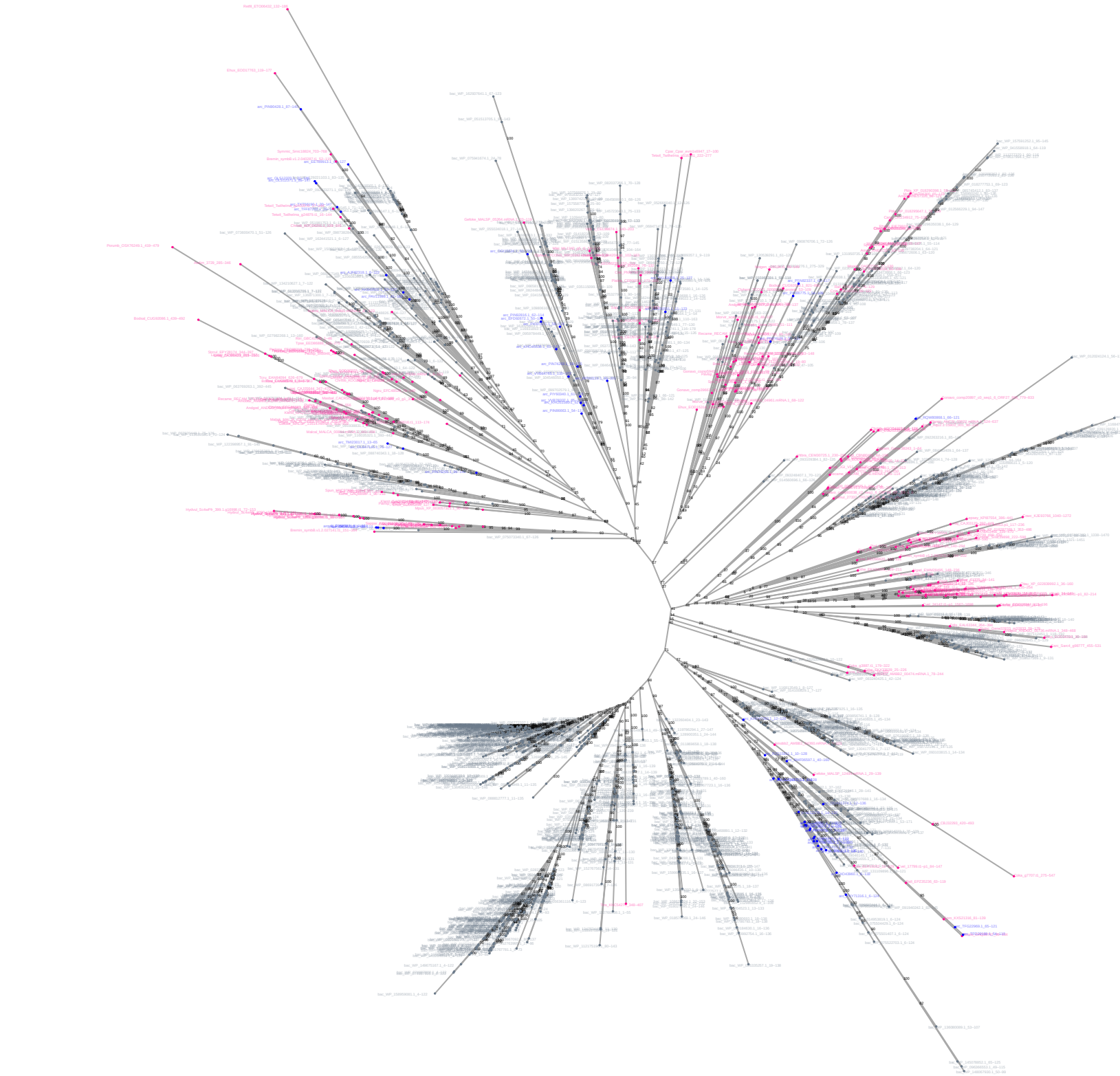
SET
euk.SET.phy.HG1.seqs.iqtree.treefile
n=1425 sequences

eukaryotes
archaea
bacteria

SET.HG3.20:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 80
SET.HG7.0:SETD7 n = 29
SET.HG3.19:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 19
SET.HG4.1:like:ASH1L/KMT2E/NSD1/NSD2/NSD3/SETD2/SETD5:likeclu:5/9/10/11 n = 19
other n = 82

0.5

Bathyarchaeota n = 2
Crenarchaeota n = 1
Diapherotrites n = 1
Euryarchaeota n = 5
Lokiarchaeota n = 6
Marsarchaeota n = 1
Micrarchaeota n = 2
NA n = 18
Parvarchaeota n = 2
Thaumarchaeota n = 1
Woesearchaeota n = 18



