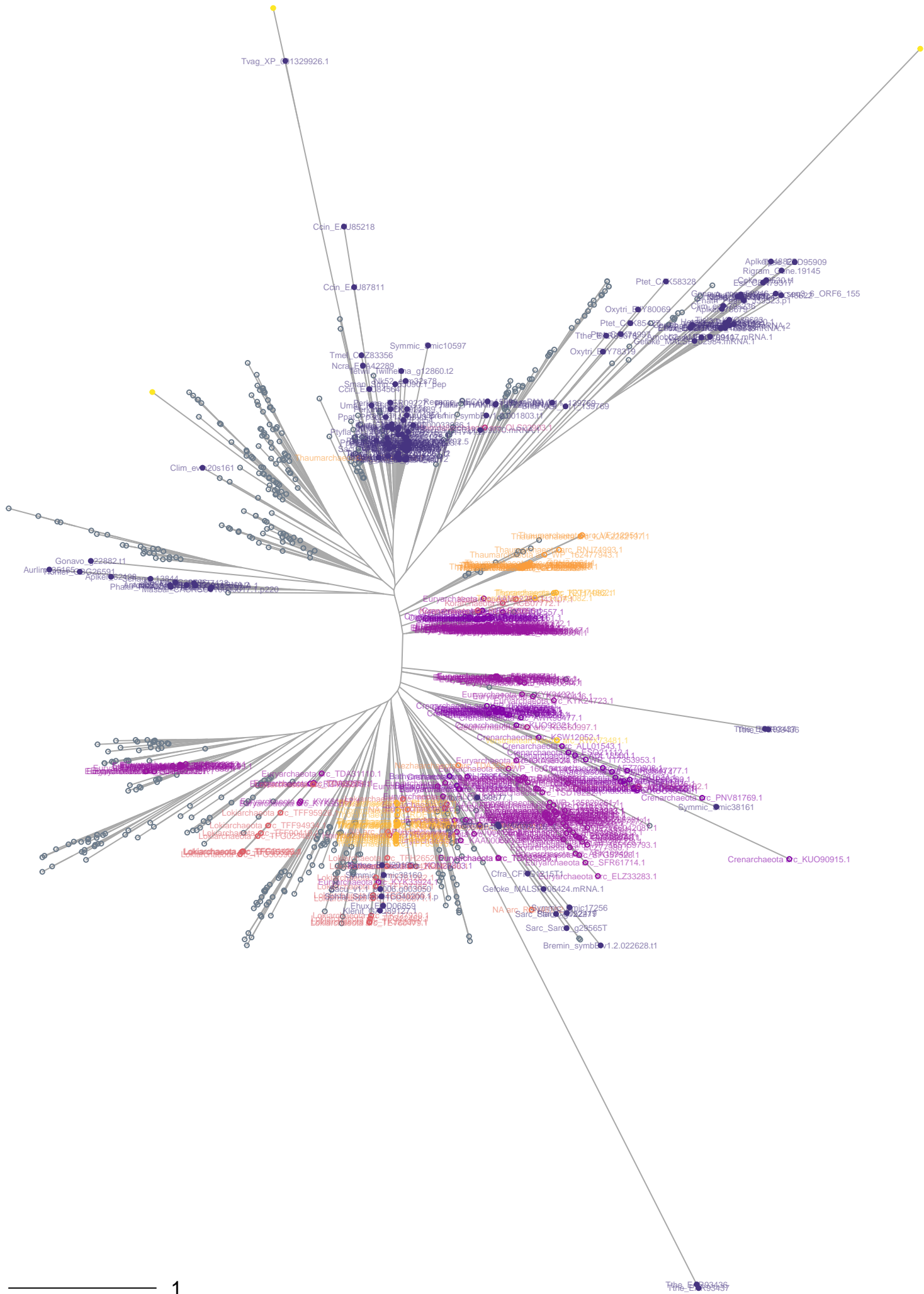


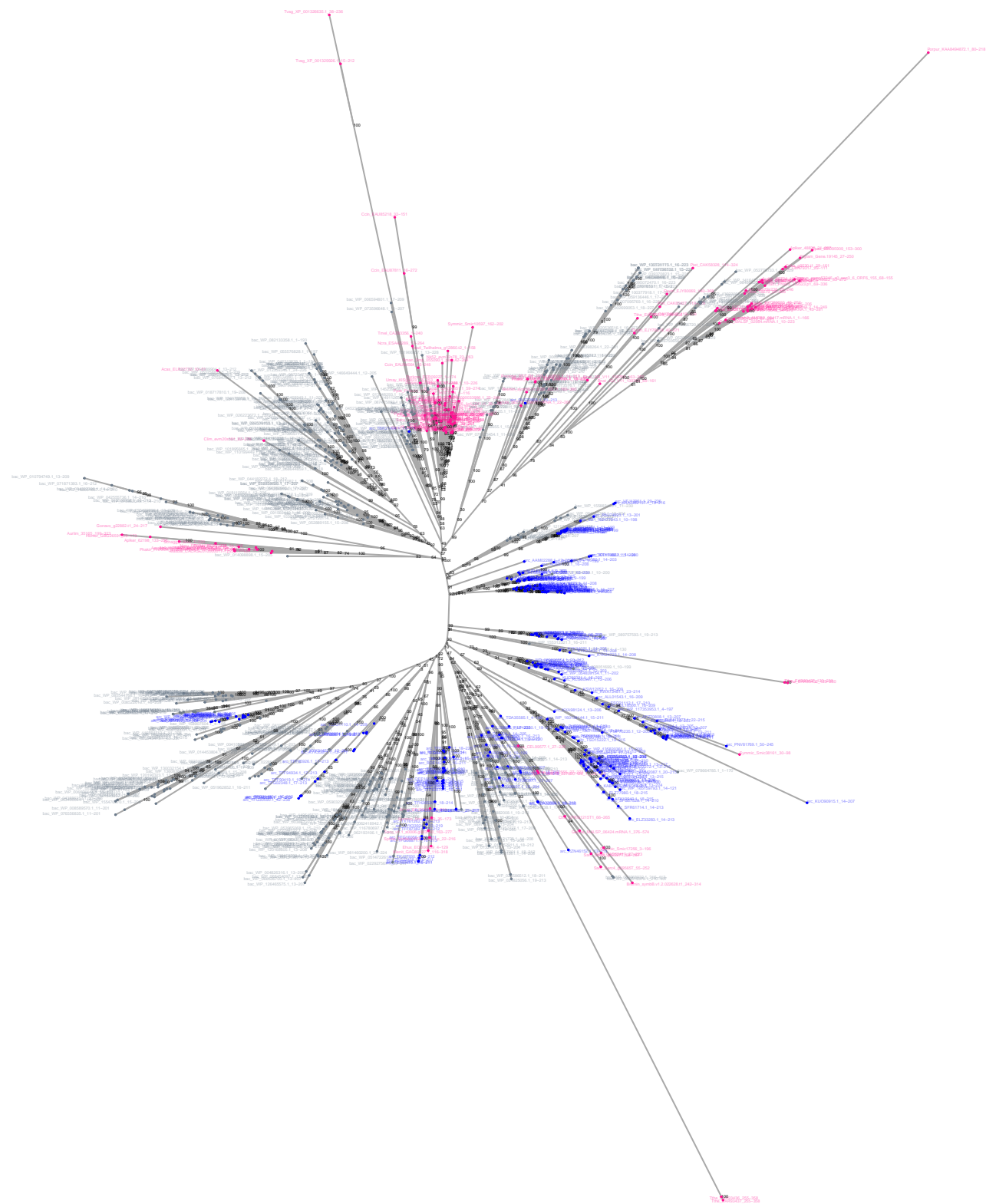
SIR2
euk.SIR2.phy.HG1.seqs.iqtree.treefile
n=884 sequences

