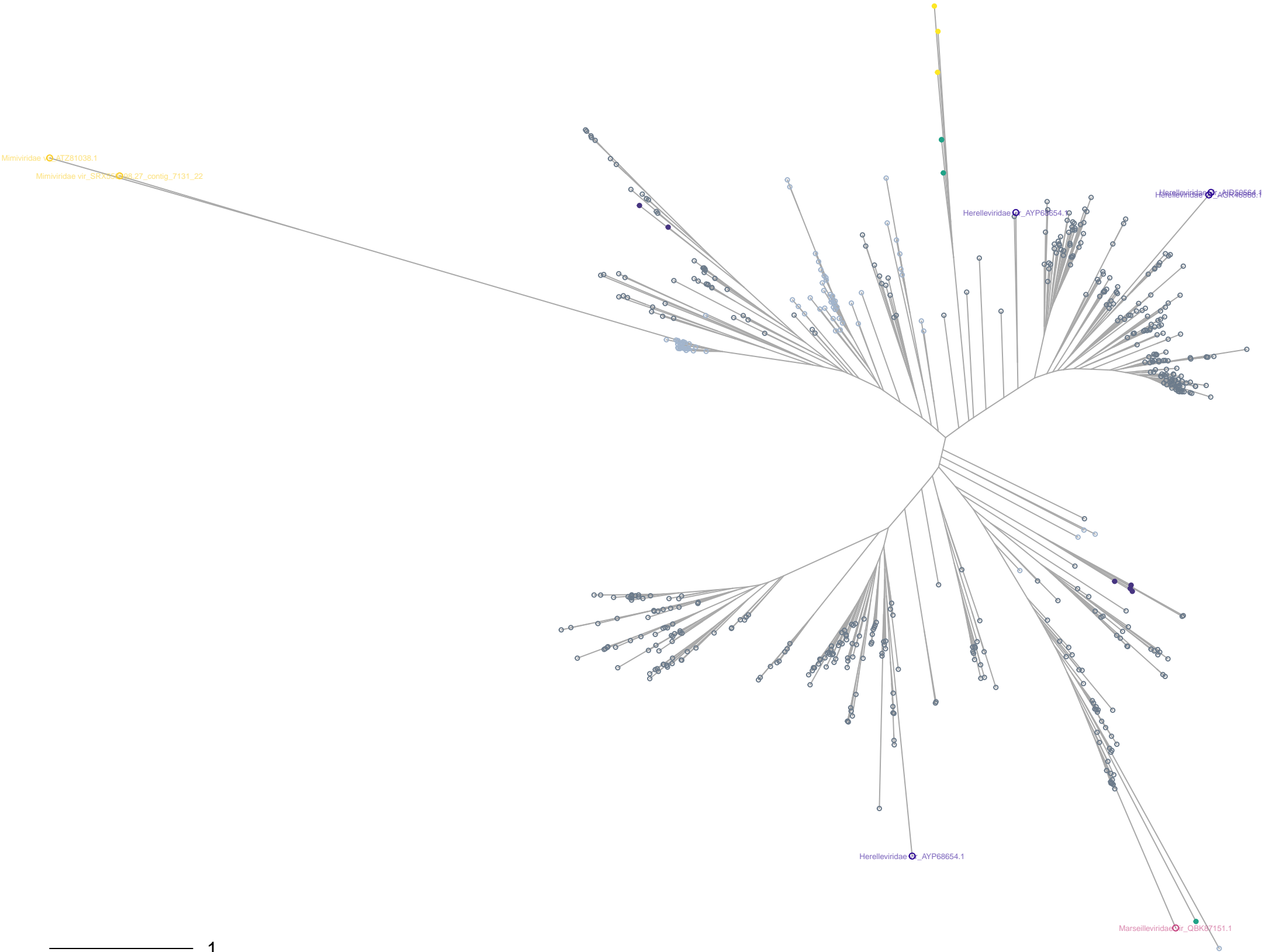


SIR2  
vir.SIR2.phy.HG1.seqs.iqtree.treefile  
n=574 sequences

- eukaryotes
- archaea
- bacteria