0.5

SET
euk.SET.phy.HG13.seqs.iqtree.treefile
n=11 sequences

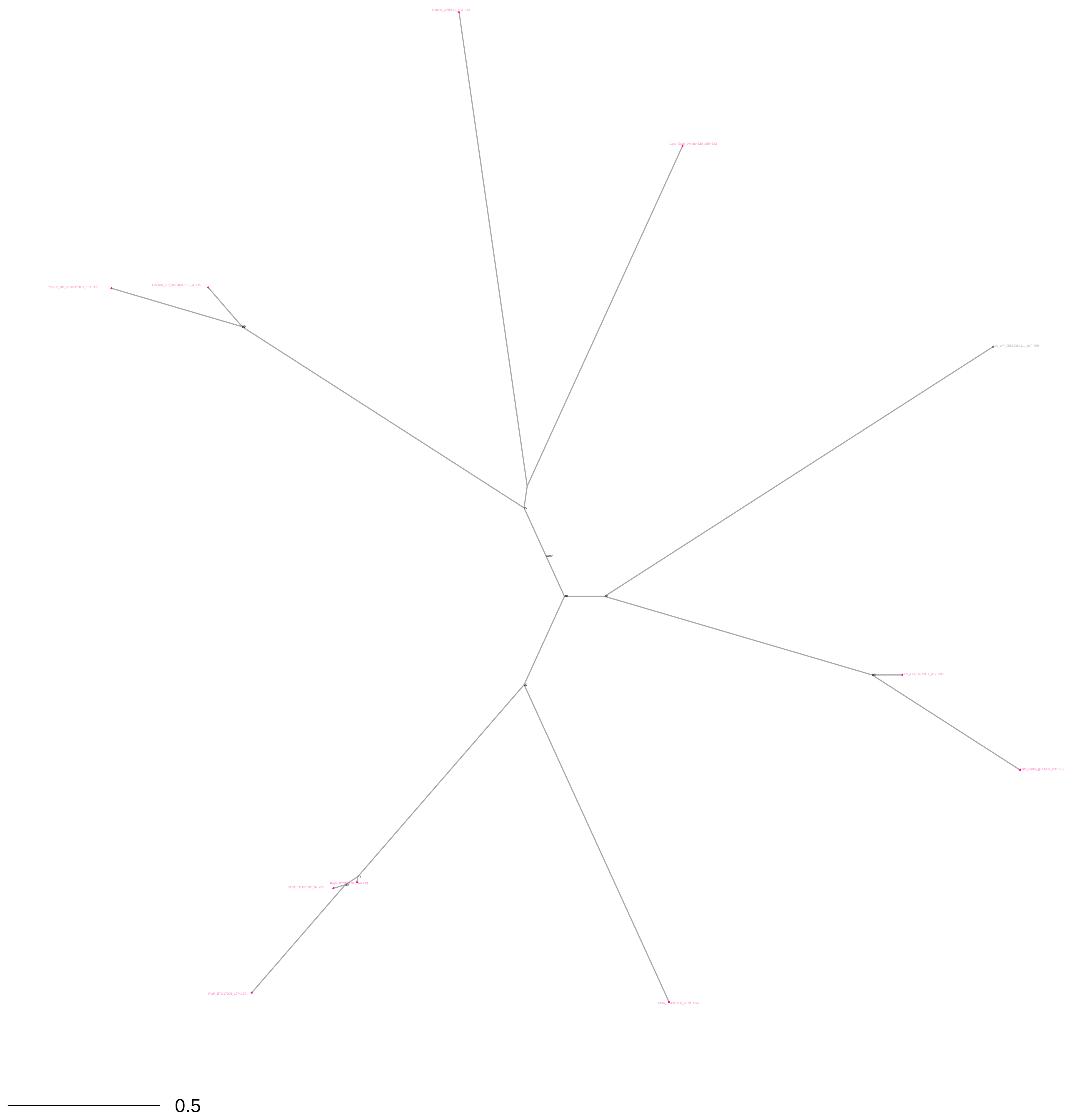
eukaryotes
archaea
bacteria

Caulen_12954.t1
Cpar_Cpar_evm1s4520
Cocsub_XP_005651532.1
Cocsub_XP_005646852.1
Cfra_CFRG6909T1
Sarc_Sarc_g11433T
Retfil_EOO06770
Retfil_EOO20332
Retfil_EOO17906
Aano_EAB07480

0.5

SET.HG11.0:NA n = 10
other n = 0

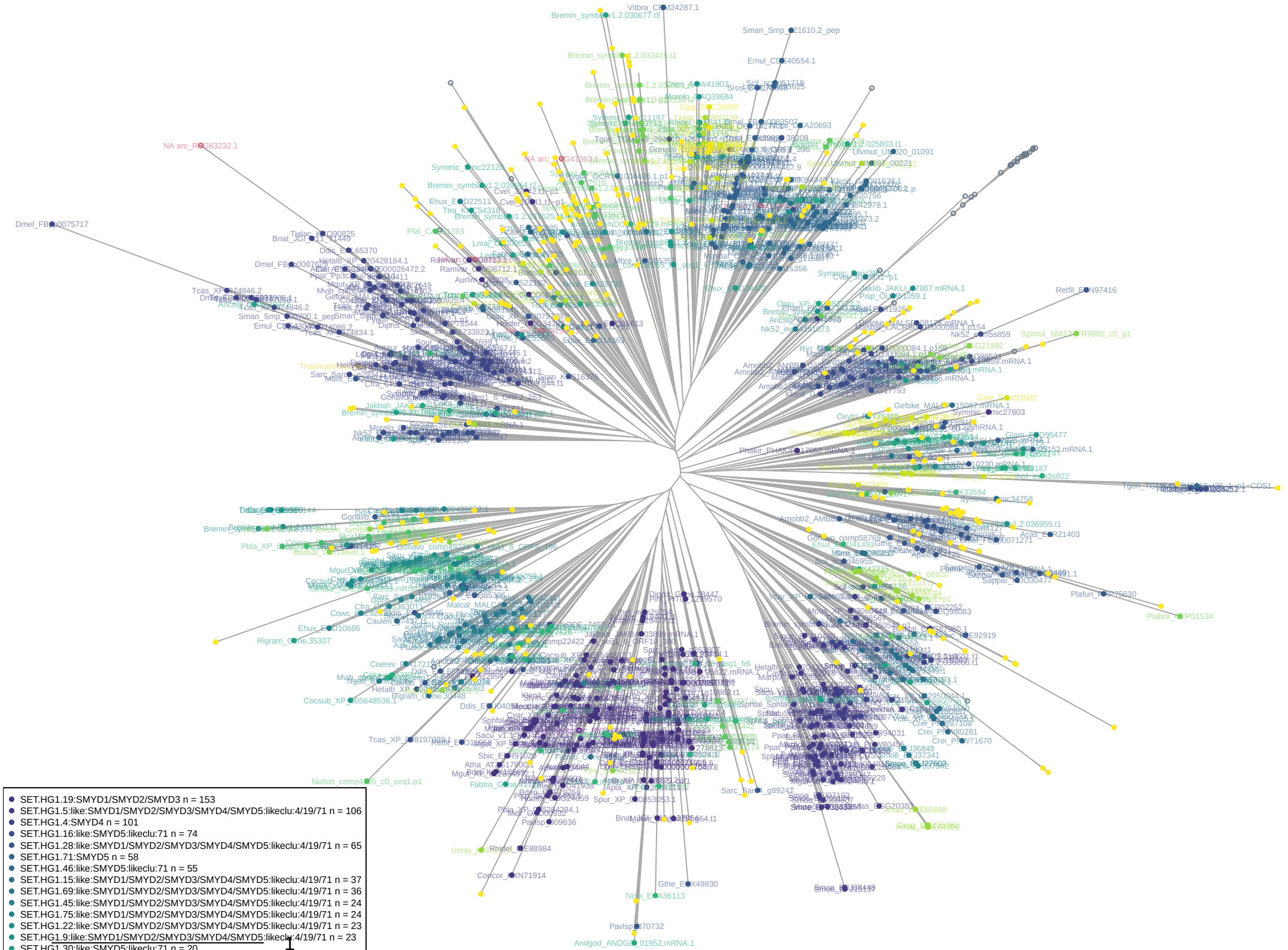