- eukaryotes
- archaea
- bacteria

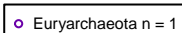


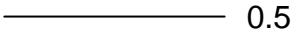
1

SIR2.HG2.1:SIRT4/SIRT5 n = 138
other n = 3

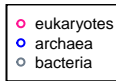


SIRZ

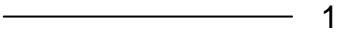




SIRZ

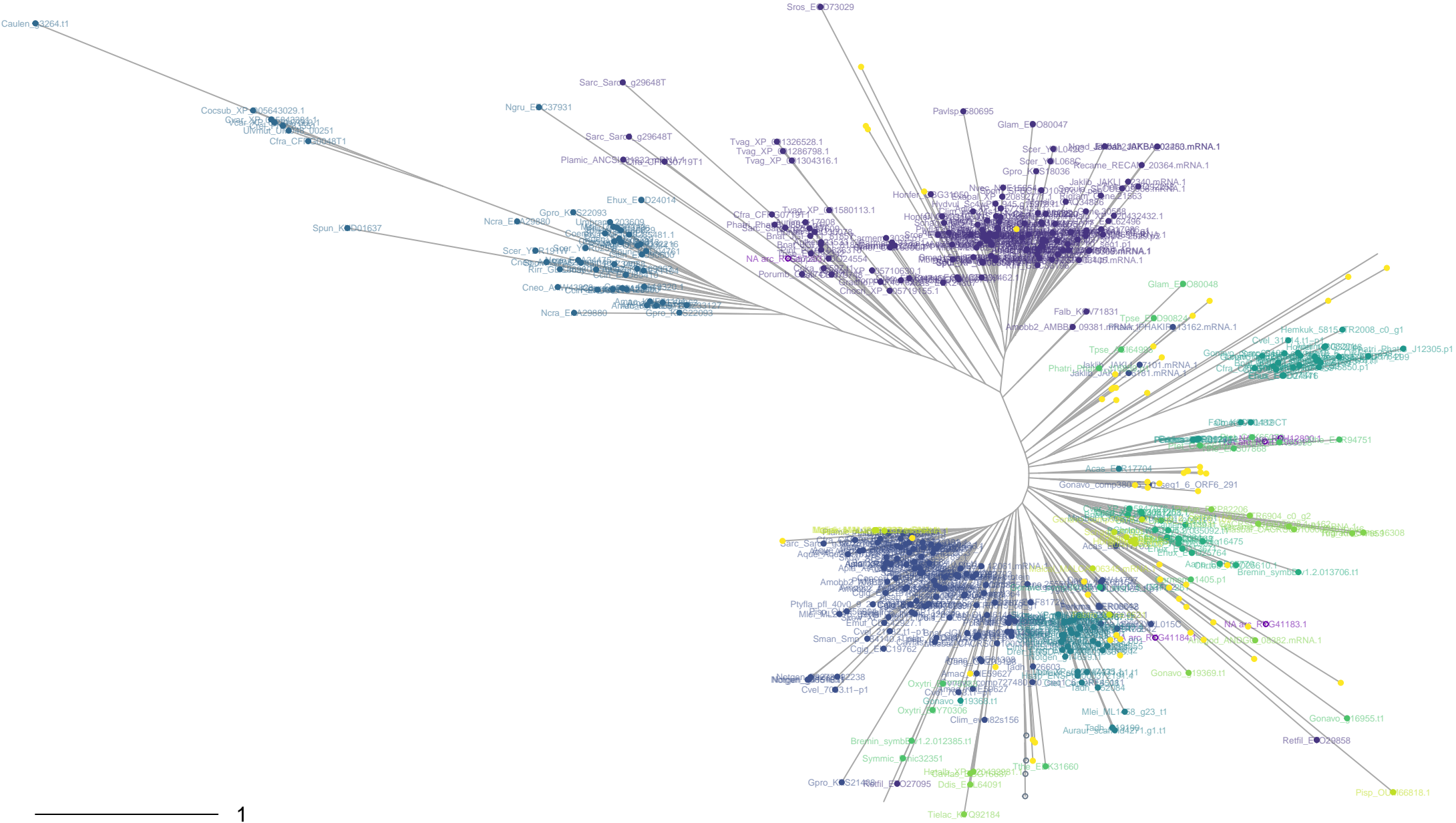


1



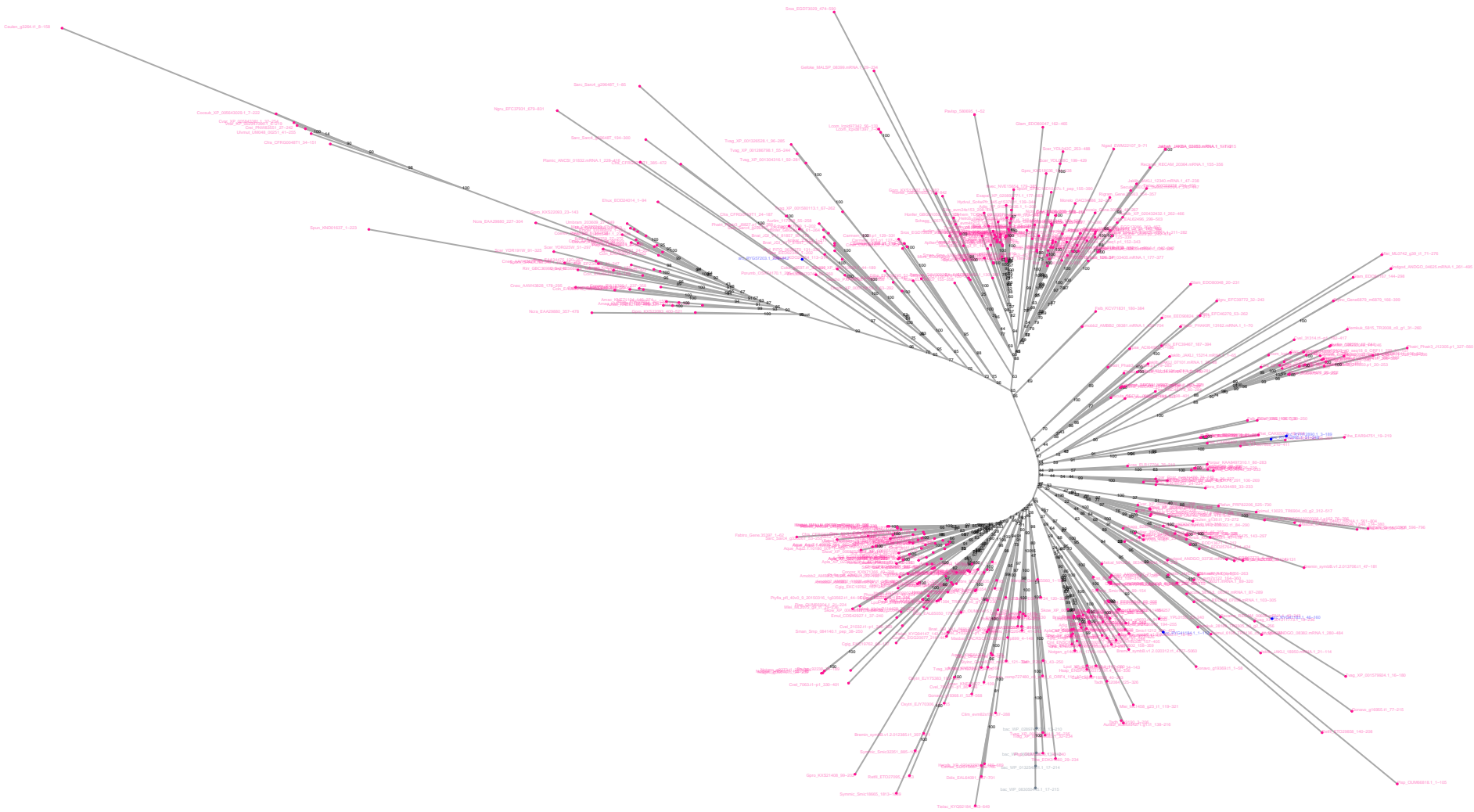
euk.SIR2.phy.HG4.seqs.iqtree.treefile
n=516 sequences

