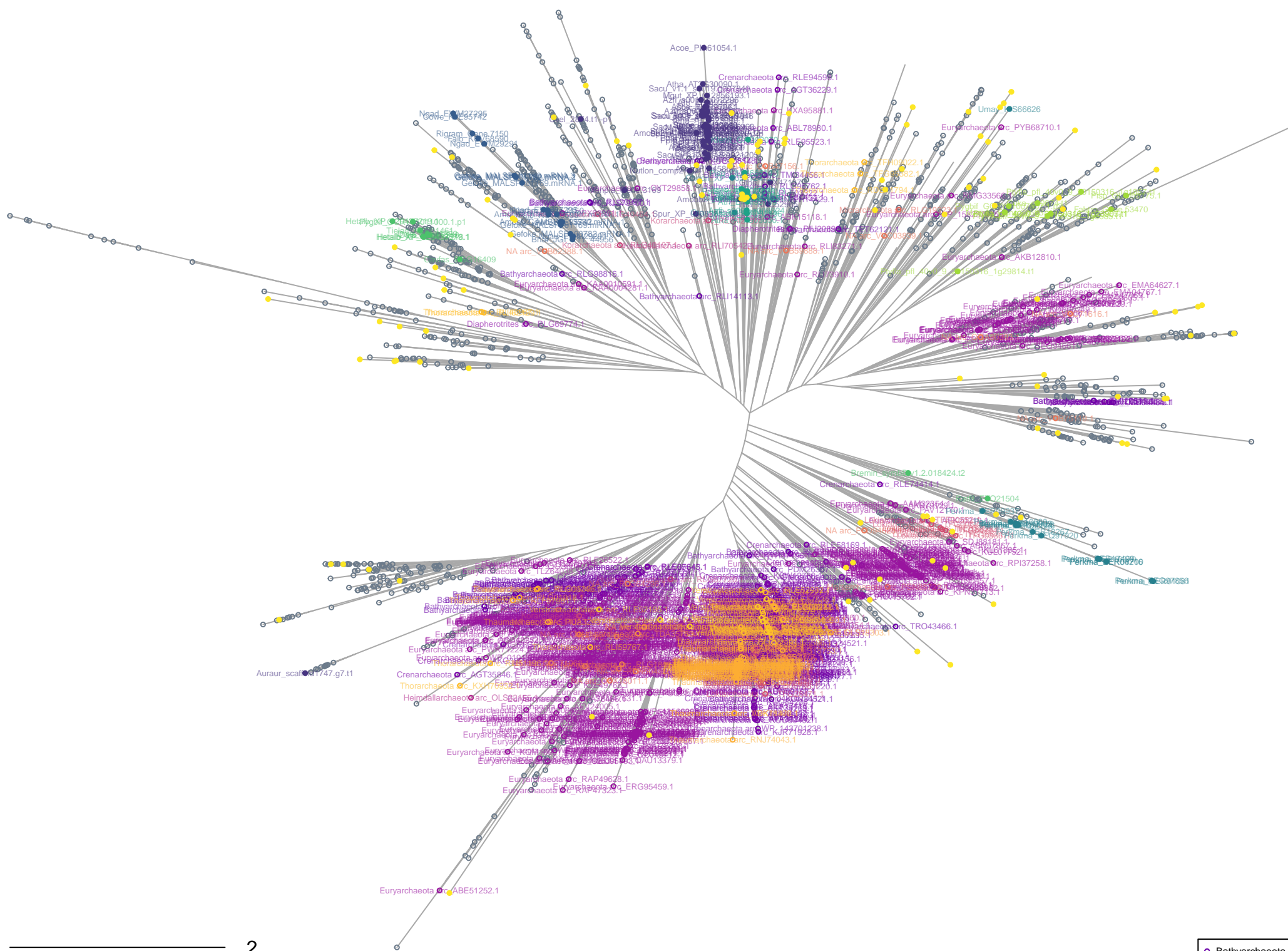
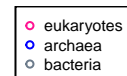


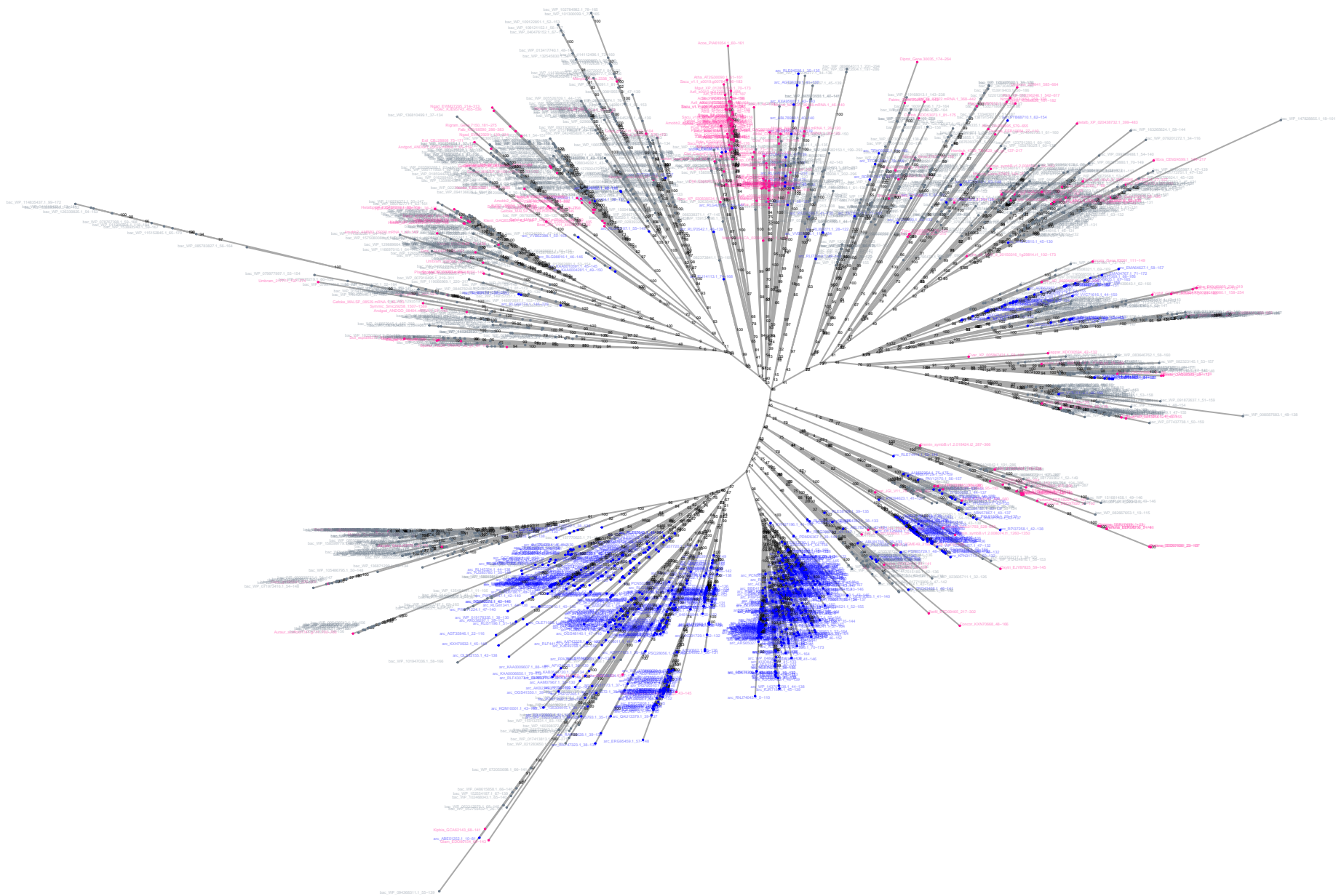
euk.Acetyltransf_1.phy.HG1.seqs.iqtree.treefile
n=2157 sequences



2

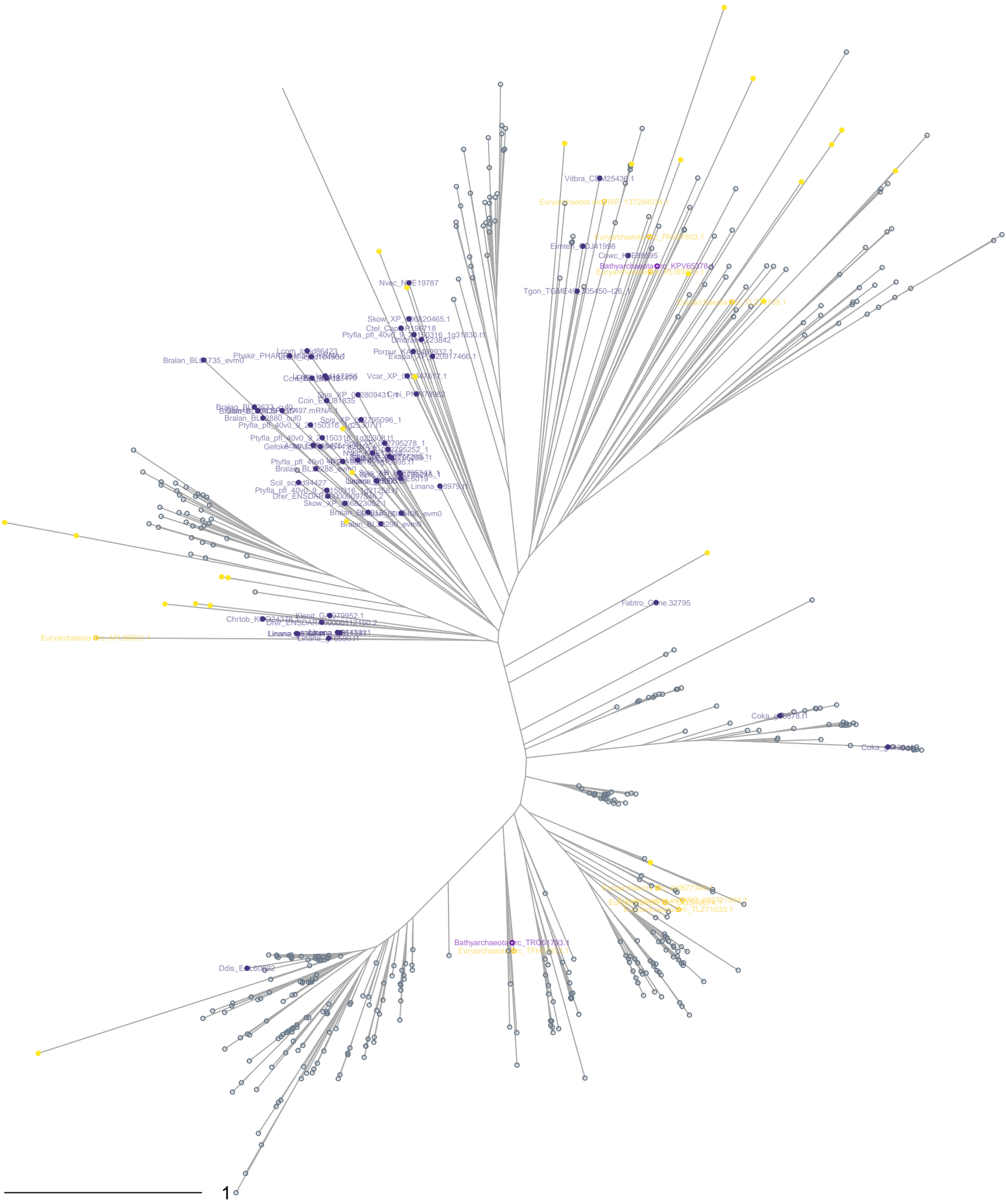
- Acetyltransf_1.HG21.0:NA n = 50
- Acetyltransf_1.HG1.13:like:NAA30:likeclu:14 n = 19
- Acetyltransf_1.HG2.4:like:NAA50:NAA60:likeclu:8/17 n = 17
- Acetyltransf_1.HG1.0:like:NAA30/NAT8/NAT8L/NAT14:likeclu:14/23/38 n = 13
- Acetyltransf_1.HG2.10:like:NAA50:likeclu:17 n = 10
- Acetyltransf_1.HG26.0:NA n = 10
- other n = 107

- Bathyarchaeota n = 92
- Crenarchaeota n = 175
- Diapherotrites n = 2
- Euryarchaeota n = 346
- Geothermarchaeota n = 8
- Heimdallarchaeota n = 8
- Hydrothermarchaeota n = 1
- Korarchaeota n = 14
- Lokiarchaeota n = 11
- Marsarchaeota n = 2
- Micrarchaeota n = 1
- NA n = 29
- Nanoarchaeota n = 1
- Nezharchaeota n = 2
- Odinarchaeota n = 2
- Thaumarchaeota n = 63
- Thorarchaeota n = 20
- Verstraetearchaeota n = 9



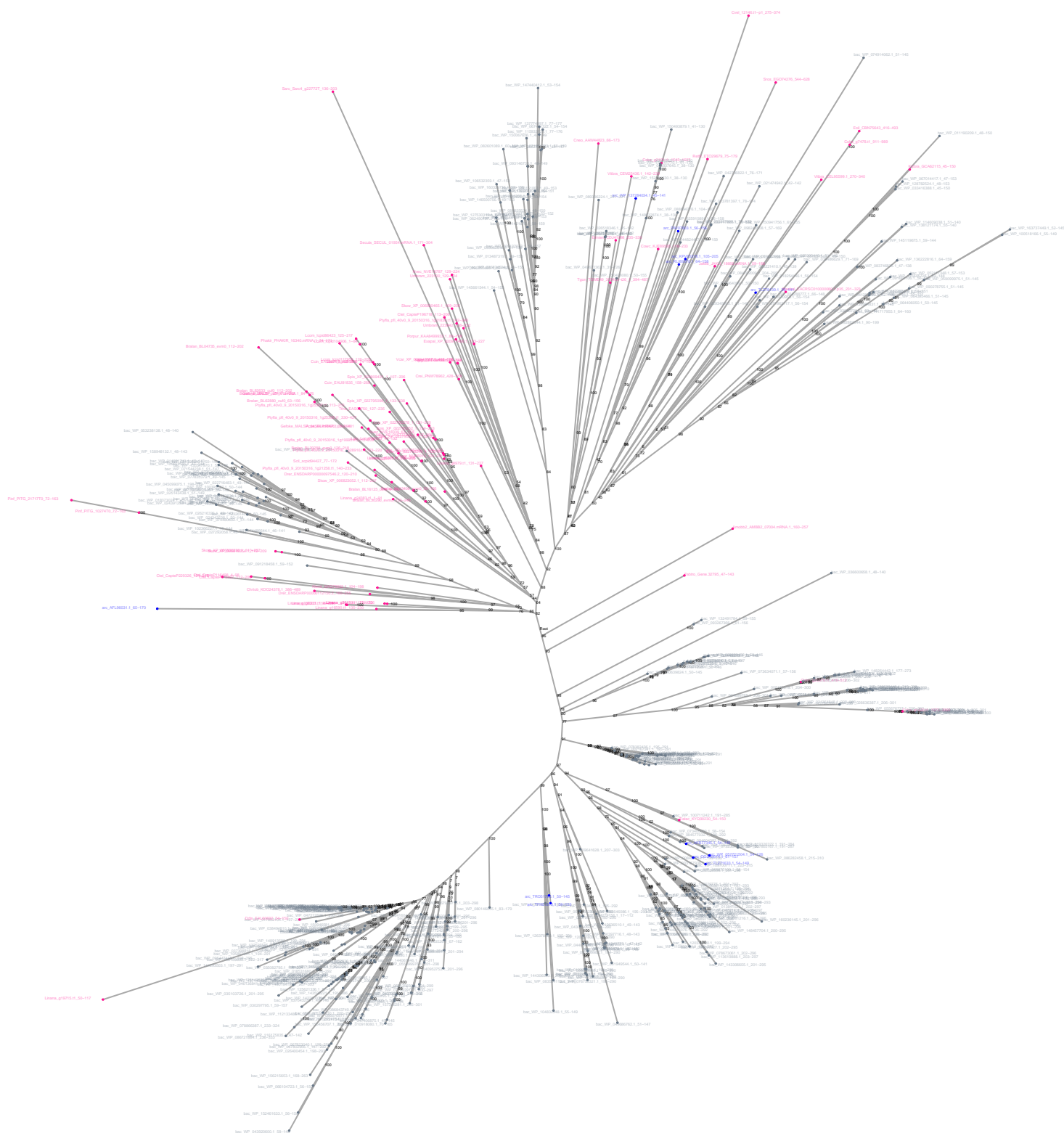
Acetyltransf_1
euk.Acetyltransf_1.phy.HG10.seqs.iqtree.treefile
n=534 sequences

- eukaryotes
- archaea
- bacteria



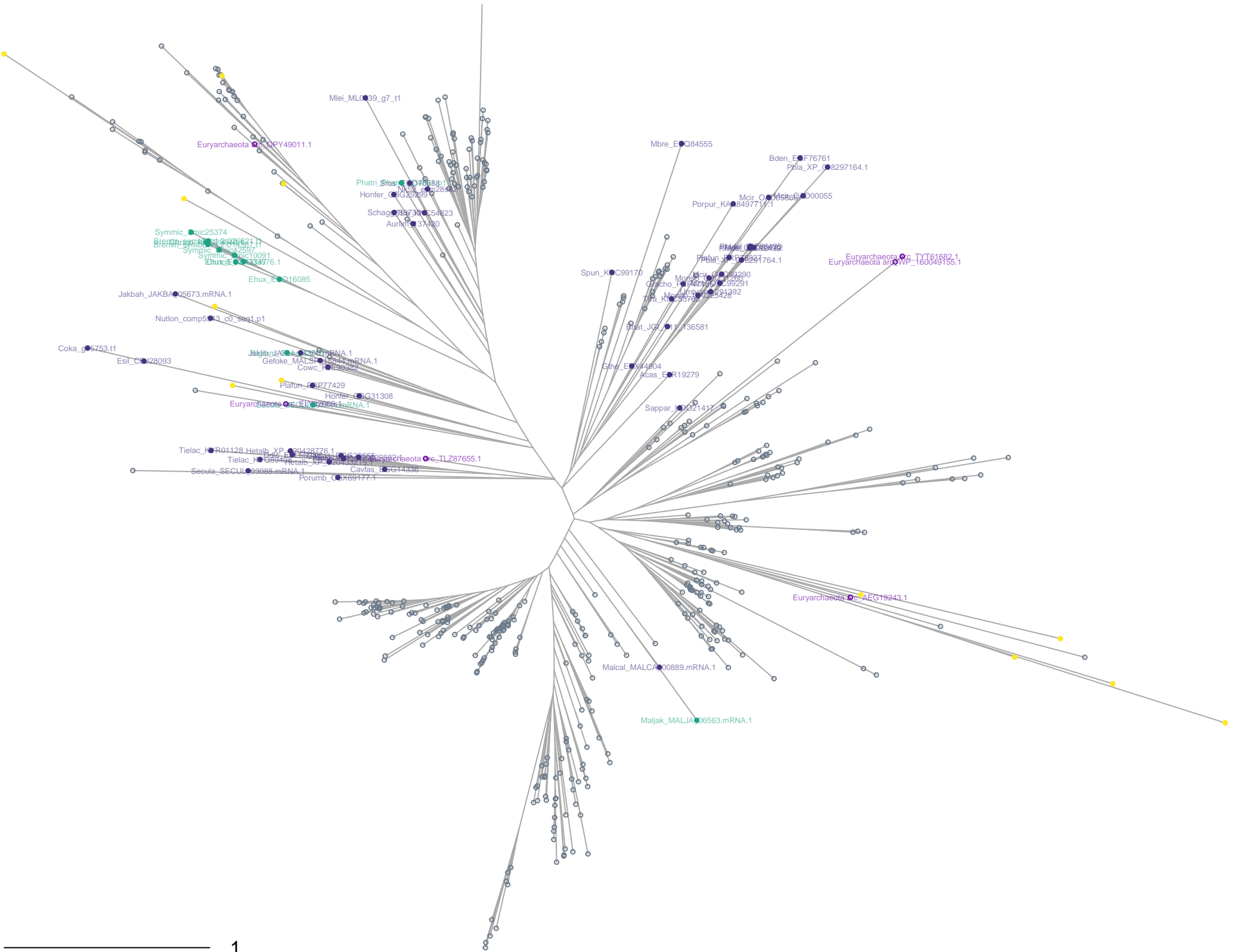
Acetyltransf_1.HG1.38:NAT8/NAT8L n = 64
other n = 28

Bathyarchaeota n = 2
Euryarchaeota n = 10



euk.Acetyltransf_1.phy.HG11.seqs.iqtree.treefile
n=511 sequences

eukaryotes
archaea
bacteria



Acetyltransf_1.HG15.1:NA n = 51
Acetyltransf_1.HG36.0:NA n = 13
other n = 12

Euryarchaeota n = 6

Acetyltransf_1
euk.Acetyltransf_1.phy.HG12.seqs.iqtree.treefile
n=506 sequences

- eukaryotes
- archaea
- bacteria



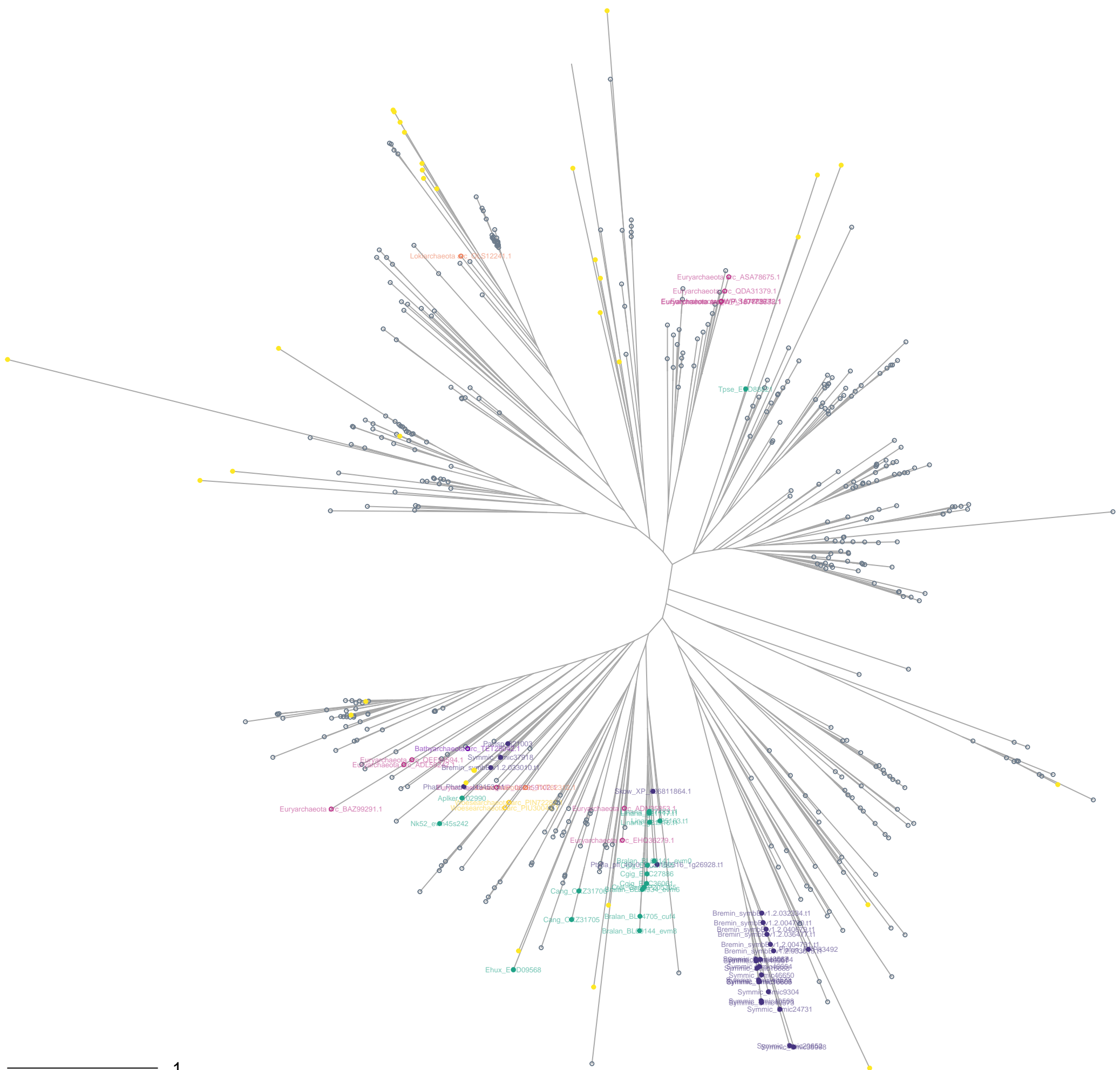
- Acetyltransf_1.HG19.1:NA n = 57
- Acetyltransf_1.HG15.0:NA n = 15
- other n = 10

- Crenarchaeota n = 1
- Euryarchaeota n = 8
- NA n = 2
- Thorarchaeota n = 1



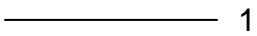
Acetyltransf_1
euk.Acetyltransf_1.phy.HG13.seqs.iqtree.treefile
n=498 sequences

eukaryotes
archaea
bacteria



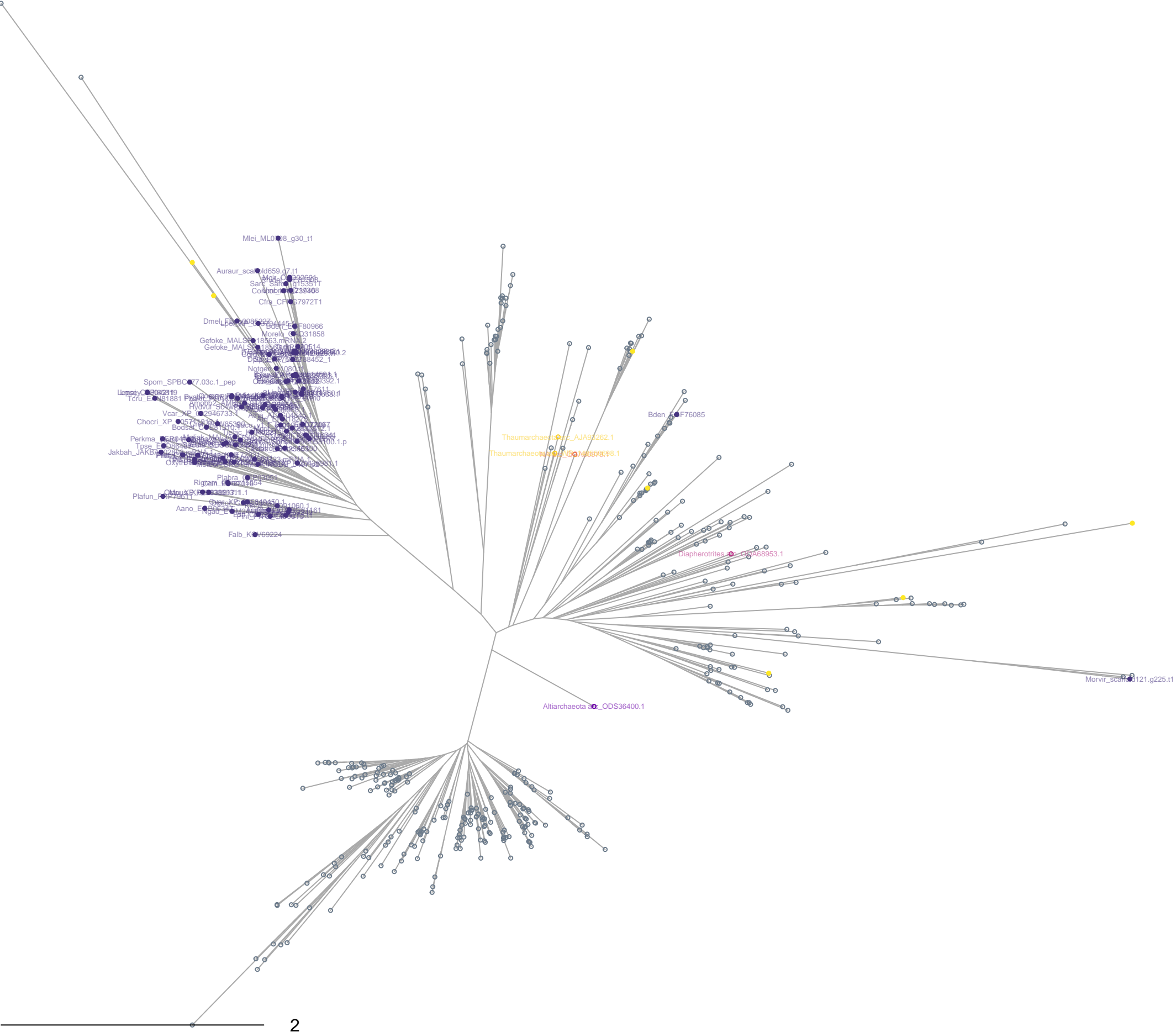
Acetyltransf_1.HG22.0:NA n = 28
Acetyltransf_1.HG1.12:like:NAA30/NAT8/NAT8L/NAT14:likeclu:14/23/38 n = 18
other n = 33

Bathyarchaeota n = 1
Euryarchaeota n = 11
Lokiarchaeota n = 2
Woesearchaeota n = 2



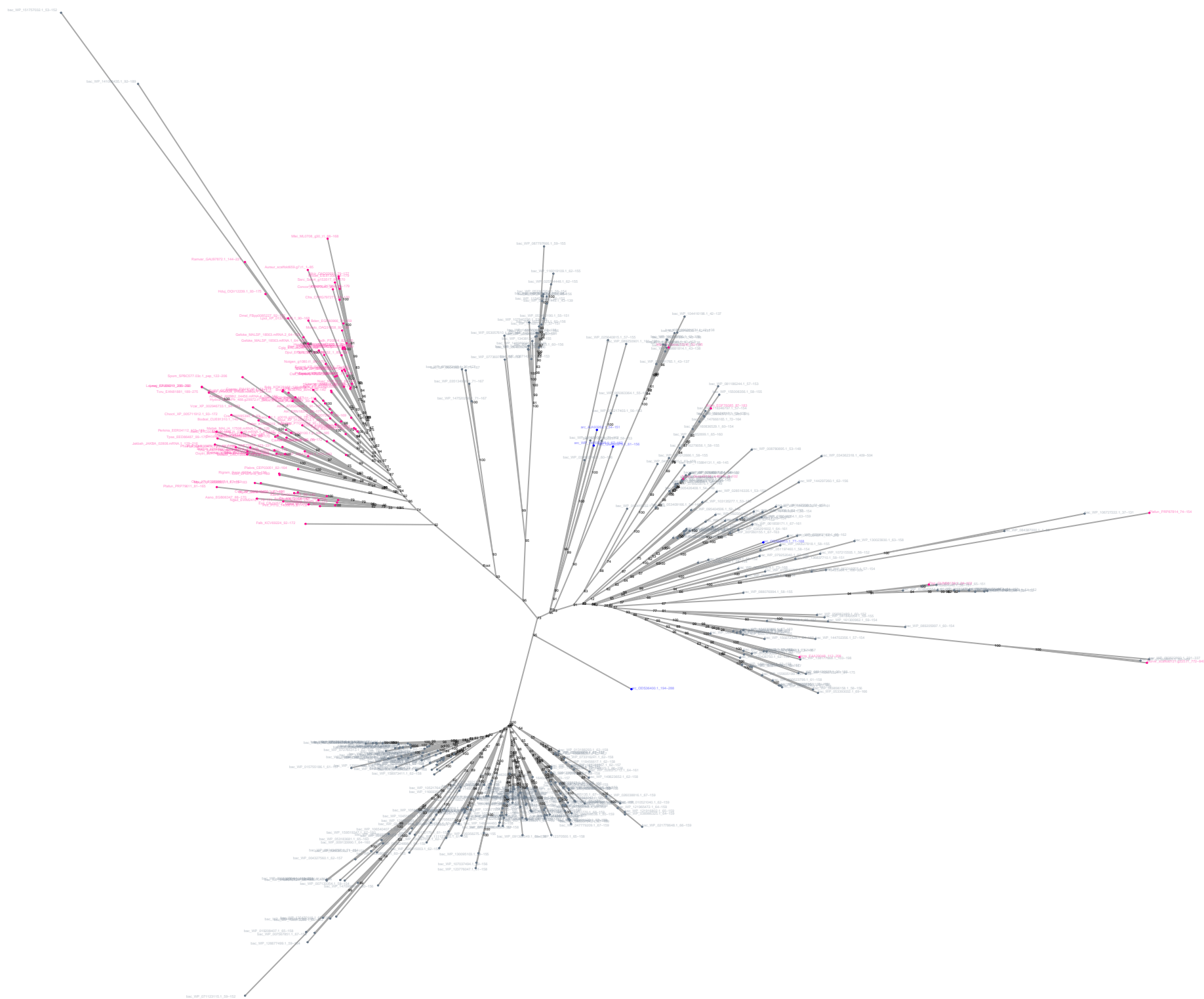
euk.Acetyltransf_1.phy.HG14.seqs.iqtree.treefile
n=485 sequences

- eukaryotes
- archaea
- bacteria



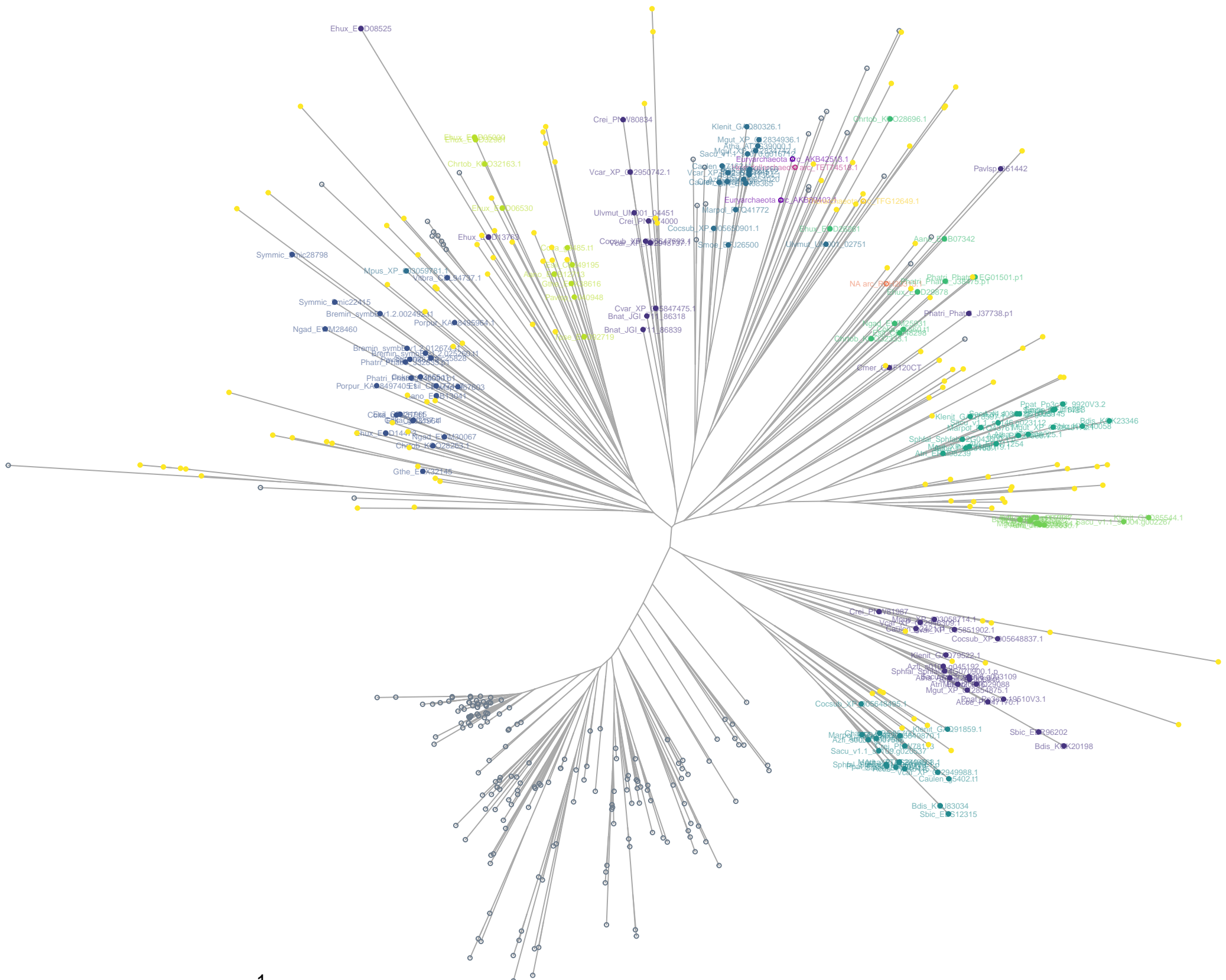
- Acetyltransf_1.HG14.1:NAT9 n = 106
- other n = 7