n =



Caulen_g2954.t1_103−278
Cpar_Cpar_evm1s4520_189−243
Cocsub_XP_005651532.1_151−303
Cocsub_XP_005646852.1_64−215
99
bac_WP_058533841.1_107−259
89
Cfra_CFRG6909T1_417−599
Sarc_Sarc4_g11433T_595−917
87
49
Retfil_ETO00332_96−285
Retfil_ETO17906_107−170
Root
0.5

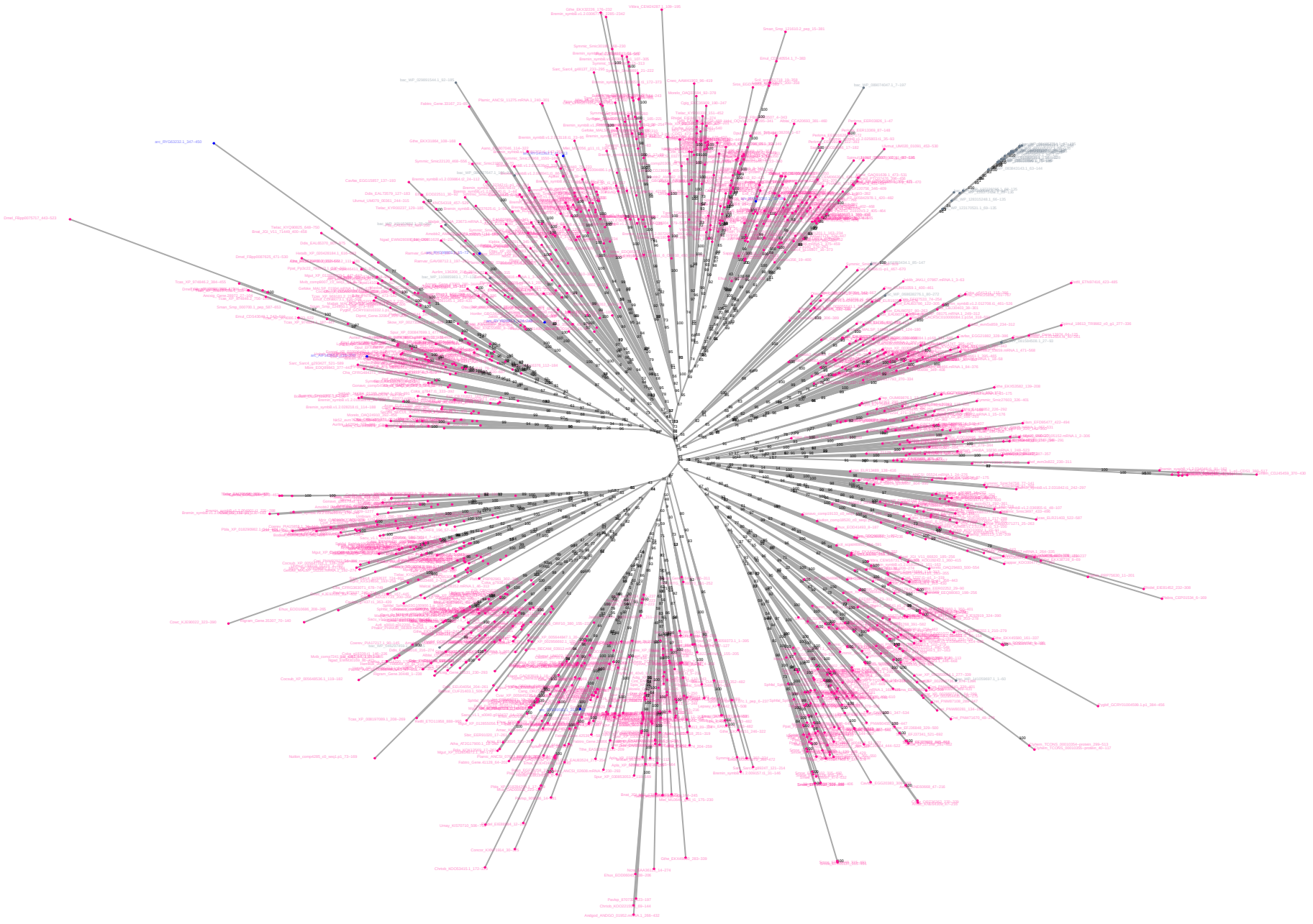
SET
euk.SET.phy.HG2.seqs.iqtree.treefile
n=1298 sequences