- eukaryotes
- archaea
- bacteria



- SIR2.HG1.3:SIRT1 n = 141
- SIR2.HG1.14:SIRT2 n = 130
- SIR2.HG1.0:like:SIRT1/SIRT2/SIRT3:likeclu:3/12/14 n = 49
- SIR2.HG1.12:SIRT3 n = 38
- SIR2.HG1.7:like:SIRT2/SIRT3:likeclu:12/14 n = 31
- SIR2.HG1.13:like:SIRT2/SIRT3:likeclu:12/14 n = 19
- SIR2.HG1.6:like:SIRT2/SIRT3:likeclu:12/14 n = 16
- SIR2.HG1.16:like:SIRT2/SIRT3:likeclu:12/14 n = 13
- SIR2.HG1.10:like:SIRT2/SIRT3:likeclu:12/14 n = 12
- other n = 56

- NA n = 5

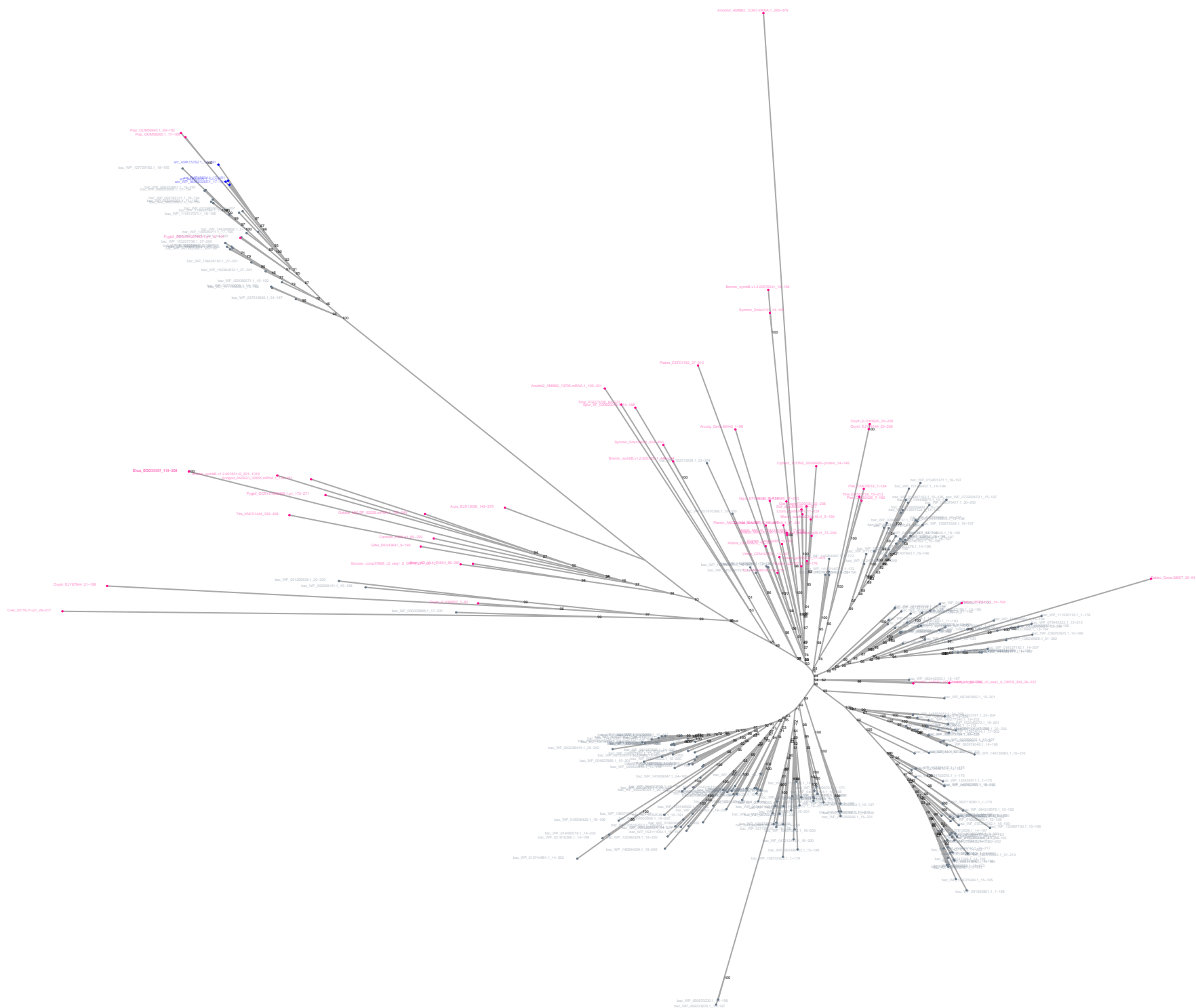


SIRZ



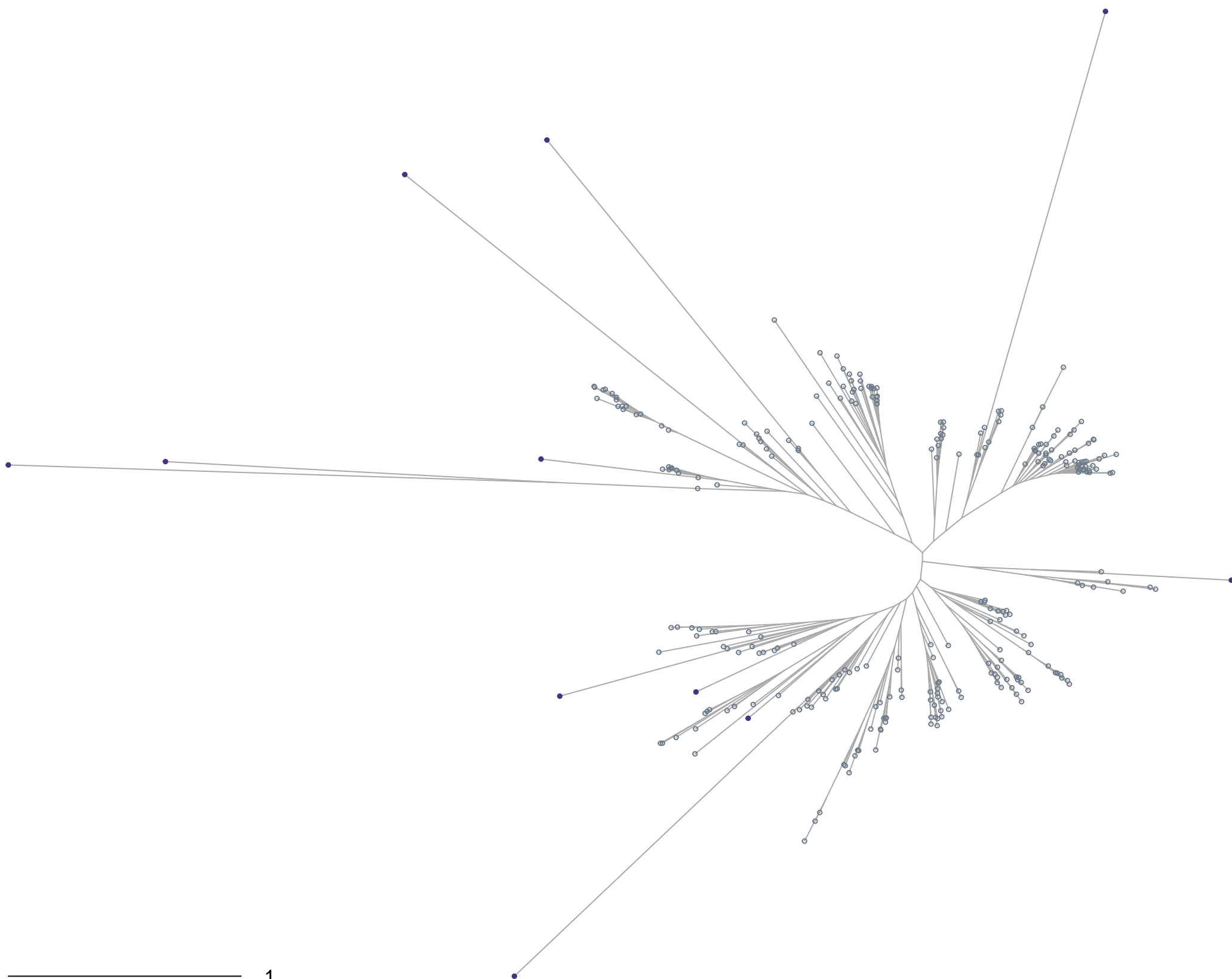
- SIR2.HG2.0:like:SIRT4/SIRT5:likeclu:1 n = 51
- other n = 4