- Altiarchaeota n = 1
- Diapherotrites n = 1
- NA n = 1
- Thaumarchaeota n = 2



Acetyltransf_1.phy.HG15.seqs.iqtree.treefile
n=469 sequences

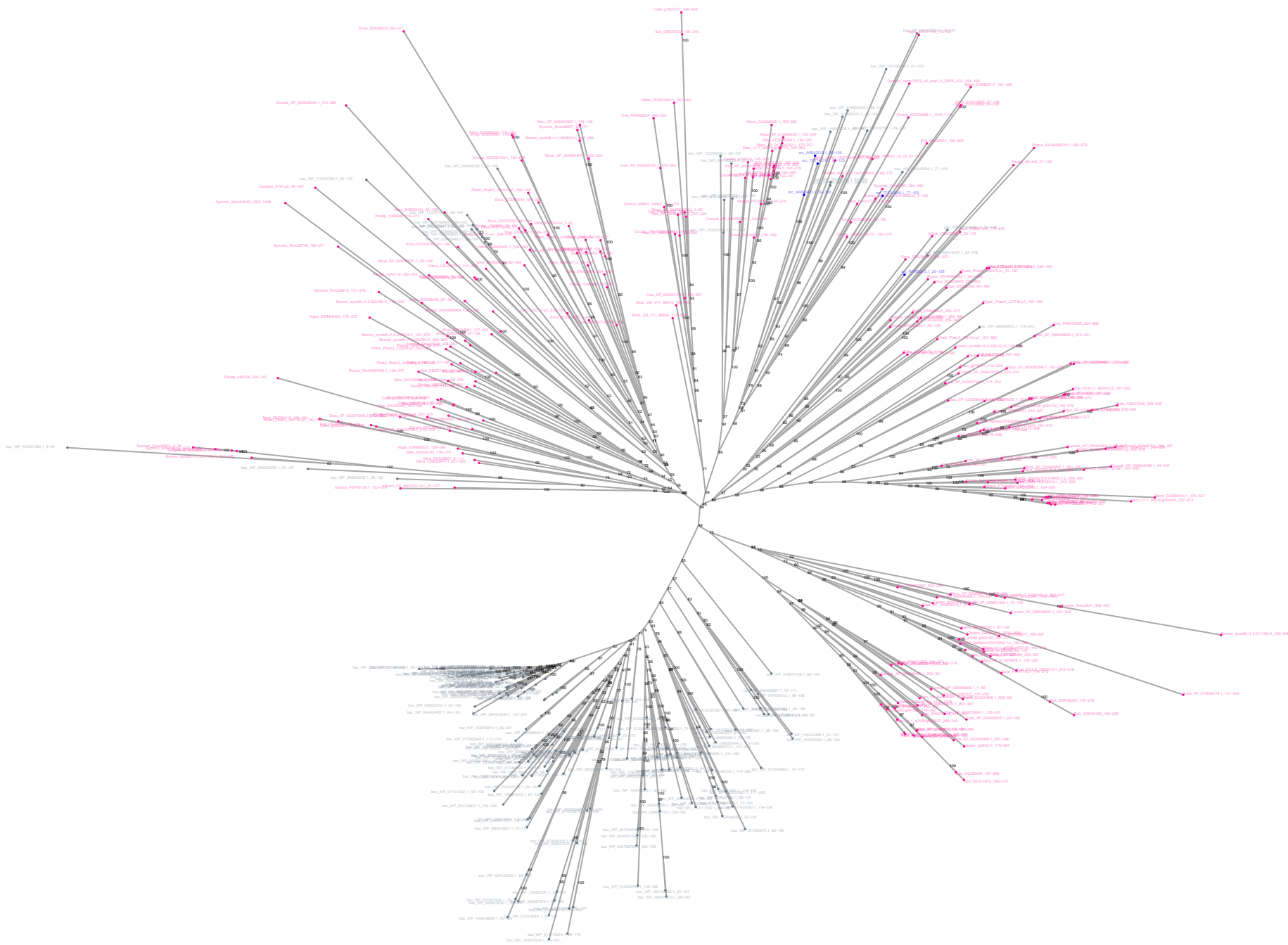
- eukaryotes
- archaea
- bacteria



1

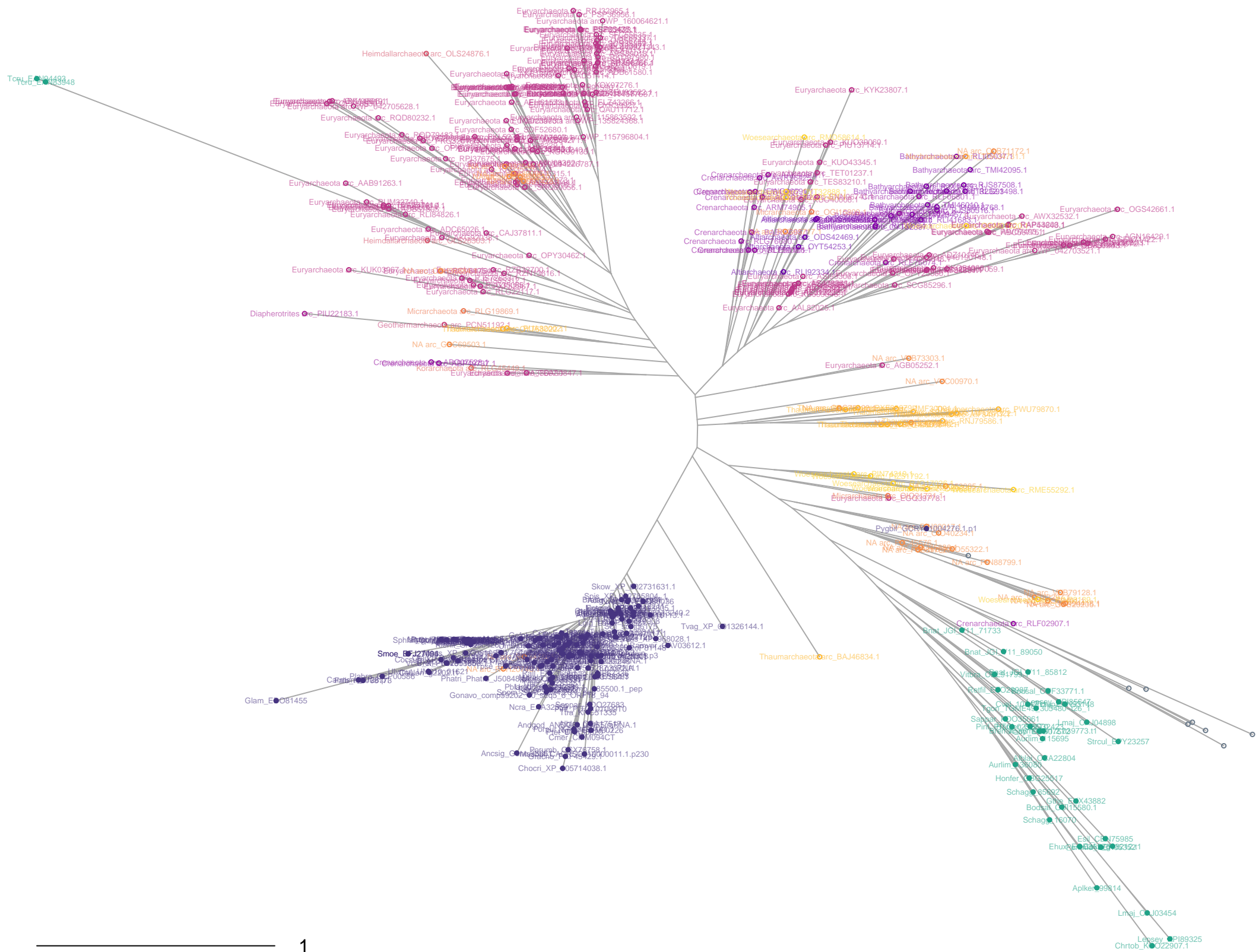
- Acetyltransf_1.HG1.18:like:NAT14:likeclu:23 n = 33
- Acetyltransf_1.HG1.22:like:NAT14:likeclu:23 n = 25
- Acetyltransf_1.HG1.23:NAT14 n = 19
- Acetyltransf_1.HG1.37:like:NAT14:likeclu:23 n = 19
- Acetyltransf_1.HG1.27:like:NAT14:likeclu:23 n = 18
- Acetyltransf_1.HG1.20:like:NAT14:likeclu:23 n = 10
- Acetyltransf_1.HG1.42:like:NAT14:likeclu:23 n = 10
- Acetyltransf_1.HG1.46:like:NAT14:likeclu:23 n = 10
- other n = 122

- Euryarchaeota n = 2
- Heimdallarchaeota n = 1
- NA n = 1
- Thorarchaeota n = 1



Acetyltransf_1.phy.HG16.seqs.iqtree.treefile
n=428 sequences

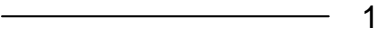
- eukaryotes
- archaea
- bacteria



1

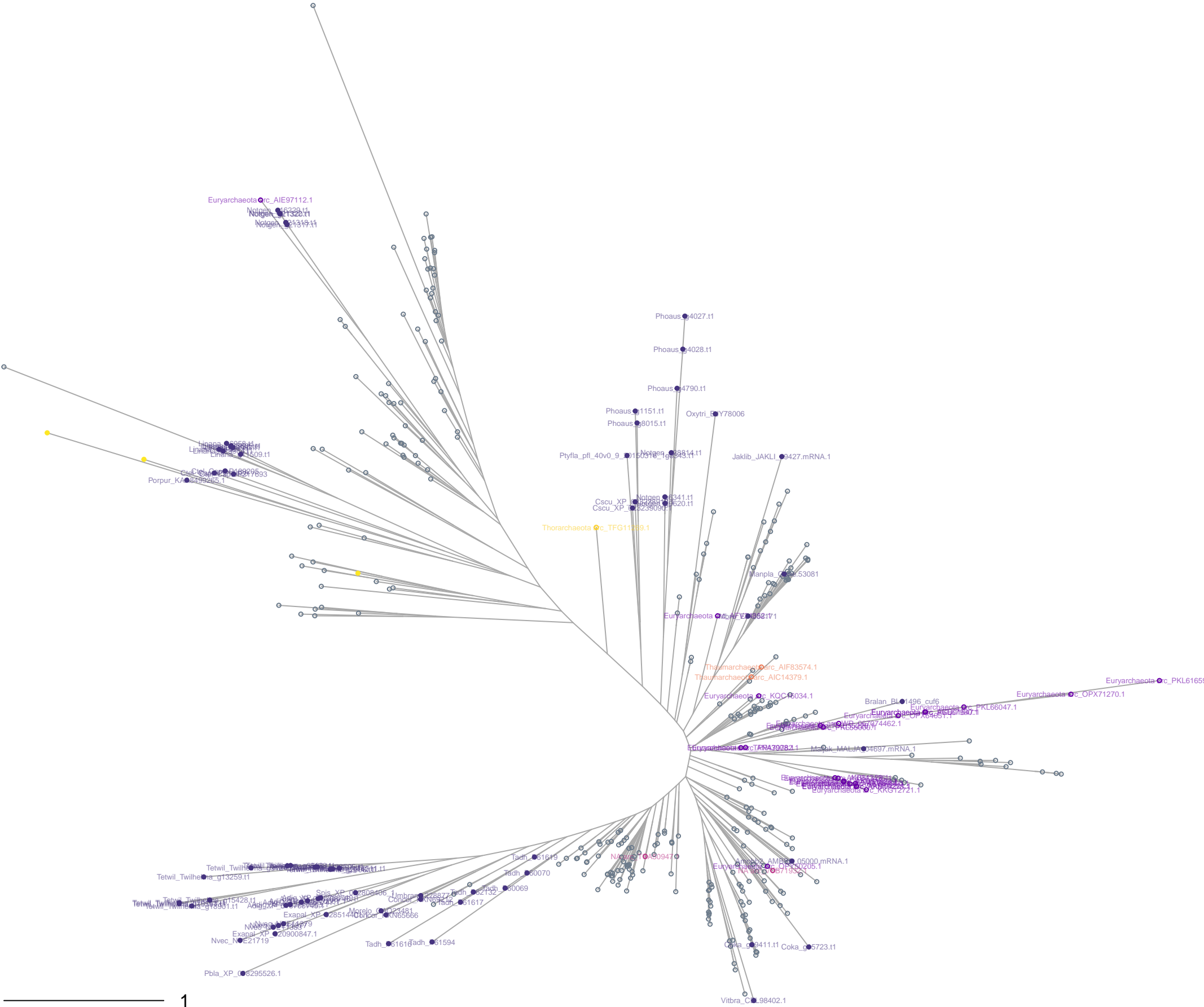
- Acetyltransf_1.HG9.1:ELP3 n = 144
- Acetyltransf_1.HG9.0:like:ELP3:likeclu:1 n = 35
- other n = 0

- Altiarchaeota n = 5
- Bathyarchaeota n = 17
- Crenarchaeota n = 16
- Diapherotrites n = 1
- Euryarchaeota n = 141
- Geothermarchaeota n = 1
- Heimdallarchaeota n = 2
- Korarchaeota n = 1
- Micrarchaeota n = 3
- NA n = 28
- Nezhaarchaeota n = 1
- Thaumarchaeota n = 14
- Woesearchaeota n = 11



euk.Acetyltransf_1.phy.HG17.seqs.iqtree.treefile
n=413 sequences

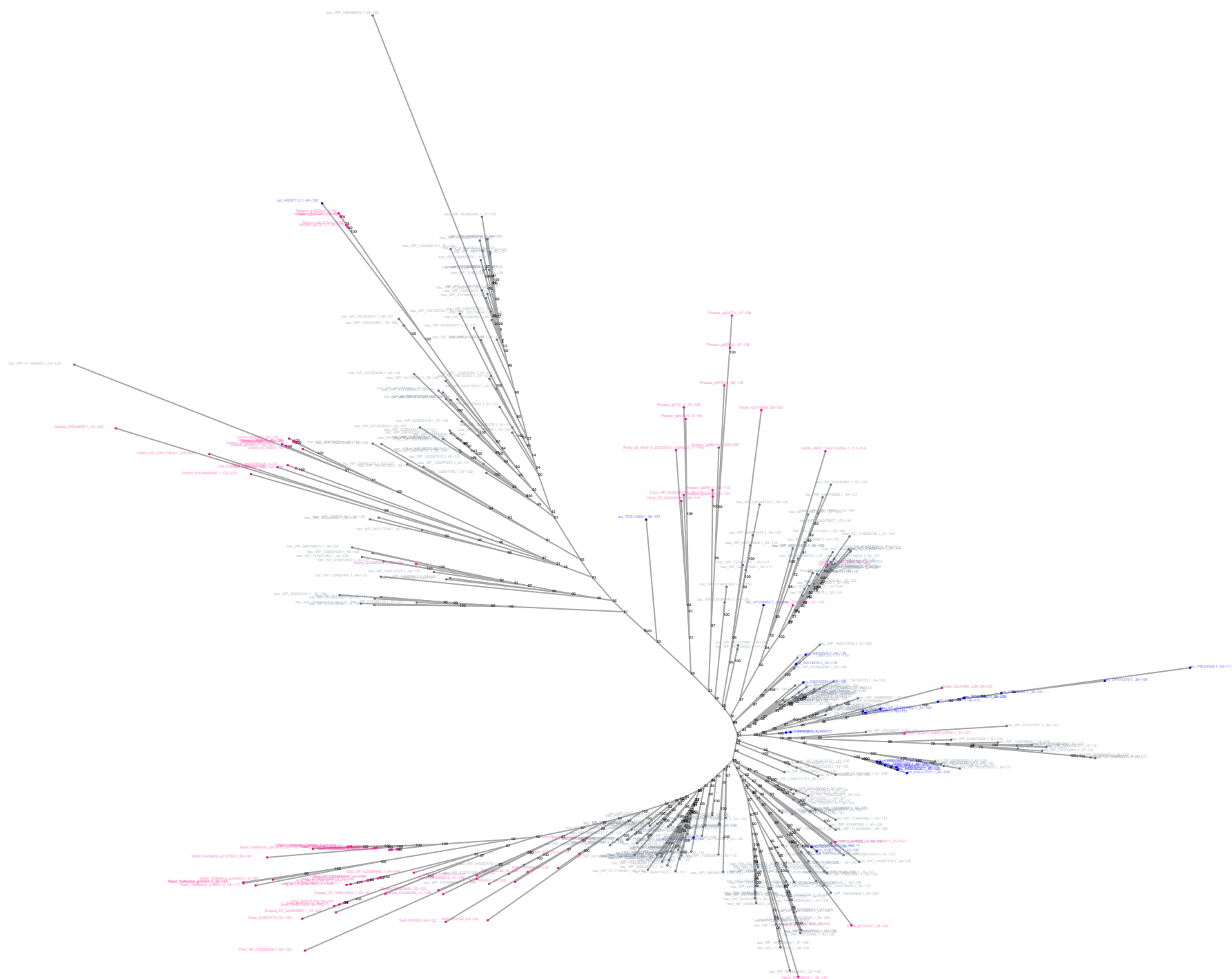
- eukaryotes
- archaea
- bacteria



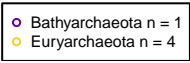
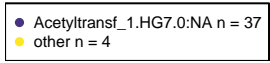
1

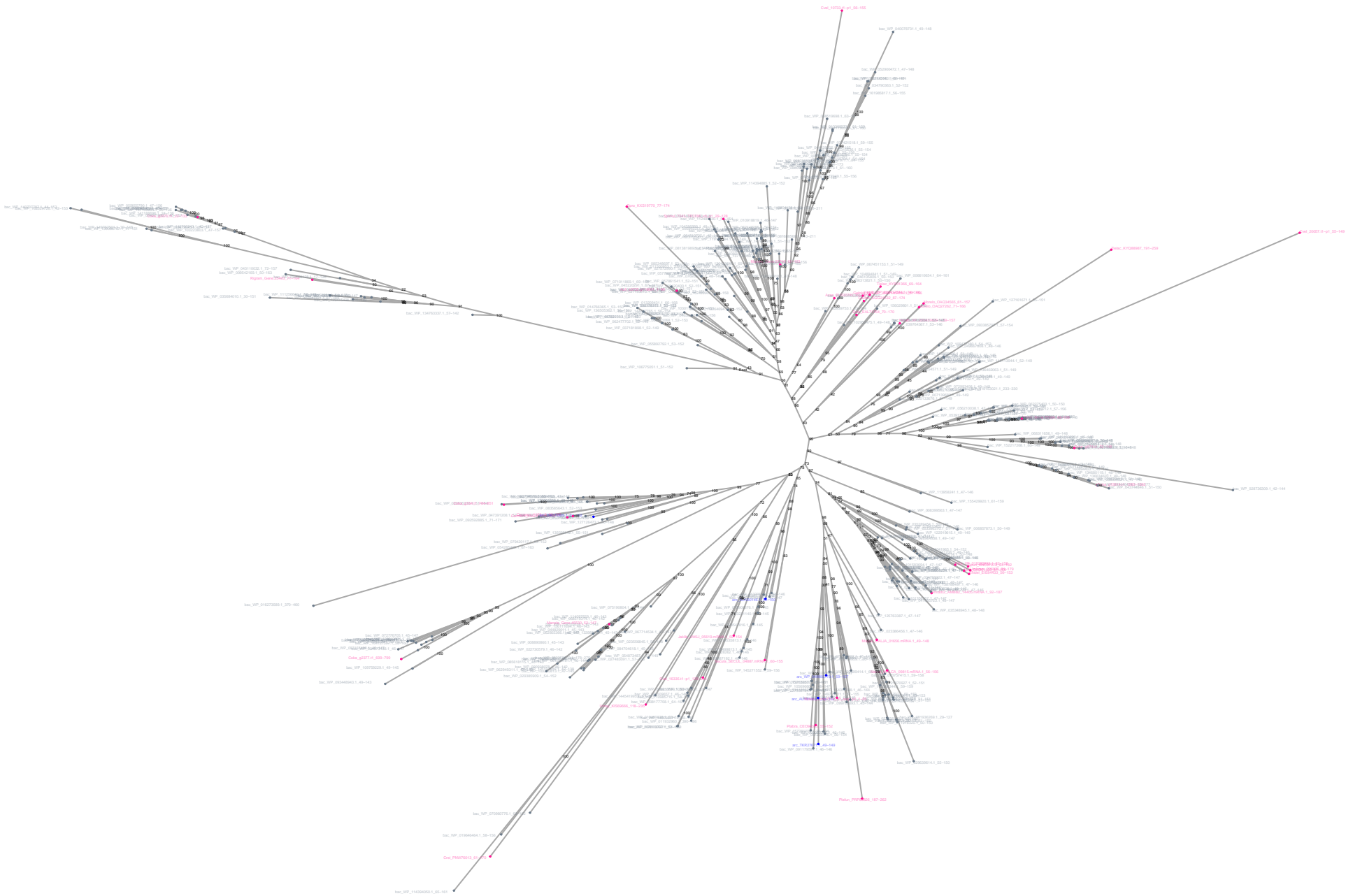
- Acetyltransf_1.HG18.0:NA n = 75
- other n = 3

- Euryarchaeota n = 24
- NA n = 2
- Thaumarchaeota n = 2
- Thorarchaeota n = 1



- eukaryotes
- archaea
- bacteria





euk.Acetyltransf_1.phy.HG19.seqs.iqtree.treefile
n=409 sequences

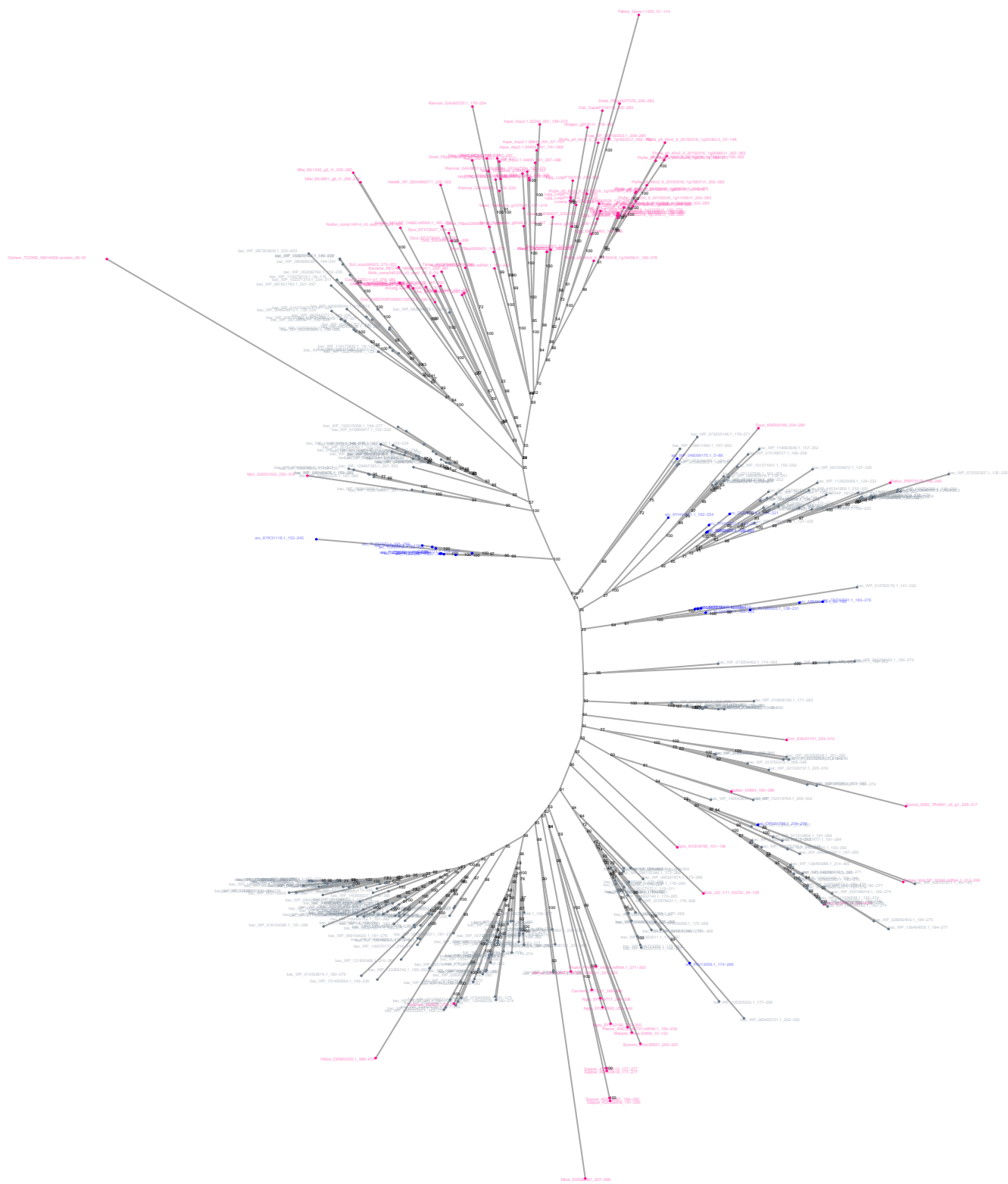
- eukaryotes
- archaea
- bacteria



1

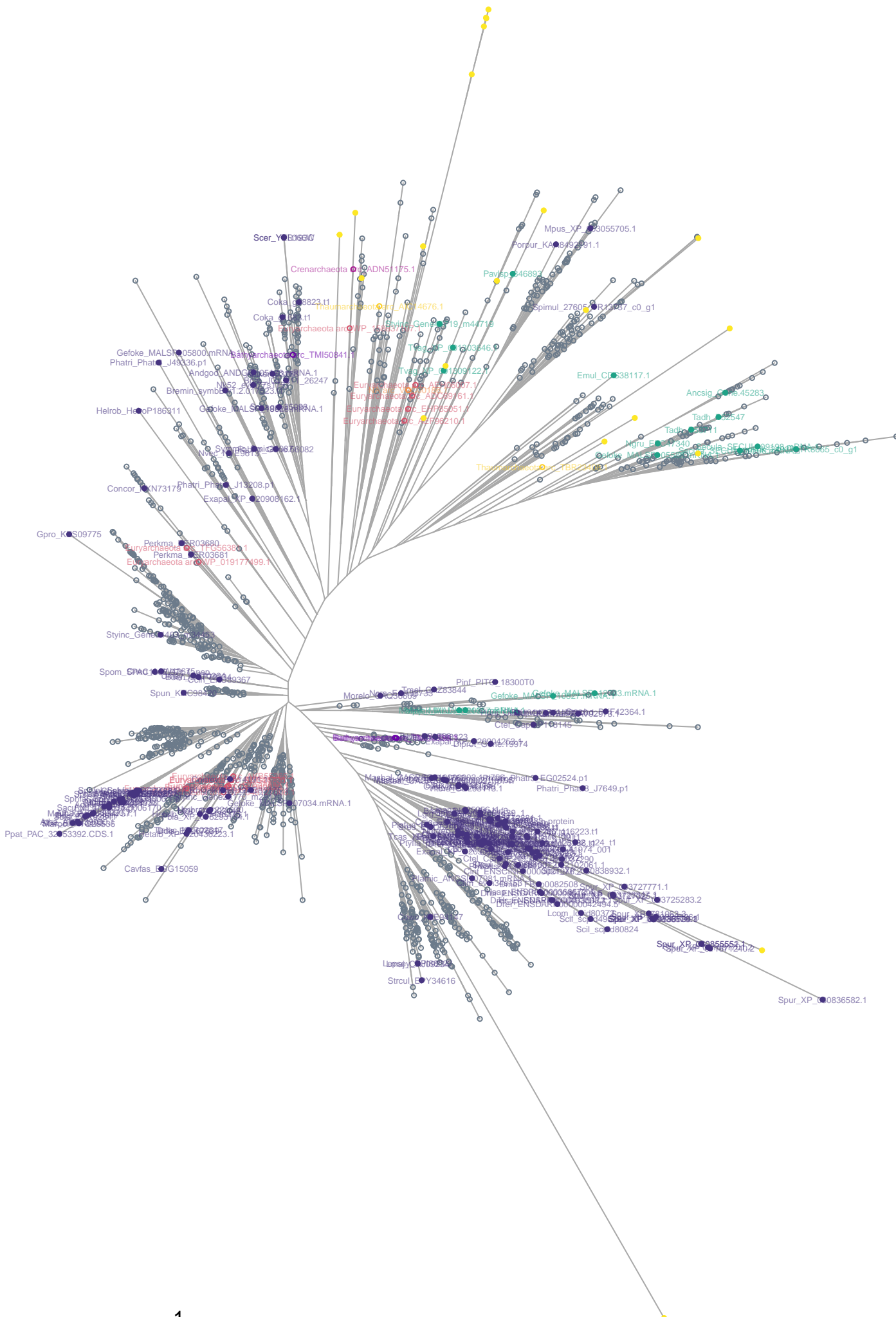
- Acetyltransf_1.HG17.2:NA n = 32
- Acetyltransf_1.HG17.0:NA n = 29
- Acetyltransf_1.HG17.1:NA n = 21
- Acetyltransf_1.HG25.1:NA n = 10
- other n = 12

- Bathyarchaeota n = 4
- Crenarchaeota n = 8
- Euryarchaeota n = 11
- Korarchaeota n = 1



Acetyltransf_1.phy.HG2.seqs.iqtree.treefile
n=1609 sequences

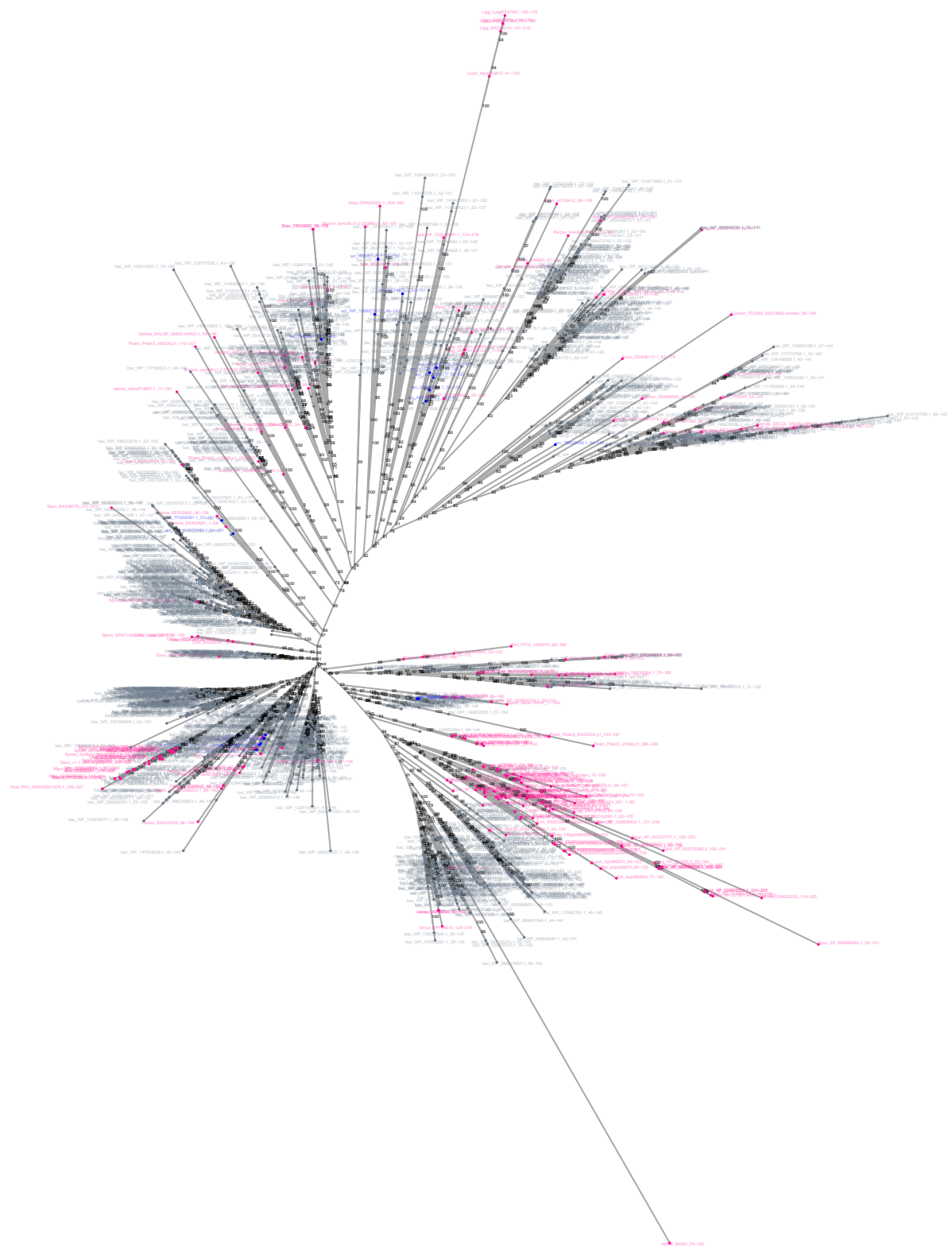
- eukaryotes
- archaea
- bacteria



1

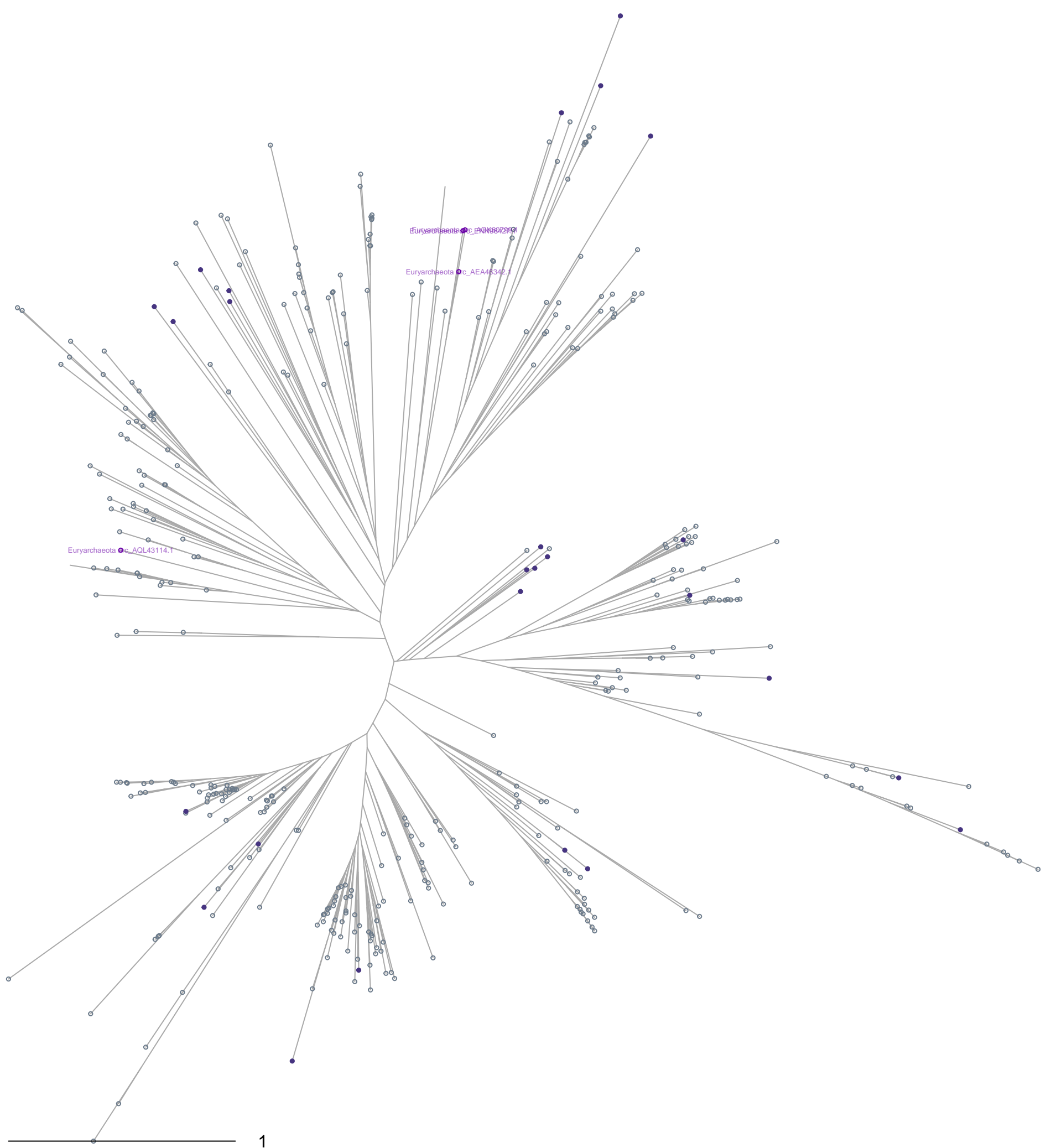
- Acetyltransf_1.HG4.1:SAT1/SAT2/SATL1 n = 185
- Acetyltransf_1.HG4.0:like:SAT1/SAT2/SATL1:likeclu:1 n = 17
- other n = 21

