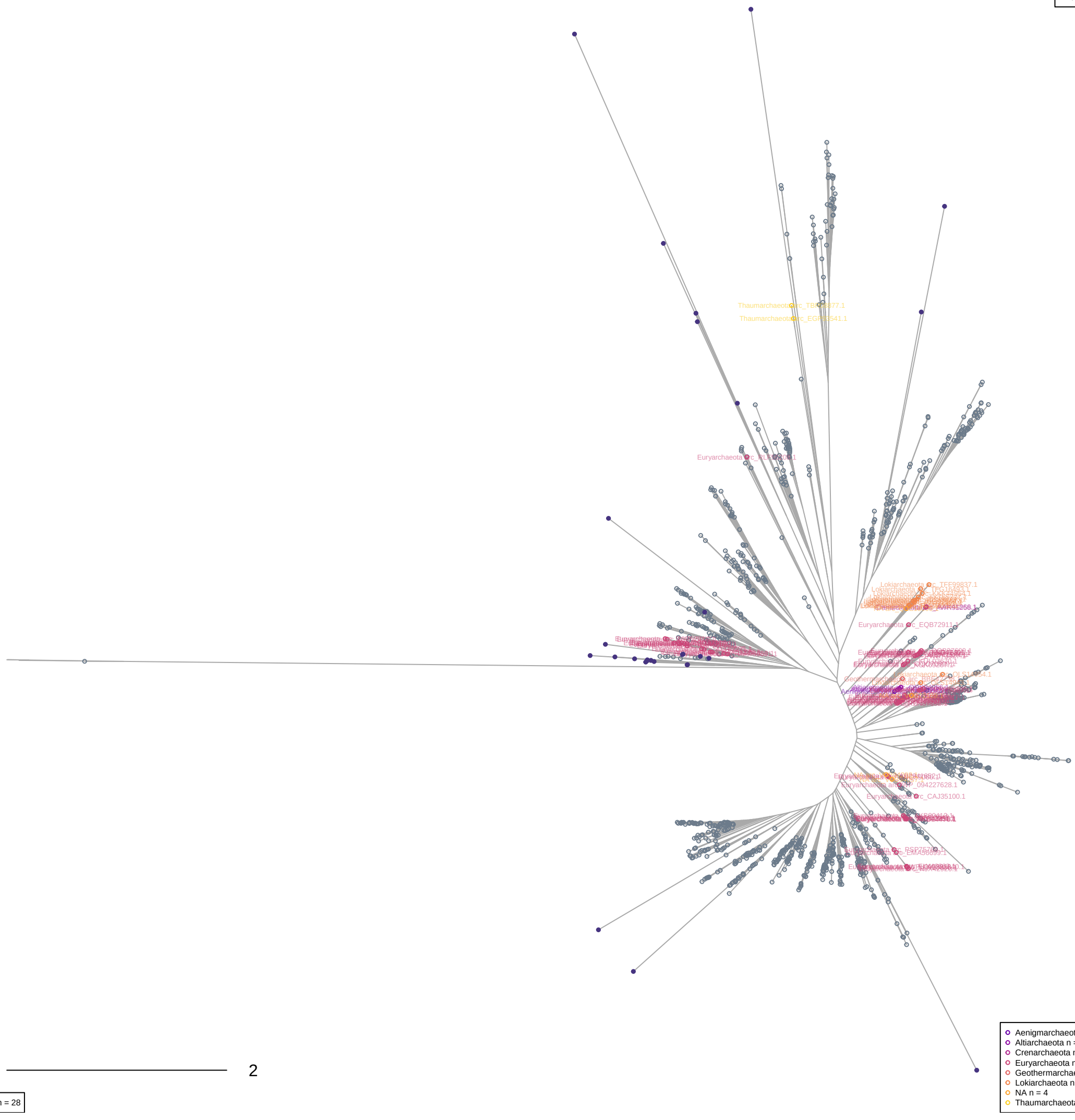