- Euryarchaeota n = 4



SIR2
euk.SIR2.phy.HG6.seqs.iqtree.treefile
n=294 sequences

● eukaryotes
● archaea
● bacteria



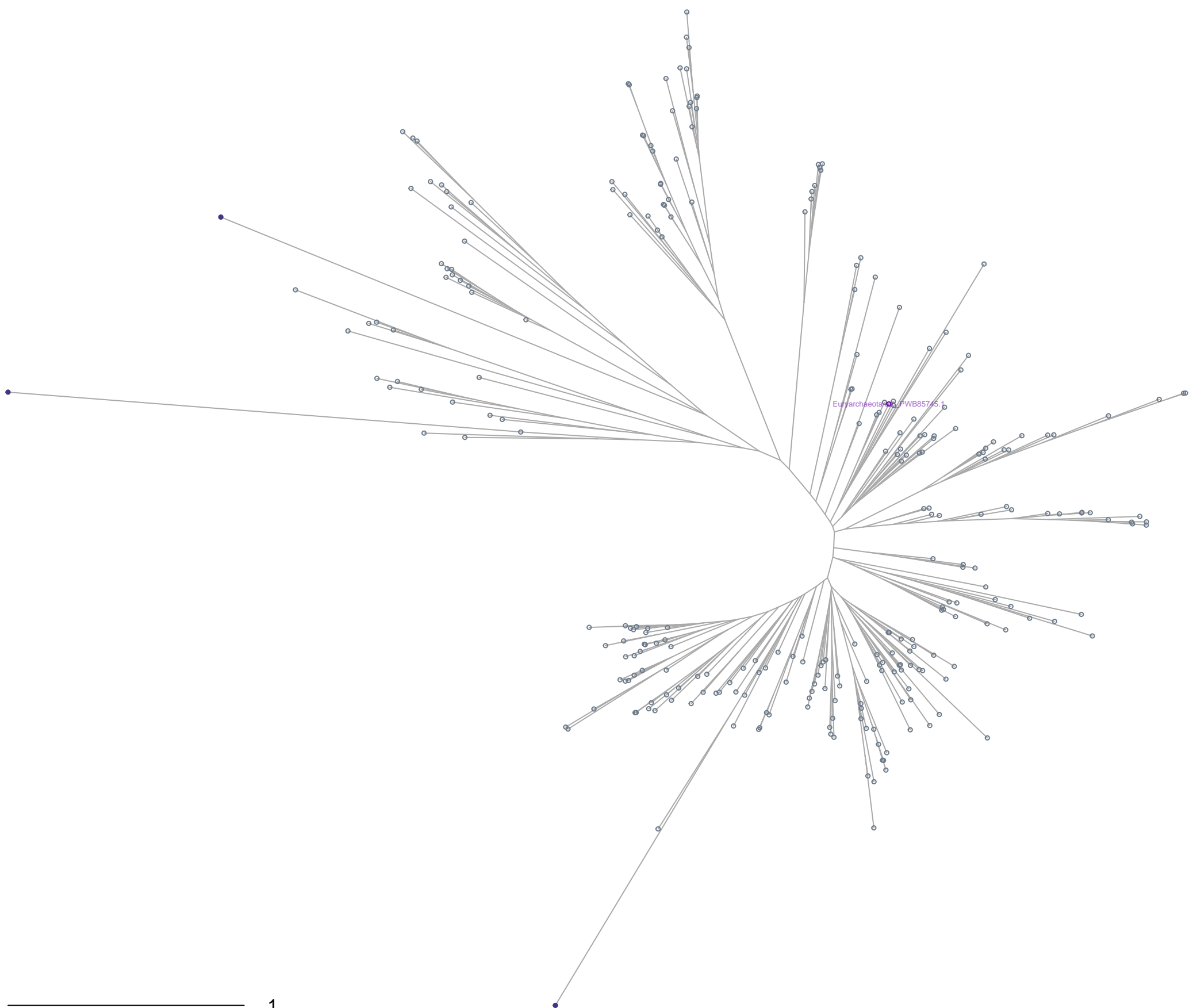
