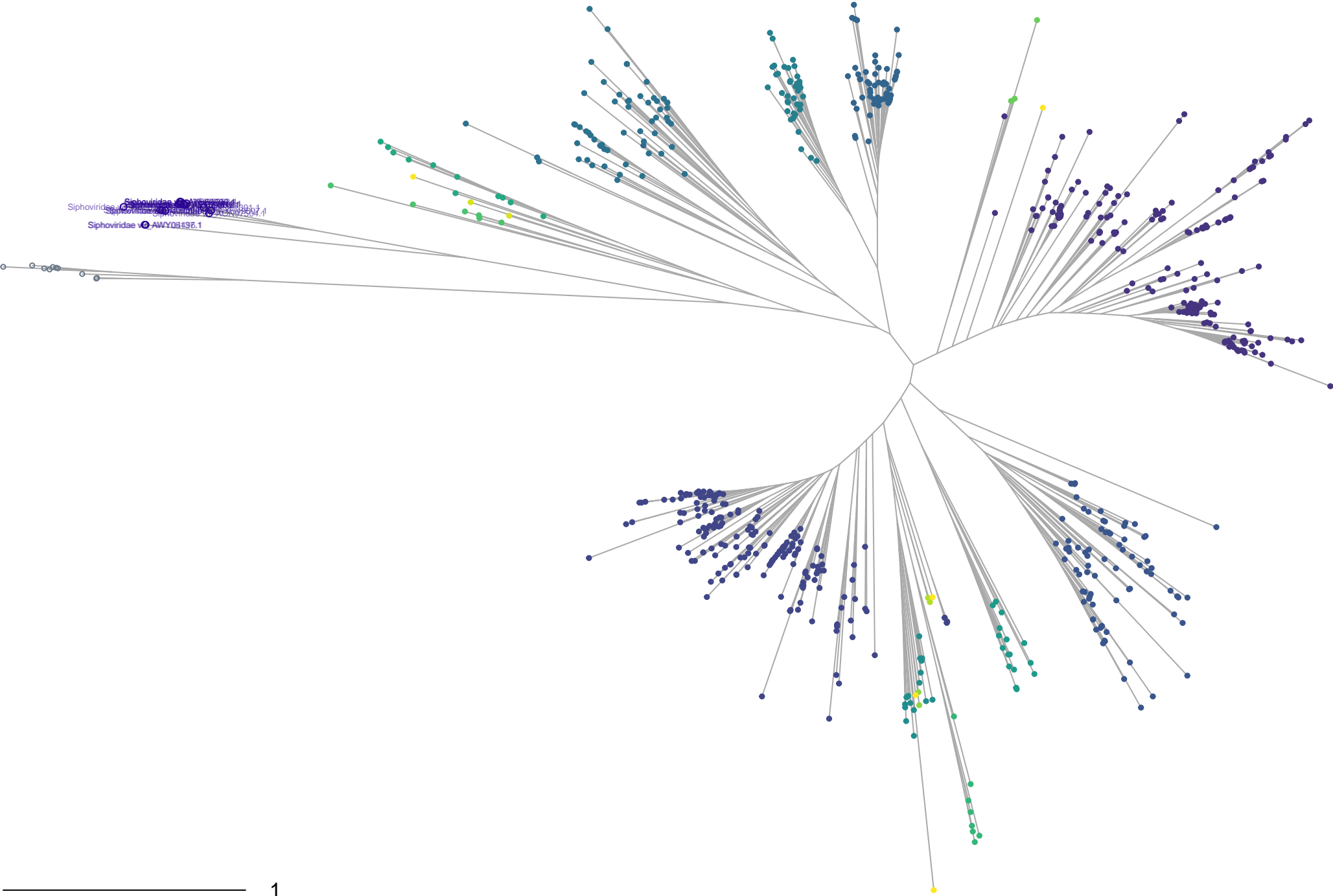
- NA n = 2
- Siphoviridae n = 4

## SNF2\_N



SNF2\_N  
vir.SNF2\_N.phy.HG3.seqs.iqtree.treefile  
n=737 sequences

- eukaryotes
- archaea
- bacteria
- viruses

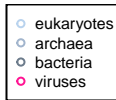


1

- SNF2\_N.HG6.0:SMARCA2/SMARCA4 n = 193
- SNF2\_N.HG2.10:SMARCA1/SMARCA5 n = 189
- SNF2\_N.HG2.3:HELLS n = 80
- SNF2\_N.HG12.0:AC106886.6/EP400/SRCAP n = 65
- SNF2\_N.HG2.7:SMARCA1 n = 58
- SNF2\_N.HG13.0:INO80 n = 44
- SNF2\_N.HG2.15:like:SMARCA1/SMARCA5:likeclu:10 n = 18
- SNF2\_N.HG2.0:CHD1L n = 17
- SNF2\_N.HG3.3:ERCC6 n = 11
- SNF2\_N.HG2.12:like:SMARCA1/SMARCA5:likeclu:10 n = 8
- SNF2\_N.HG3.1:ERCC6L2 n = 6
- SNF2\_N.HG6.1:like:SMARCA2/SMARCA4:likeclu:0 n = 3
- SNF2\_N.HG2.13:like:SMARCA1/SMARCA5:likeclu:10 n = 2
- SNF2\_N.HG2.8:like:SMARCA1/SMARCA5:likeclu:10 n = 2
- SNF2\_N.HG3.5:ERCC6L n = 2
- other n = 5