eukaryotes
archaea
bacteria



- SET.HG1.19:SMYD1/SMYD2/SMYD3 n = 153
- SET.HG1.5:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 106
- SET.HG1.4:SMYD4 n = 101
- SET.HG1.16:like:SMYD5:likeclu:71 n = 74
- SET.HG1.28:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 65
- SET.HG1.71:SMYD5 n = 58
- SET.HG1.46:like:SMYD5:likeclu:71 n = 55
- SET.HG1.15:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 37
- SET.HG1.69:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 36
- SET.HG1.45:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 24
- SET.HG1.75:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 24
- SET.HG1.22:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 23
- SET.HG1.9:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 23
- SET.HG1.30:like:SMYD5:likeclu:71 n = 20
- SET.HG1.50:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 20
- SET.HG1.2:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 17
- SET.HG1.61:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 17
- SET.HG1.18:like:SMYD1/SMYD2/SMYD3:likeclu:19 n = 15
- SET.HG1.66:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 15
- SET.HG1.58:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 14
- SET.HG1.26:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 13
- SET.HG1.38:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 13
- SET.HG1.44:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 13
- SET.HG1.14:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 12
- SET.HG1.36:like:SMYD5:likeclu:71 n = 11
- SET.HG1.53:like:SMYD5:likeclu:71 n = 11
- SET.HG1.8:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 11
- SET.HG1.70:like:SMYD5:likeclu:71 n = 10
- other n = 262

- Euryarchaeota n = 1
- NA n = 5
- Thaumarchaeota n = 1



1

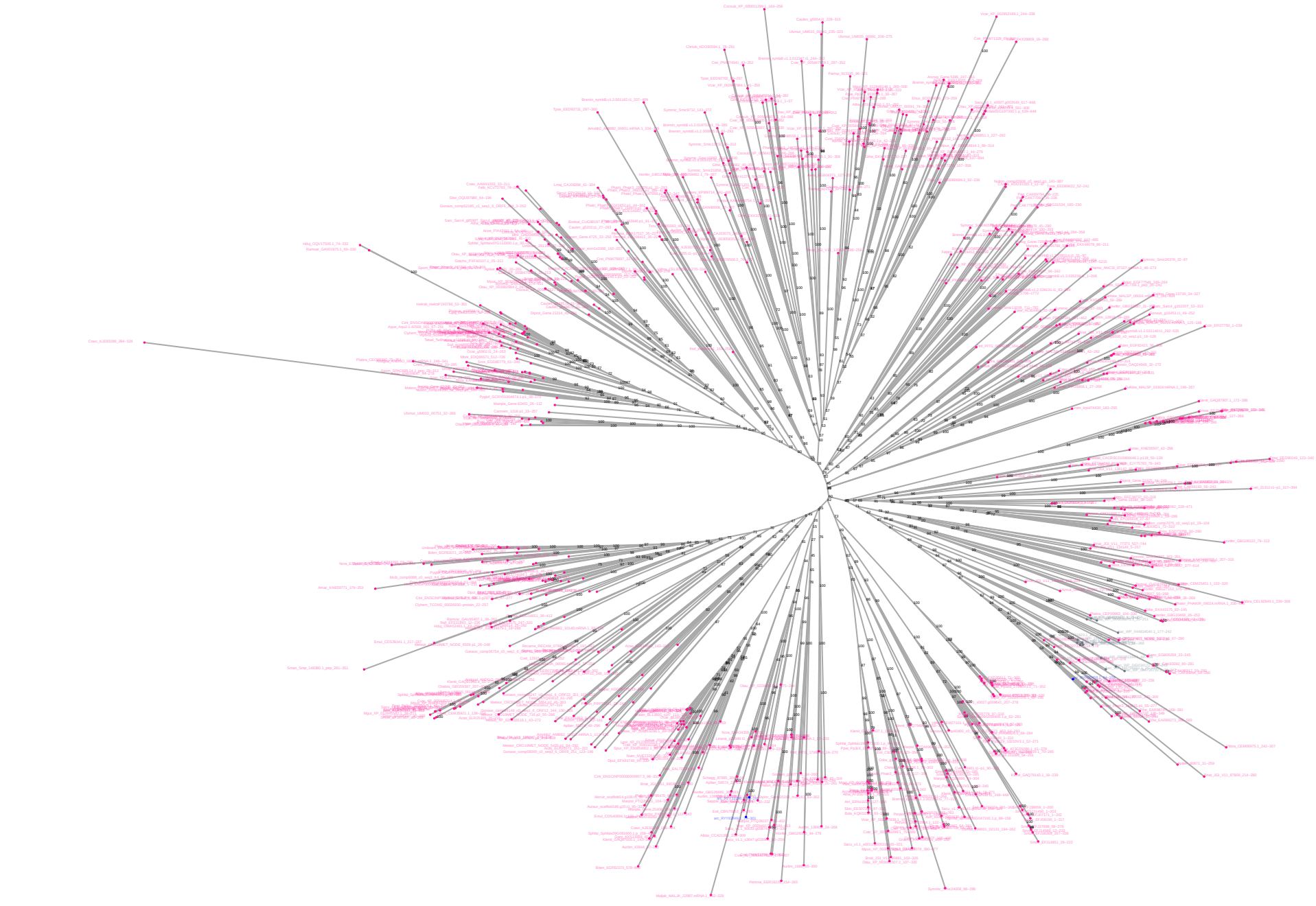
SET
euk.SET.phy.HG3.seqs.iqtree.treefile
n=723 sequences

eukaryotes
archaea
bacteria

SET.HG2.19:like:SETD3/SETD4:likeclu:16/17 n = 101
SET.HG2.17:SETD4 n = 81
SET.HG2.8:SETD6 n = 51
SET.HG2.16:SETD3 n = 41
SET.HG2.7:like:SETD6:likeclu:8 n = 36
SET.HG2.10:like:SETD3/SETD4:likeclu:16/17 n = 33
SET.HG2.31:like:SETD3/SETD4:likeclu:16/17 n = 23
SET.HG2.4:like:SETD6:likeclu:8 n = 23
SET.HG2.42:like:SETD3/SETD4:likeclu:16/17 n = 23
SET.HG2.5:like:SETD3/SETD4:likeclu:16/17 n = 21
SET.HG2.18:like:SETD3/SETD4:likeclu:16/17 n = 18
SET.HG2.24:like:SETD3/SETD4:likeclu:16/17 n = 18
SET.HG2.41:like:SETD3/SETD4:likeclu:16/17 n = 18
SET.HG2.3:like:SETD3/SETD4:likeclu:16/17 n = 16
SET.HG2.9:like:SETD3/SETD4:likeclu:16/17 n = 16
SET.HG2.26:like:SETD3/SETD4:likeclu:16/17 n = 15
SET.HG2.12:like:SETD3/SETD4:likeclu:16/17 n = 14
SET.HG2.35:like:SETD3/SETD4:likeclu:16/17 n = 14
SET.HG2.34:like:SETD3/SETD4:likeclu:16/17 n = 12
SET.HG2.39:like:SETD3/SETD4:likeclu:16/17 n = 10
other n = 121