- viruses

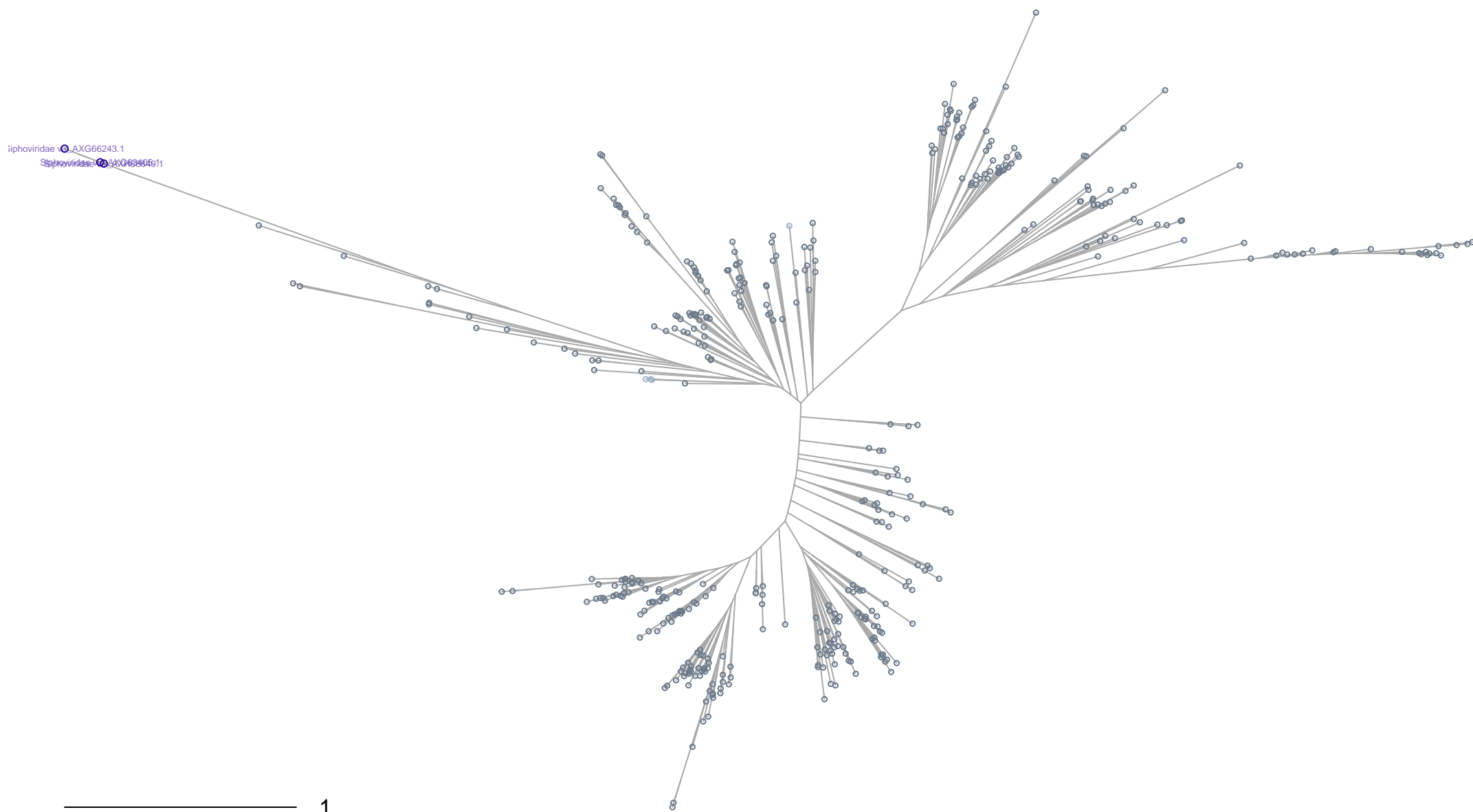


- SIR2.HG2.1:SIRT4/SIRT5 n = 6
- SIR2.HG3.10:like:SIRT6:likeclu:1 n = 4
- other n = 3