- Bathyarchaeota n = 3
- Crenarchaeota n = 1
- Euryarchaeota n = 14
- NA n = 1
- Thaumarchaeota n = 2



euk.Acetyltransf_1.phy.HG20.seqs.iqtree.treefile
n=388 sequences

eukaryotes
archaea
bacteria



other n = 26

Euryarchaeota n = 4



Acetyltransf_1



- Acetyltransf_1.HG16.0:AANAT n = 86
- other n = 3

- NA $n = 2$

Acetyltransf_1.phy.HG22.seqs.iqtree.treefile
n=352 sequences

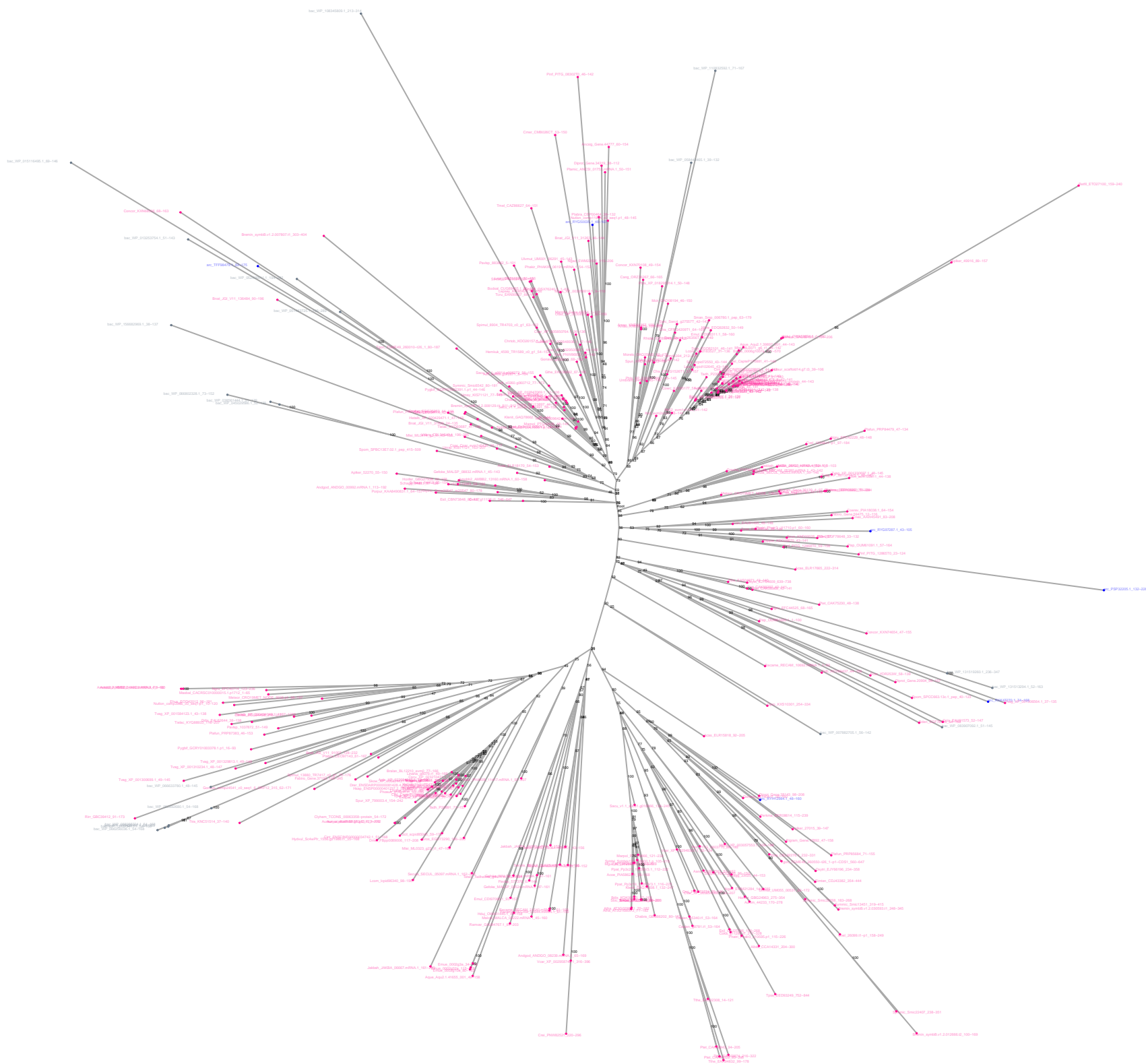
- eukaryotes
- archaea
- bacteria



- Acetyltransf_1.HG2.8:NAA60 n = 131
- Acetyltransf_1.HG2.17:NAA50 n = 116
- Acetyltransf_1.HG2.16:like:NAA50:likeclu:17 n = 35
- Acetyltransf_1.HG2.14:like:NAA50:likeclu:17 n = 12
- other n = 31

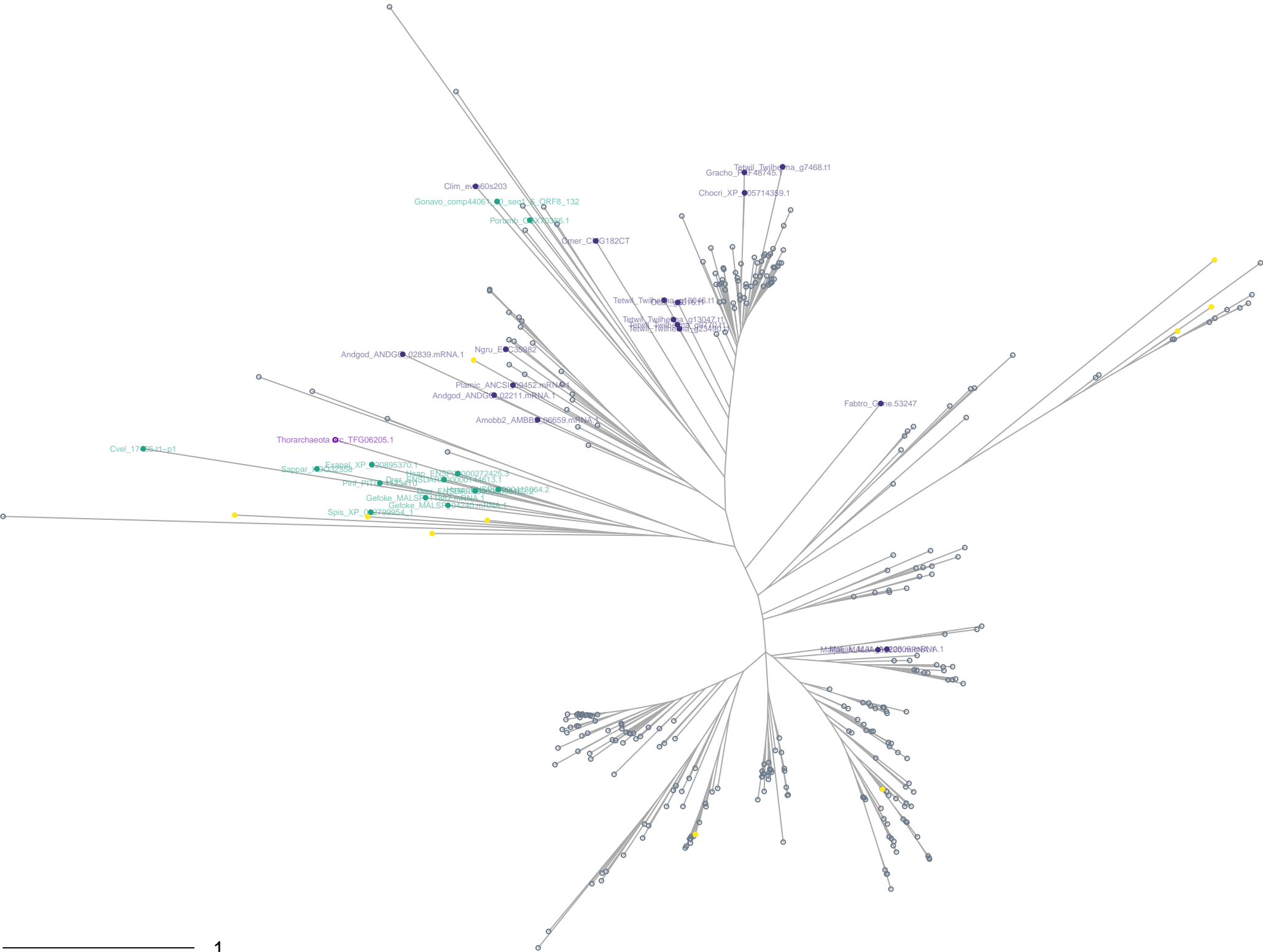
1

- Euryarchaeota n = 2
- Lokiarchaeota n = 1
- NA n = 3



Acetyltransf_1
euk.Acetyltransf_1.phy.HG23.seqs.iqtree.treefile
n=341 sequences

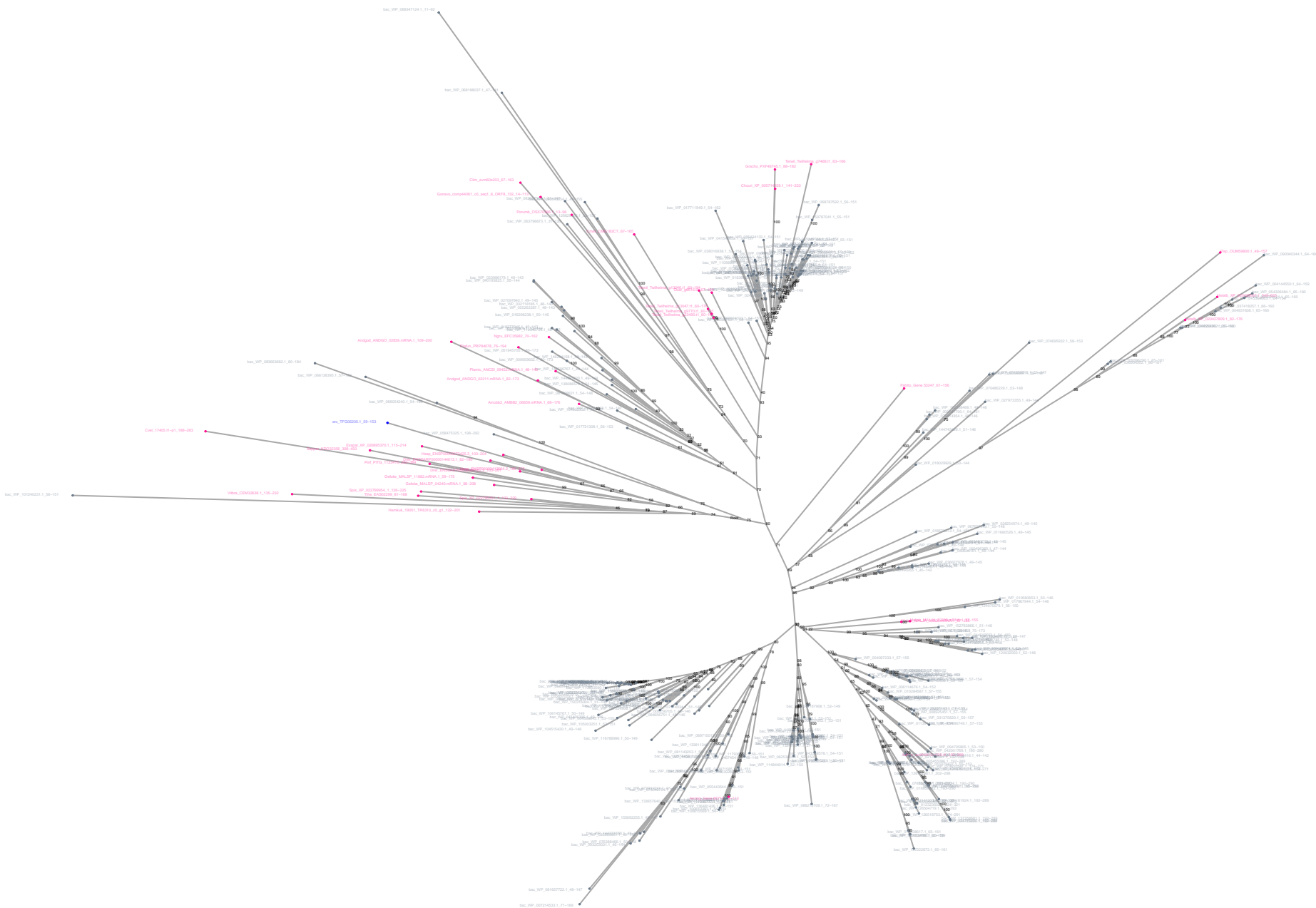
eukaryotes
archaea
bacteria



1

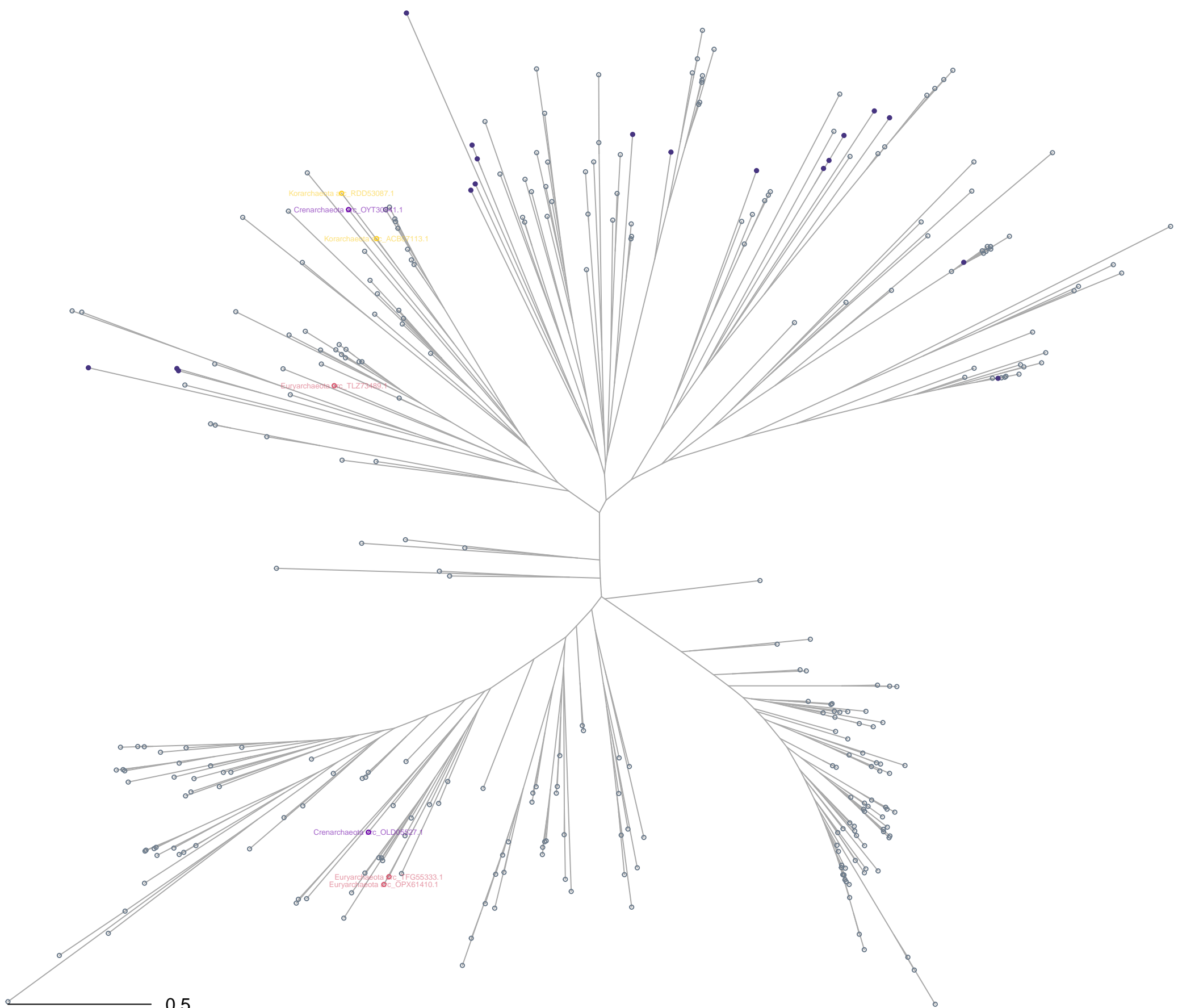
Acetyltransf_1.HG1.19:like:NAT8/NAT8L:likeclu:38 n = 18
Acetyltransf_1.HG1.38:NAT8/NAT8L n = 13
other n = 10

Thorarchaeota n = 1



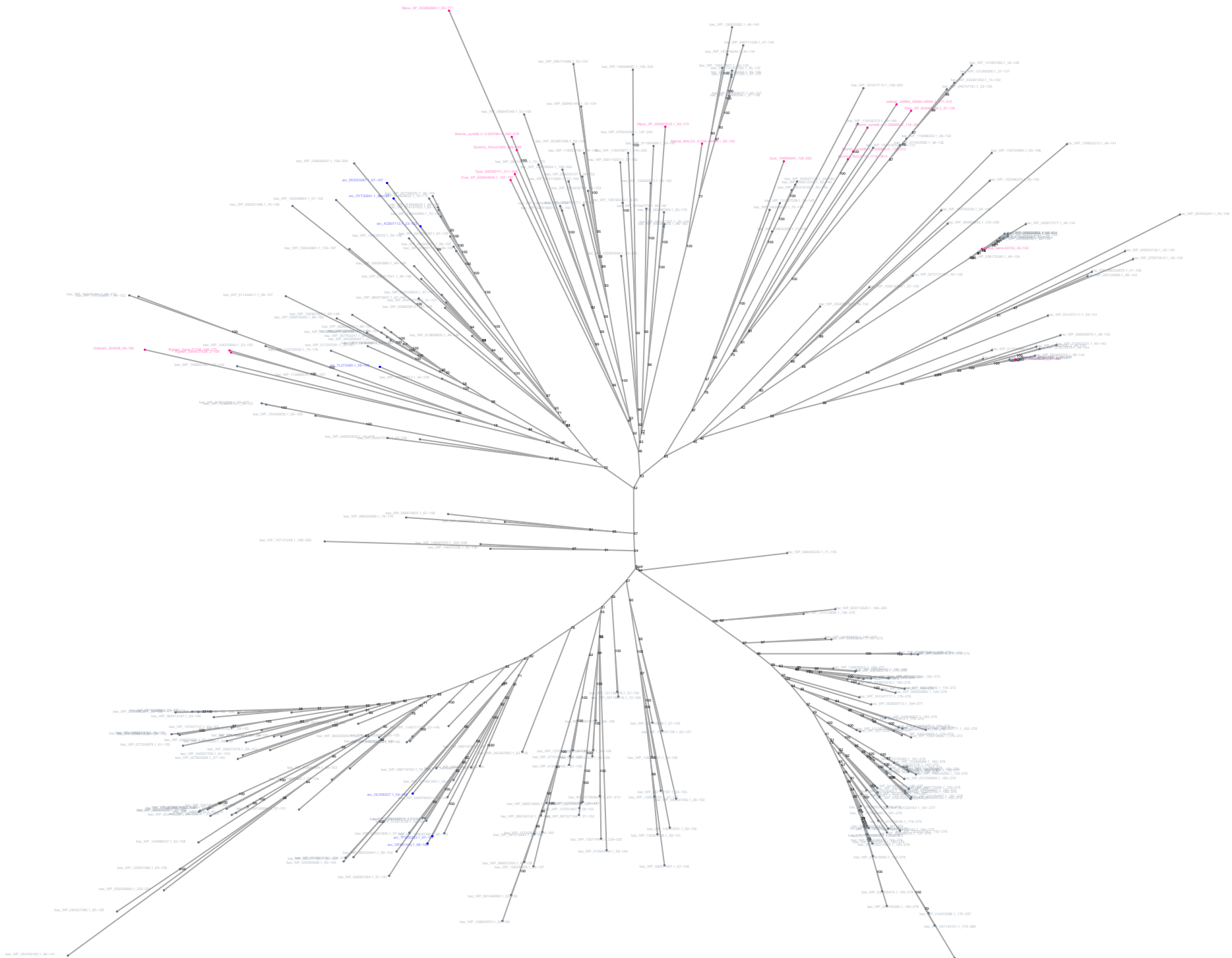
Acetyltransf_1
euk.Acetyltransf_1.phy.HG24.seqs.iqtree.treefile
n=323 sequences

eukaryotes
archaea
bacteria



other n = 18

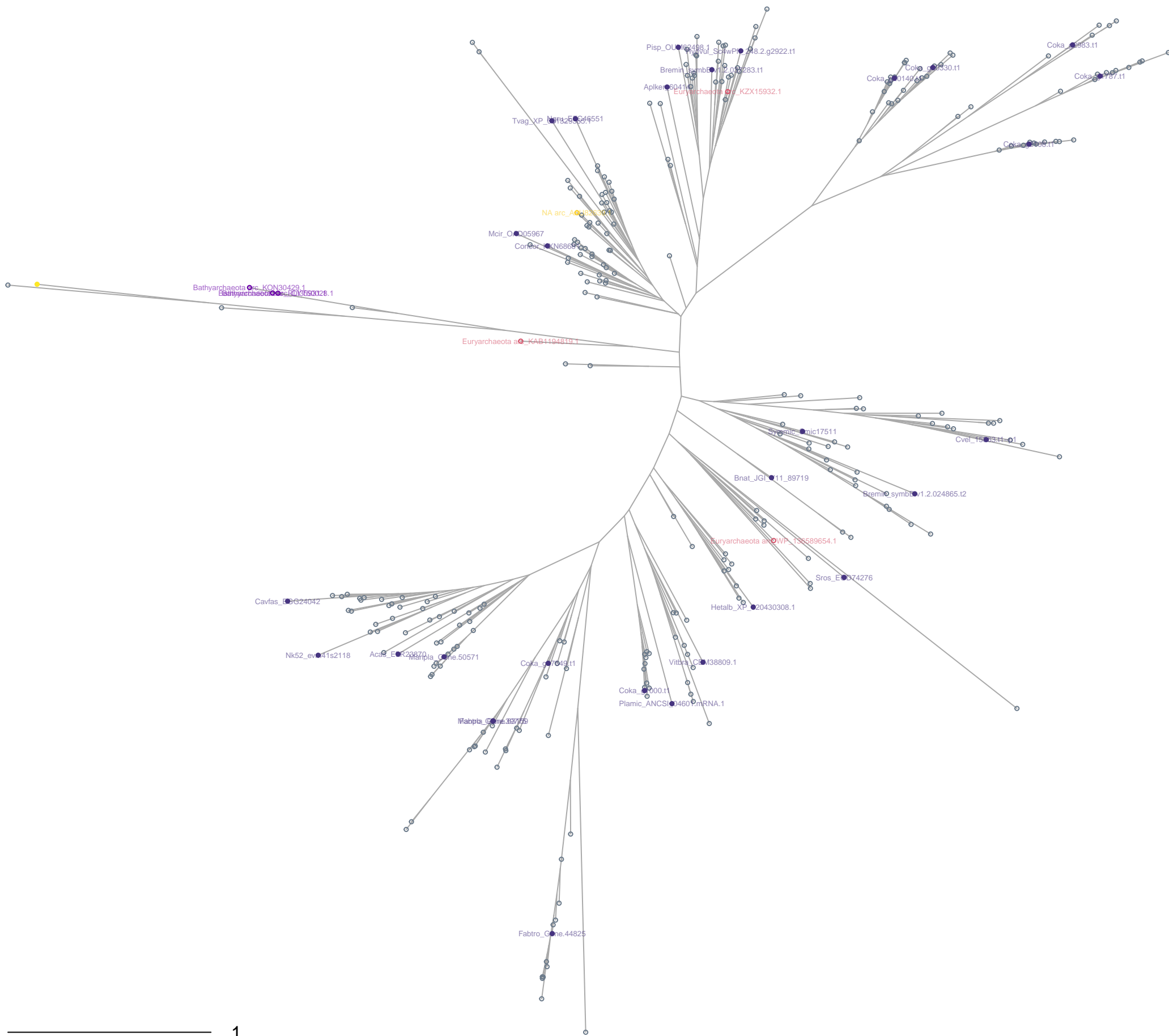
Crenarchaeota n = 2
Euryarchaeota n = 3
Korarchaeota n = 2



0.5

Acetyltransf_1
euk.Acetyltransf_1.phy.HG25.seqs.iqtree.treefile
n=321 sequences

eukaryotes
archaea
bacteria



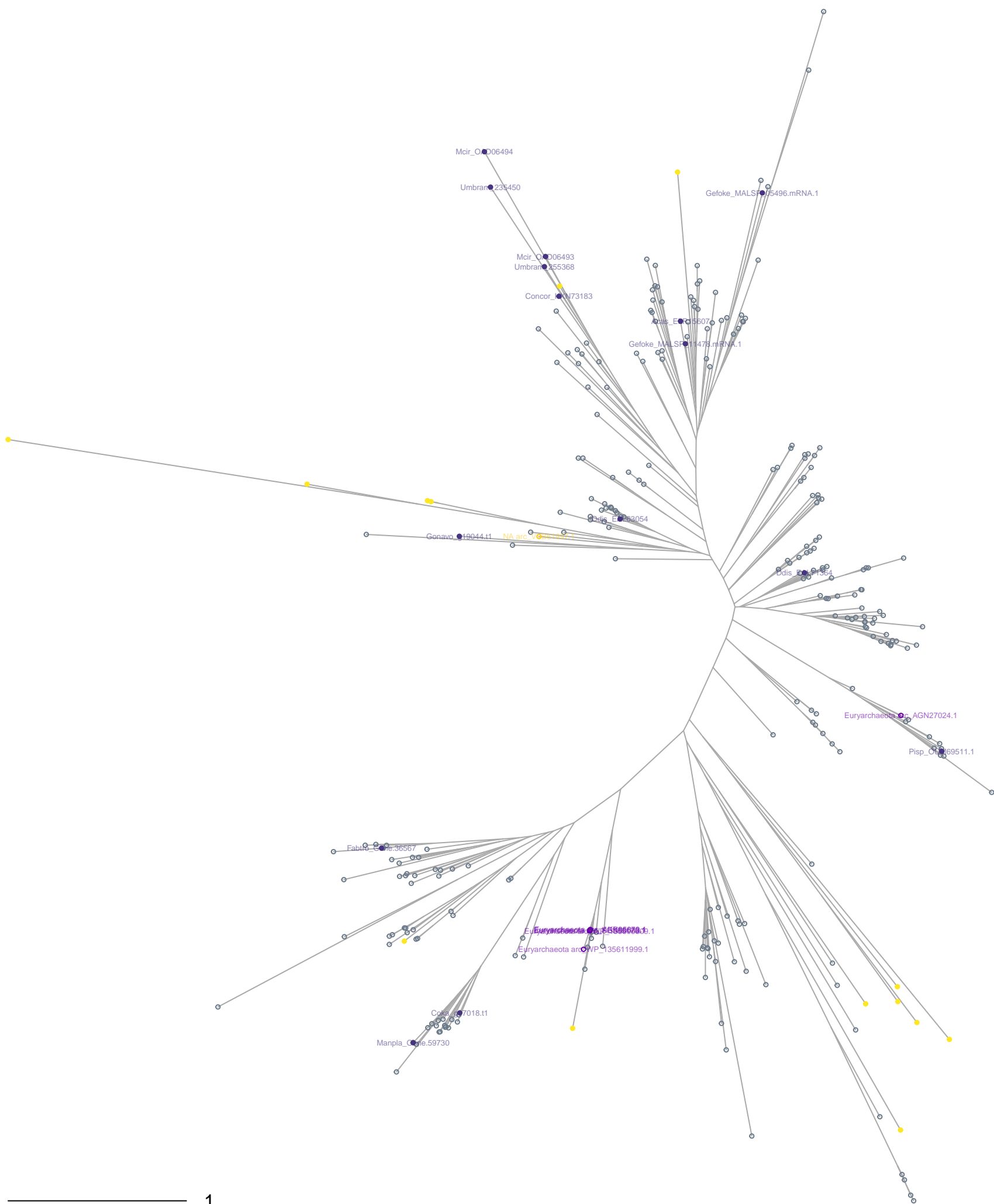
Acetyltransf_1.HG7.0:NA n = 30
other n = 1

Bathyarchaeota n = 3
Euryarchaeota n = 3
NA n = 1



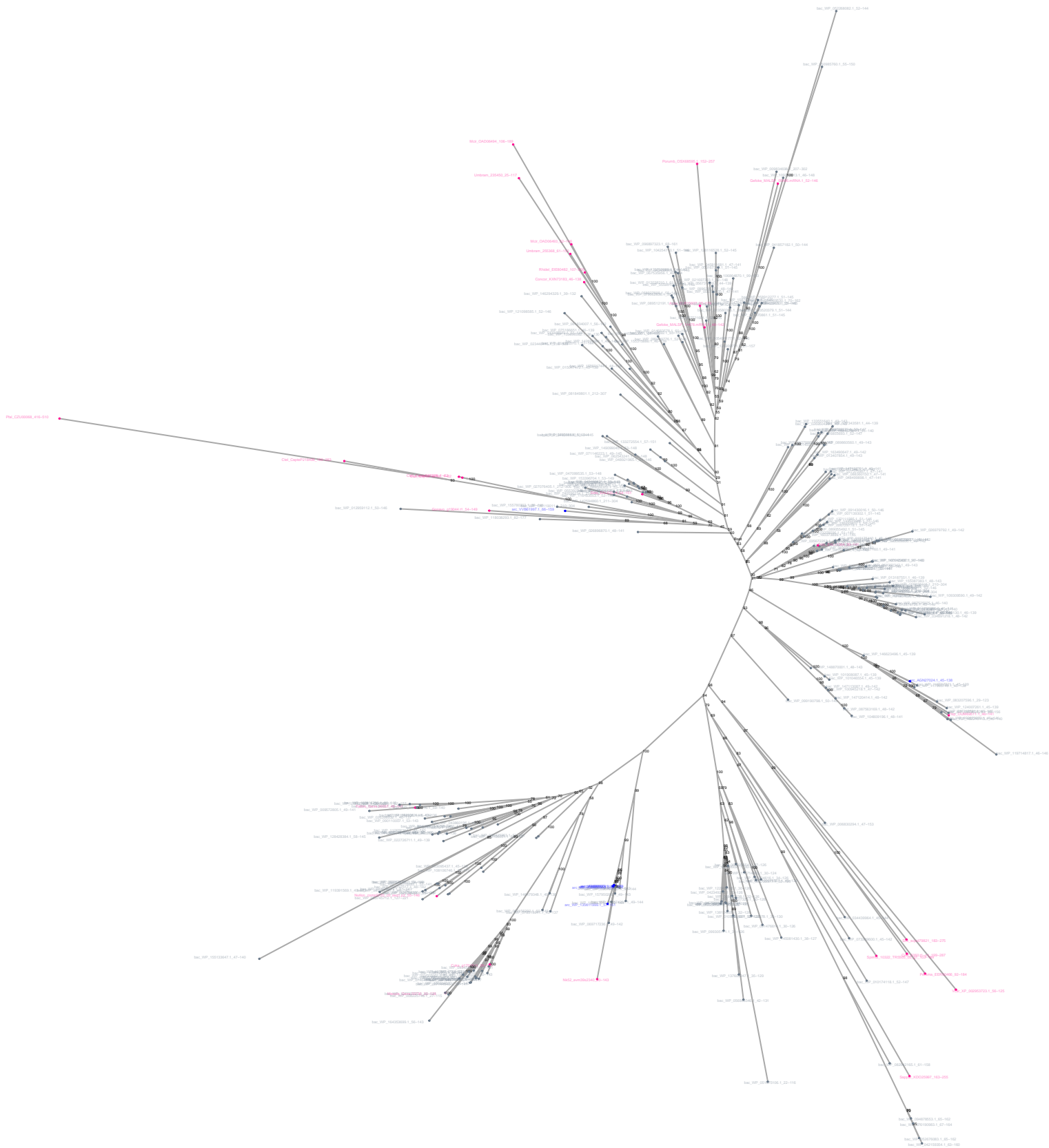
Acetyltransf_1
euk.Acetyltransf_1.phy.HG26.seqs.iqtree.treefile
n=302 sequences

eukaryotes
archaea
bacteria



Acetyltransf_1.HG1.19:like:NAT8/NAT8L:likeclu:38 n = 15
other n = 14

Euryarchaeota n = 6
NA n = 1



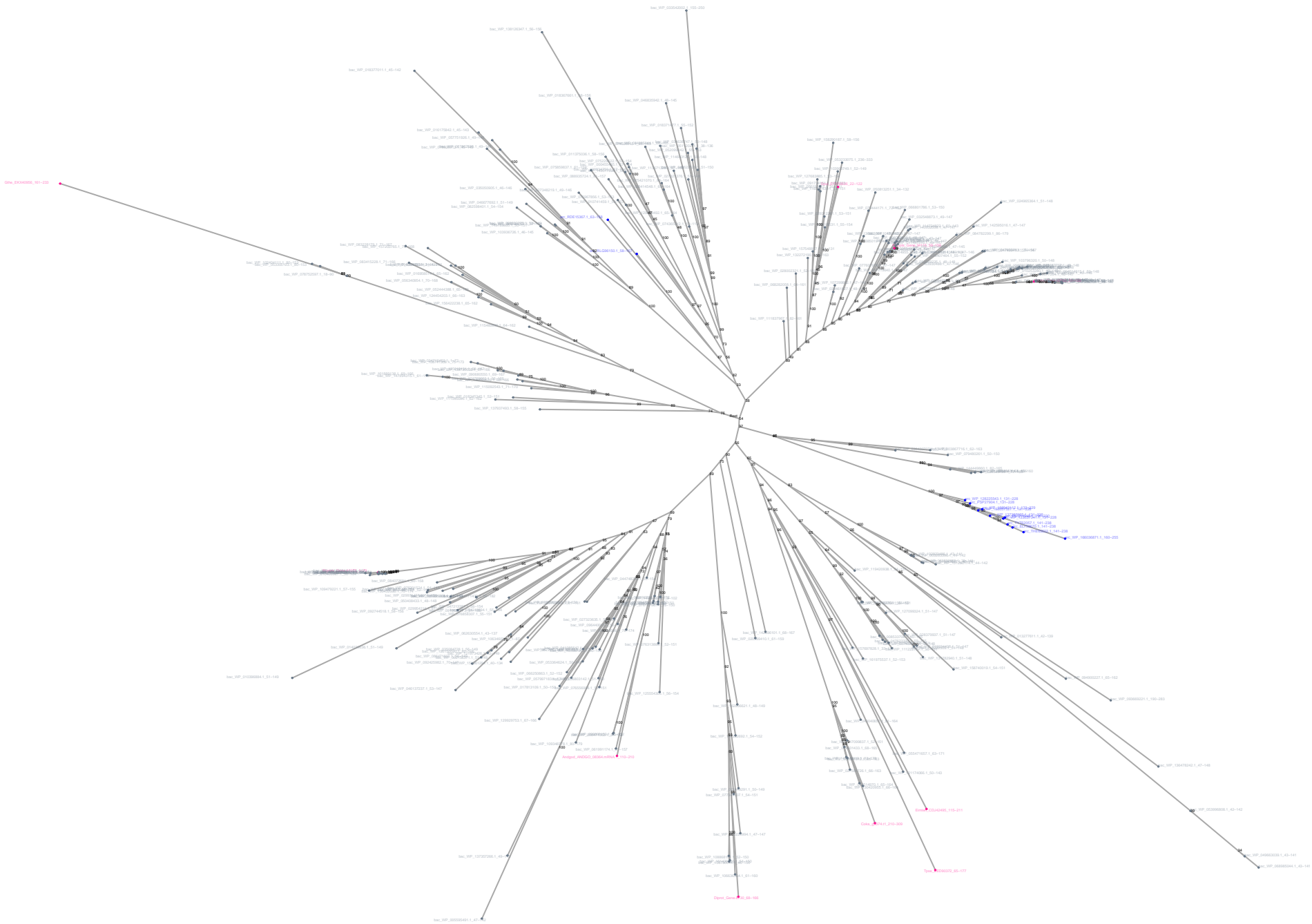
Acetyltransf_1
euk.Acetyltransf_1.phy.HG27.seqs.iqtree.treefile
n=293 sequences