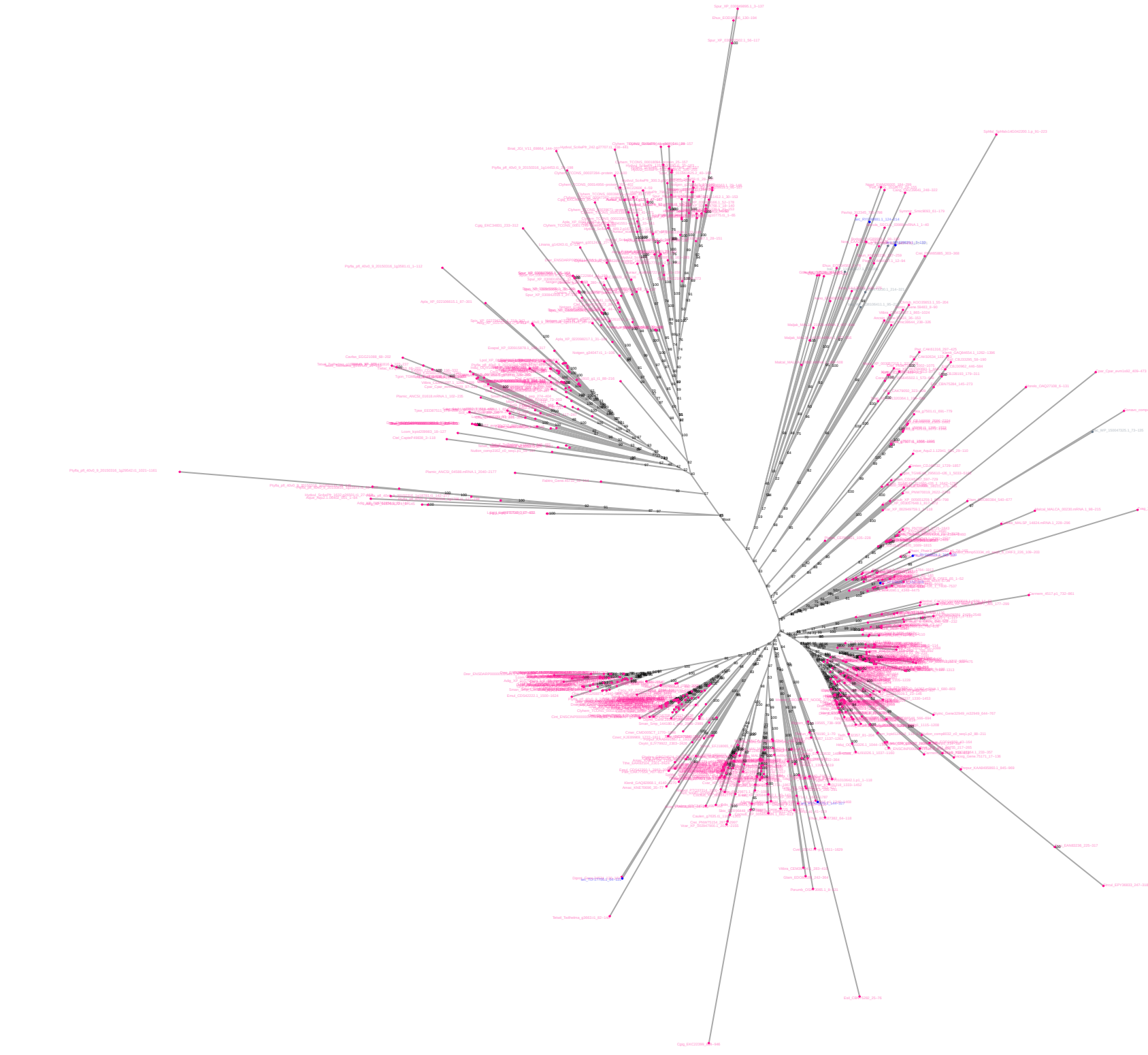
1

NA n = 3



1

SET
euk.SET.phy.HG4.seqs.iqtree.treefile
n=656 sequences



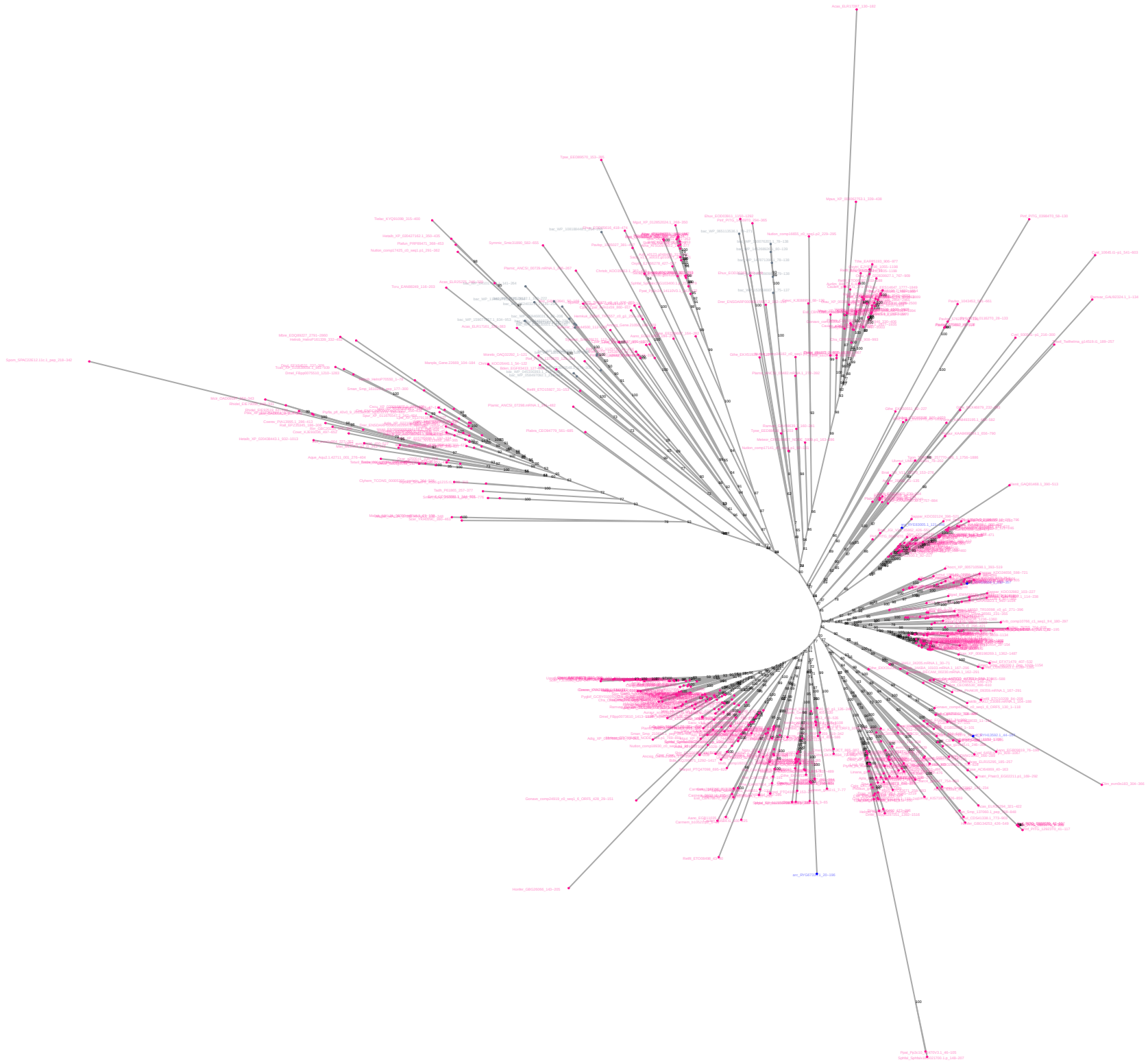
1

SET
euk.SET.phy.HG5.seqs.iqtree.treefile
n=609 sequences

eukaryotes
archaea
bacteria

SET.HG4.11:SETD2 n = 164
SET.HG4.9:NSD1/NSD2/NSD3 n = 133
SET.HG4.5:KMT2E/SETD5 n = 70
SET.HG4.10:ASH1L n = 50
SET.HG4.3:like:KMT2E/SETD5:likeclu:5 n = 45
SET.HG4.7:like:ASH1L/NSD1/NSD2/NSD3/SETD2:likeclu:9/10/11 n = 27
SET.HG4.6:like:ASH1L/NSD1/NSD2/NSD3/SETD2:likeclu:9/10/11 n = 18
SET.HG4.8:like:NSD1/NSD2/NSD3:likeclu:9 n = 15
SET.HG4.1:like:ASH1L/KMT2E/NSD1/NSD2/NSD3/SETD2/SETD5:likeclu:5/9/10/11 n = 12
other n = 48