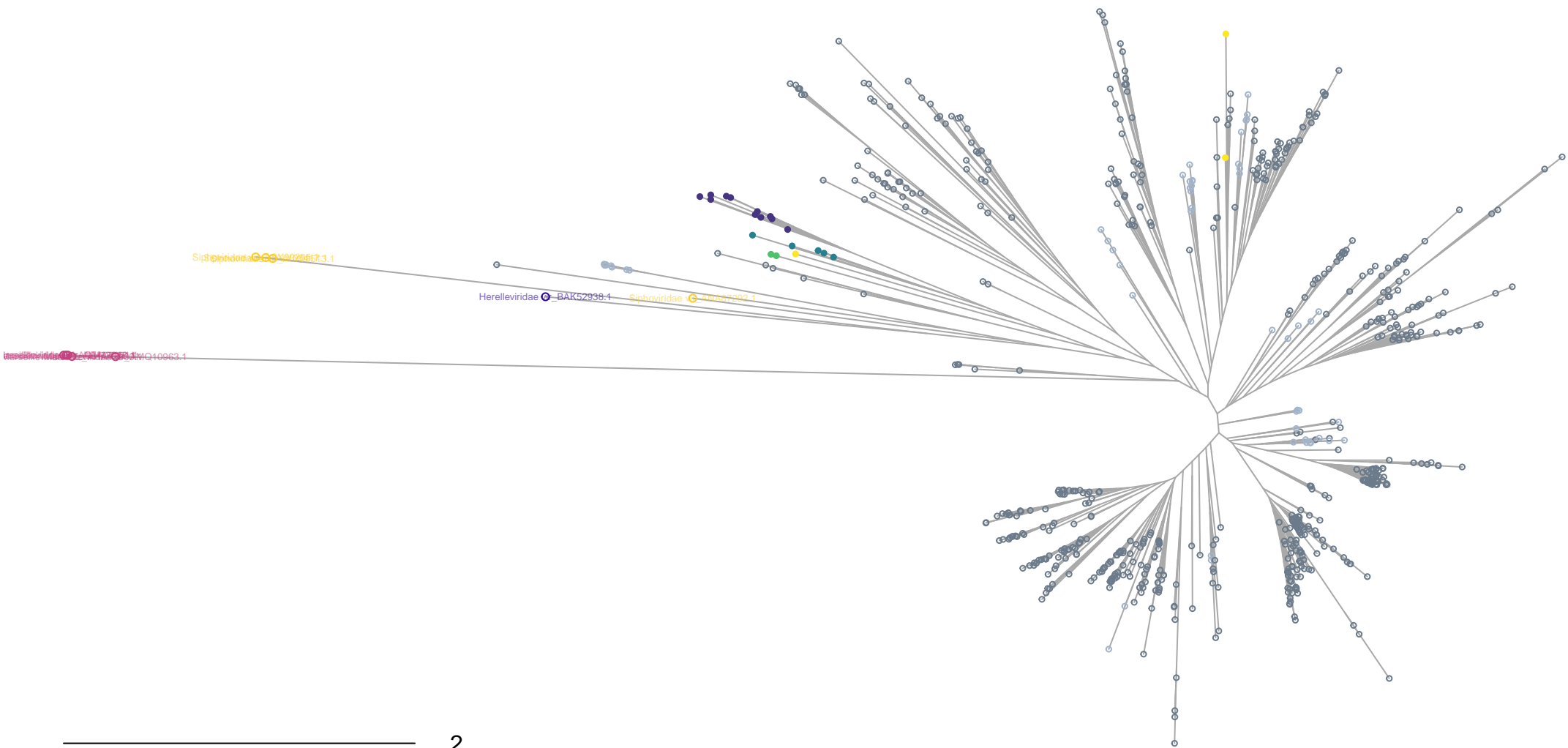
Siphoviridae n = 18

## SNF2\_N



SNF2\_N  
vir.SNF2\_N.phy.HG5.seqs.iqtree.treefile  
n=689 sequences

- eukaryotes
- archaea