eukaryotes
archaea
bacteria



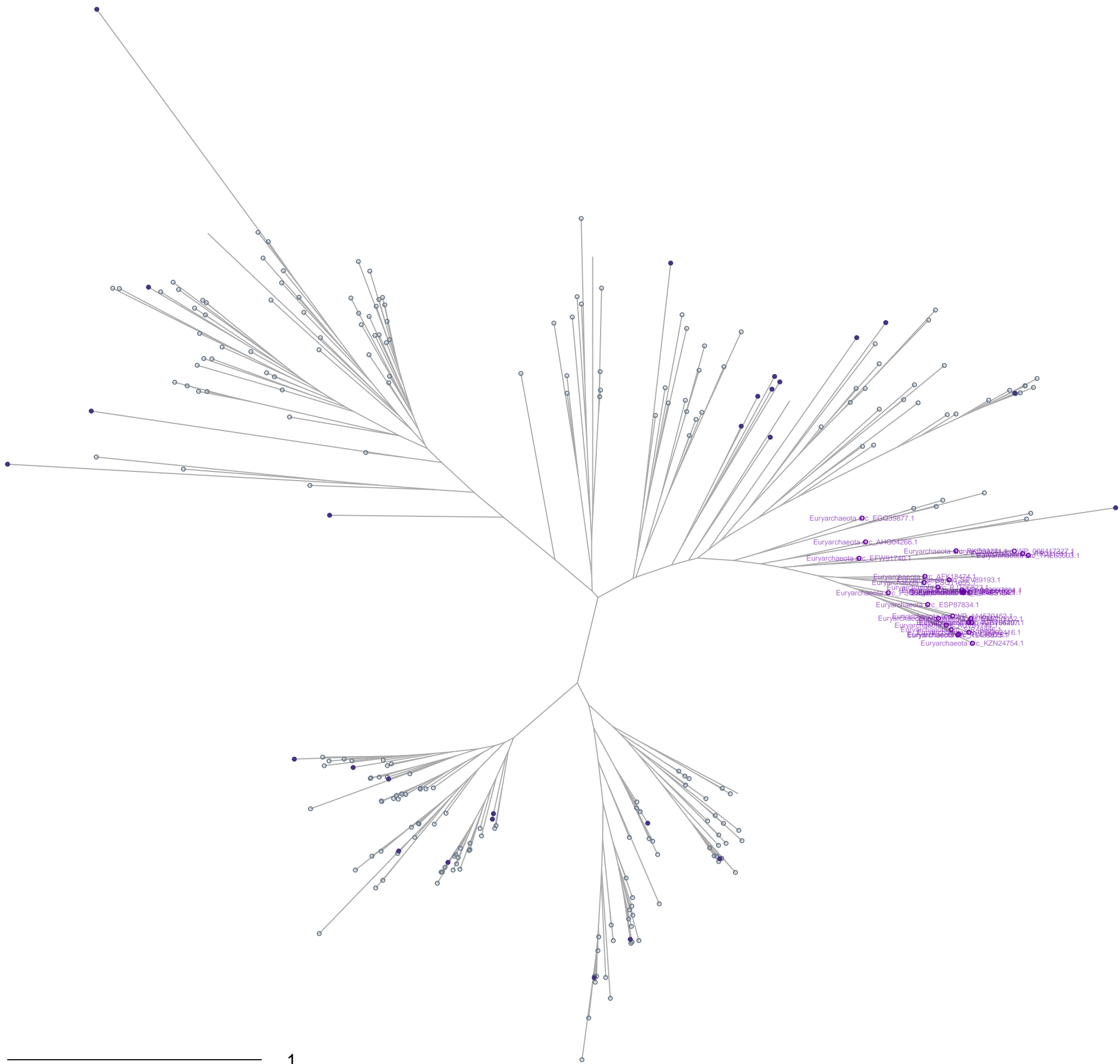
other n = 10

Bathyarchaeota n = 1
Euryarchaeota n = 11
Thorarchaeota n = 1



Acetyltransf_1
euk.Acetyltransf_1.phy.HG28.seqs.iqtree.treefile
n=278 sequences

eukaryotes
archaea
bacteria

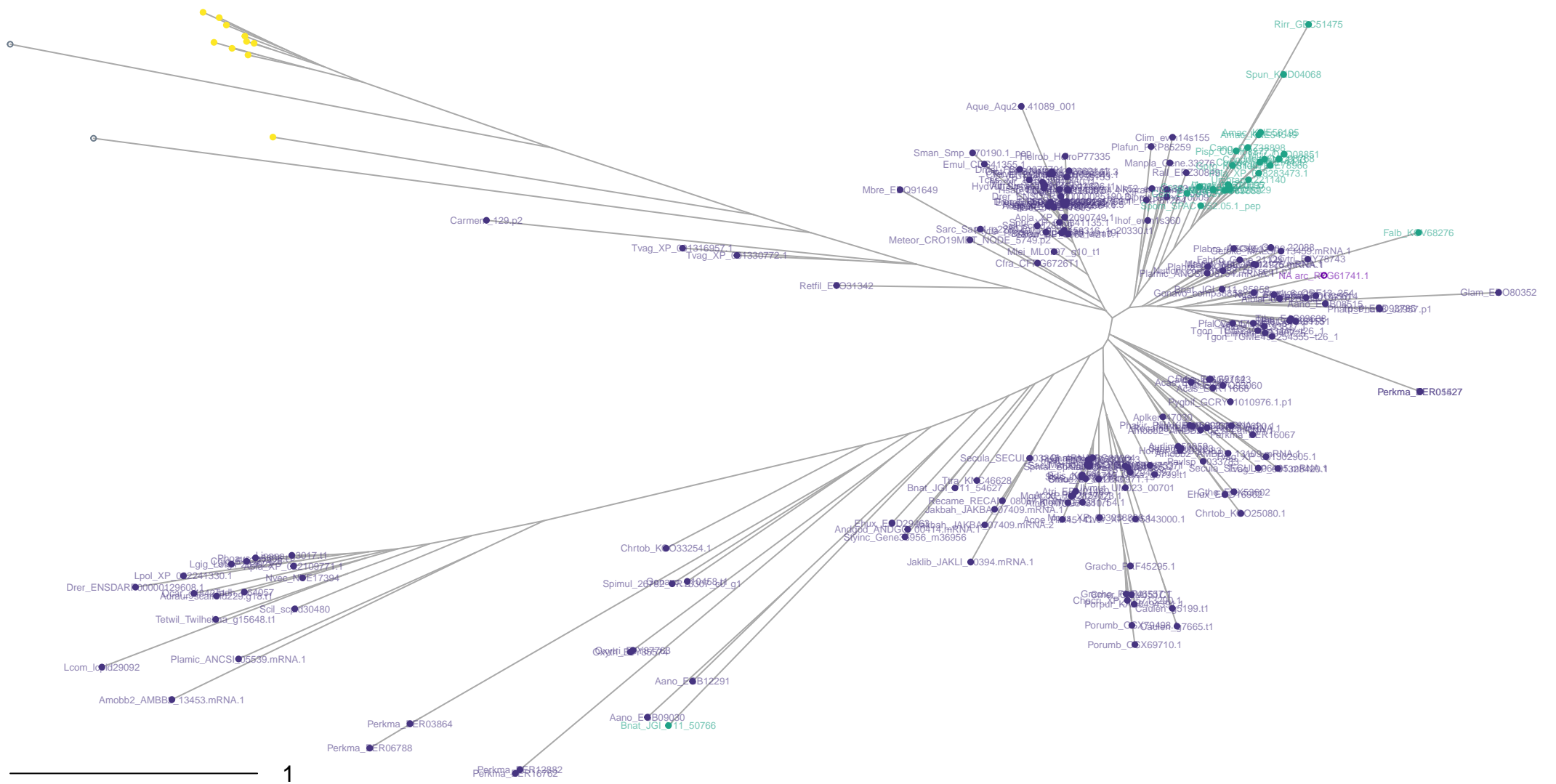


other n = 27

Euryarchaeota n = 29

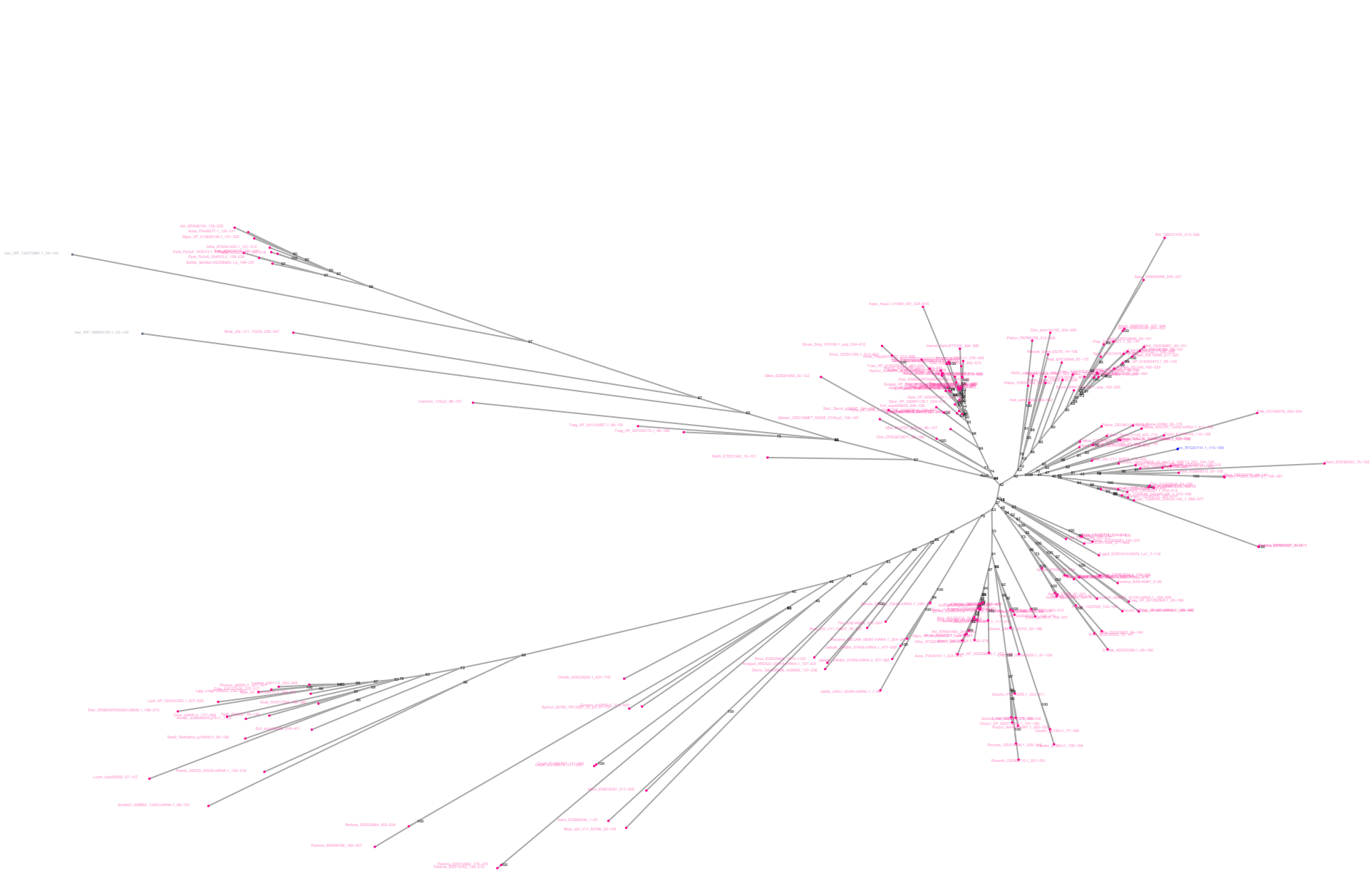
Acetyltransf_1
euk.Acetyltransf_1.phy.HG29.seqs.iqtree.treefile
n=216 sequences

eukaryotes
archaea
bacteria



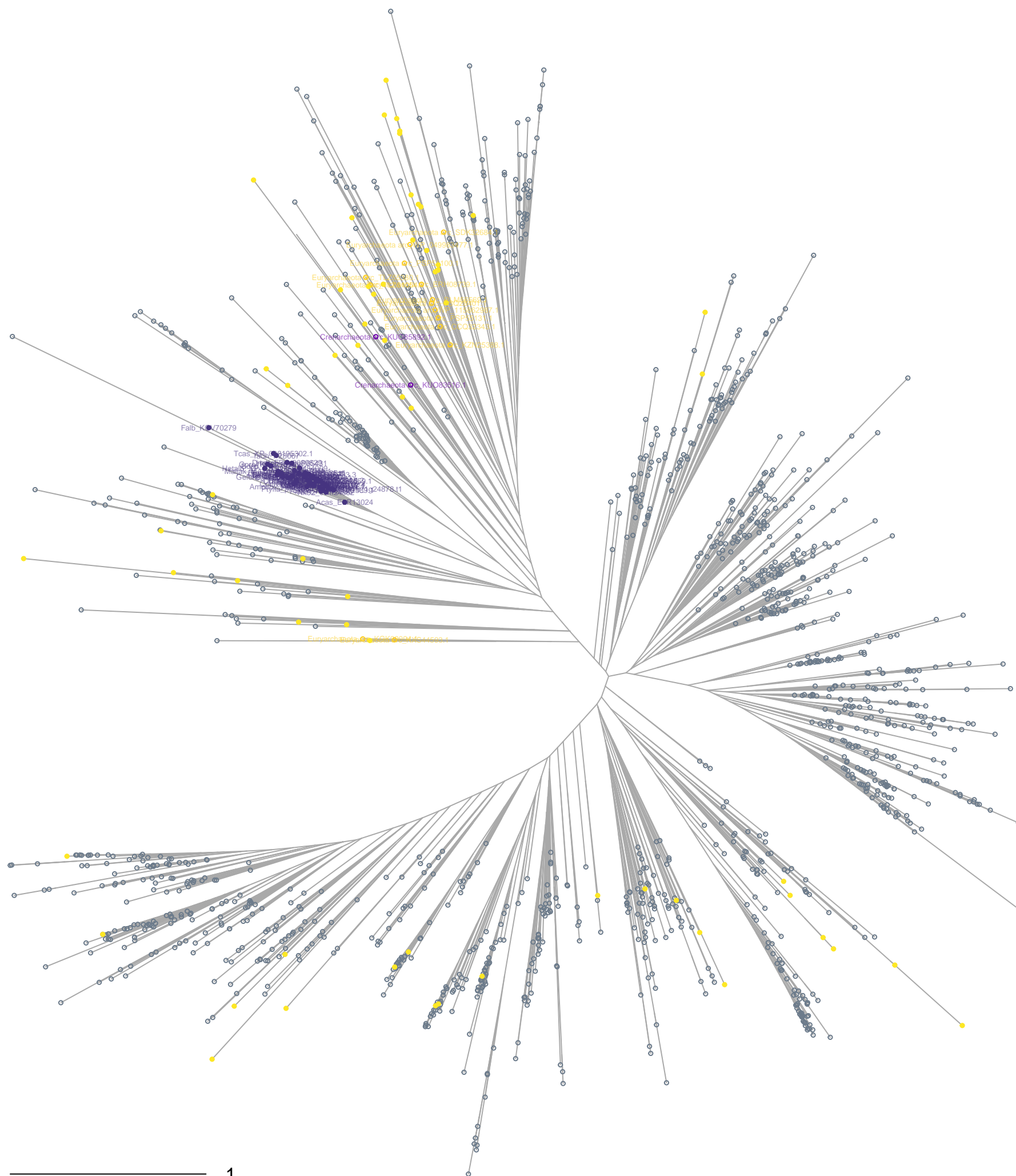
Acetyltransf_1.HG5.1:KAT2A/KAT2B n = 179
Acetyltransf_1.HG5.0:like:KAT2A/KAT2B:likeclu:1 n = 24
other n = 10

NA n = 1



Acetyltransf_1
euk.Acetyltransf_1.phy.HG3.seqs.iqtree.treefile
n=1523 sequences

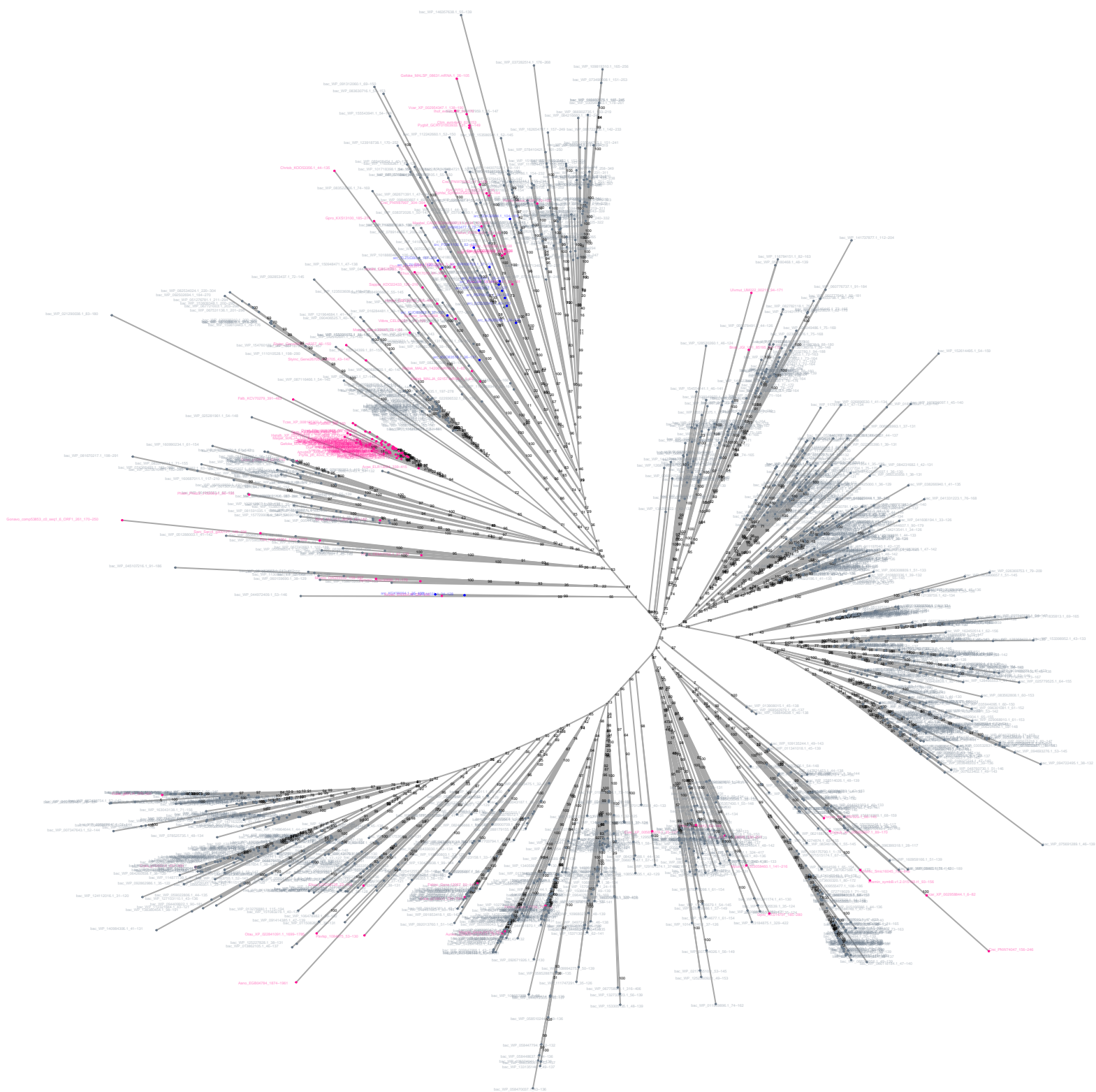
eukaryotes
archaea
bacteria



1

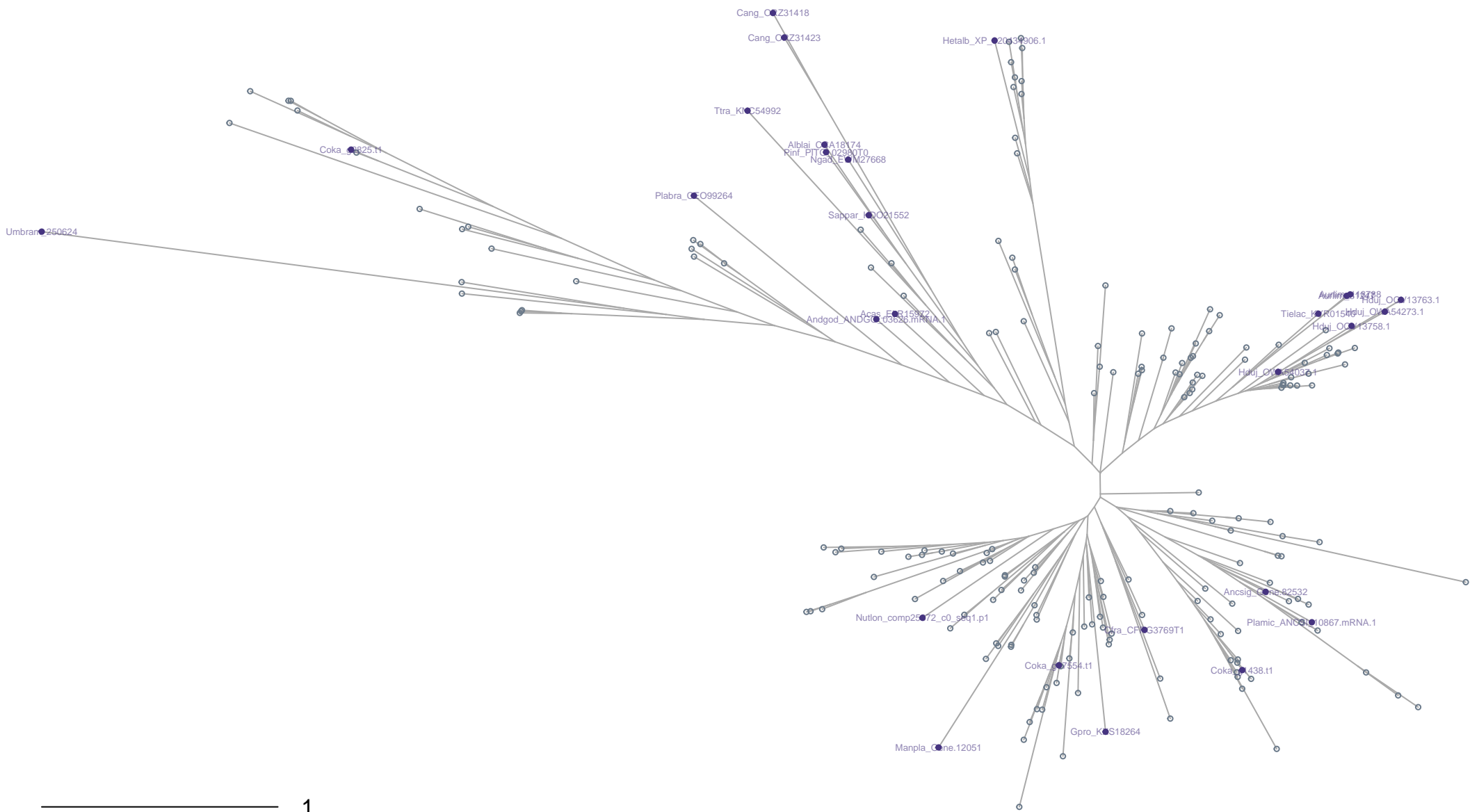
Acetyltransf_1.HG2.0:KAT14 n = 54
other n = 64

Crenarchaeota n = 2
Euryarchaeota n = 14



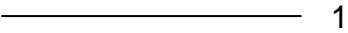
Acetyltransf_1
euk.Acetyltransf_1.phy.HG30.seqs.iqtree.treefile
n=216 sequences

eukaryotes
archaea
bacteria



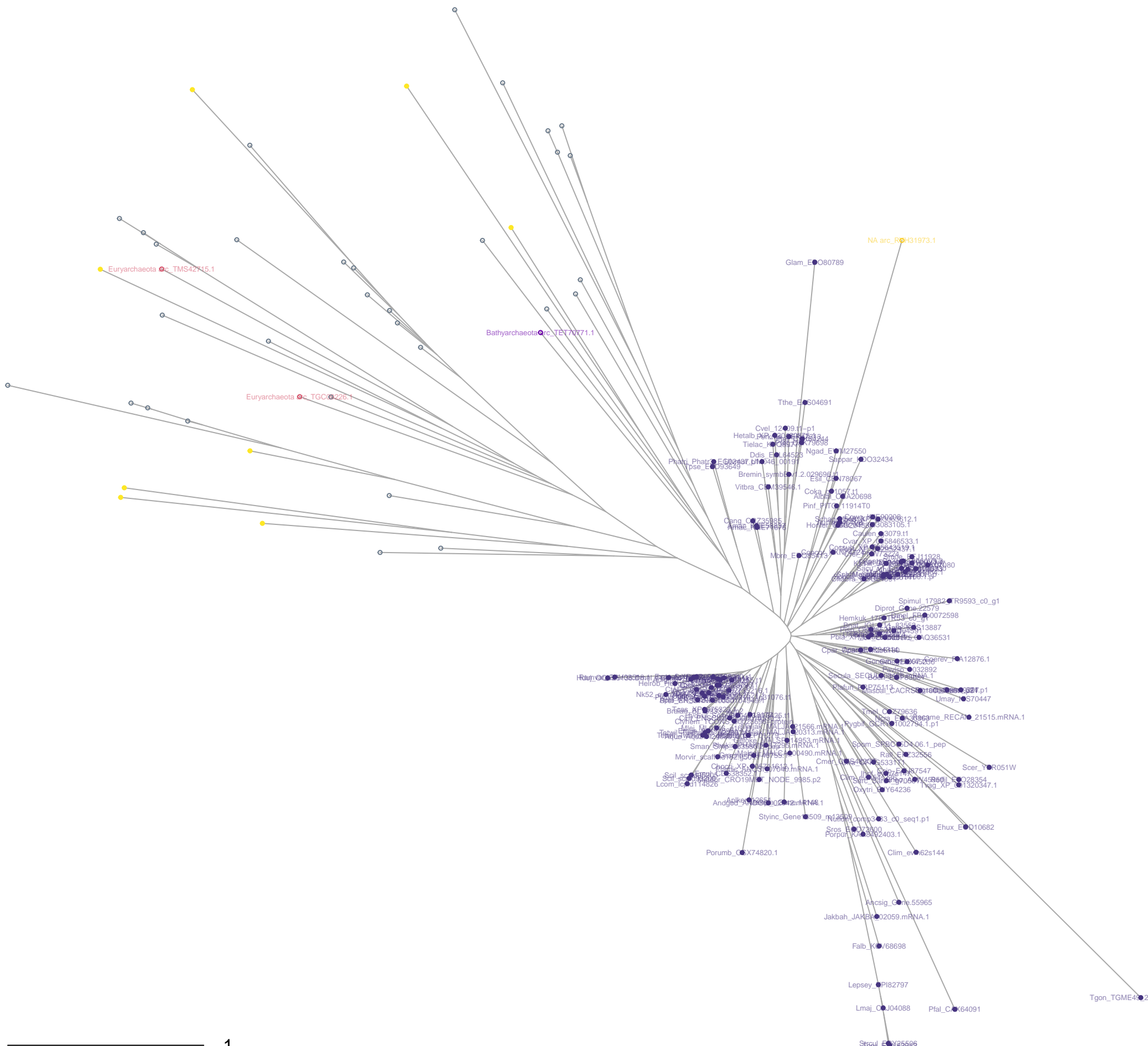
Acetyltransf_1.HG11.1:NA n = 28
other n = 0

n =



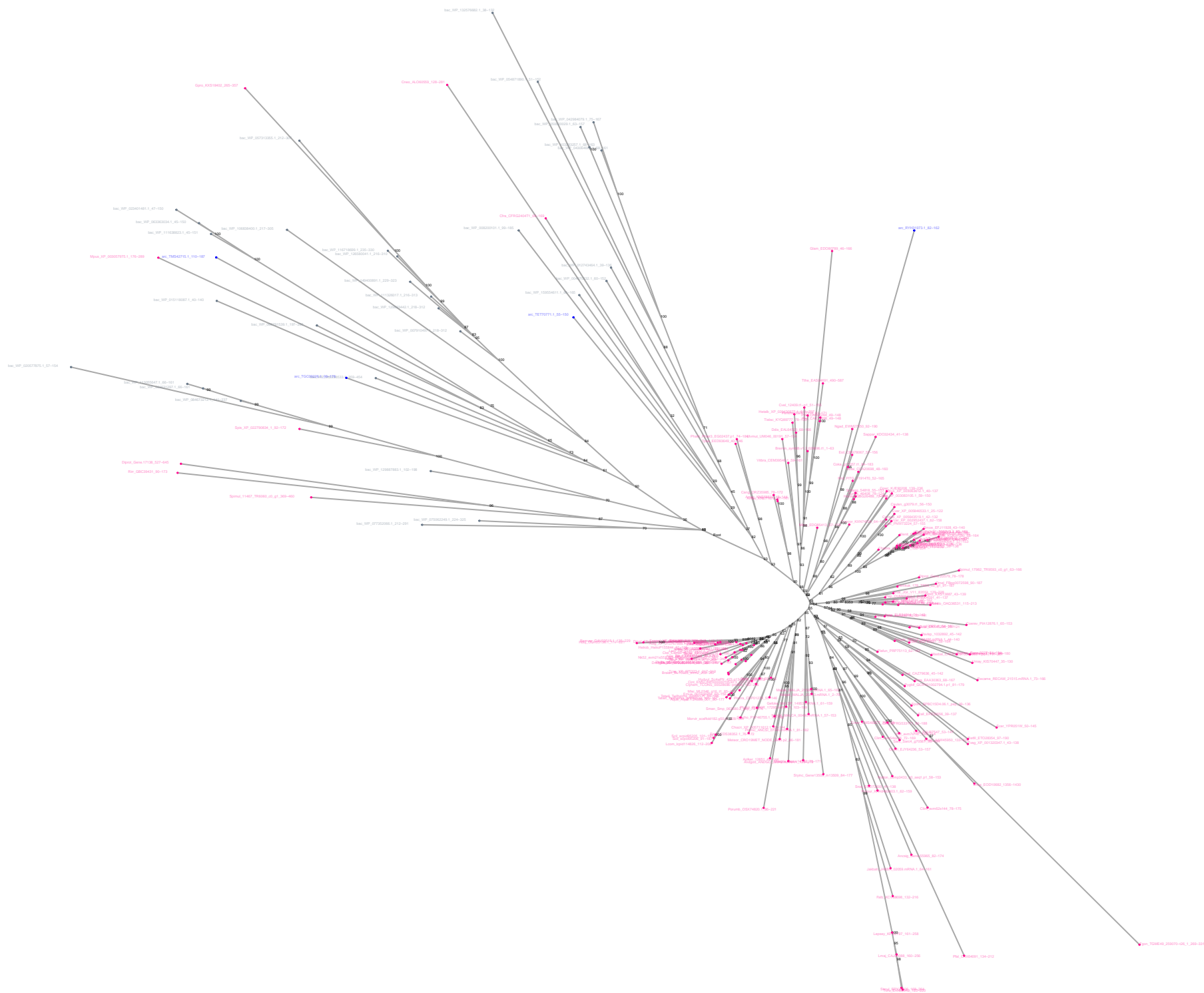
euk.Acetyltransf_1.phy.HG31.seqs.iqtree.treefile
n=209 sequences

eukaryotes
archaea
bacteria



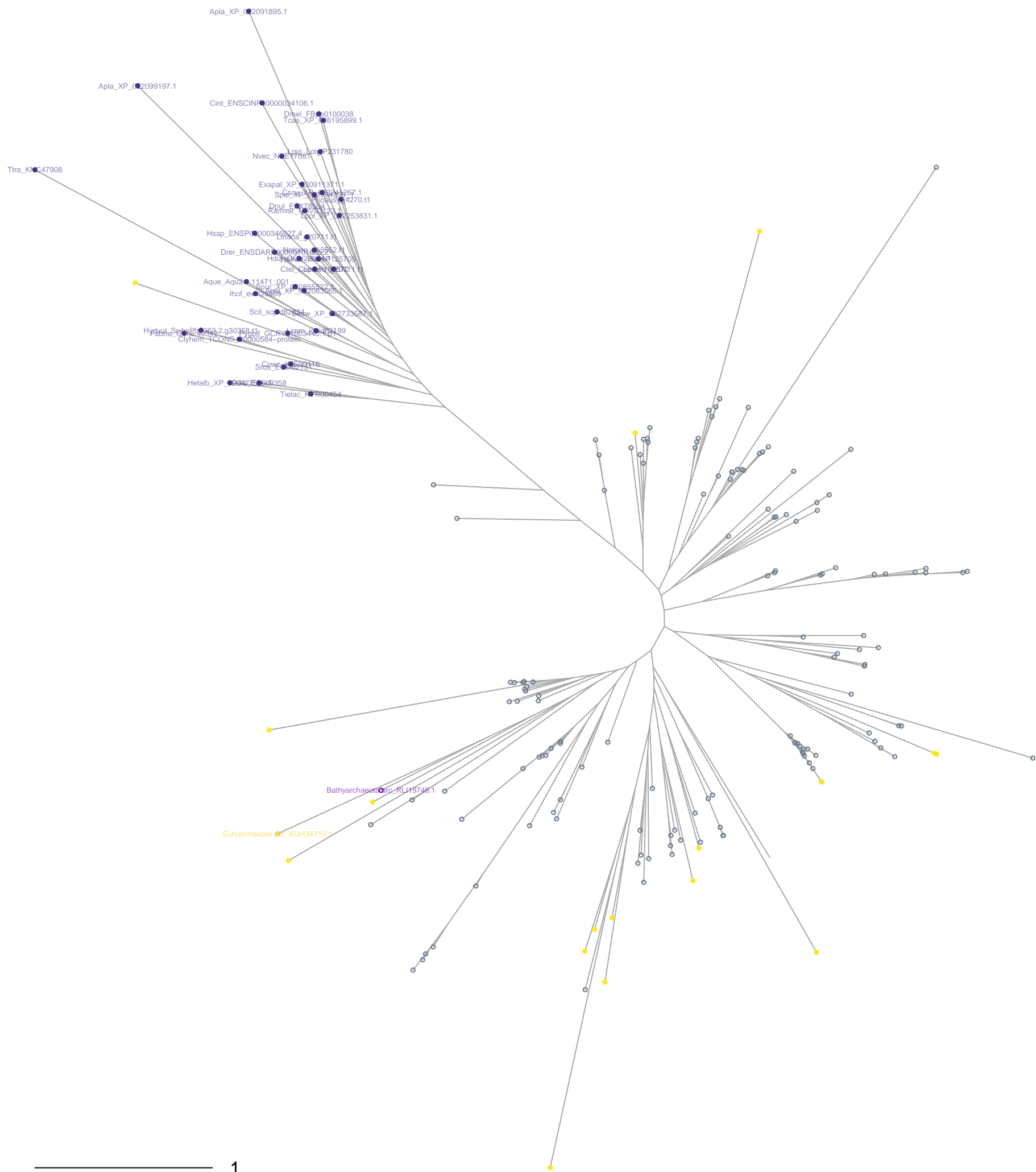
Acetyltransf_1.HG1.14:NAA30 n = 166
other n = 8

Bathyarchaeota n = 1
Euryarchaeota n = 2
NA n = 1



euk.Acetyltransf_1.phy.HG32.seqs.iqtree.treefile
n=197 sequences

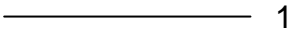
eukaryotes
archaea
bacteria



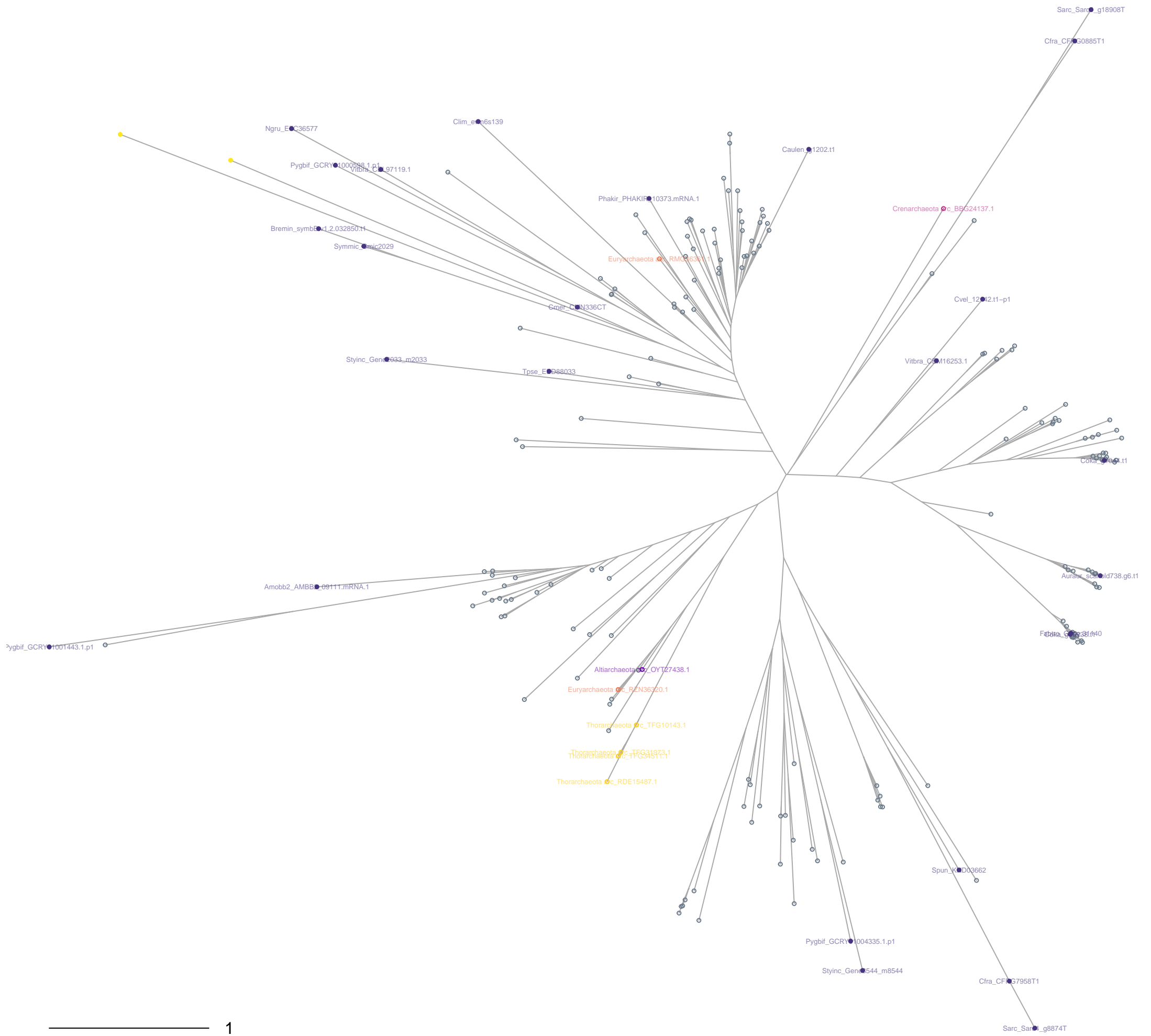
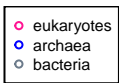
1