● other n = 11

○ n =



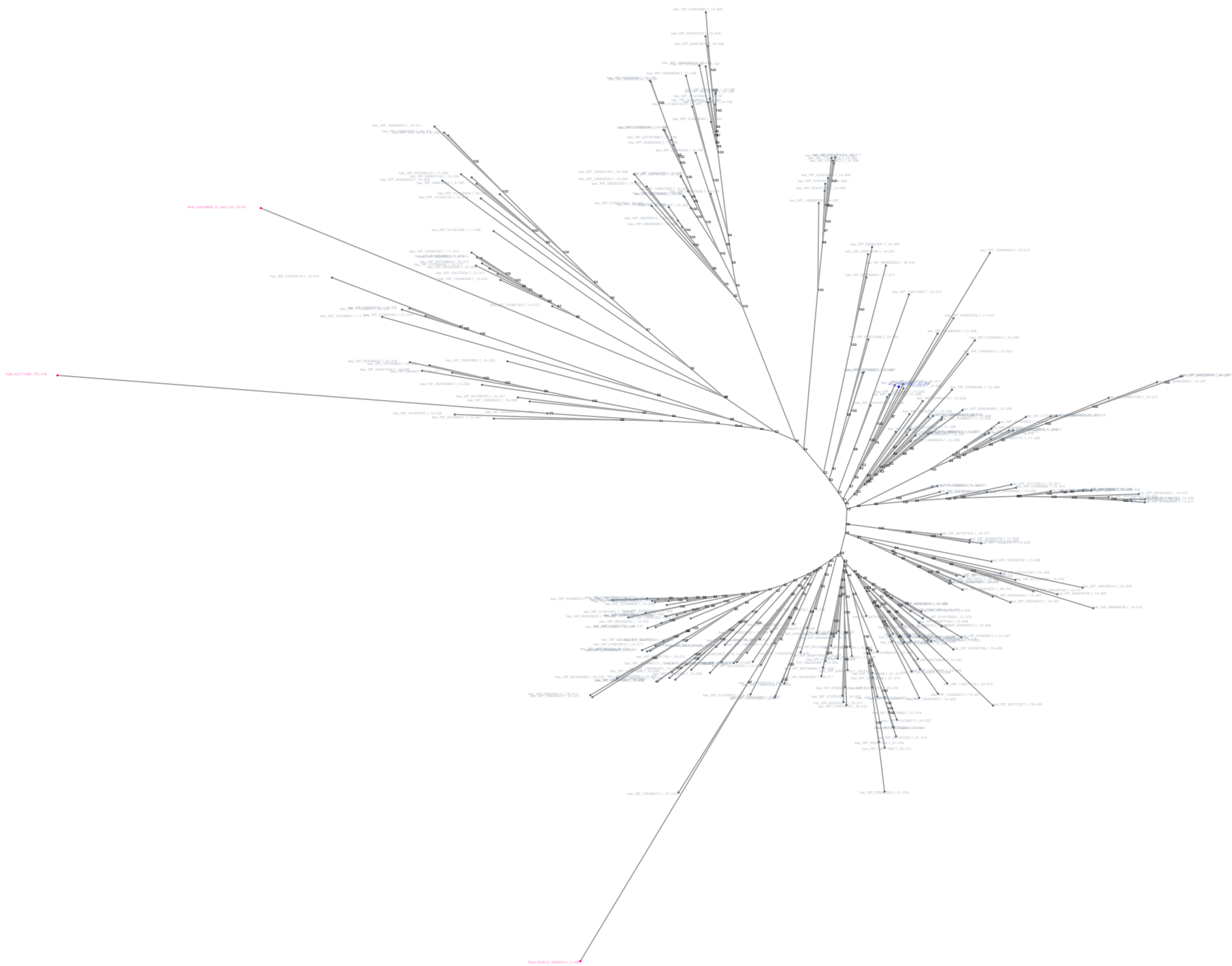
SIR2
euk.SIR2.phy.HG7.seqs.iqtree.treefile
n=284 sequences