Euryarchaeota n = 1
NA n = 3

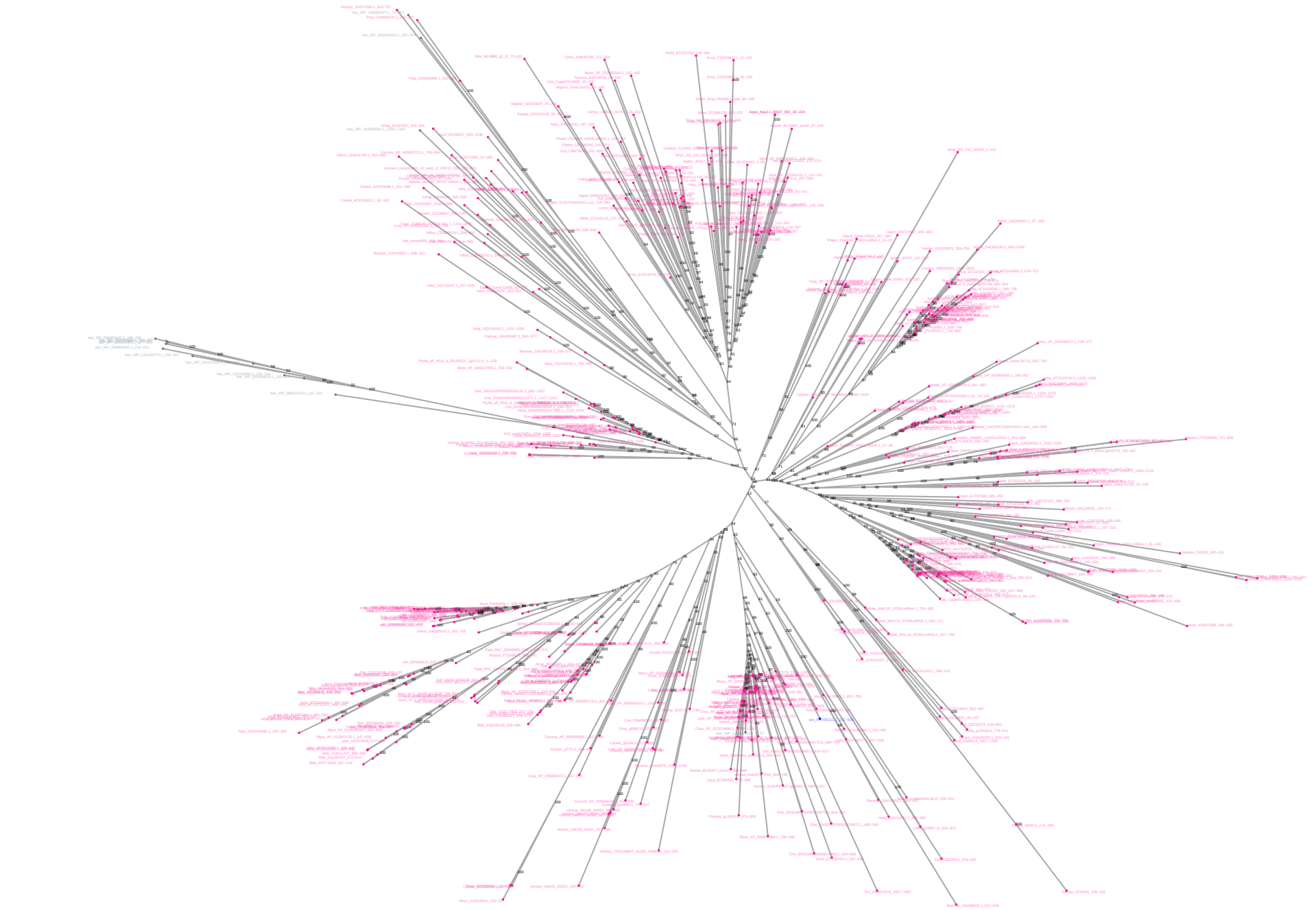


1

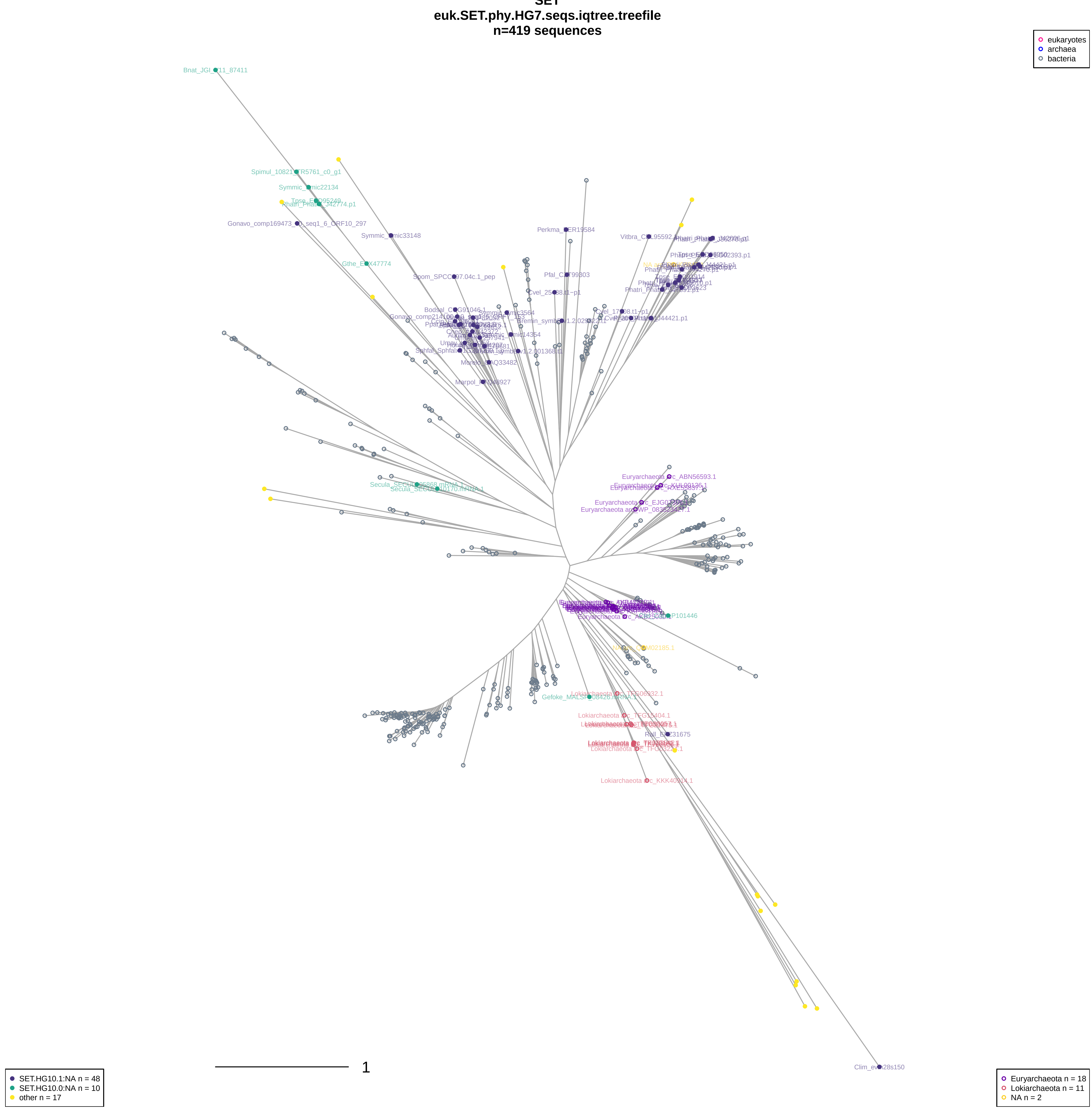
SET
euk.SET.phy.HG6.seqs.iqtree.treefile
n=570 sequences

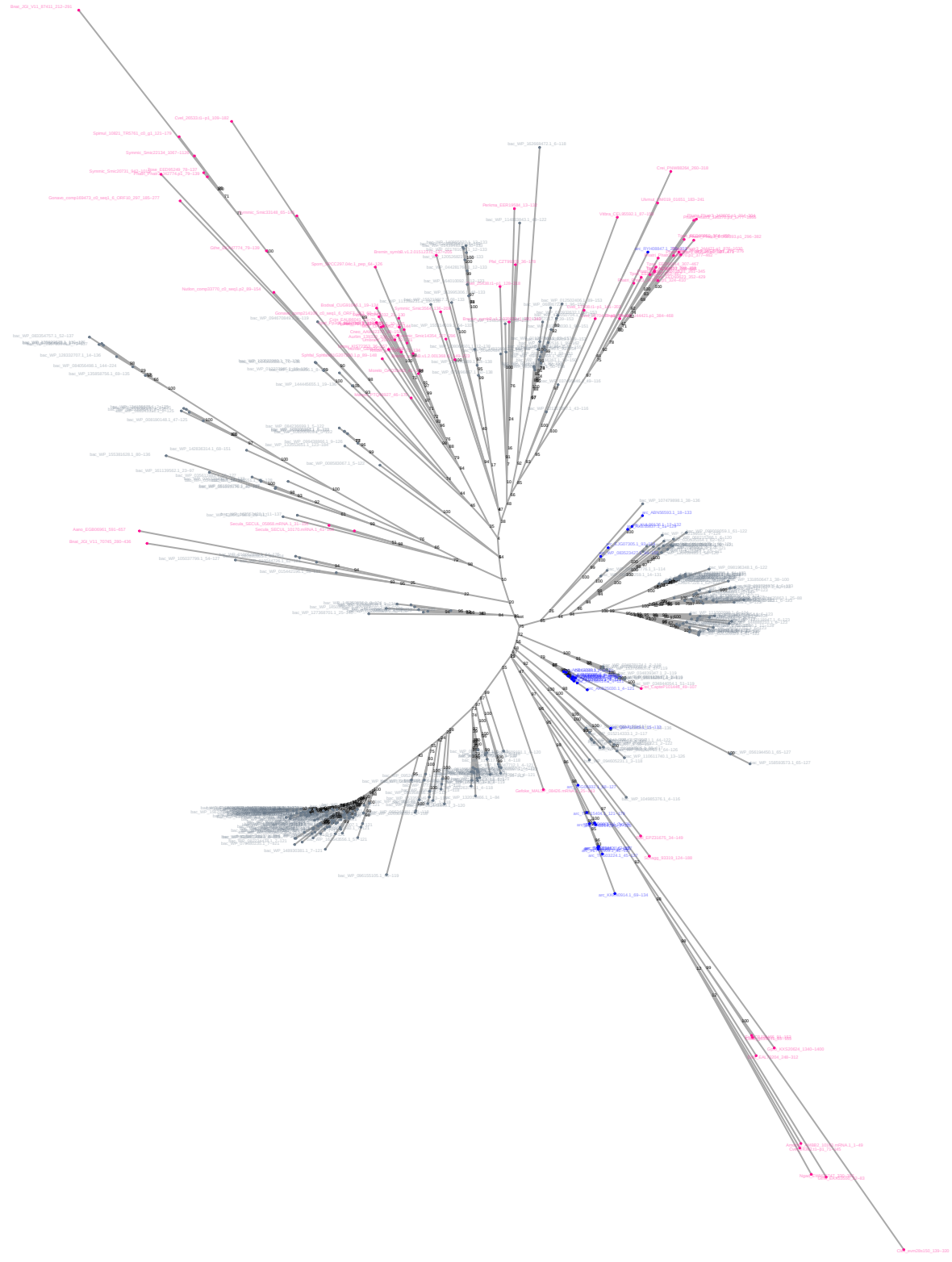
SET.HG5.7:SETDB1/SETDB2 n = 200
SET.HG5.1:SUV39H1/SUV39H2 n = 106
SET.HG5.6:EHMT1/EHMT2 n = 99
SET.HG5.3:SETMAR n = 88
SET.HG5.2like:SETMAR:likeclu:3 n = 15
SET.HG5.4:like:EHMT1/EHMT2/SETDB1/SETDB2/SUV39H1/SUV39H2:likeclu:1/6/7 n = 14
SET.HG5.5:like:EHMT1/EHMT2/SETDB1/SETDB2/SUV39H1/SUV39H2:likeclu:1/6/7 n = 11
other n = 21