Acetyltransf_1.HG3.4:NAA80 n = 39
other n = 17

Bathyarchaeota n = 1
Euryarchaeota n = 1



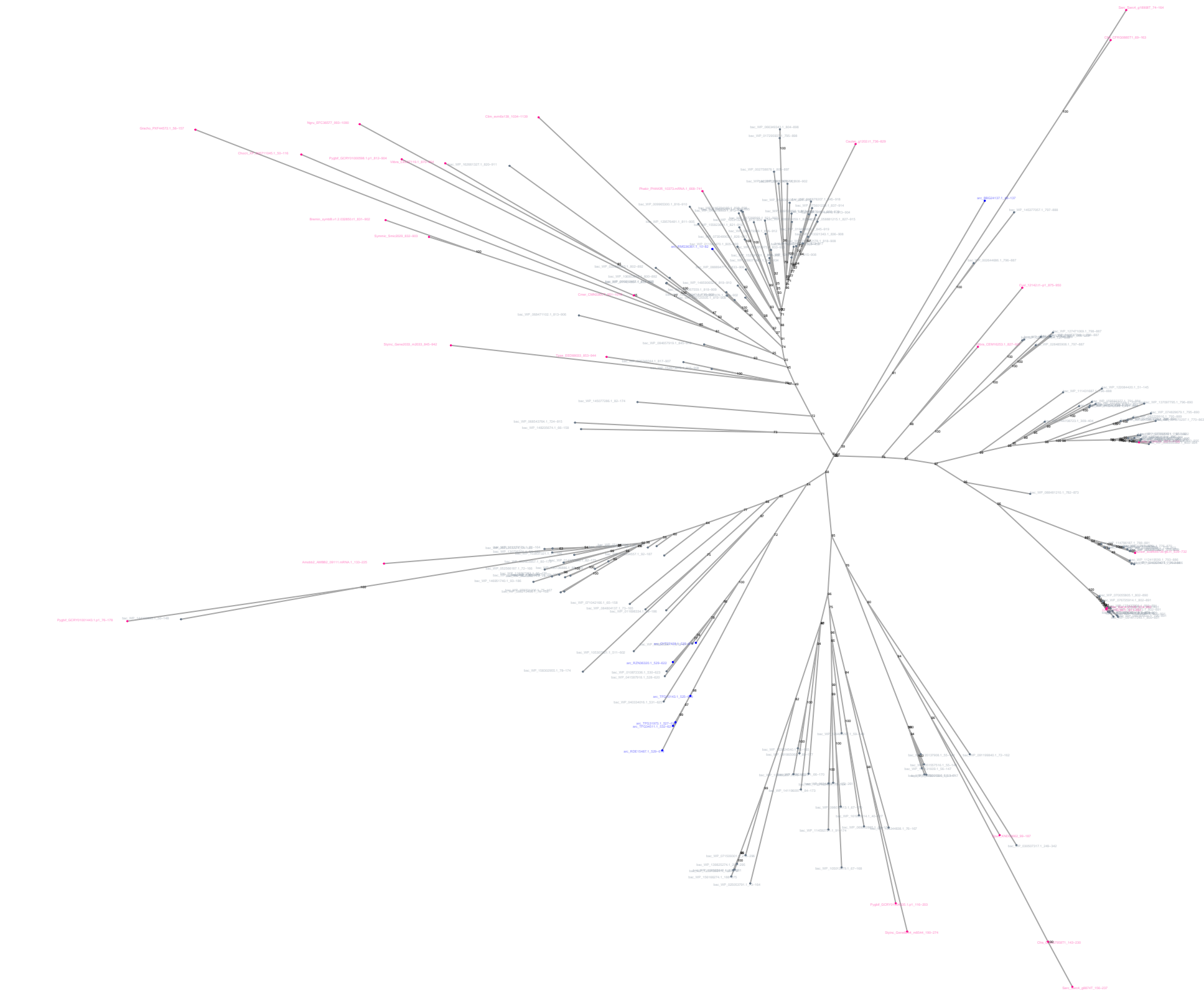
euk.Acetyltransf_1.phy.HG33.seqs.iqtree.treefile
n=196 sequences



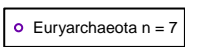
1

- Acetyltransf_1.HG7.0:NA n = 26
- other n = 2

- Altiarchaeota n = 1
- Crenarchaeota n = 1
- Euryarchaeota n = 2
- Thorarchaeota n = 4

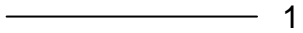


Acetyltransf_1



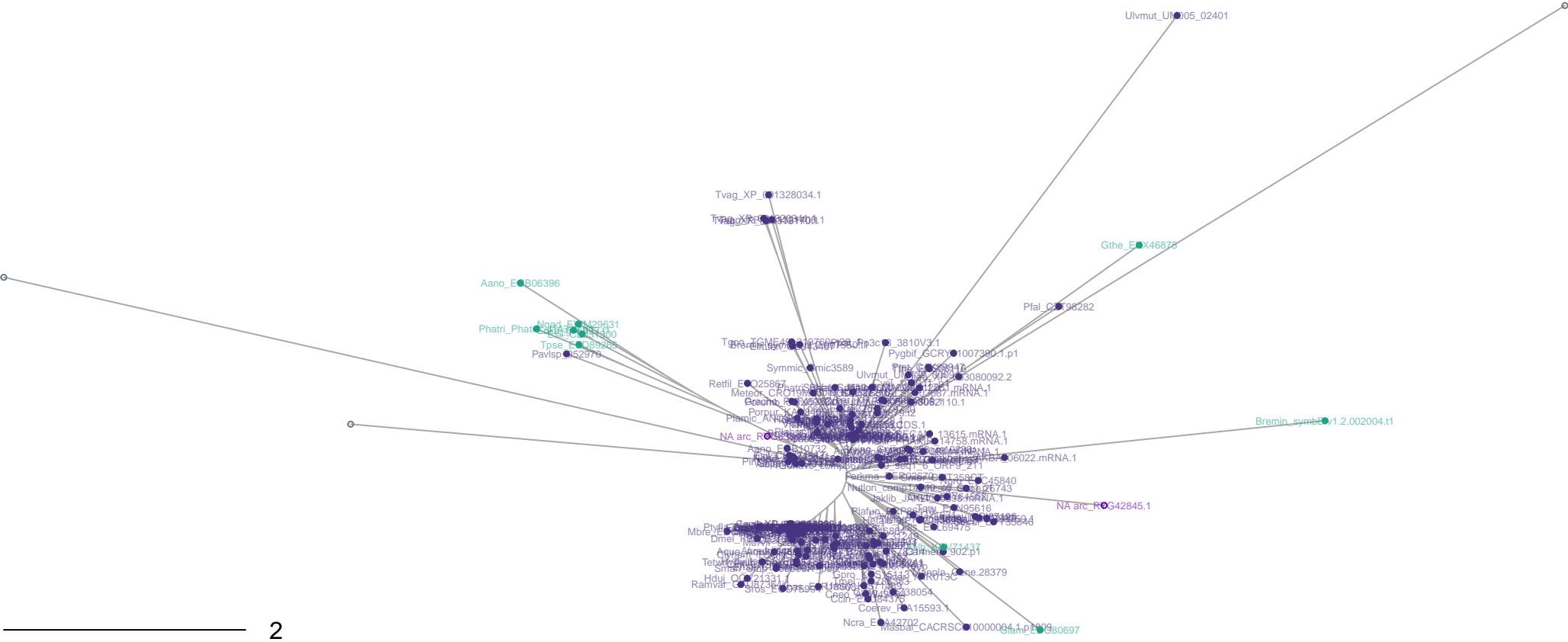
nsf_1.HG4.0:like:SAT1/SAT2/SATL1:likeclu:1 n = 28
3

- Euryarchaeota n = 7



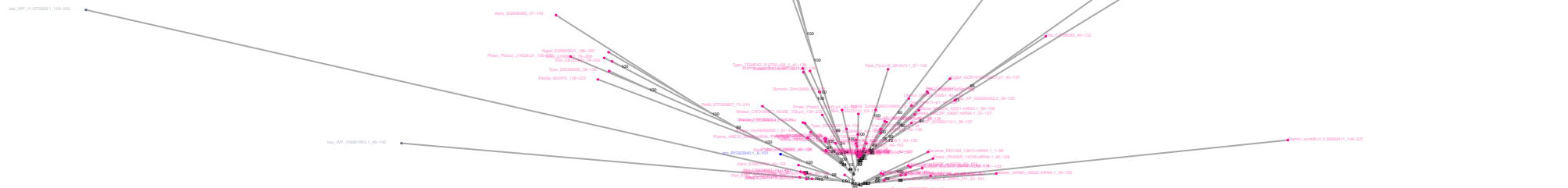
euk.Acetyltransf_1.phy.HG35.seqs.iqtree.treefile
n=183 sequences

- eukaryotes
- archaea
- bacteria

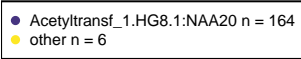


- Acetyltransf_1.HG6.1:NAA10/NAA11 n = 168
- Acetyltransf_1.HG6.0:like:NAA10/NAA11:likeclu:1 n = 10
- other n = 0

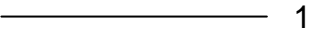
- NA n = 2



- eukaryotes
- archaea
- bacteria



- Bathyarchaeota n = 1



Acetyltransf_1.phy.HG37.seqs.iqtree.treefile
n=162 sequences

eukaryotes
archaea
bacteria



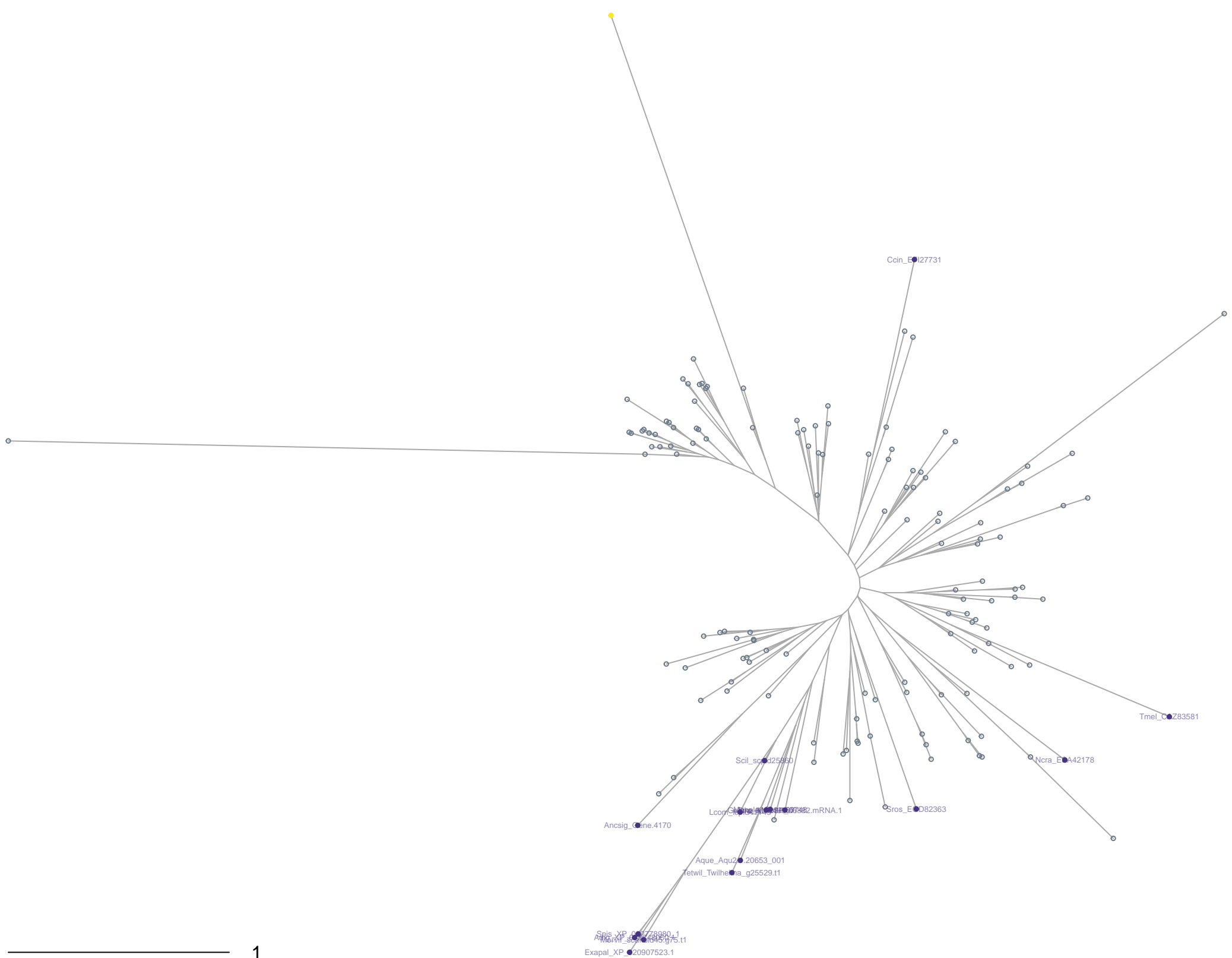
Acetyltransf_1.HG10.0:NAA40 n = 138
other n = 16

NA n = 1
Thaumarchaeota n = 1



Acetyltransf_1
euk.Acetyltransf_1.phy.HG38.seqs.iqtree.treefile
n=150 sequences

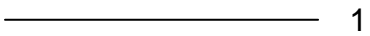
eukaryotes
archaea
bacteria



1

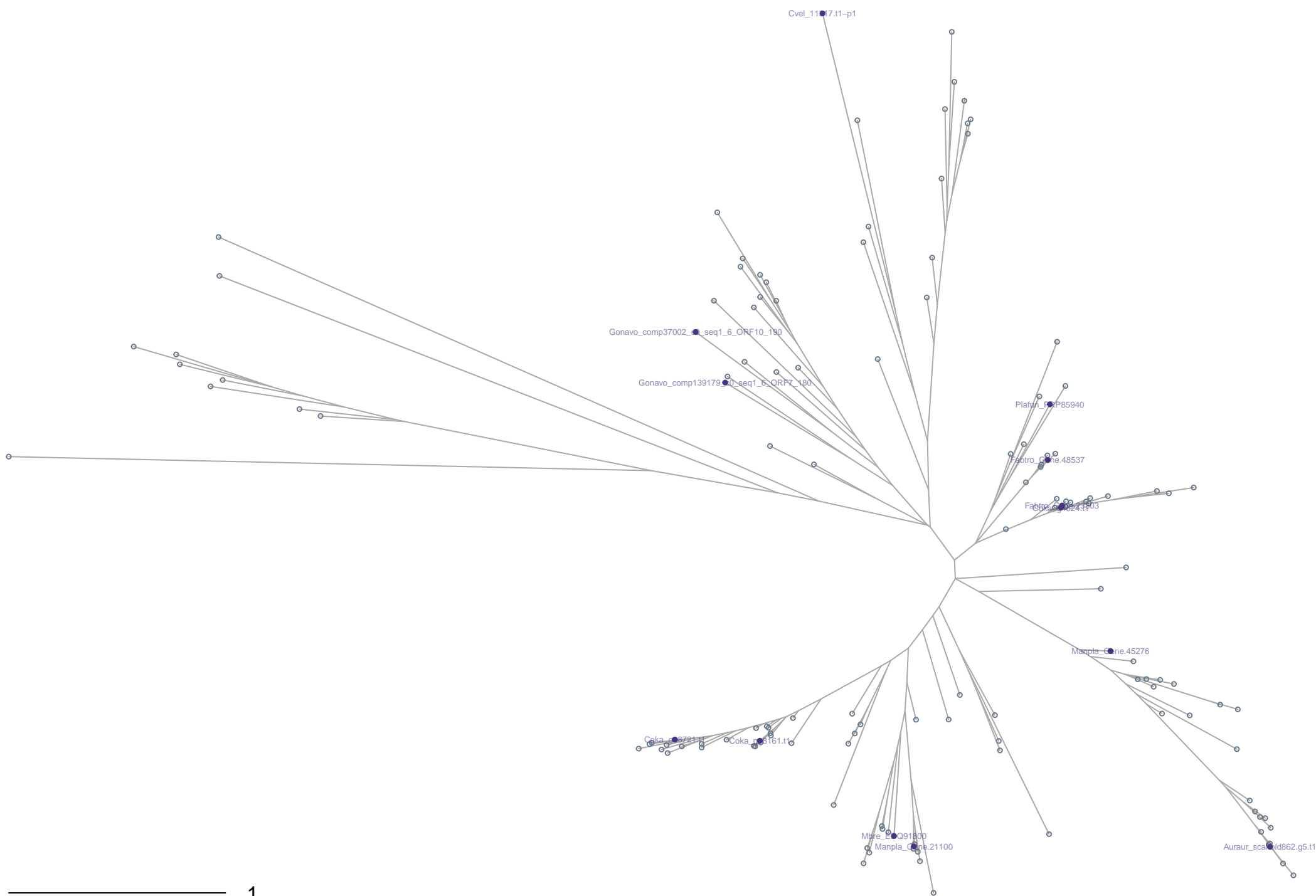
Acetyltransf_1.HG28.1:NA n = 16
other n = 1

n =



Acetyltransf_1
euk.Acetyltransf_1.phy.HG39.seqs.iqtree.treefile
n=144 sequences

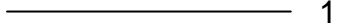
eukaryotes
archaea
bacteria



1

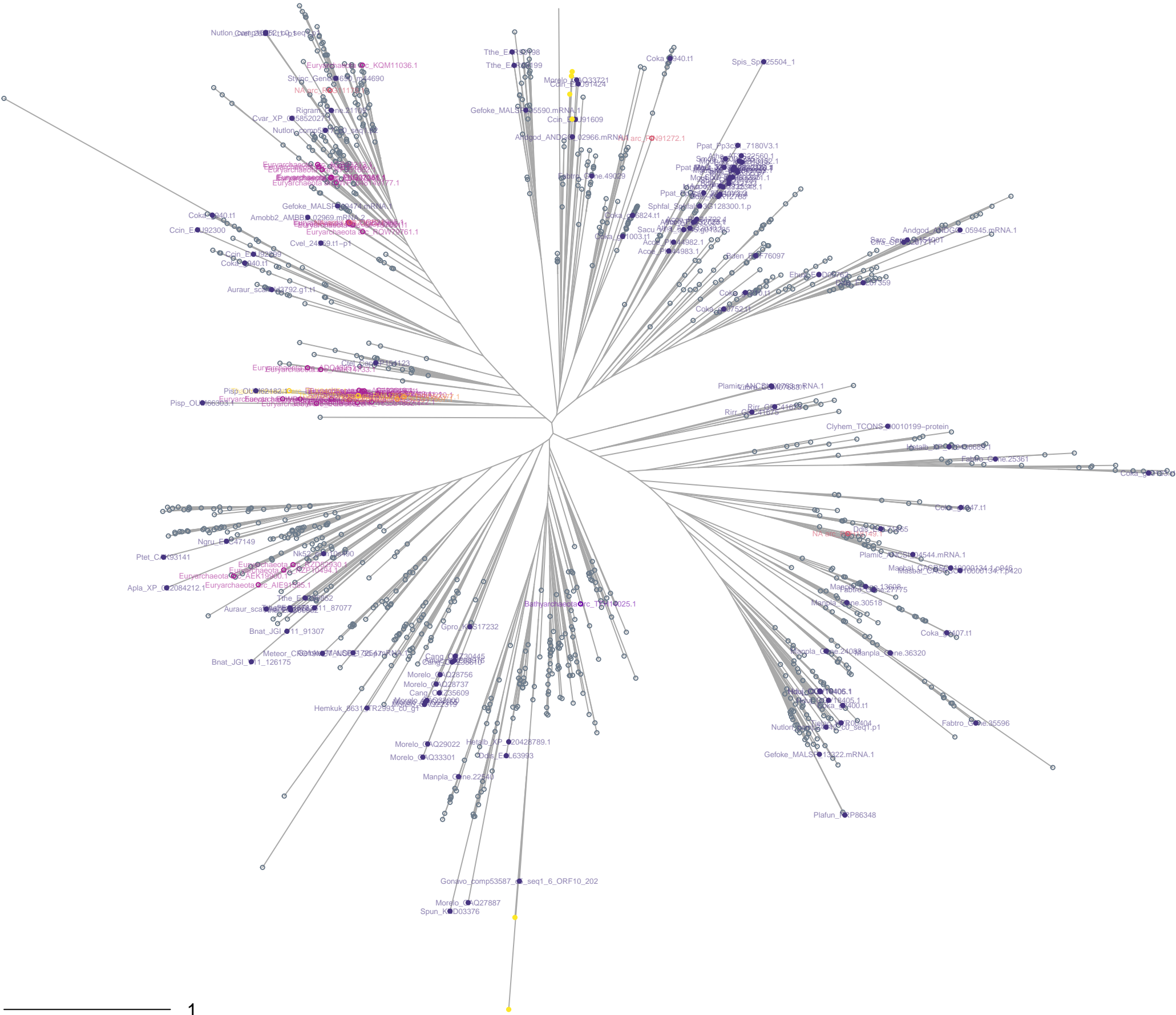
Acetyltransf_1.HG12.0:NA n = 13
other n = 0

n =



euk.Acetyltransf_1.phy.HG4.seqs.iqtree.treefile
n=1183 sequences

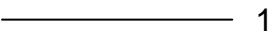
- eukaryotes
- archaea
- bacteria



1

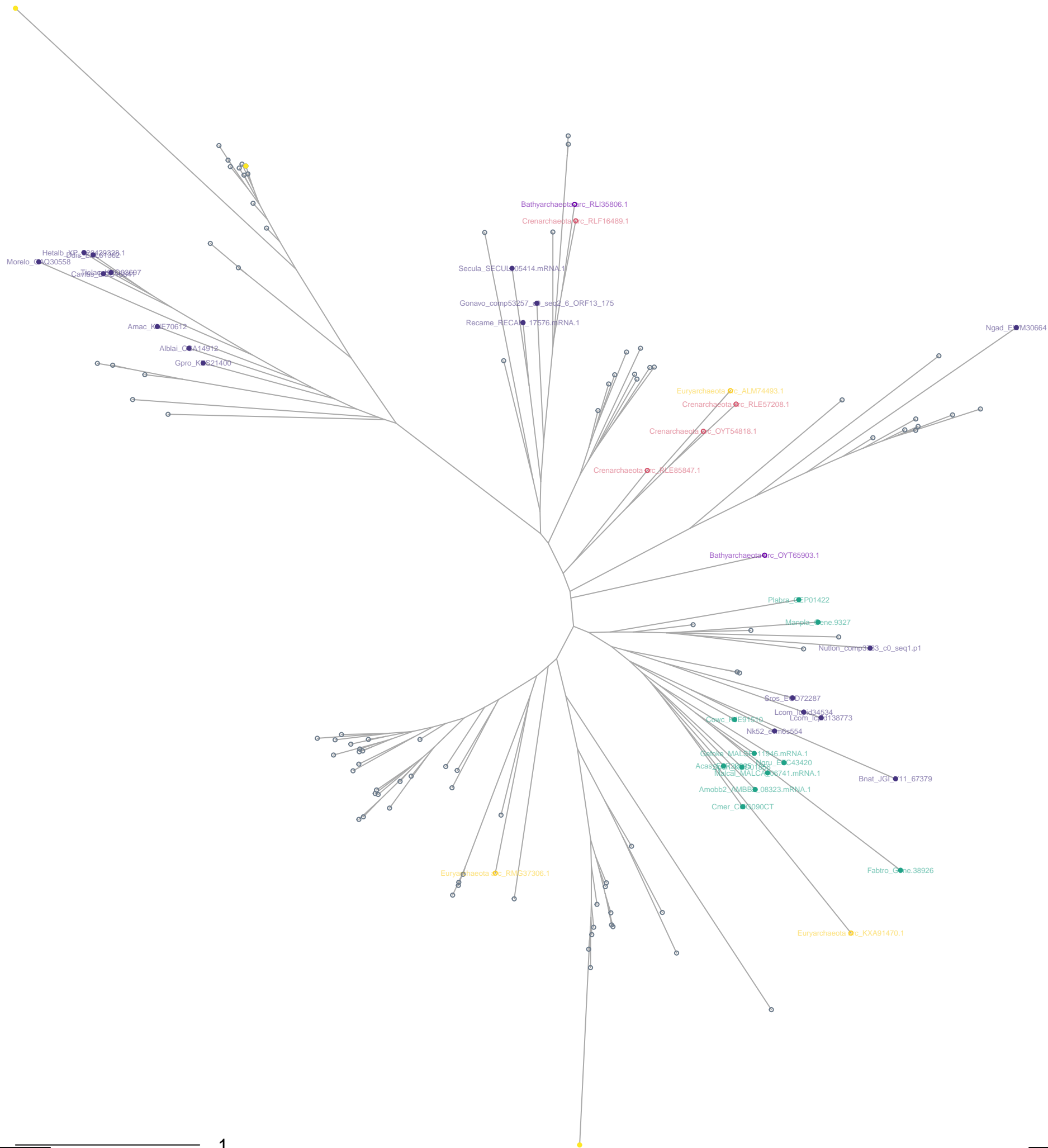
- Acetyltransf_1.HG11.1:NA n = 125
- other n = 6

- Bathyarchaeota n = 1
- Euryarchaeota n = 33
- NA n = 4
- Nanoarchaeota n = 2
- Thaumarchaeota n = 2



Acetyltransf_1
euk.Acetyltransf_1.phy.HG40.seqs.iqtree.treefile
n=130 sequences

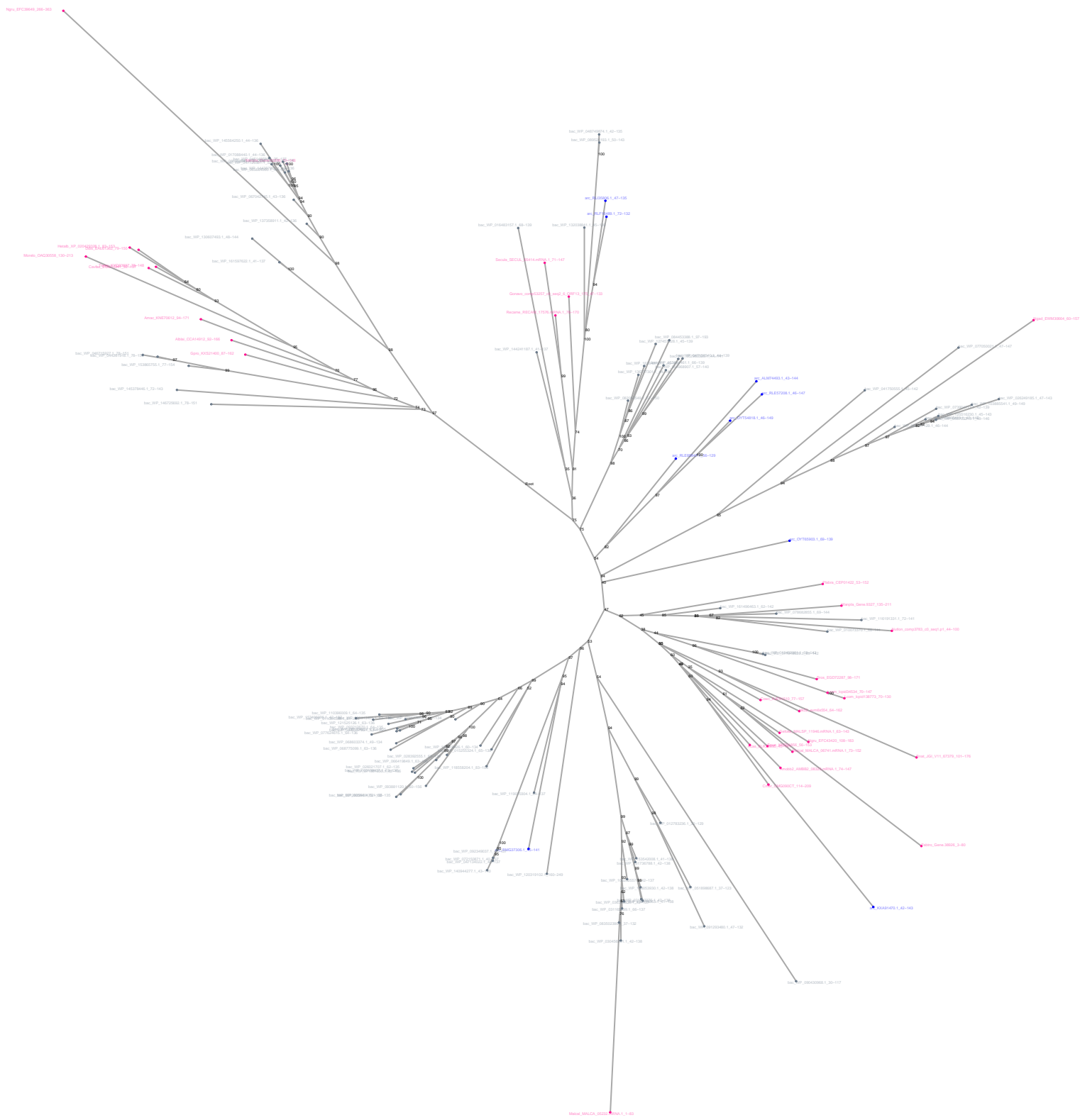
eukaryotes
archaea
bacteria



1

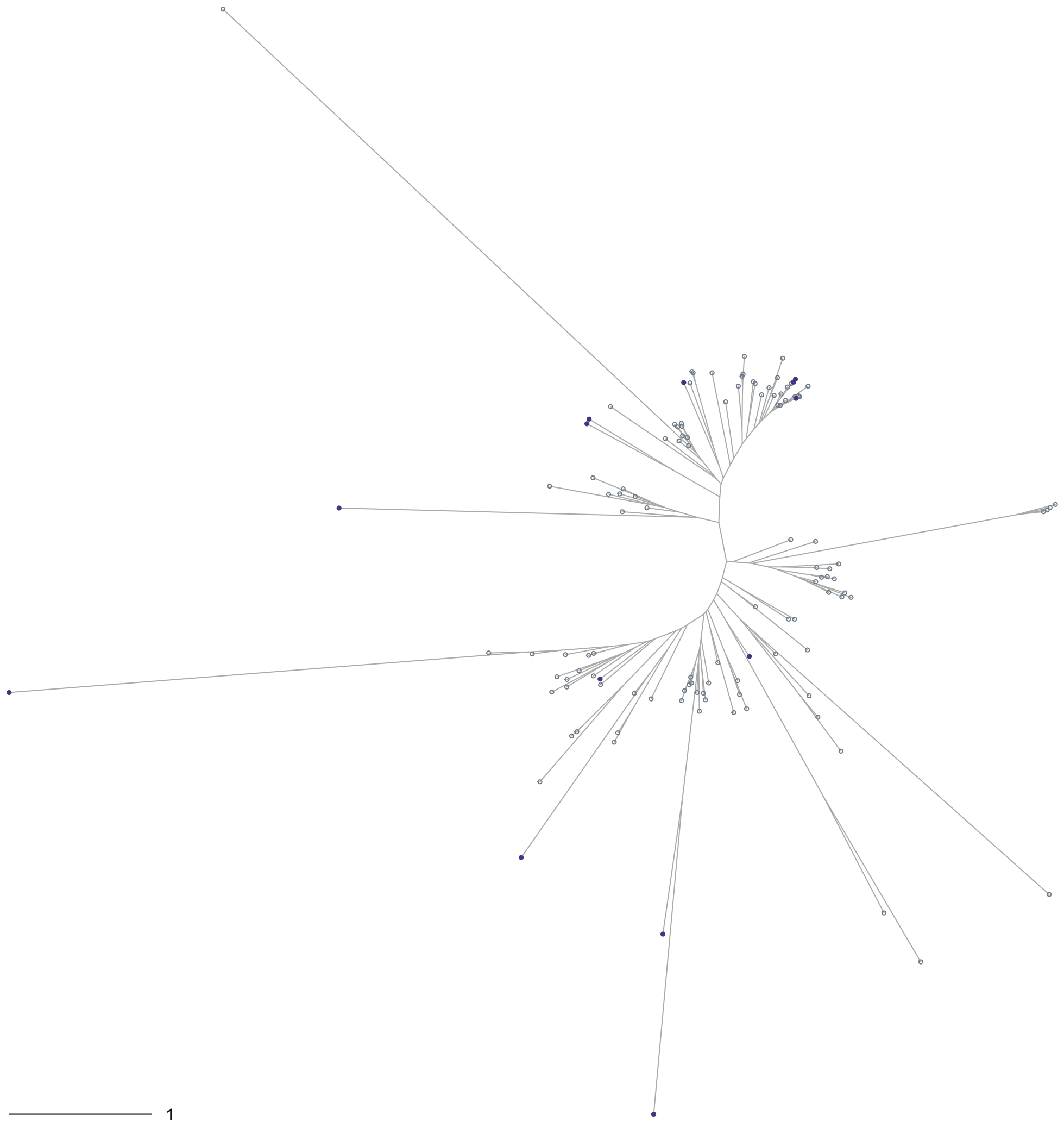
Acetyltransf_1.HG23.1:NA n = 18
Acetyltransf_1.HG23.0:NA n = 11
other n = 3