● eukaryotes
● archaea
● bacteria



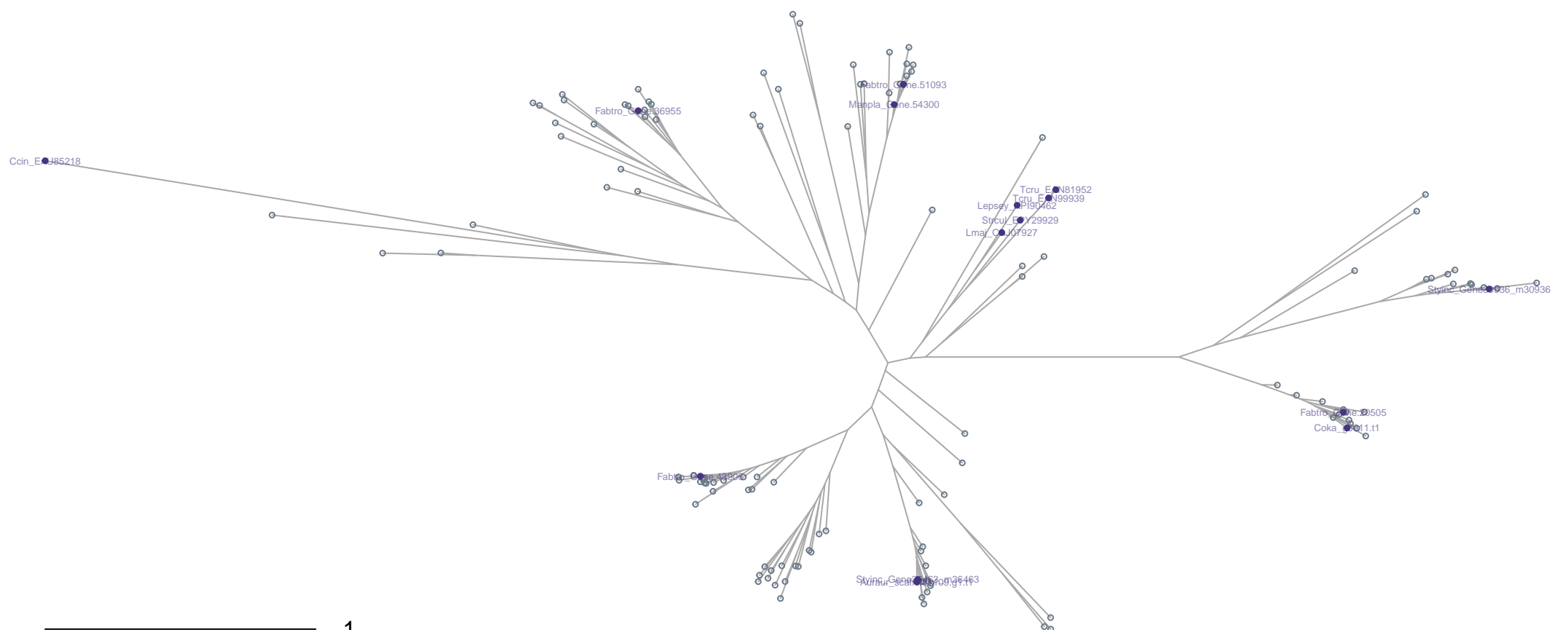
● other n = 3

○ Euryarchaeota n = 1



SIRZ

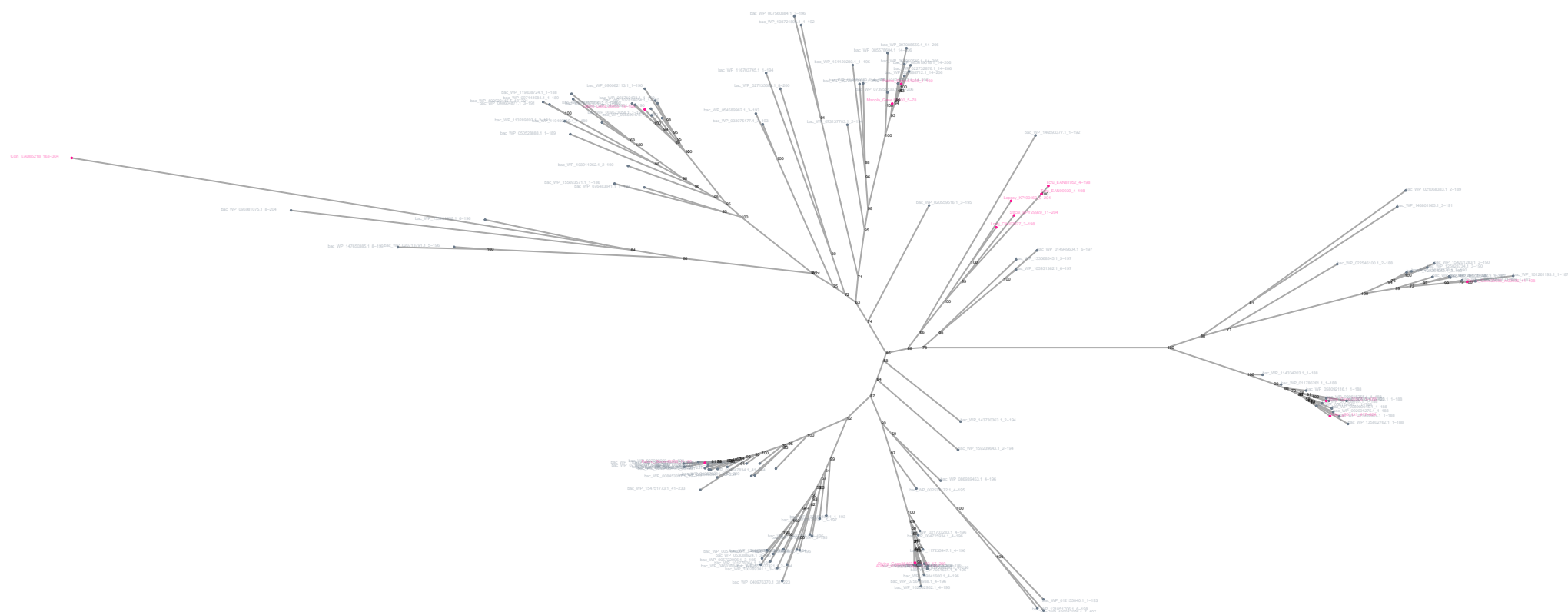
- eukaryotes
- archaea
- bacteria



1

- SIR2.HG2.1:SIRT4/SIRT5 n = 15
- other n = 0

○ $n =$



SIRZ

- other $n = 3$

○ $n =$