- Herelleviridae n = 4
- Marseilleviridae n = 1
- Mimiviridae n = 2

SIR2  
vir.SIR2.phy.HG2.seqs.iqtree.treefile  
n=436 sequences

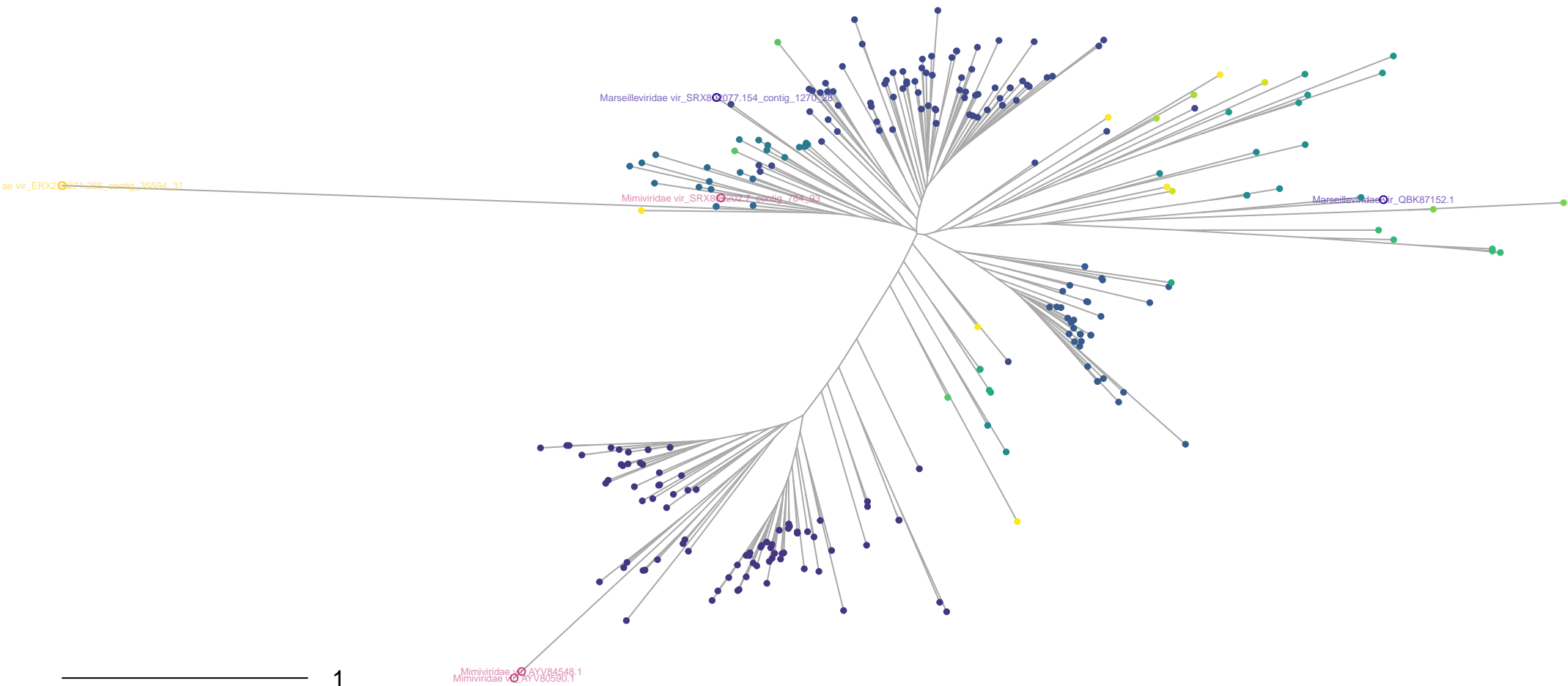
- eukaryotes
- archaea
- bacteria
- viruses