Bathyarchaeota n = 2
Crenarchaeota n = 4
Euryarchaeota n = 3



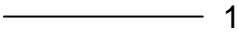
Acetyltransf_1
euk.Acetyltransf_1.phy.HG41.seqs.iqtree.treefile
n=121 sequences

eukaryotes
archaea
bacteria



other n = 13

n =



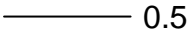
euk.Acetyltransf_1.phy.HG42.seqs.iqtree.treefile
n=113 sequences

eukaryotes
archaea
bacteria

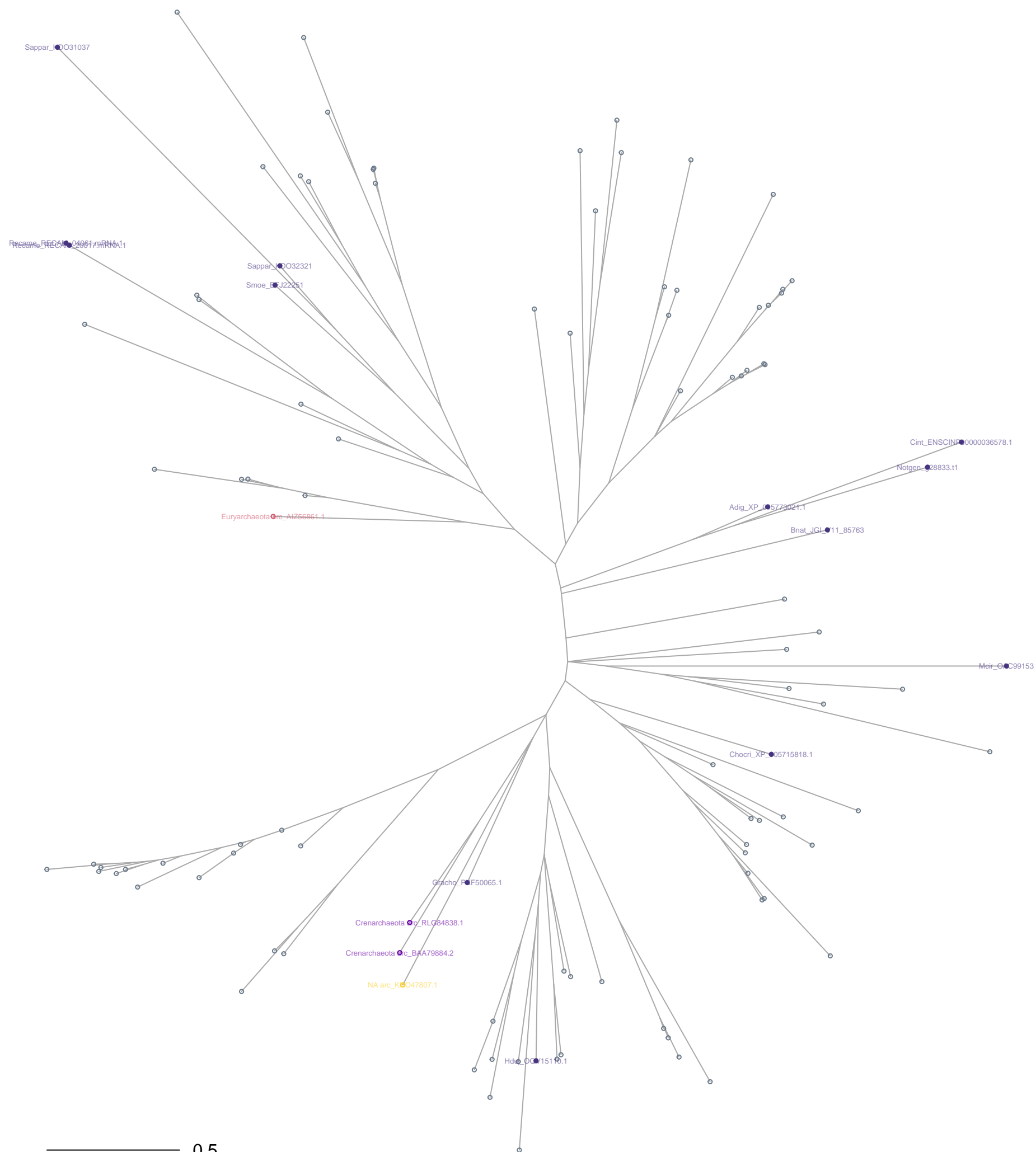


Acetyltransf_1.HG7.2:NA n = 34
other n = 6

n =



euk.Acetyltransf_1.phy.HG43.seqs.iqtree.treefile
n=107 sequences

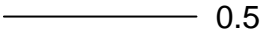


- eukaryotes
- archaea
- bacteria

_____ 0.5

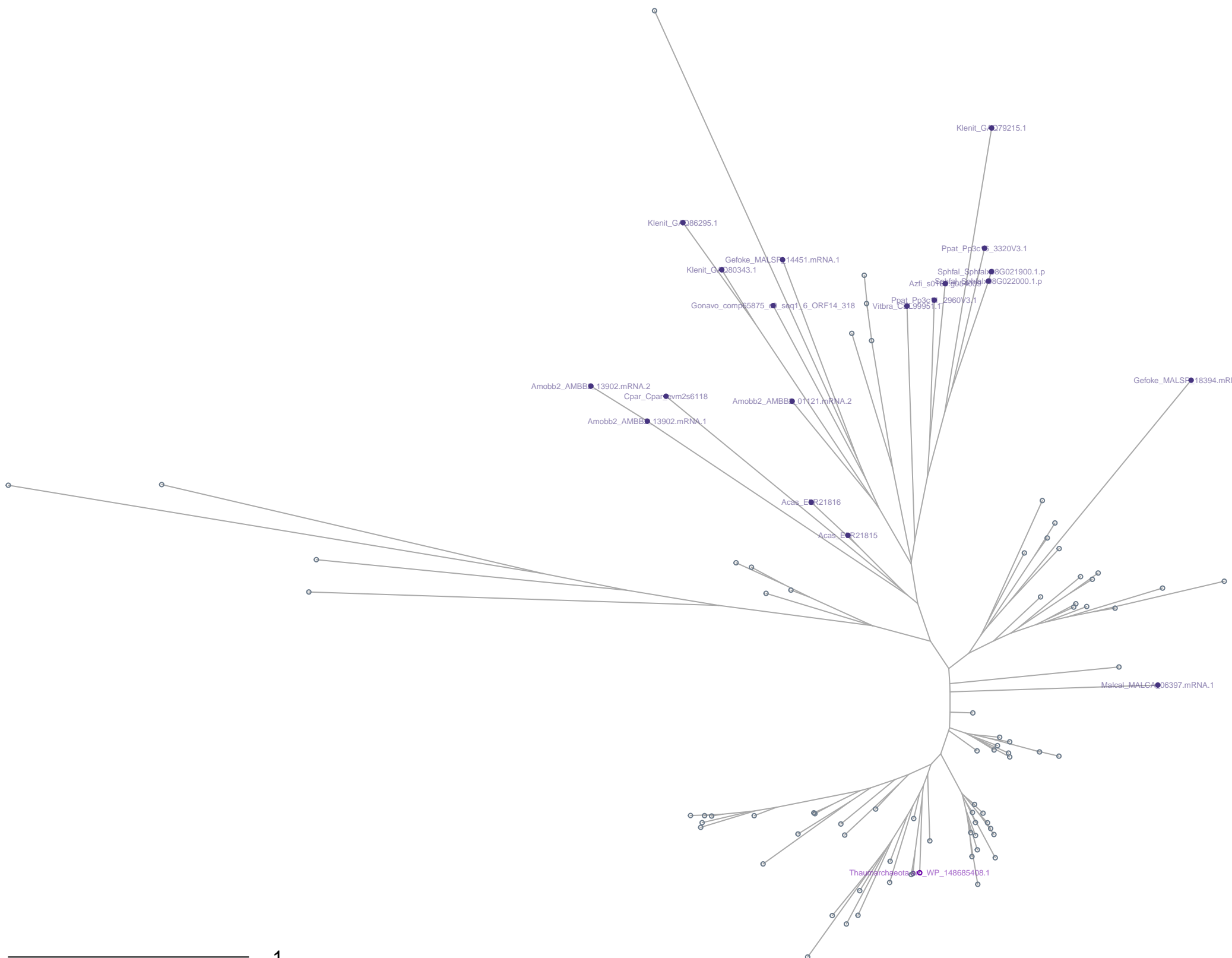
- Acetyltransf_1.HG33.0:NA n = 13
- other n = 0

- Crenarchaeota n = 2
- Euryarchaeota n = 1
- NA n = 1



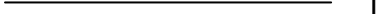
Acetyltransf_1
euk.Acetyltransf_1.phy.HG44.seqs.iqtree.treefile
n=96 sequences

- eukaryotes
- archaea
- bacteria



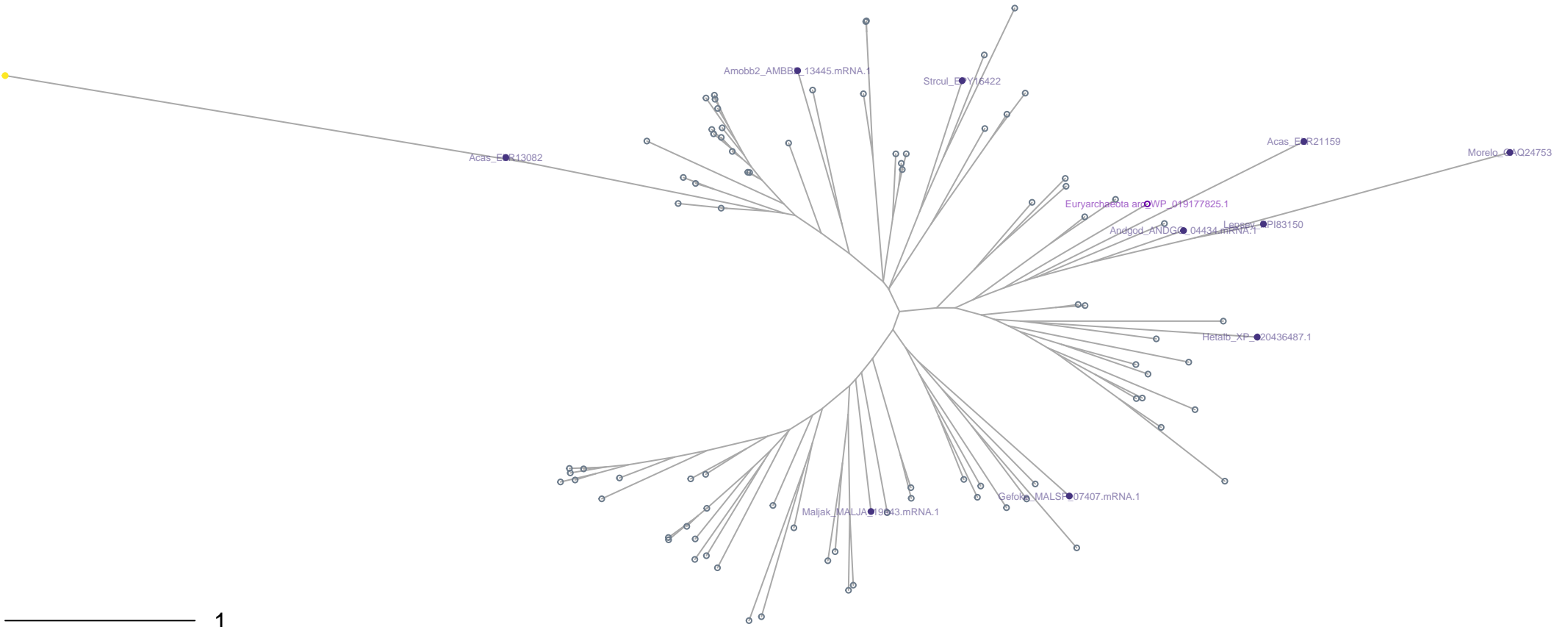
Acetyltransf_1.HG7.0:NA n = 19
other n = 0

Thaumarchaeota n = 1



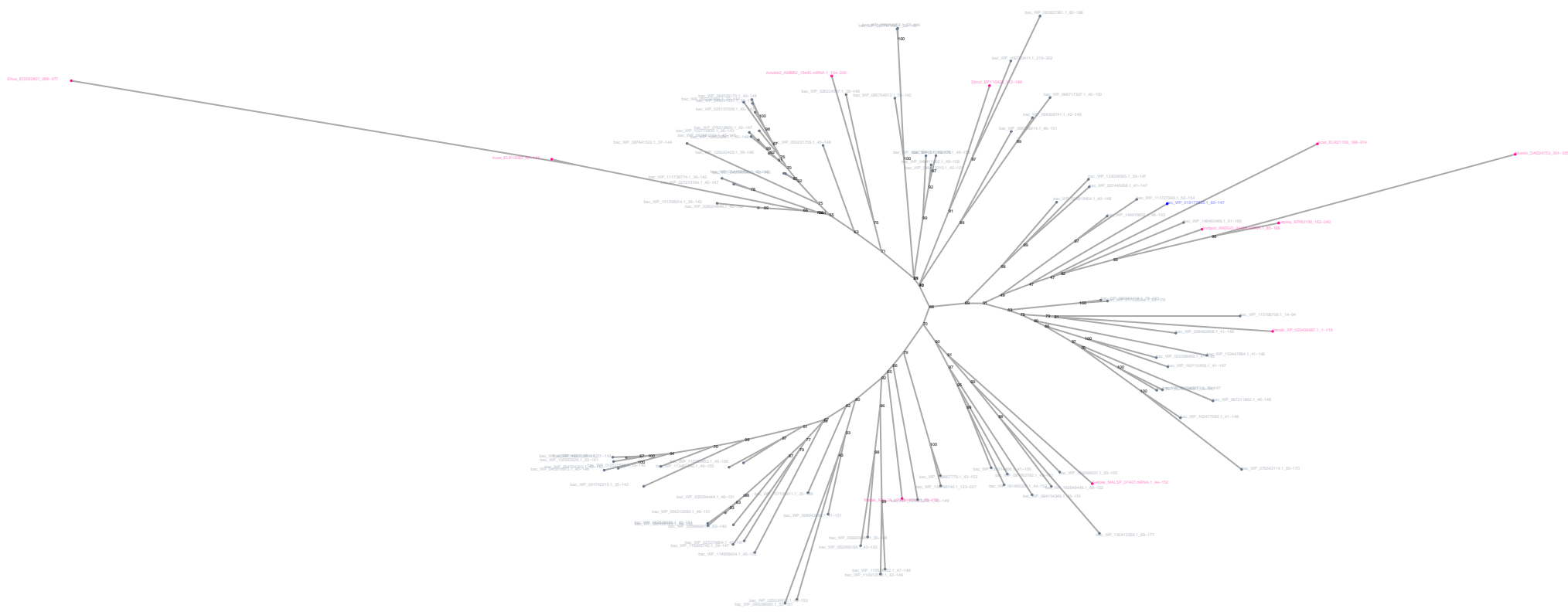
Acetyltransf_1
euk.Acetyltransf_1.phy.HG45.seqs.iqtree.treefile
n=95 sequences

eukaryotes
archaea
bacteria



Acetyltransf_1.HG31.0:NA n = 10
other n = 1

Euryarchaeota n = 1



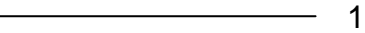
Acetyltransf_1
euk.Acetyltransf_1.phy.HG46.seqs.iqtree.treefile
n=89 sequences

eukaryotes
archaea
bacteria



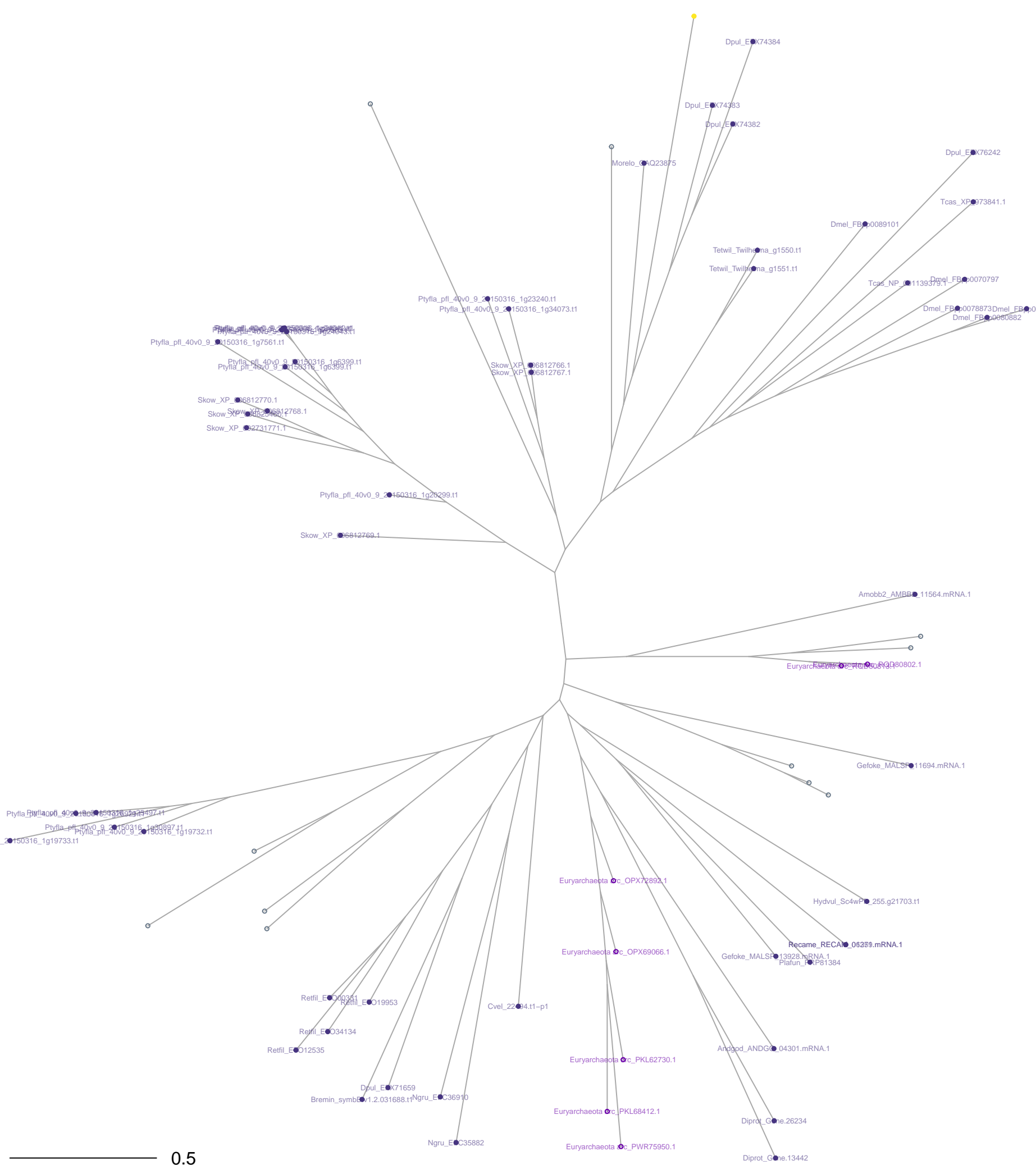
other n = 10

Euryarchaeota n = 1



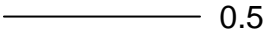
Acetyltransf_1
euk.Acetyltransf_1.phy.HG47.seqs.iqtree.treefile
n=74 sequences

- eukaryotes
- archaea
- bacteria



Acetyltransf_1.HG20.1:NA n = 55
other n = 1

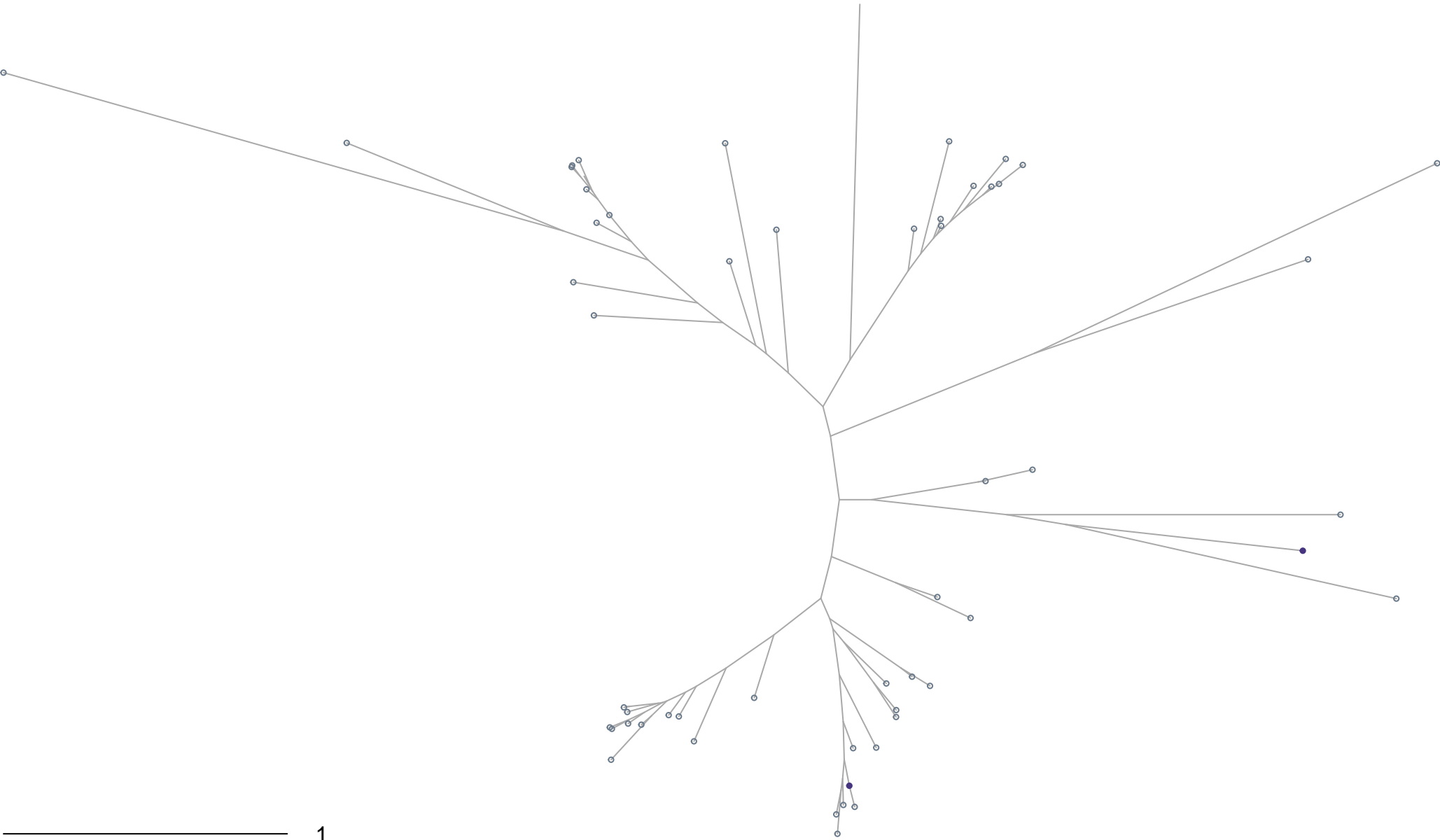
Euryarchaeota n = 7



_____ 0.5

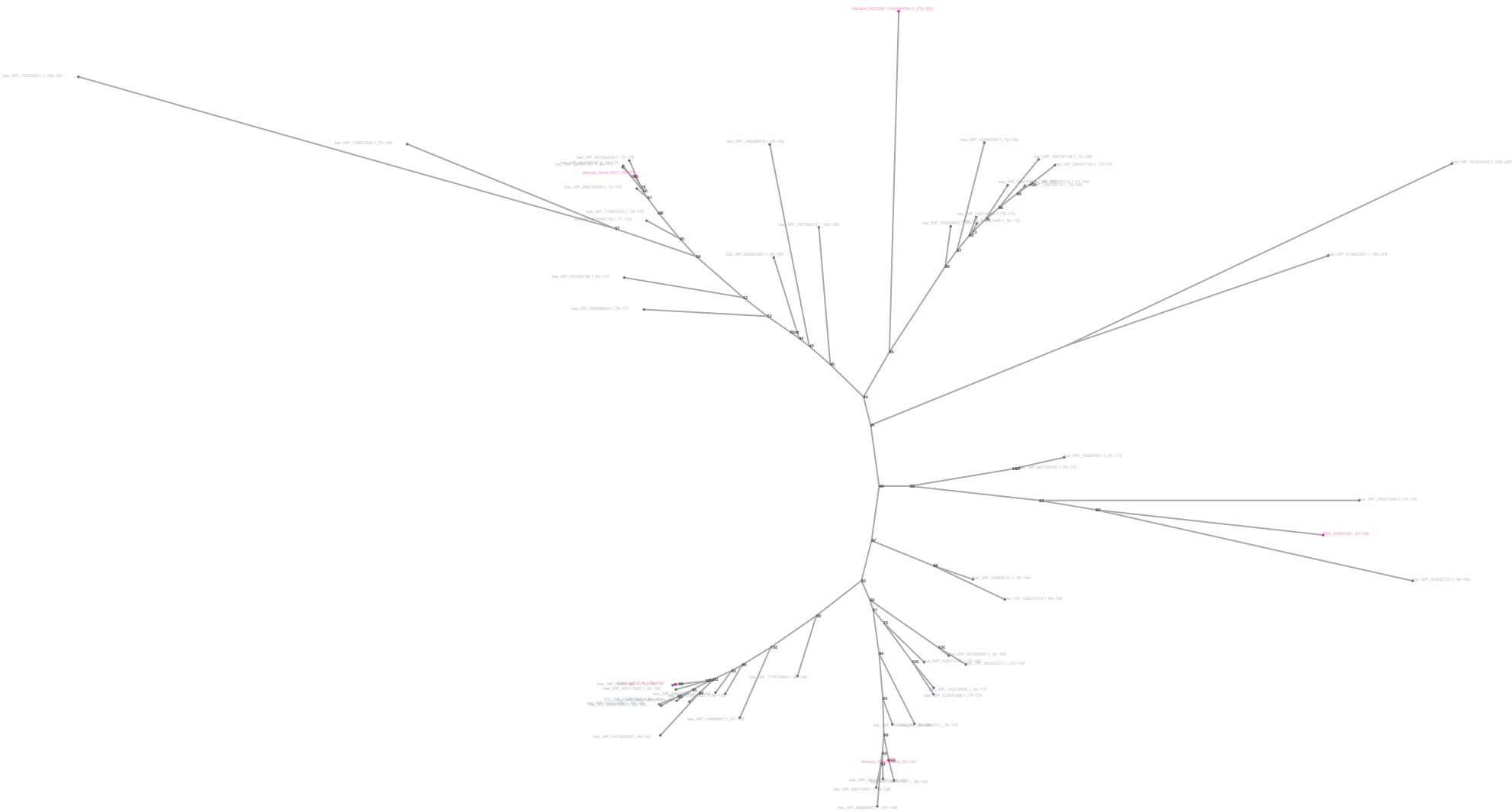
Acetyltransf_1
euk.Acetyltransf_1.phy.HG48.seqs.iqtree.treefile
n=57 sequences

eukaryotes
archaea
bacteria



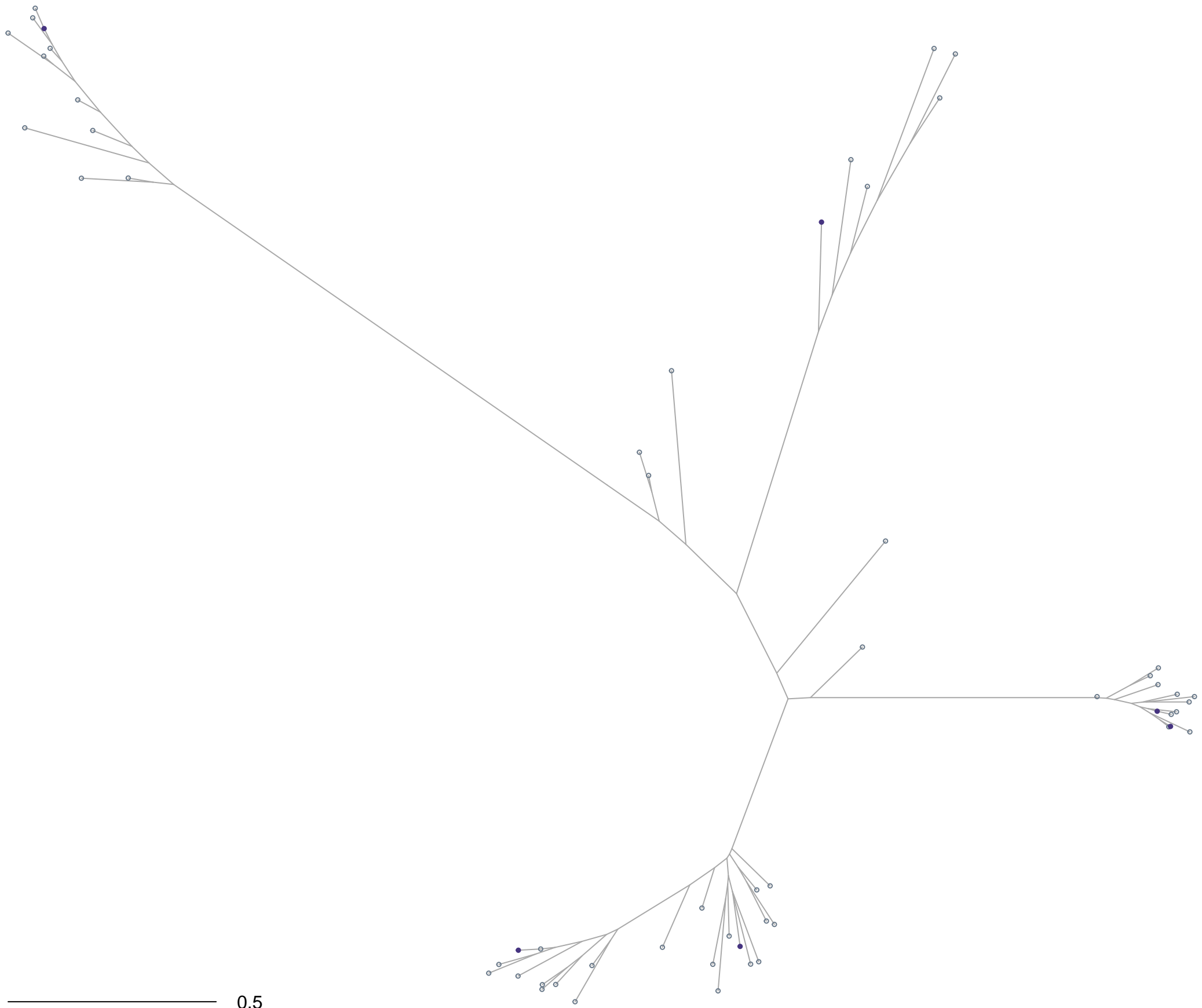
other n = 2

n =



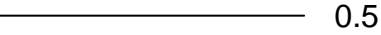
Acetyltransf_1
euk.Acetyltransf_1.phy.HG49.seqs.iqtree.treefile
n=57 sequences

eukaryotes
archaea
bacteria



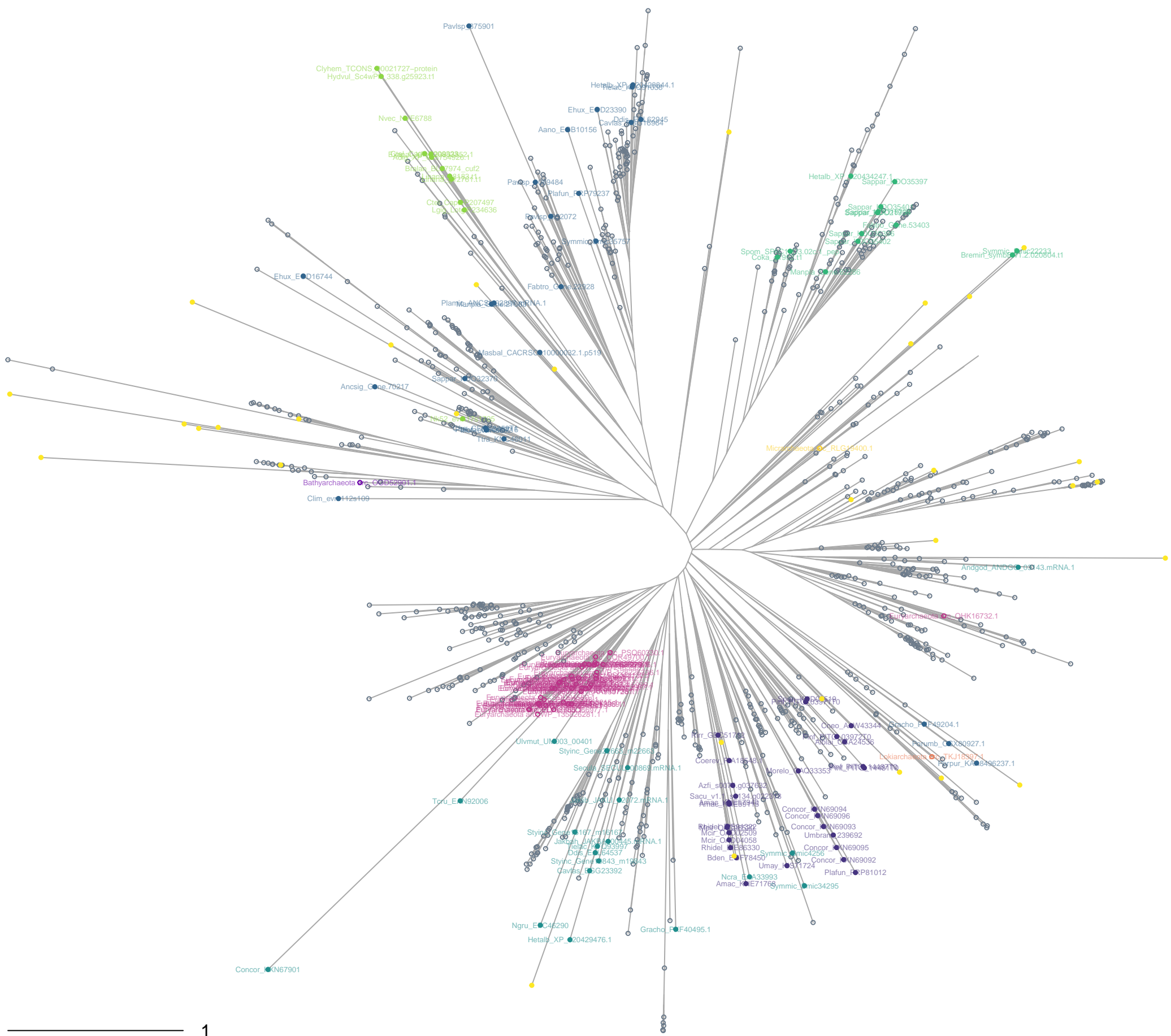
other n = 6

n =



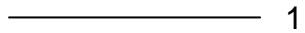
euk.Acetyltransf_1.phy.HG5.seqs.iqtree.treefile
n=1000 sequences

- eukaryotes
- archaea
- bacteria



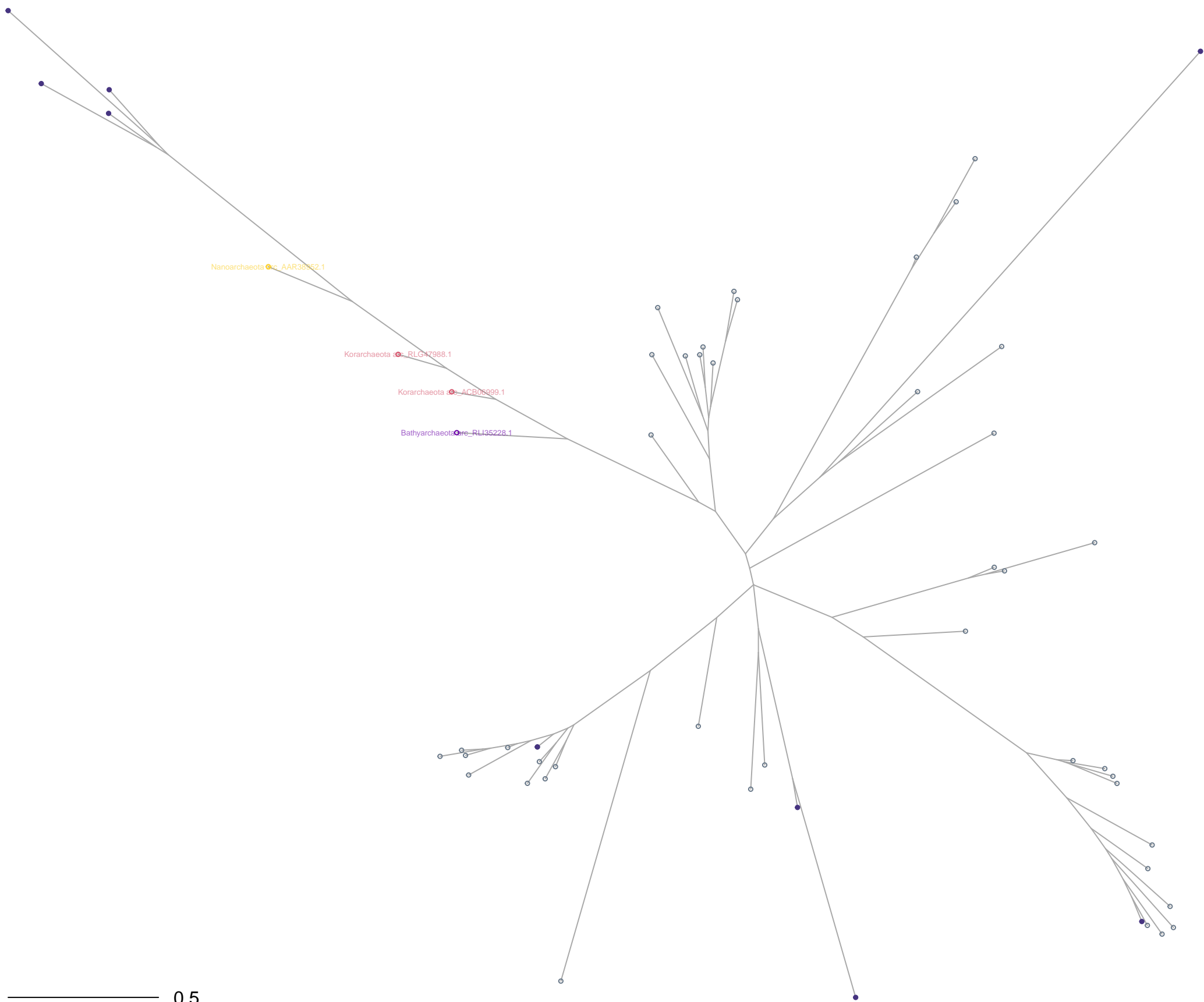
- Acetyltransf_1.HG13.4:NA n = 29
- Acetyltransf_1.HG13.0:NA n = 26
- Acetyltransf_1.HG13.3:NA n = 19
- Acetyltransf_1.HG13.6:NA n = 13
- Acetyltransf_1.HG26.0:NA n = 12
- other n = 31

- Bathyarchaeota n = 1
- Euryarchaeota n = 45
- Lokiarchaeota n = 1
- Micrarchaeota n = 1