- bacteria
- viruses

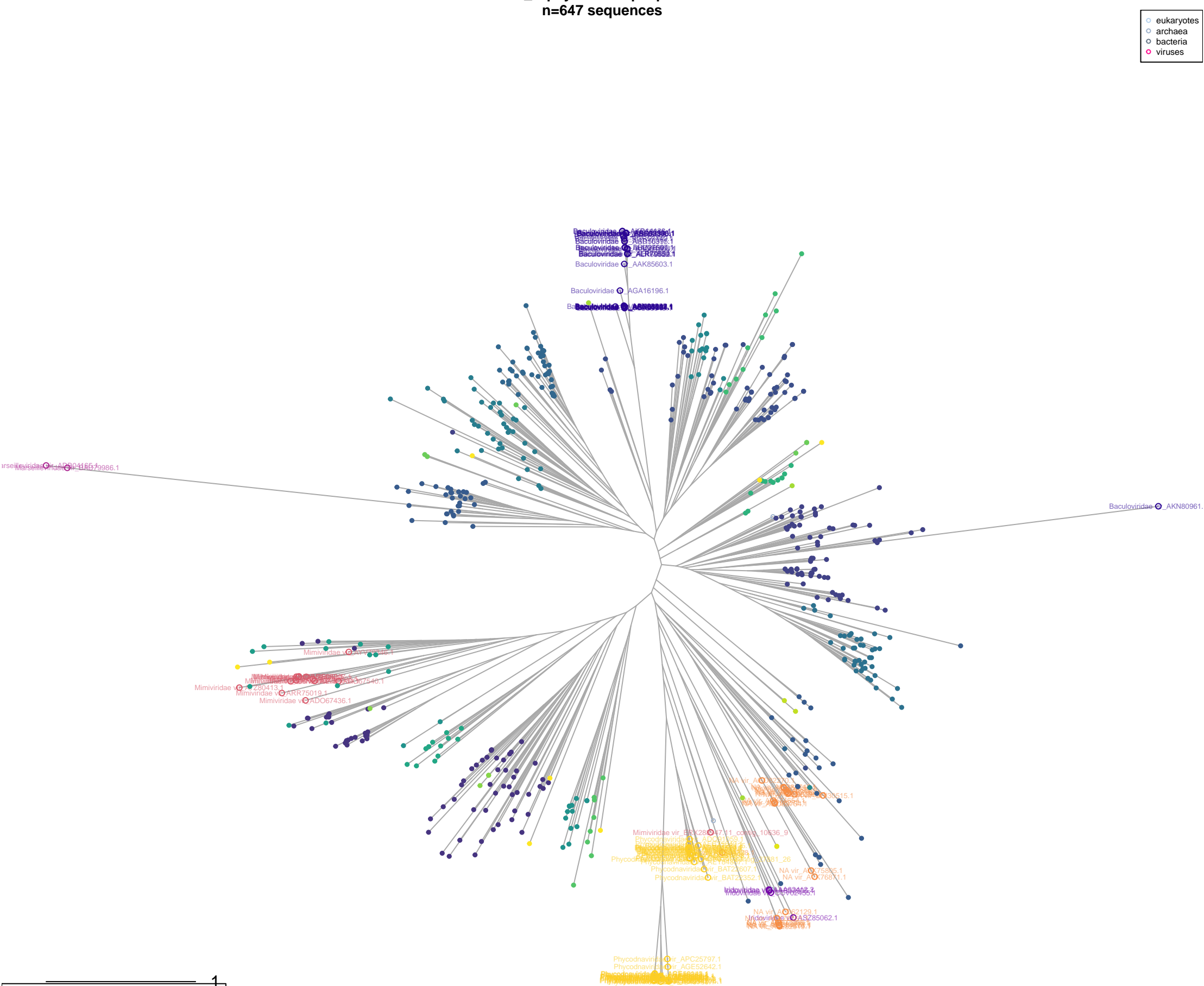


- SNF2\_N.HG3.3:ERCC6 n = 11
- SNF2\_N.HG3.5:ERCC6L n = 5
- SNF2\_N.HG3.1:ERCC6L2 n = 2
- other n = 3