Siphoviridae n = 3

SIR2  
vir.SIR2.phy.HG4.seqs.iqtree.treefile  
n=269 sequences

- eukaryotes
- archaea
- bacteria
- viruses



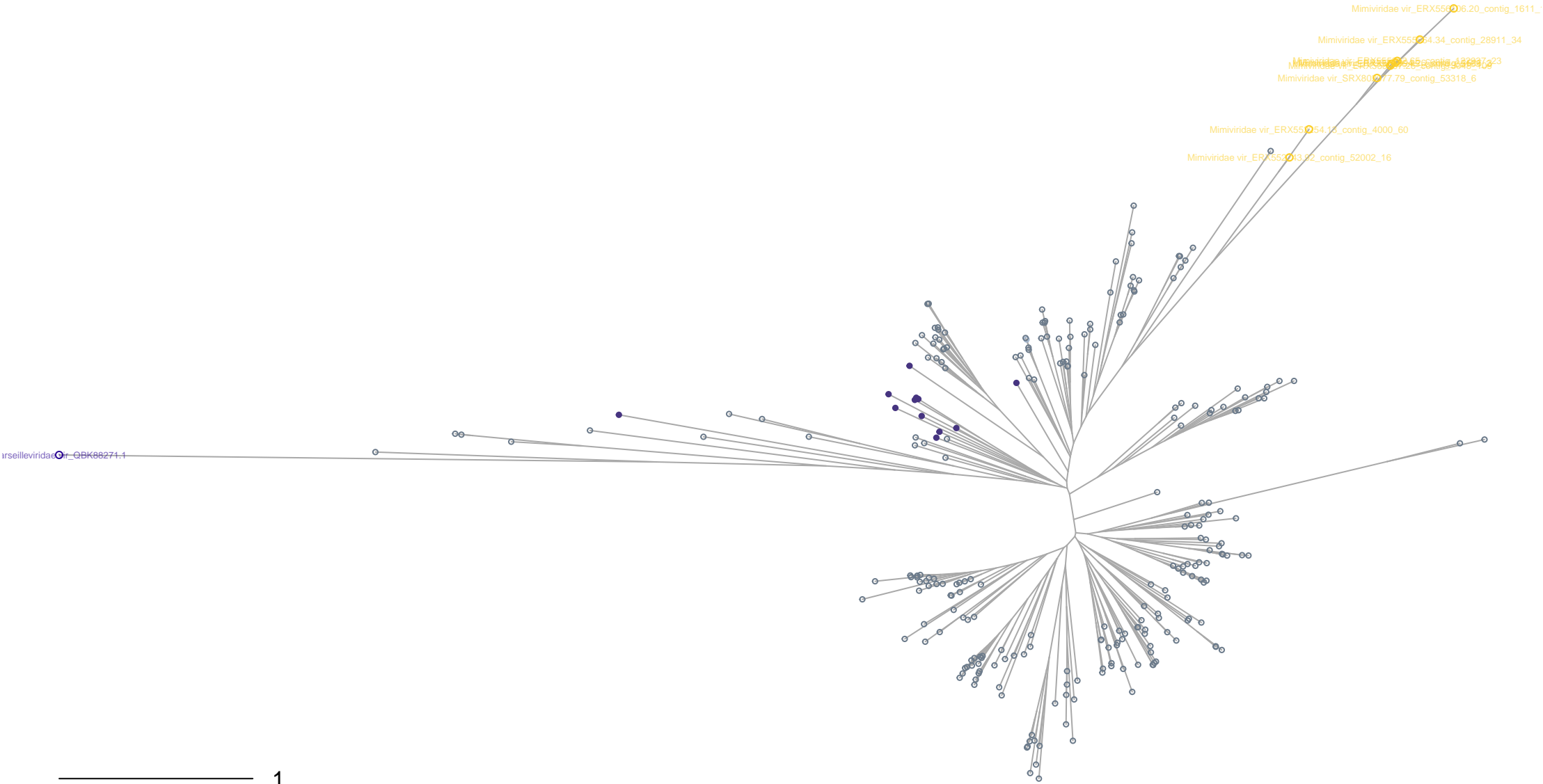
1

- SIR2.HG1.3:SIRT1 n = 84
- SIR2.HG1.14:SIRT2 n = 82
- SIR2.HG1.12:SIRT3 n = 32
- SIR2.HG1.13:like:SIRT2/SIRT3:likeclu:12/14 n = 13
- SIR2.HG1.10:like:SIRT2/SIRT3:likeclu:12/14 n = 10
- SIR2.HG1.6:like:SIRT2/SIRT3:likeclu:12/14 n = 9
- SIR2.HG1.16:like:SIRT2/SIRT3:likeclu:12/14 n = 6
- SIR2.HG1.4:like:SIRT2/SIRT3:likeclu:12/14 n = 5
- SIR2.HG1.7:like:SIRT2/SIRT3:likeclu:12/14 n = 5
- SIR2.HG1.9:like:SIRT2/SIRT3:likeclu:12/14 n = 3
- SIR2.HG1.0:like:SIRT1/SIRT2/SIRT3:likeclu:3/12/14 n = 2
- SIR2.HG1.17:like:SIRT2/SIRT3:likeclu:12/14 n = 2
- SIR2.HG1.5:like:SIRT2/SIRT3:likeclu:12/14 n = 2
- other n = 6