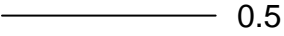
Acetyltransf_1
euk.Acetyltransf_1.phy.HG50.seqs.iqtree.treefile
n=56 sequences

eukaryotes
archaea
bacteria



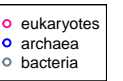
other n = 9

Bathyarchaeota n = 1
Korarchaeota n = 2
Nanoarchaeota n = 1



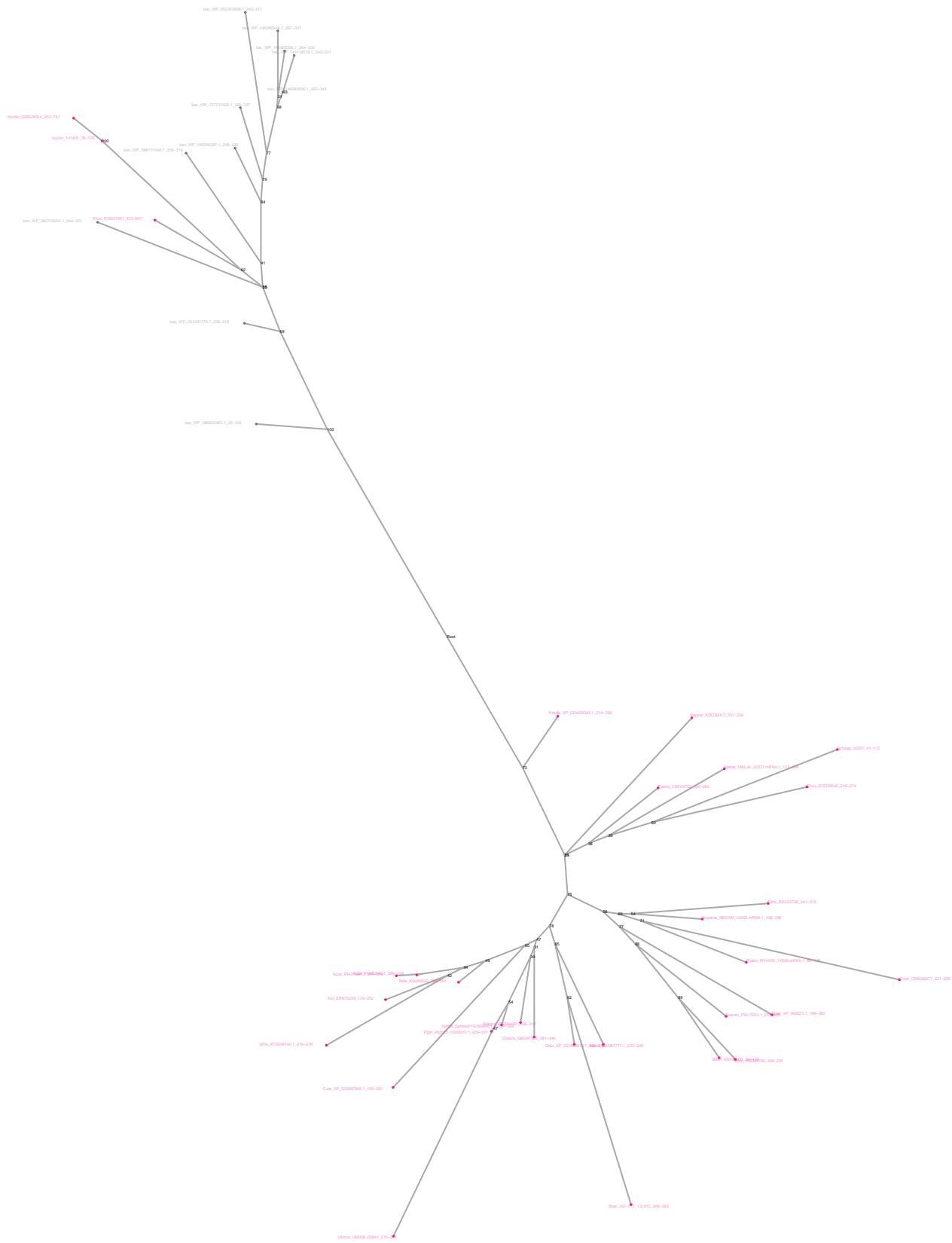
0.5

euk.Acetyltransf_1.phy.HG51.seqs.iqtree.treefile
n=42 sequences



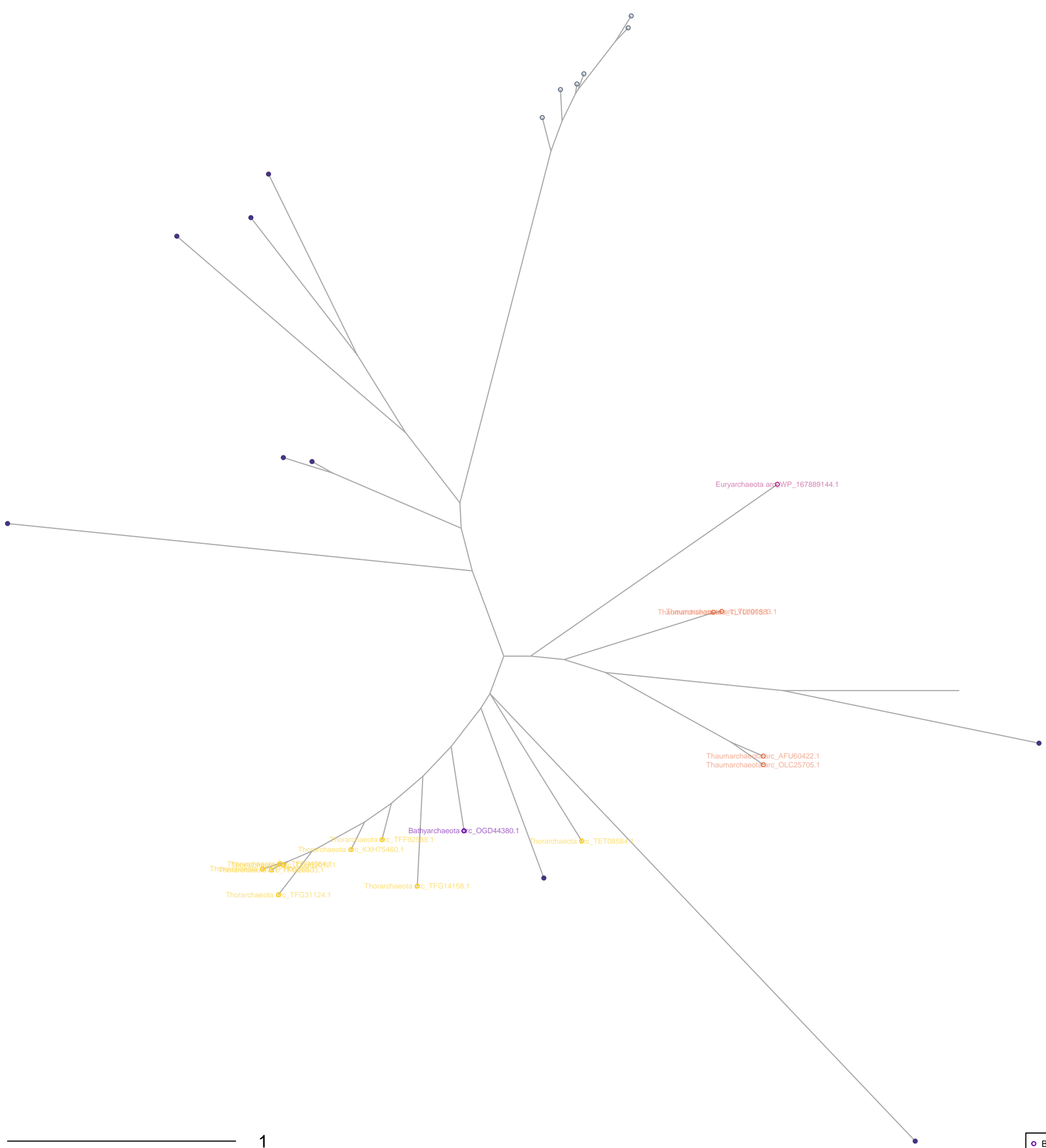
- Acetyltransf_1.HG27.0:NA n = 28
- other n = 0

○ $n =$



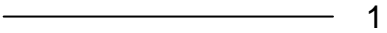
euk.Acetyltransf_1.phy.HG52.seqs.iqtree.treefile
n=31 sequences

- eukaryotes
- archaea
- bacteria



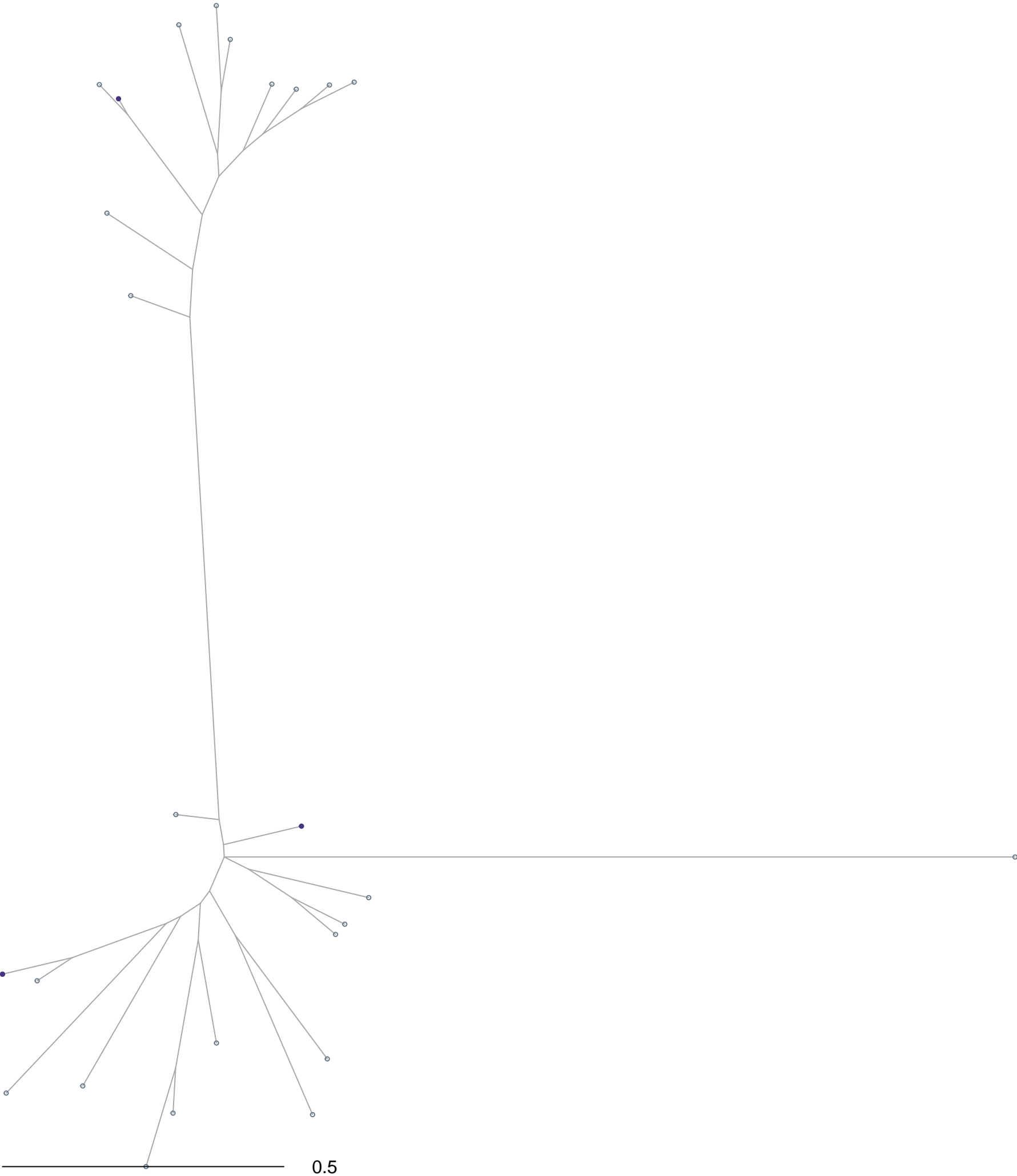
other n = 9

- Bathyarchaeota n = 1
- Euryarchaeota n = 1
- Thaumarchaeota n = 4
- Thorarchaeota n = 9



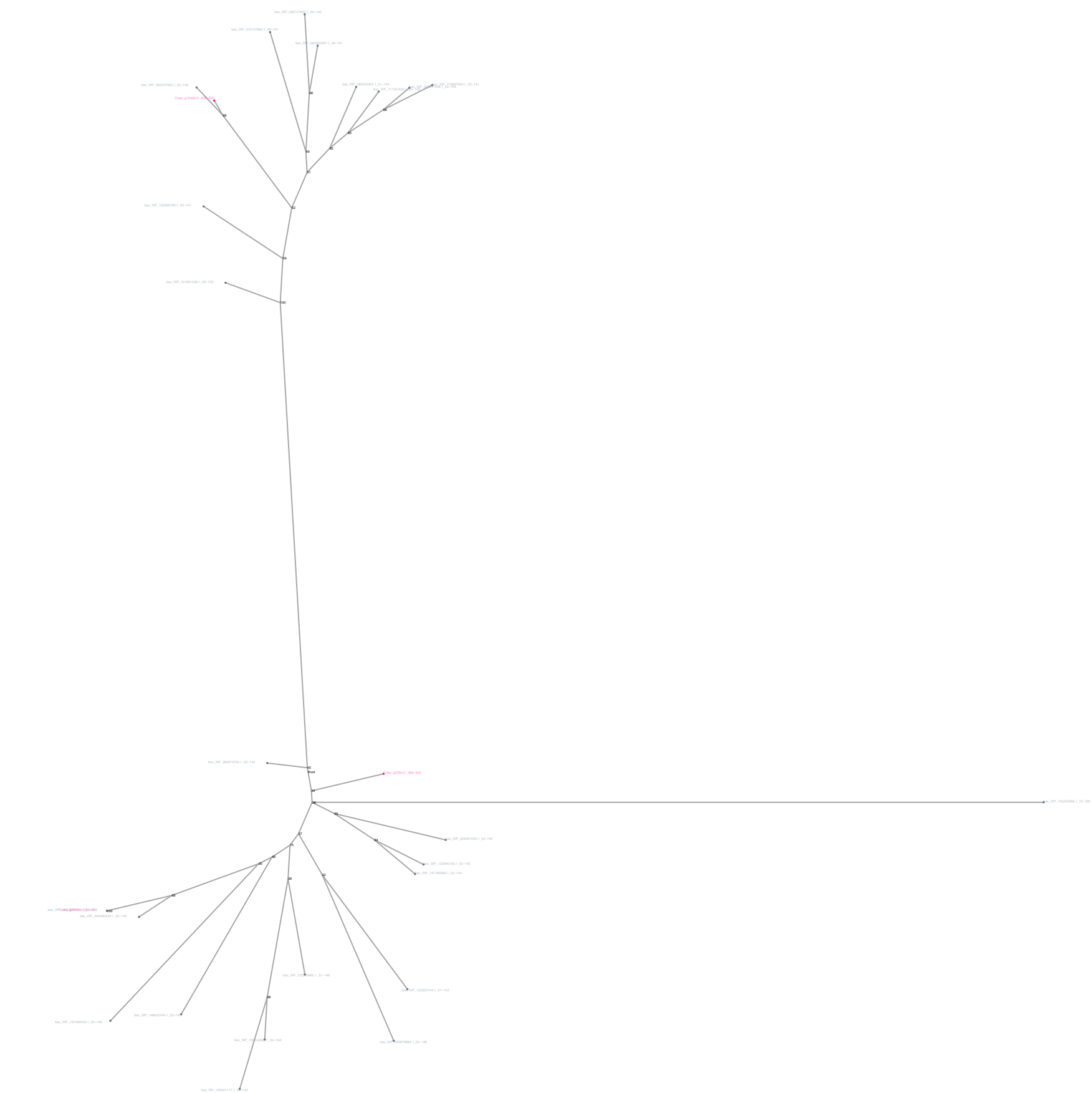
Acetyltransf_1
euk.Acetyltransf_1.phy.HG53.seqs.iqtree.treefile
n=27 sequences

eukaryotes
archaea
bacteria



other n = 3

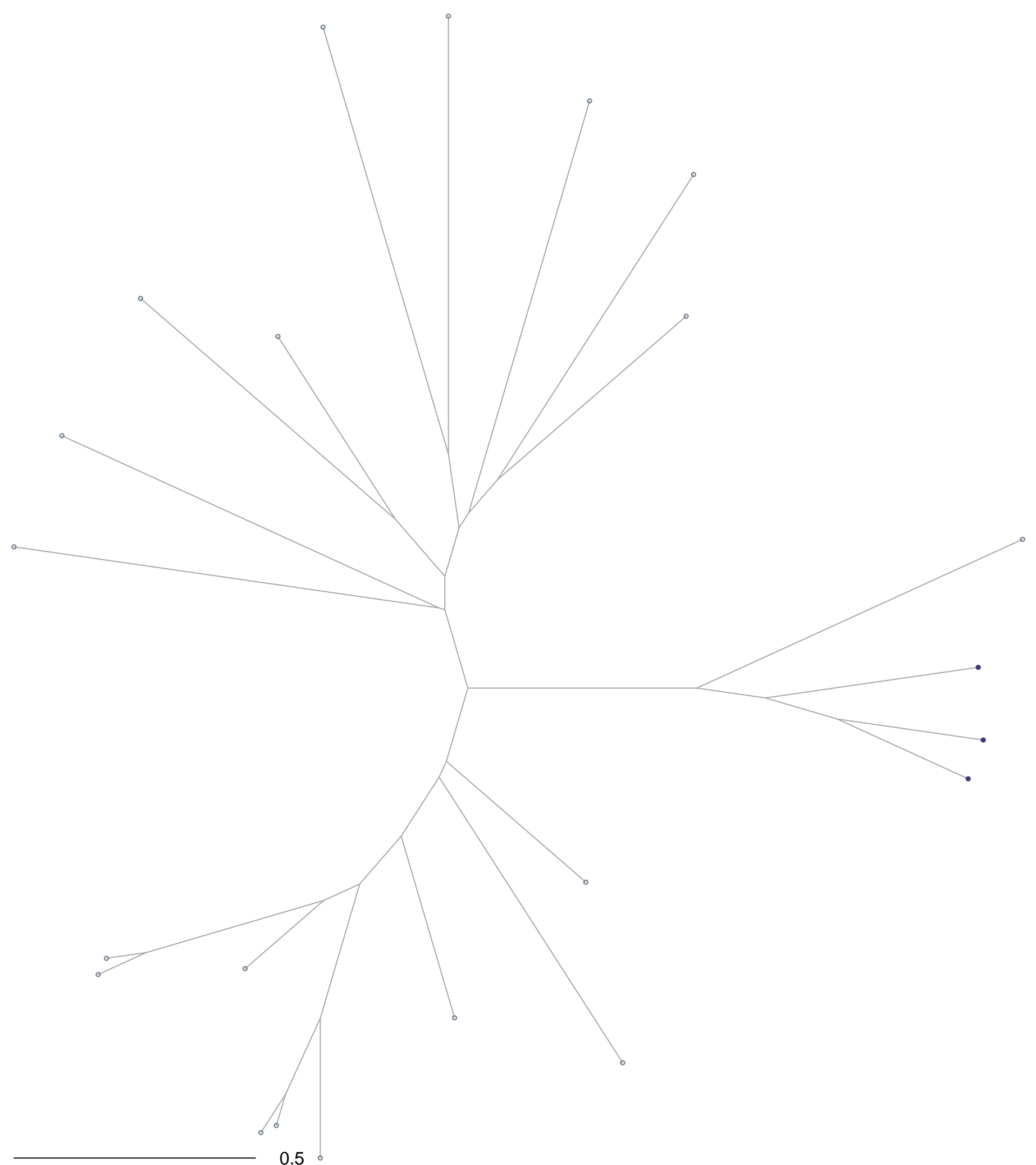
n =



0.5

Acetyltransf_1
euk.Acetyltransf_1.phy.HG54.seqs.iqtree.treefile
n=22 sequences

eukaryotes
archaea
bacteria



other n = 3

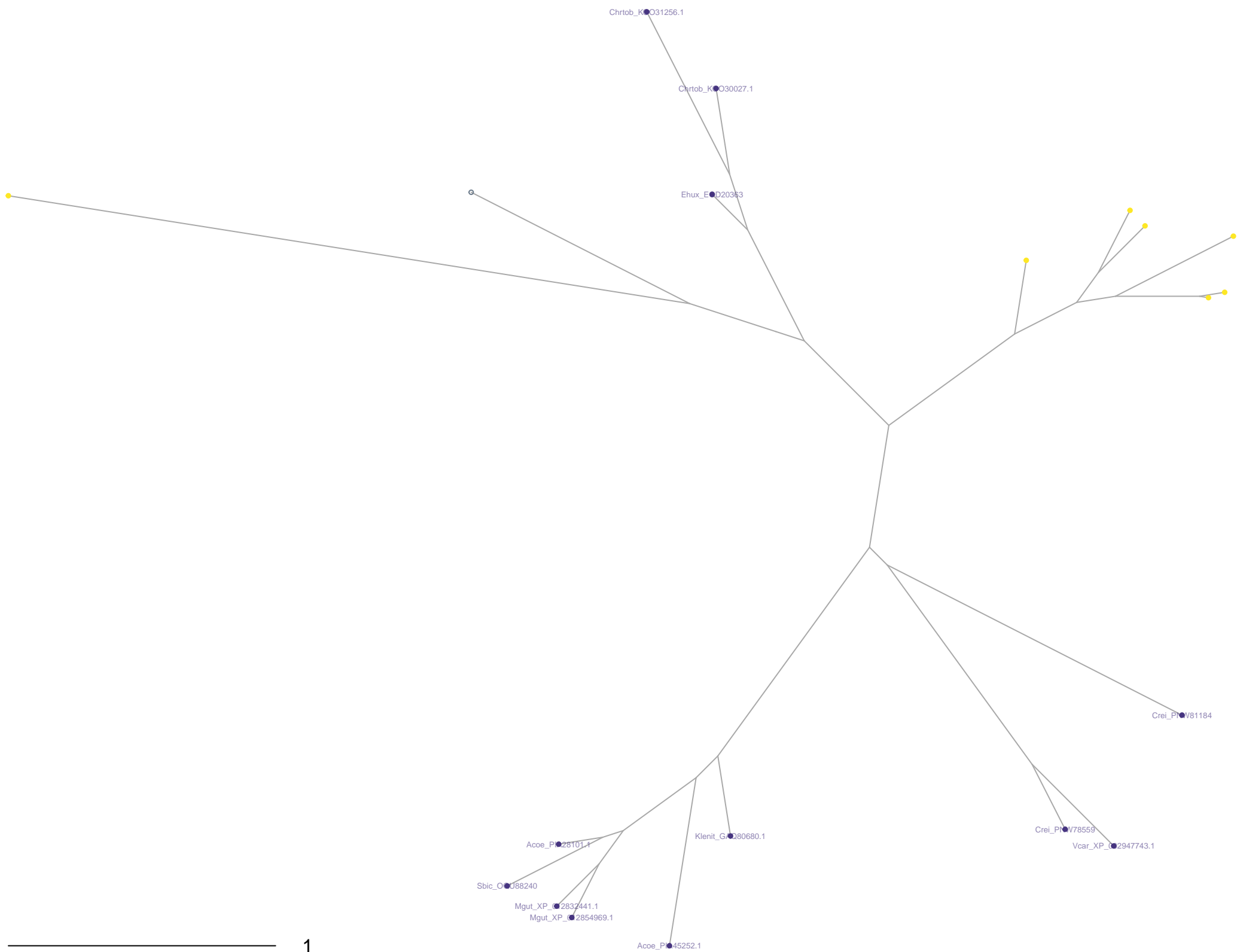
n =



0.5

Acetyltransf_1
euk.Acetyltransf_1.phy.HG55.seqs.iqtree.treefile
n=20 sequences

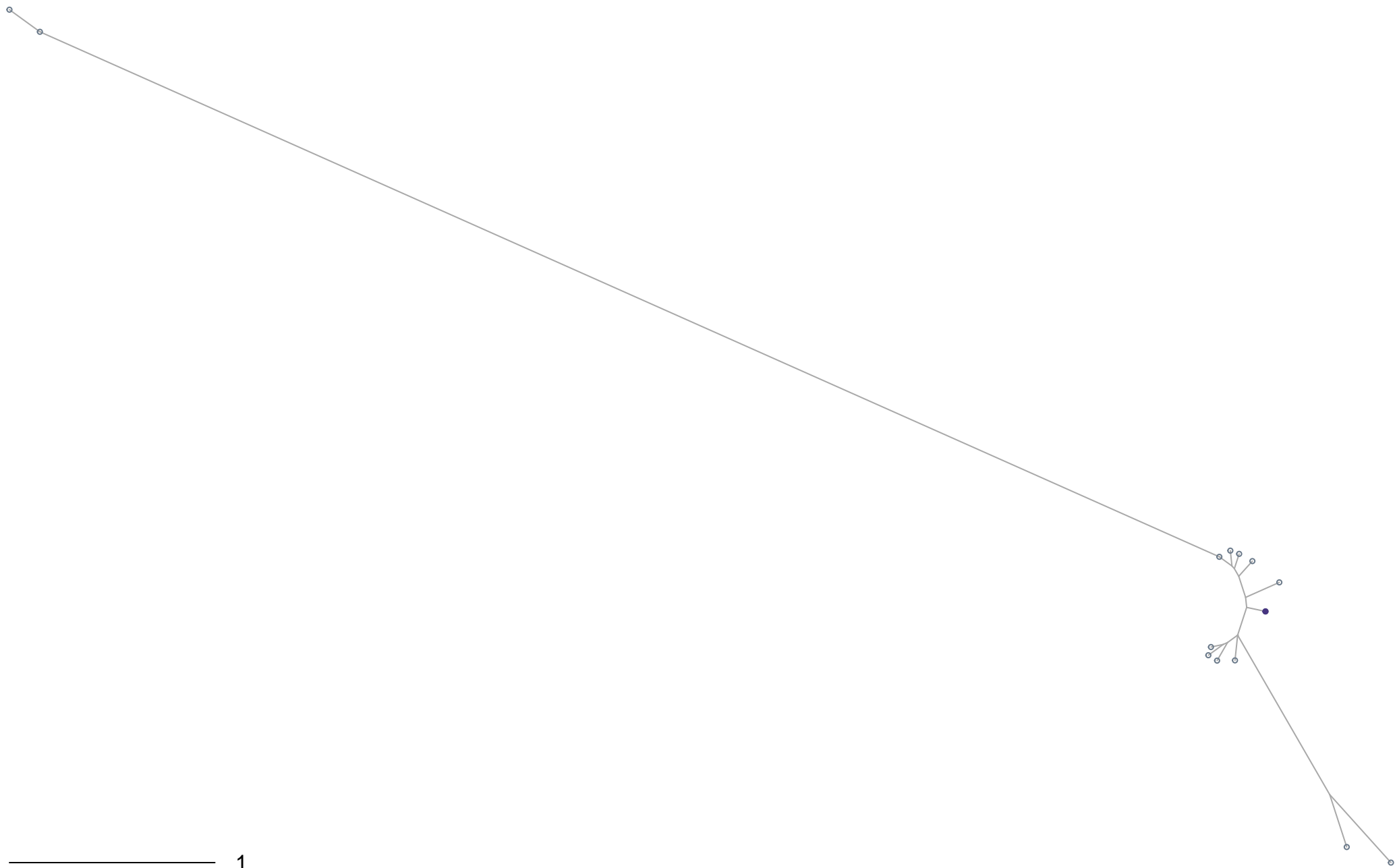
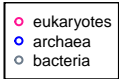
- eukaryotes
- archaea
- bacteria



1

Acetyltransf_1.HG24.1:NA n = 12
other n = 7

n =



Acetyltransf_1
euk.Acetyltransf_1.phy.HG58.seqs.iqtree.treefile
n=15 sequences

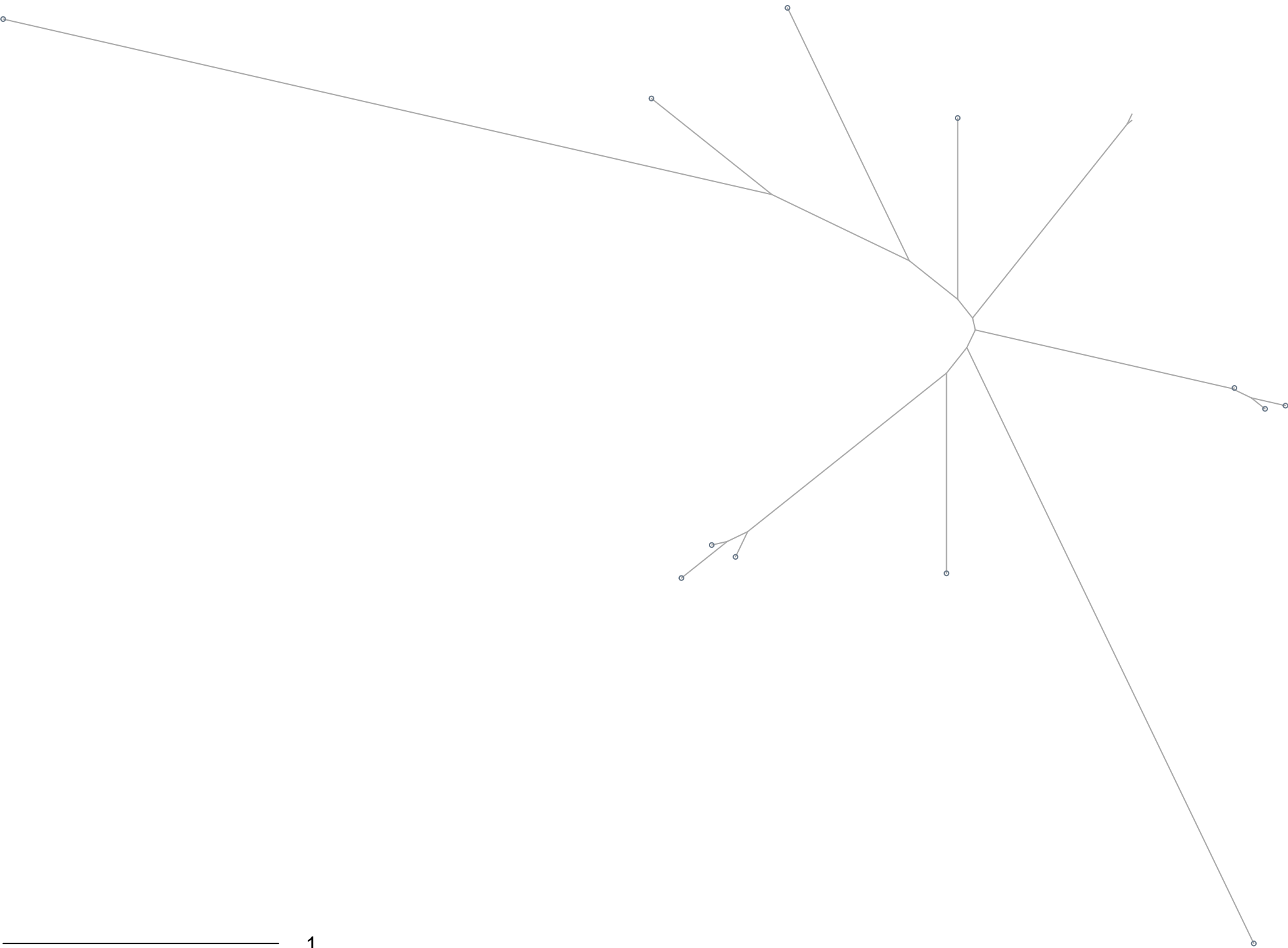
eukaryotes
archaea
bacteria



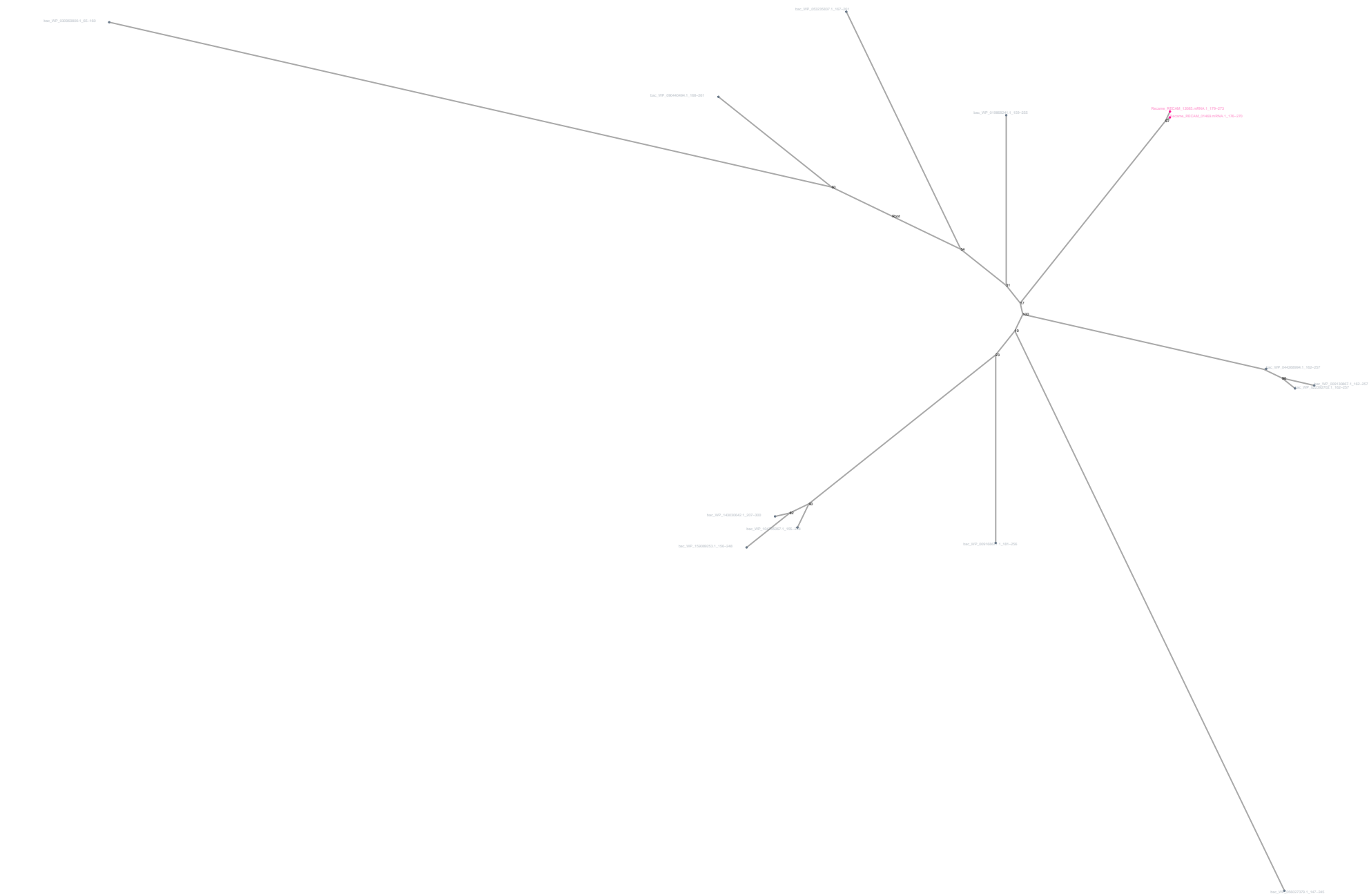
n =

Acetyltransf_1
euk.Acetyltransf_1.phy.HG59.seqs.iqtree.treefile
n=14 sequences

eukaryotes
archaea
bacteria

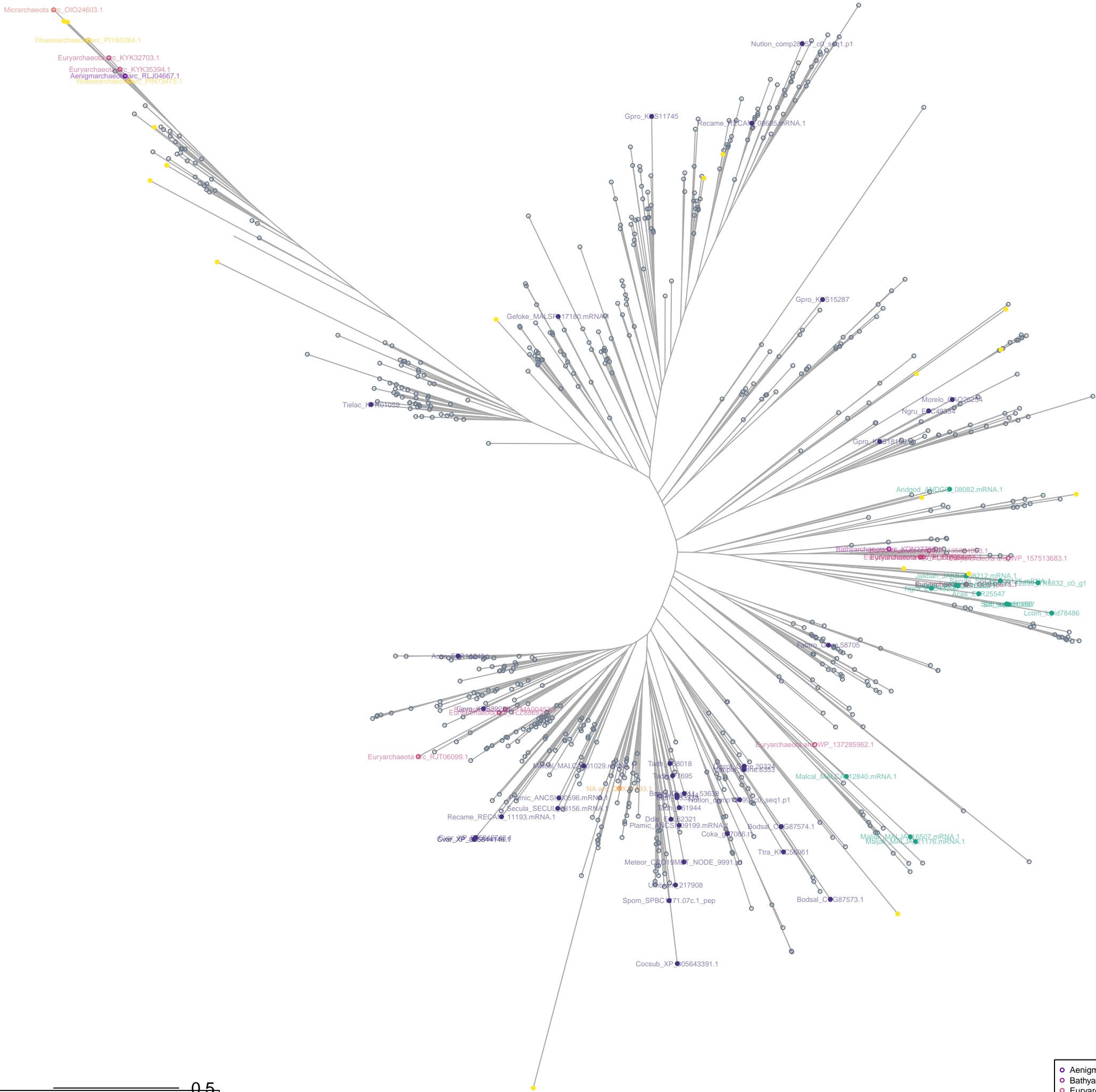


n =



euk.Acetyltransf_1.phy.HG6.seqs.iqtree.treefile
n=753 sequences

- eukaryotes
- archaea
- bacteria



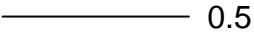
0.5

Acetyltransf_1.HG1.19:like:NAT8/NAT8L:likeclu:38 n = 38

Acetyltransf_1.HG1.38:NAT8/NAT8L n = 14

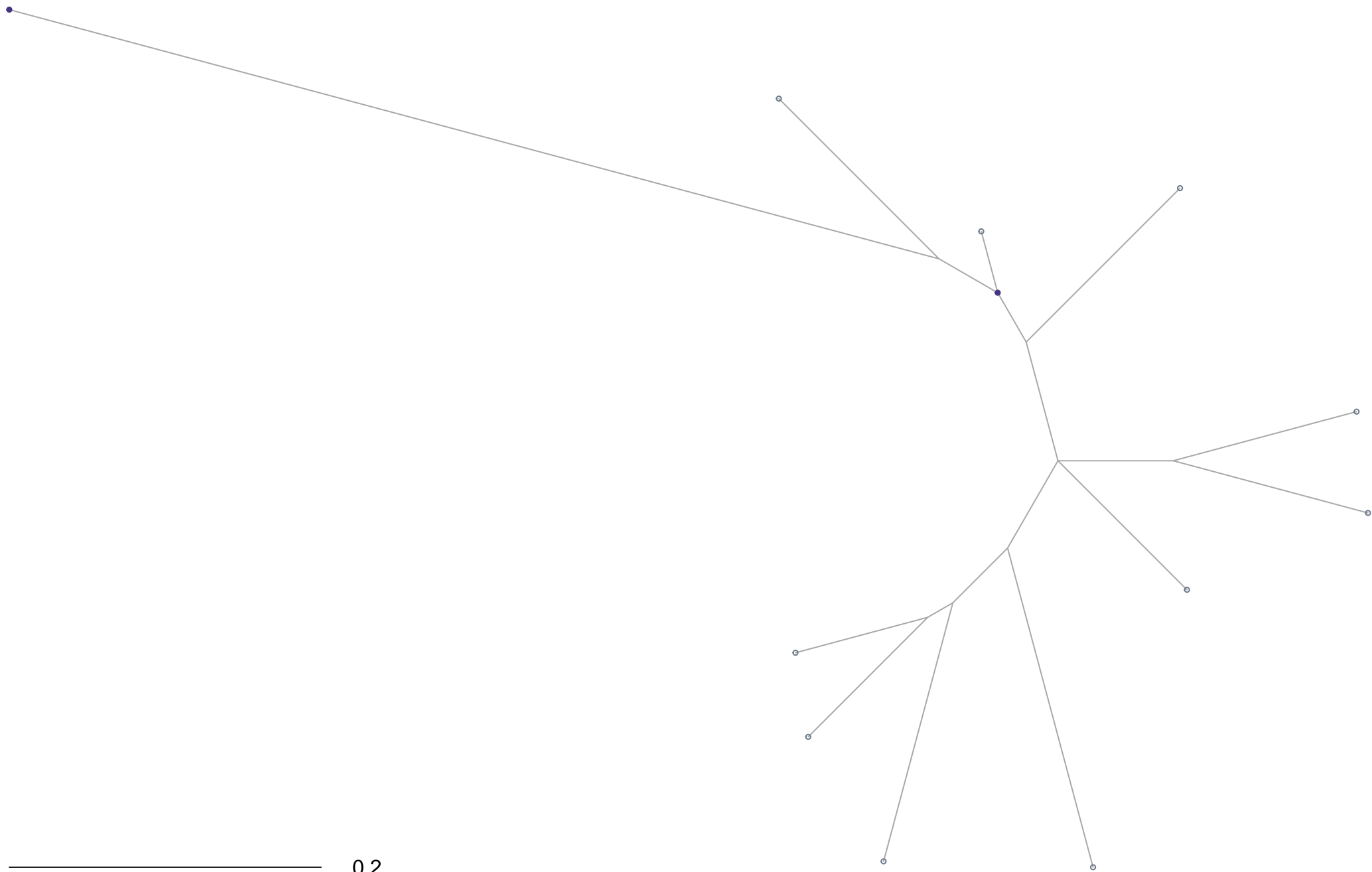
other n = 18

- Aenigmarchaeota n = 1
- Bathyarchaeota n = 1
- Euryarchaeota n = 13
- Micrarchaeota n = 1
- NA n = 1
- Woesearchaeota n = 2