- Herelleviridae n = 1
- Marseilleviridae n = 5
- Siphoviridae n = 4

vir.SNF2\_N.phy.HG6.seqs.iqtree.treefile  
n=647 sequences

- eukaryotes
- archaea
- bacteria
- viruses

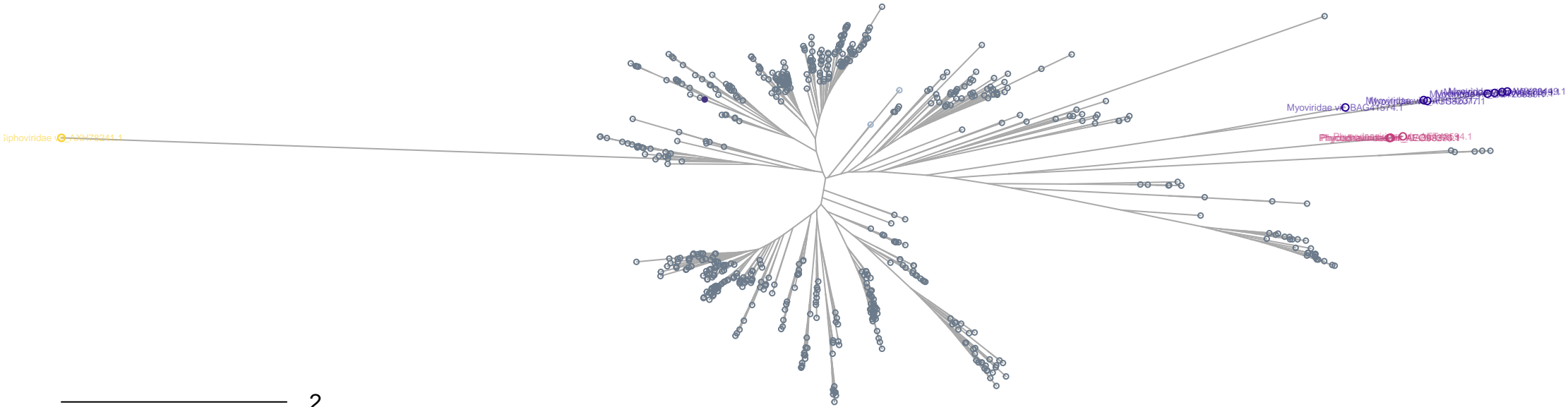


- 1
- SNF2\_N.HG10.1:SHPRH n = 75
  - SNF2\_N.HG1.16:like:HLTF/TTF2:likeclu:18/26 n = 71
  - SNF2\_N.HG1.26:HLTF n = 69
  - SNF2\_N.HG1.18:TTF2 n = 58
  - SNF2\_N.HG1.29:like:TTF2:likeclu:18 n = 46
  - SNF2\_N.HG1.17:like:HLTF/TTF2:likeclu:18/26 n = 44
  - SNF2\_N.HG1.27:like:TTF2:likeclu:18 n = 38
  - SNF2\_N.HG1.25:like:HLTF:likeclu:26 n = 17
  - SNF2\_N.HG1.7:like:HLTF/TTF2:likeclu:18/26 n = 17
  - SNF2\_N.HG1.12:like:HLTF/TTF2:likeclu:18/26 n = 13
  - SNF2\_N.HG1.4:like:HLTF/TTF2:likeclu:18/26 n = 12
  - SNF2\_N.HG1.20:like:HLTF/TTF2:likeclu:18/26 n = 11
  - SNF2\_N.HG1.23:like:HLTF:likeclu:26 n = 10
  - SNF2\_N.HG1.1:like:HLTF/TTF2:likeclu:18/26 n = 8
  - SNF2\_N.HG1.21:like:HLTF/TTF2:likeclu:18/26 n = 6
  - SNF2\_N.HG10.0:like:SHPRH:likeclu:1 n = 4
  - SNF2\_N.HG1.22:like:HLTF:likeclu:26 n = 3
  - SNF2\_N.HG1.5:like:HLTF/TTF2:likeclu:18/26 n = 2
  - SNF2\_N.HG2.11:like:SMARCAD1:likeclu:7 n = 2
  - other n = 8

- Baculoviridae n = 37
- Iridoviridae n = 4
- Marseilleviridae n = 2
- Mimiviridae n = 14
- NA n = 22
- Phycodnaviridae n = 45