- Marseilleviridae n = 2
- Mimiviridae n = 3
- Phycodnaviridae n = 1

SIR2  
vir.SIR2.phy.HG5.seqs.iqtree.treefile  
n=268 sequences

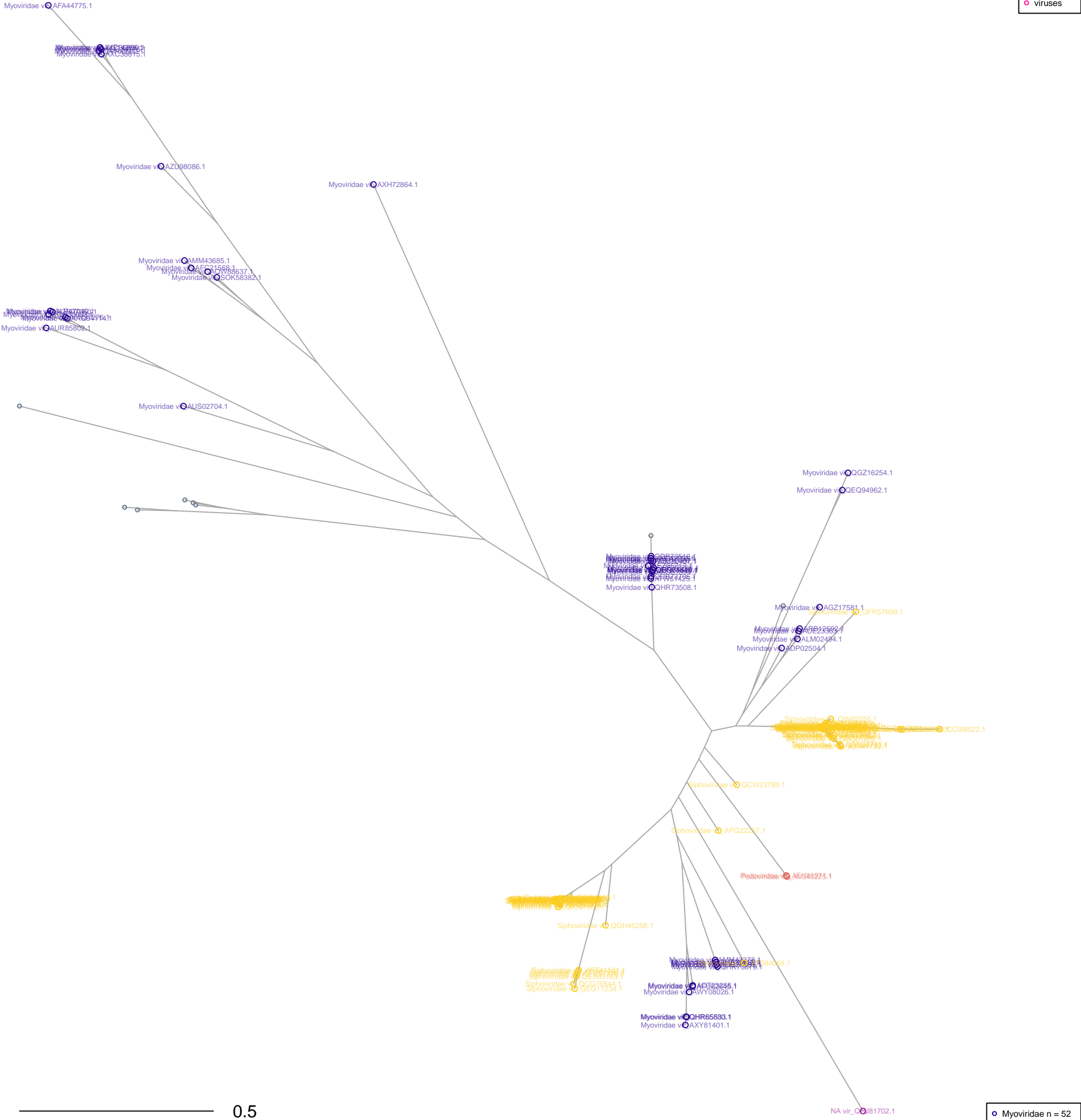
- eukaryotes
- archaea
- bacteria
- viruses



● SIR2.HG2.0:like:SIRT4/SIRT5:likeclu:1 n = 12  
● other n = 0

● Marseilleviridae n = 1  
● Mimiviridae n = 9

SIR2  
vir.SIR2.phy.HG6.seqs.iqtree.treefile  
n=139 sequences



SIR2  
vir.SIR2.phy.HG7.seqs.iqtree.treefile  
n=118 sequences

eukaryotes  
archaea  
bacteria  
viruses



Mimiviridae n = 1  
Phycodnaviridae n = 1