Acetyltransf_1
euk.Acetyltransf_1.phy.HG60.seqs.iqtree.treefile
n=12 sequences

eukaryotes
archaea
bacteria

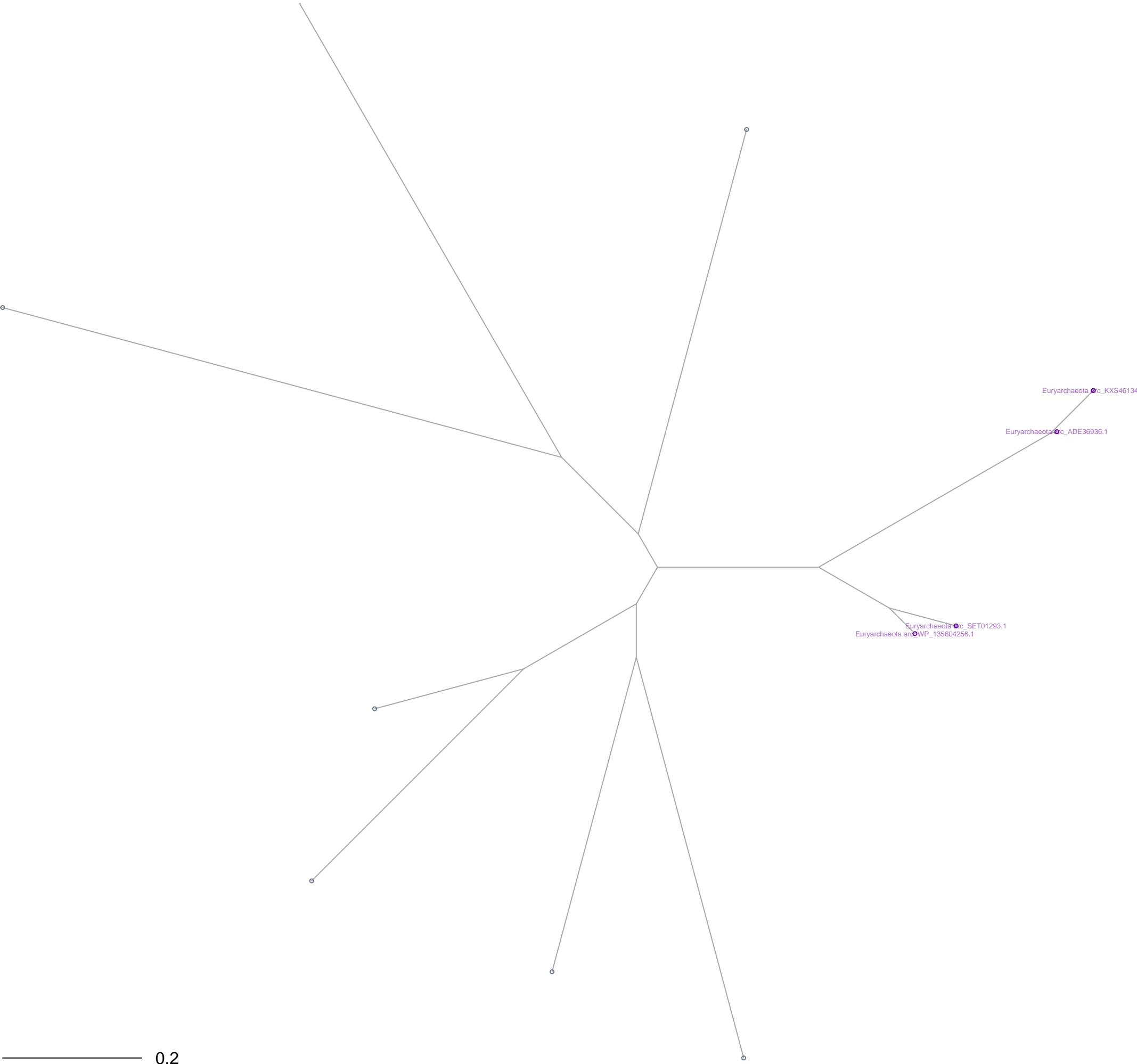


other n = 2

n =

Acetyltransf_1
euk.Acetyltransf_1.phy.HG61.seqs.iqtree.treefile
n=12 sequences

- eukaryotes
- archaea
- bacteria

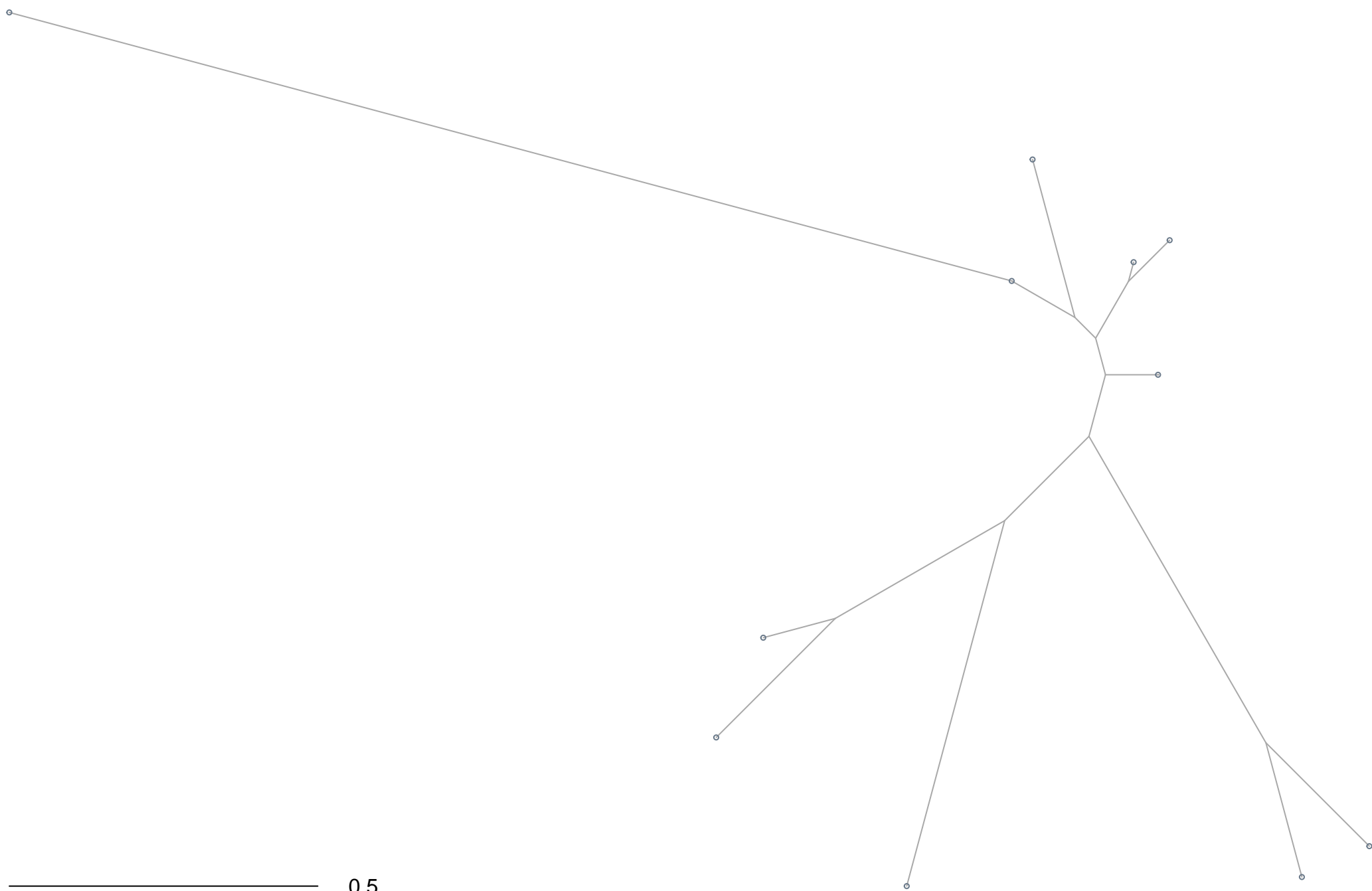


Euryarchaeota n = 4

0.2

Acetyltransf_1
euk.Acetyltransf_1.phy.HG62.seqs.iqtree.treefile
n=12 sequences

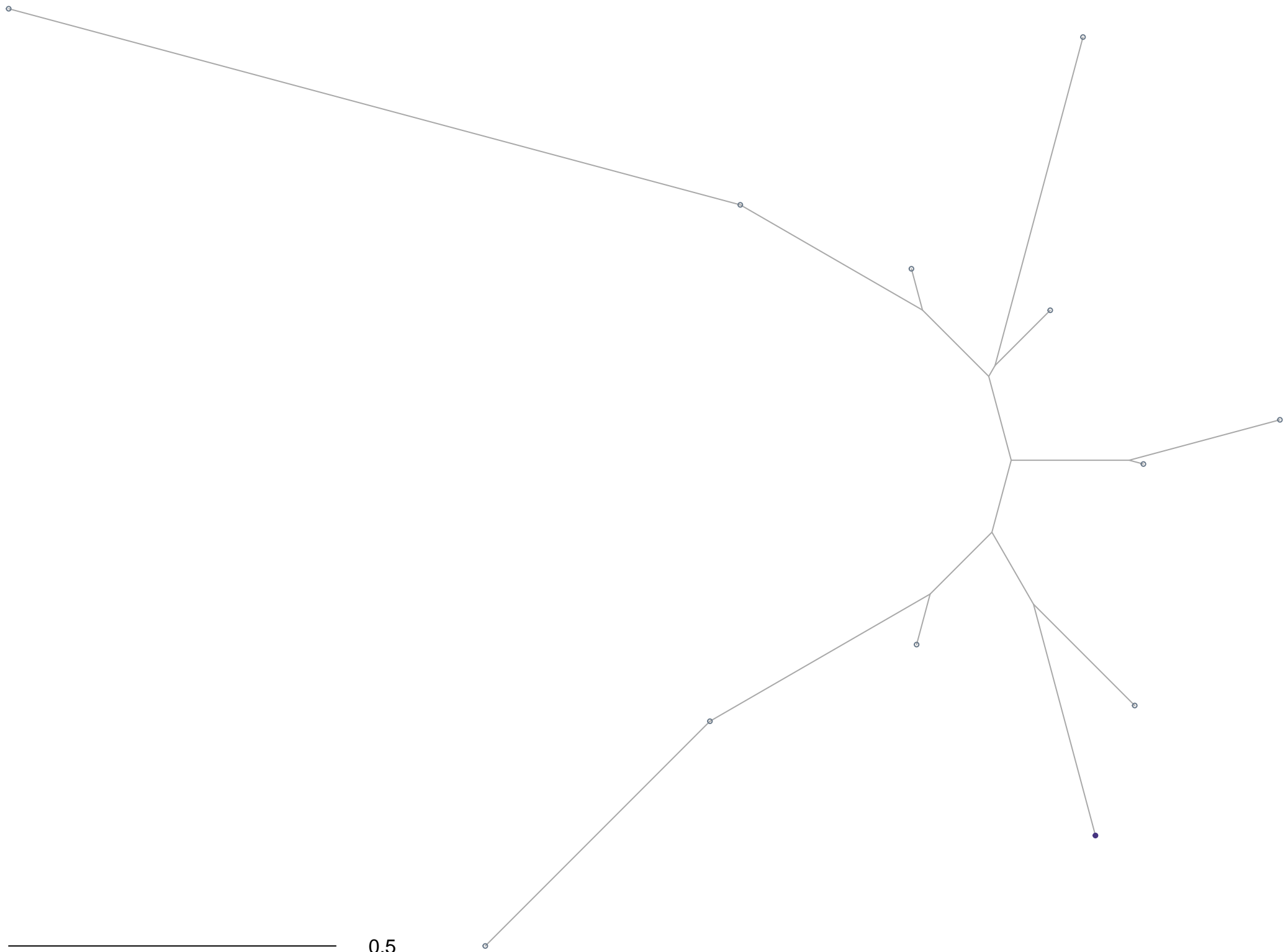
eukaryotes
archaea
bacteria



n =

Acetyltransf_1
euk.Acetyltransf_1.phy.HG63.seqs.iqtree.treefile
n=12 sequences

eukaryotes
archaea
bacteria

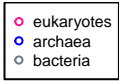


other n = 1

n =

0.5

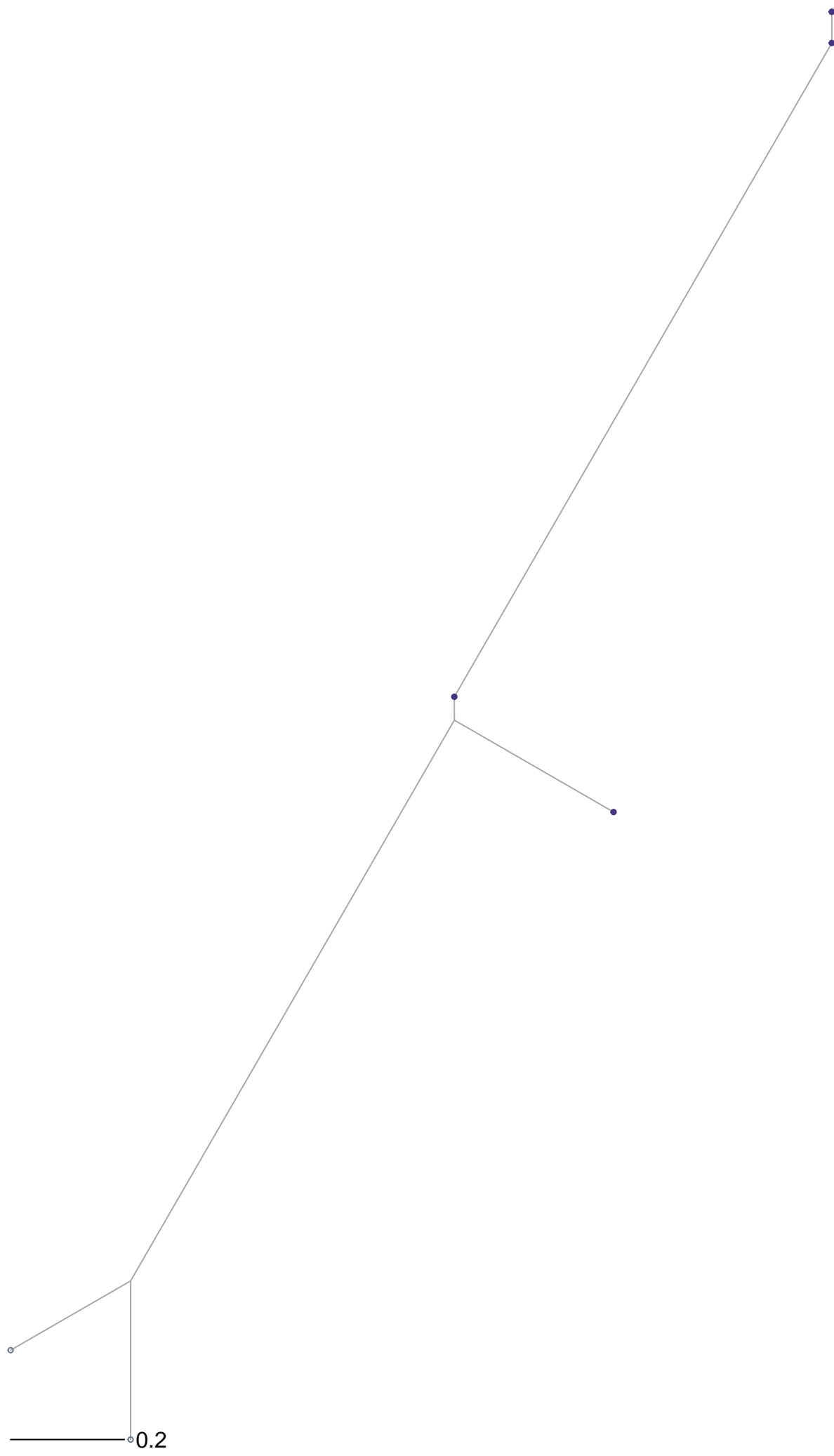
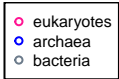
Acetyltransf_1
euk.Acetyltransf_1.phy.HG66.seqs.iqtree.treefile
n=6 sequences



other n = 5

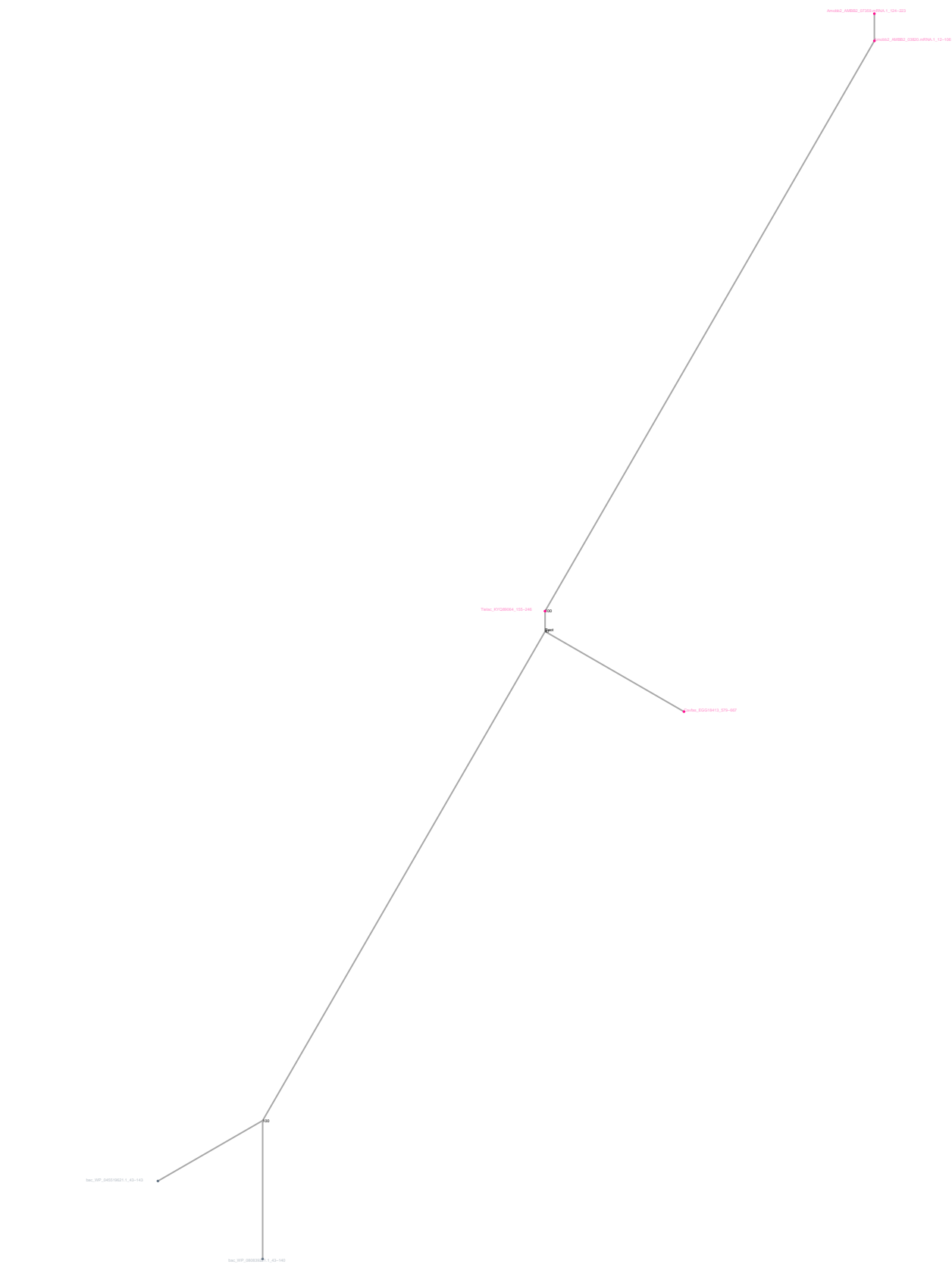
n =

Acetyltransf_1
euk.Acetyltransf_1.phy.HG68.seqs.iqtree.treefile
n=6 sequences



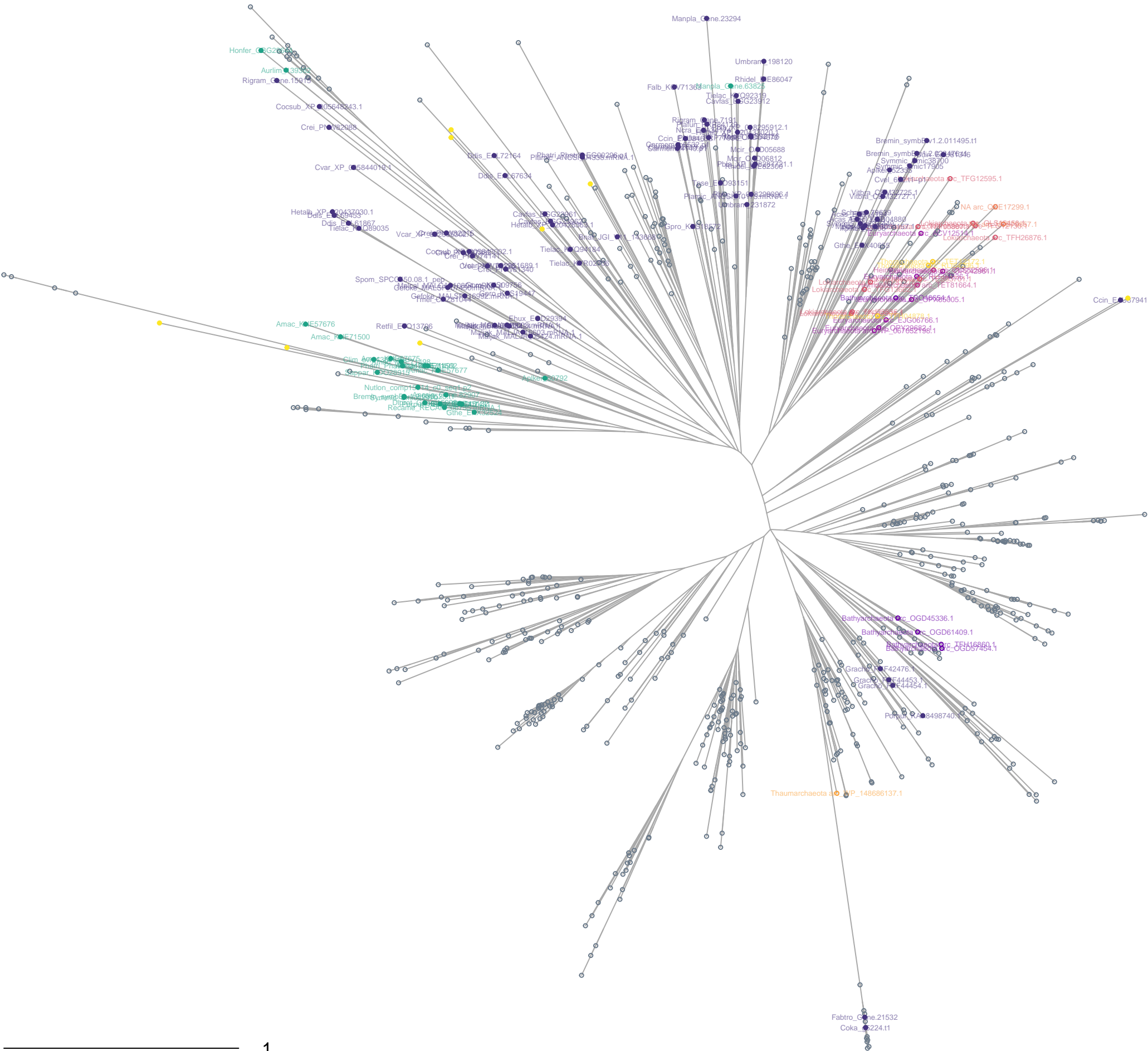
other n = 4

n =



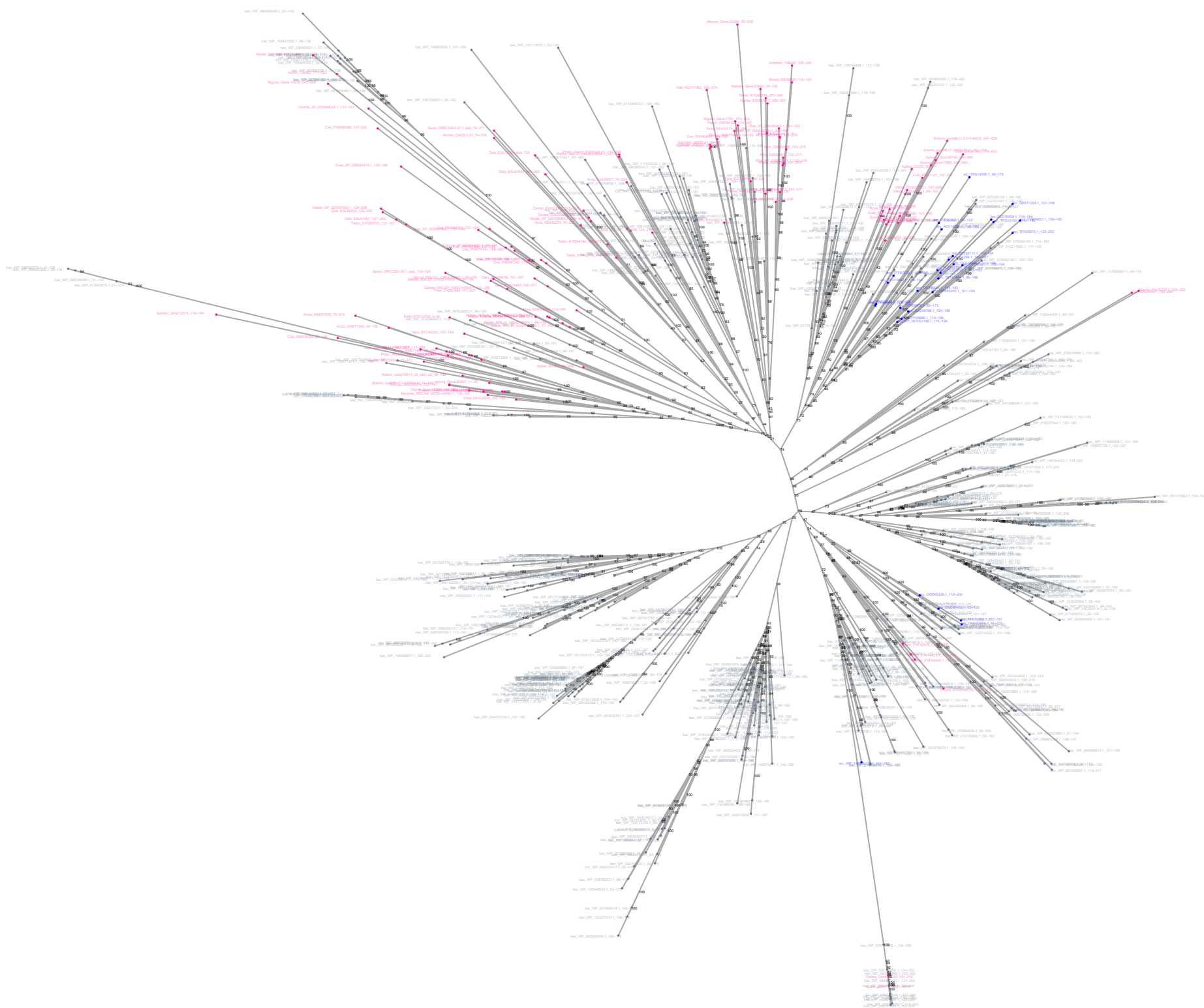
Acetyltransf_1
euk.Acetyltransf_1.phy.HG7.seqs.iqtree.treefile
n=753 sequences

- eukaryotes
- archaea
- bacteria



- Acetyltransf_1.HG12.2:NA n = 92
- Acetyltransf_1.HG12.1:NA n = 24
- other n = 8

- Bathyarchaeota n = 5
- Euryarchaeota n = 7
- Heimdallarchaeota n = 2
- Lokiarchaeota n = 10
- NA n = 2
- Thaumarchaeota n = 1
- Thorarchaeota n = 3



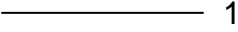
Acetyltransf_1.phy.HG8.seqs.iqtree.treefile
n=545 sequences

- eukaryotes
- archaea
- bacteria



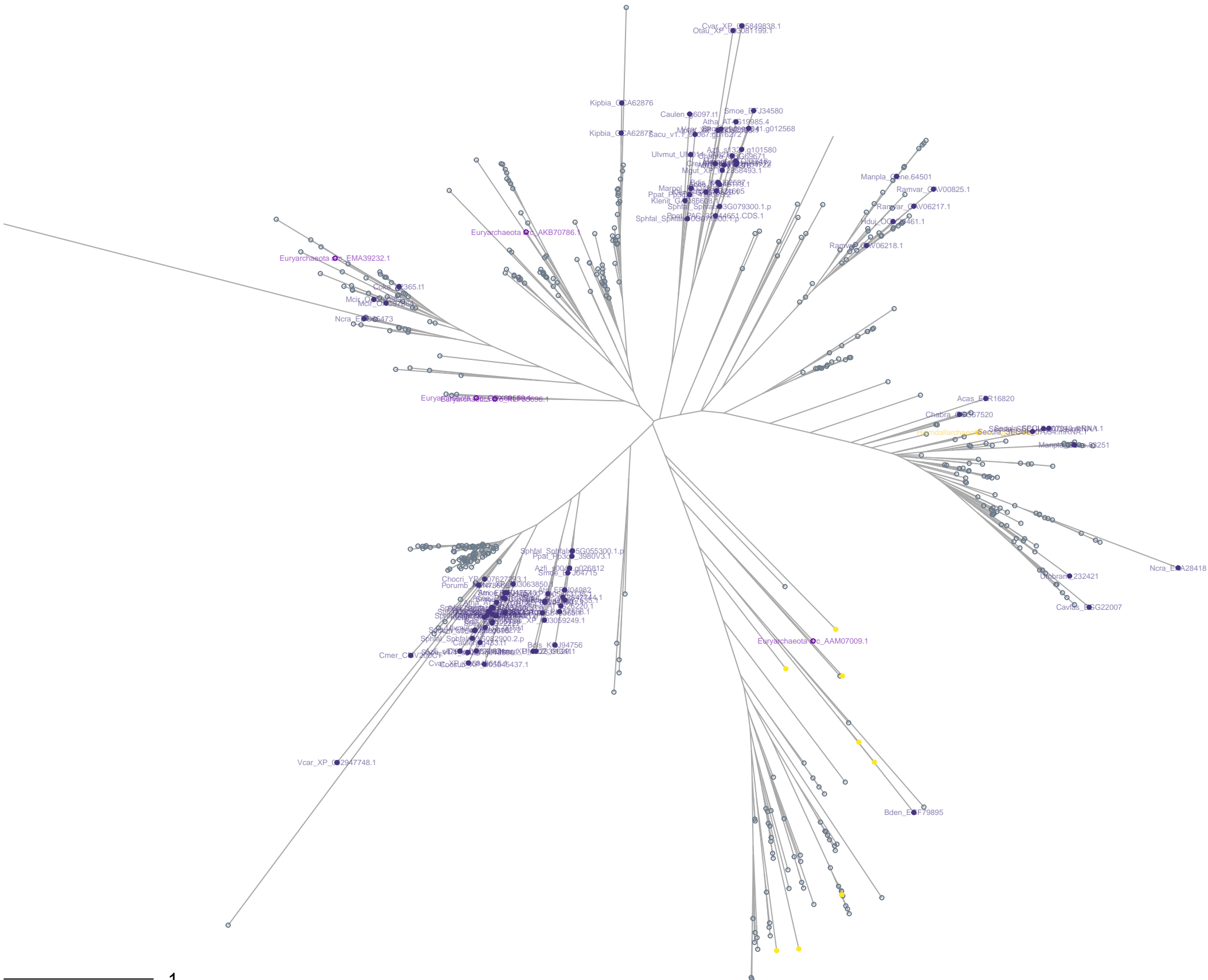
Acetyltransf_1.HG3.5:GNPNAT1 n = 176
other n = 30

Bathyarchaeota n = 1
Crenarchaeota n = 1
Euryarchaeota n = 6
NA n = 5
Thaumarchaeota n = 73



euk.Acetyltransf_1.phy.HG9.seqs.iqtree.treefile
n=537 sequences

- eukaryotes
- archaea
- bacteria



Acetyltransf_1.HG3.0:like:GNPNAT1/NAA80:likeclu:4/5 n = 100
other n = 8

Euryarchaeota n = 5
Heimdallarchaeota n = 1