NA n = 1



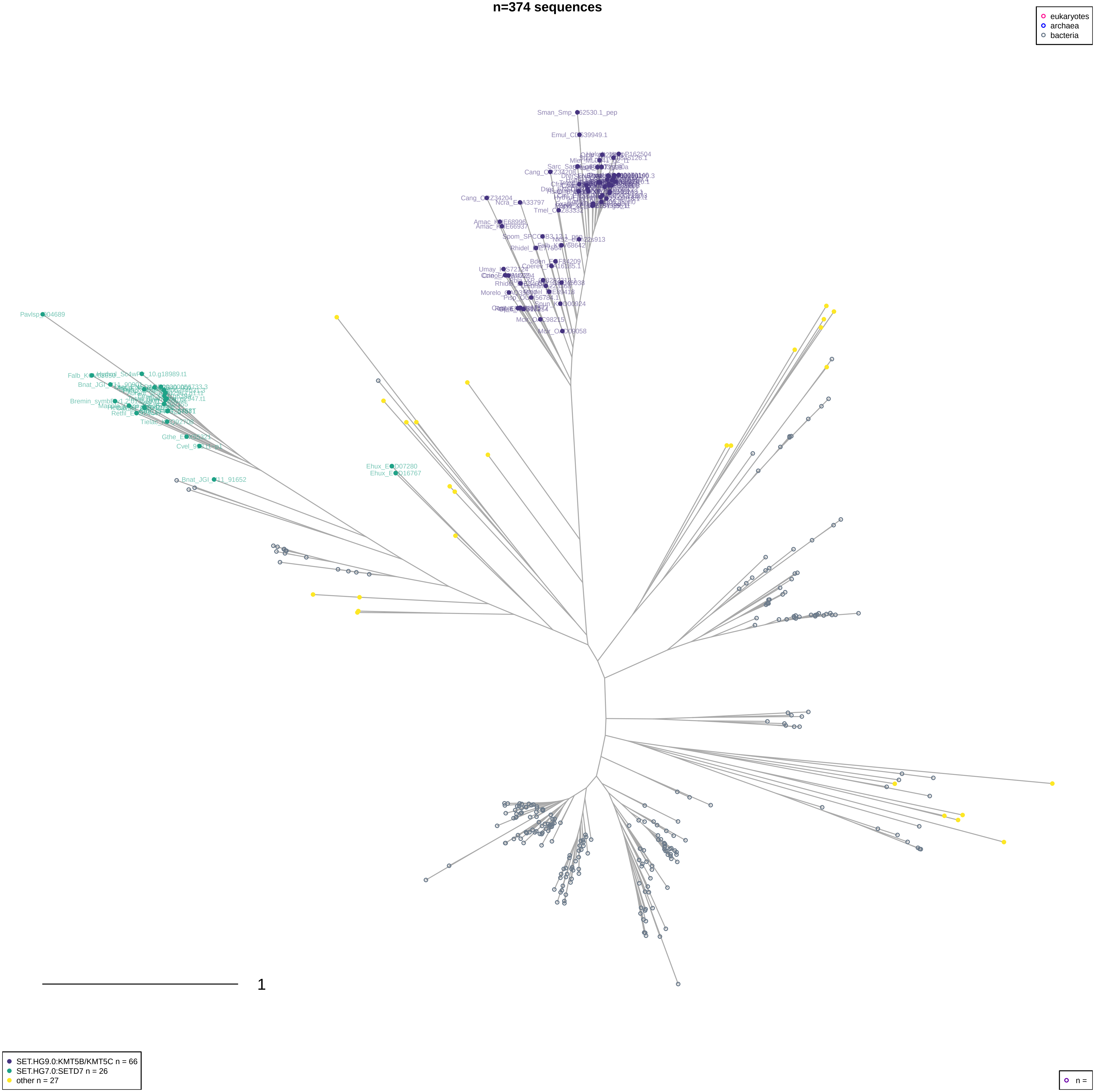
1

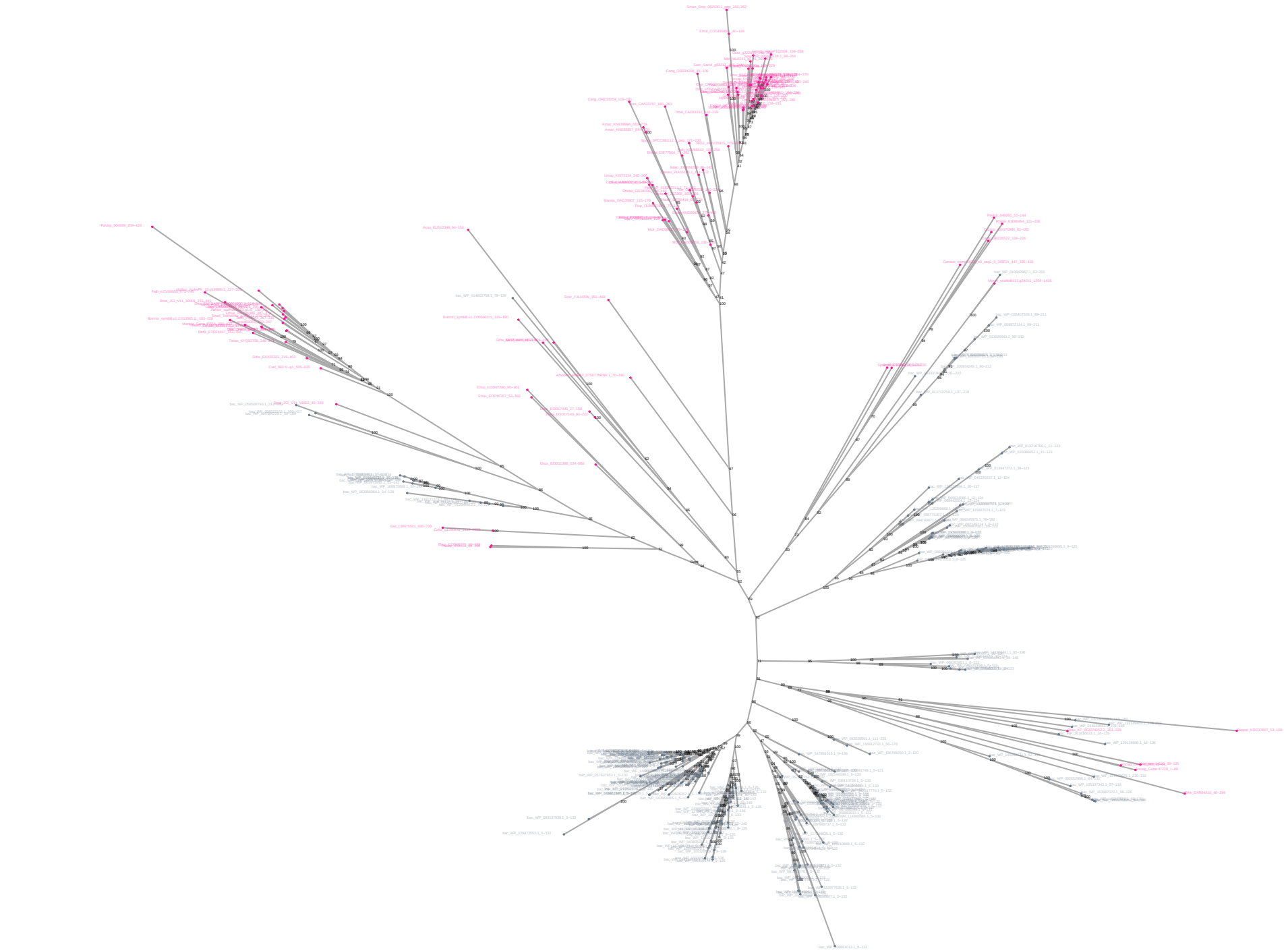

SET
euk.SET.phy.HG7.seqs.iqtree.treefile
n=419 sequences
eukaryotes
archaea
bacteria
Bnat_JGI_411_87411
Spimul_10821_TR5761_c0_g1
Symmic_mic22134
Gonavo_comp169473_c0_seq1_6_ORF10_297
Symmic_mic33148
Gthe_EKX47774
Spom_SPCC297.04c.1_pep
Perkma_EER19584
Pfal_CZT99803
Vitbra_CEL95592.1
Morelo_AAQ33482
Marpol_KYJ48927
Euryarchaeota_rc_ABN56593.1
Euryarchaeota_rc_EJG07
Lokiarchaeota_rc_TFG15404.1
Lokiarchaeota_rc_KKK40014.1
Gefoke_MALSP08426.mRNA.1
Clim_evm28s150
1
SET.HG10.1:NA n = 48
SET.HG10.0:NA n = 10
other n = 17
Euryarchaeota n = 18
Lokiarchaeota n = 11
NA n = 2