SNF2\_N  
vir.SNF2\_N.phy.HG7.seqs.iqtree.treefile  
n=633 sequences

- eukaryotes
- archaea
- bacteria
- viruses

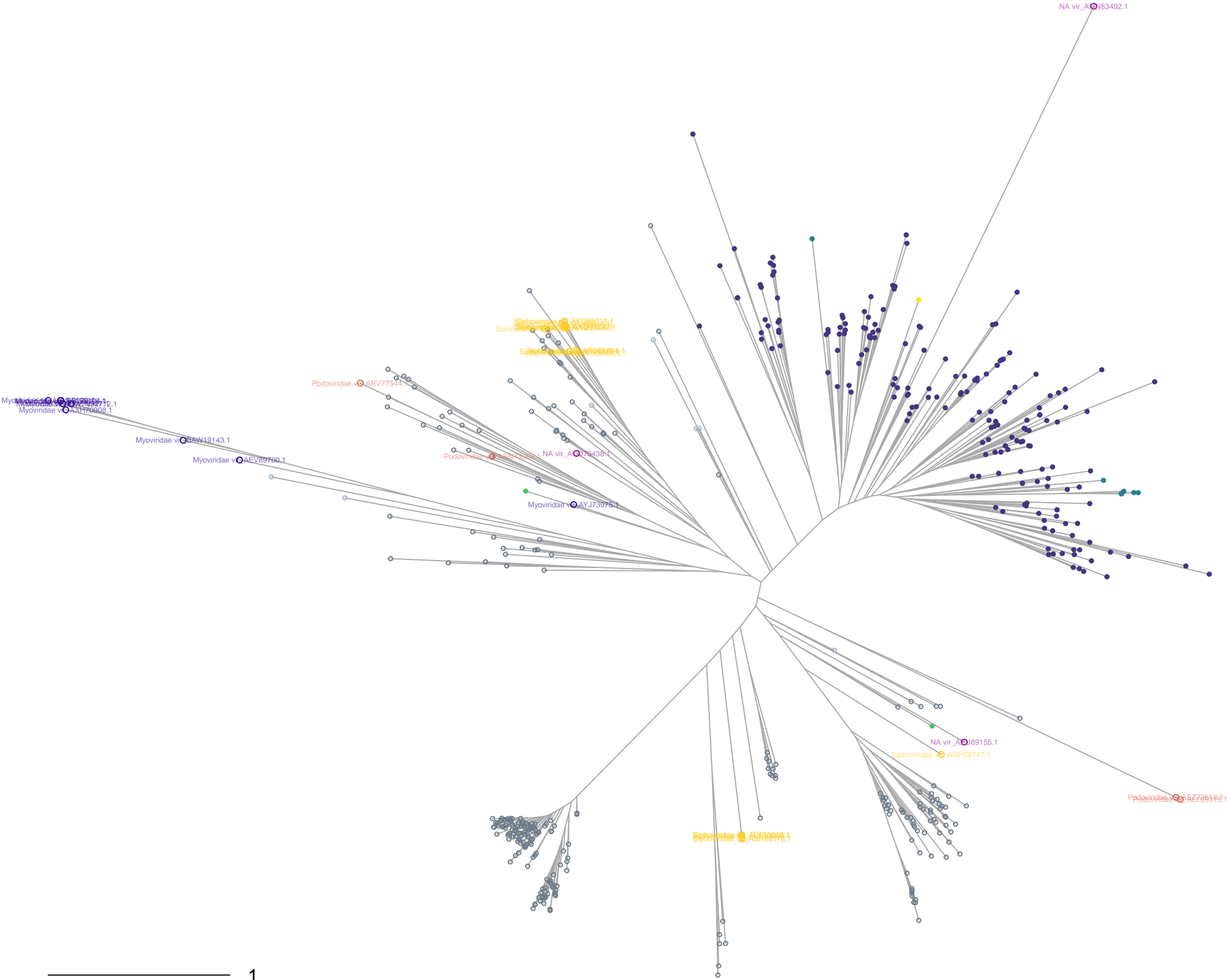


other n = 1

- Myoviridae n = 7
- Phycodnaviridae n = 4
- Siphoviridae n = 1

SNF2\_N  
vir.SNF2\_N.phy.HG8.seqs.iqtree.treefile  
n=527 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- SNF2\_N.HG9.2:SMARCA1/ZRANB3 n = 194
- SNF2\_N.HG9.0:like:SMARCA1/ZRANB3:likeclu:2 n = 7
- SNF2\_N.HG9.3:like:SMARCA1/ZRANB3:likeclu:2 n = 2
- other n = 1

- Myoviridae n = 9
- NA n = 3
- Podoviridae n = 4
- Siphoviridae n = 19



## SNF2\_N



- other  $n = 1$

- ☐ eukaryotes
- ☐ archaea
- ☐ bacteria
- ☒ viruses

- Myoviridae n = 35
- NA n = 3
- Podoviridae n = 7
- Siphoviridae n = 75