1

SET
euk.SET.phy.HG8.seqs.iqtree.treefile
n=374 sequences

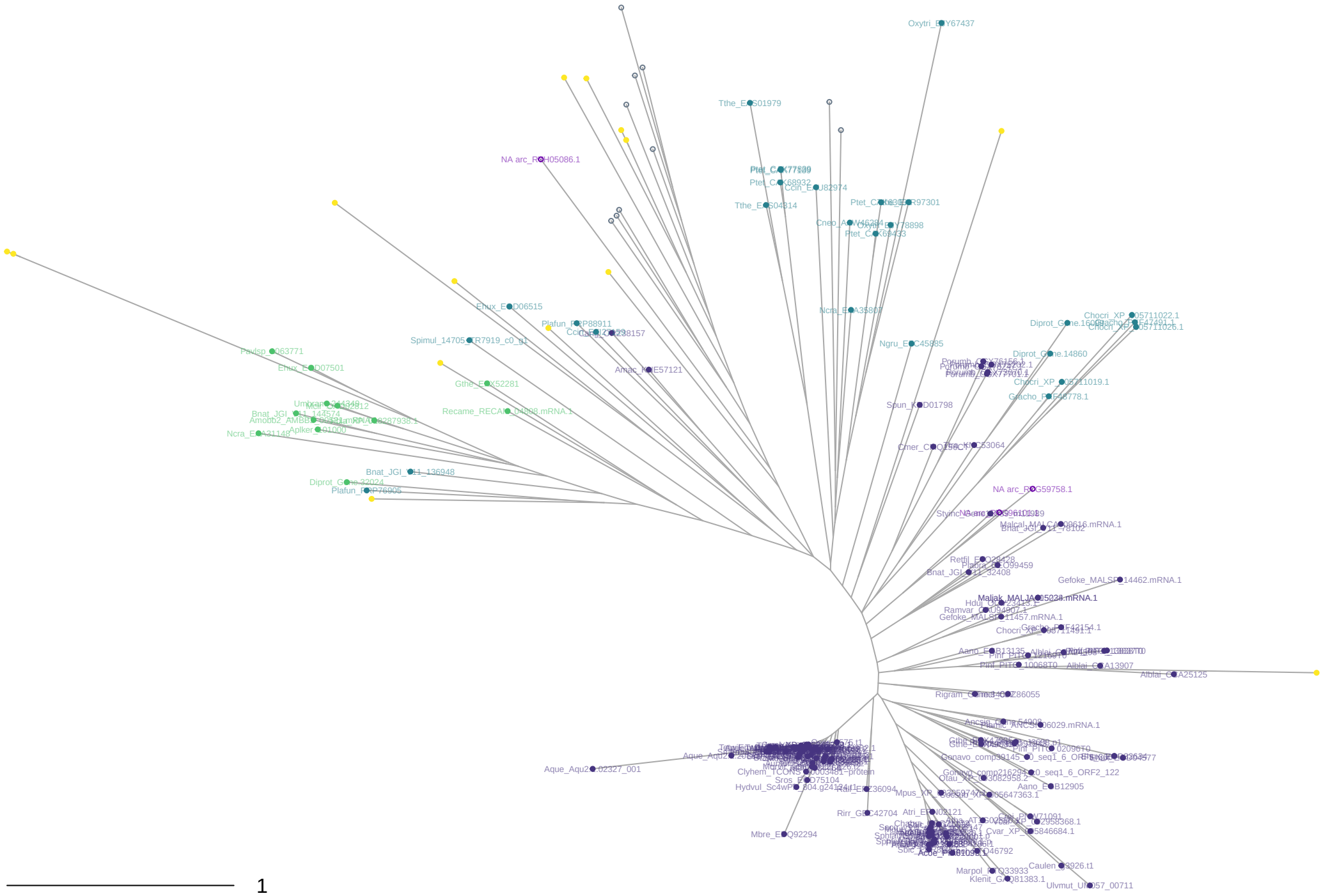




1

SET
euk.SET.phy.HG9.seqs.iqtree.treefile
n=192 sequences

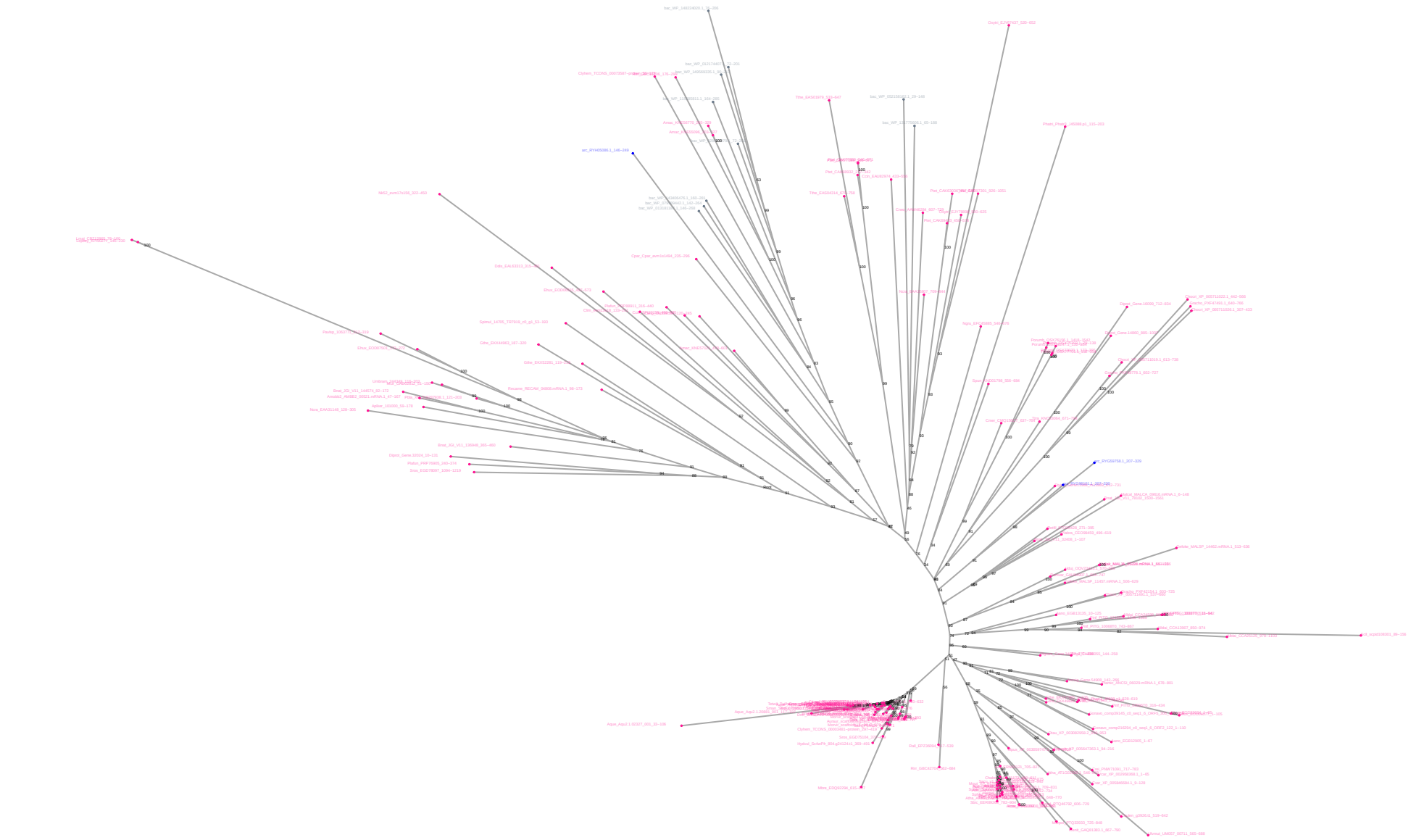
eukaryotes
archaea
bacteria



1

SET.HG8.1:EZH1/EZH2 n = 126
SET.HG8.0:like:EZH1/EZH2:likeclu:1 n = 27
SET.HG3.8:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 12
other n = 14

NA n = 3



1