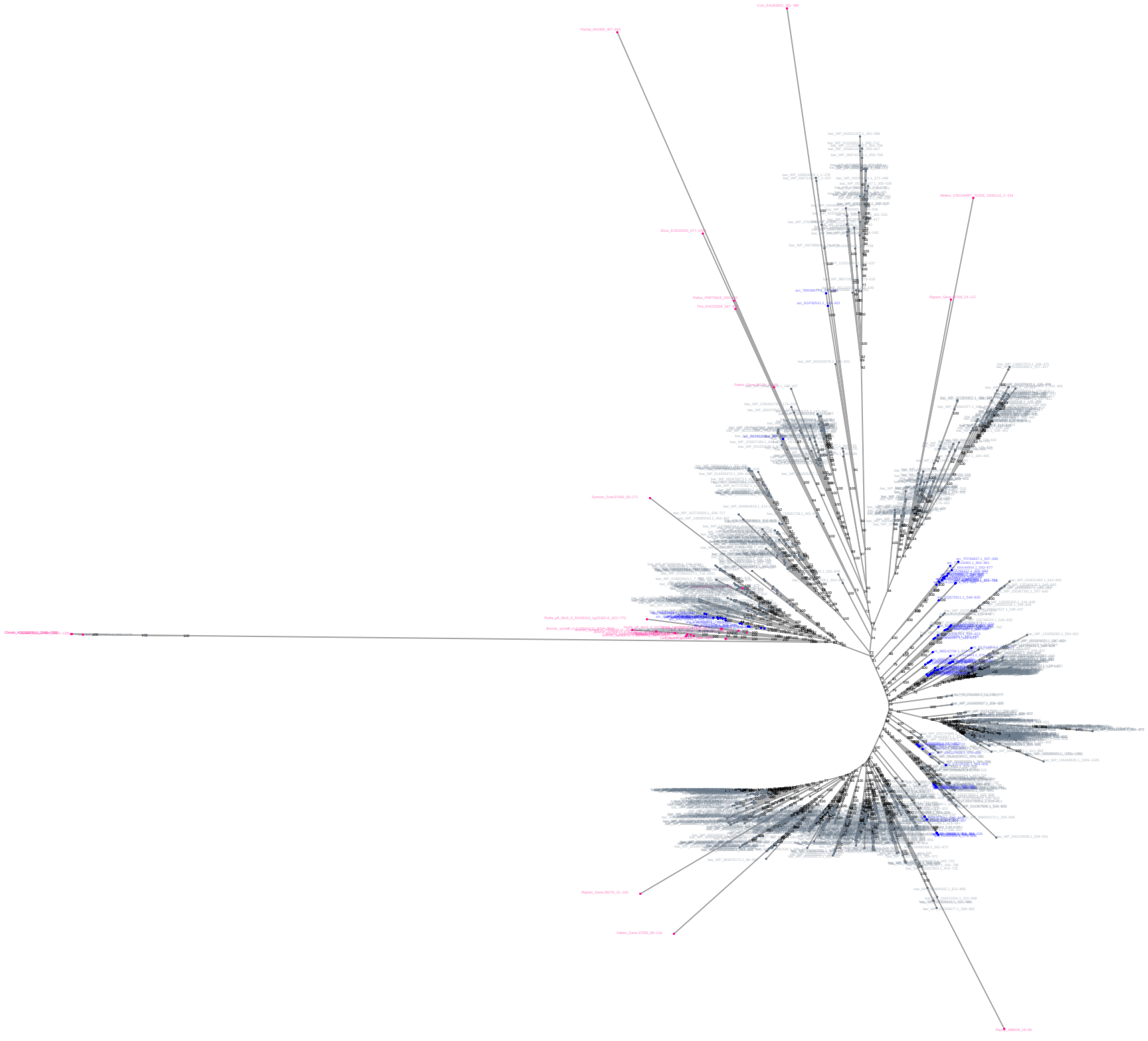
SNF2_N
euk.SNF2_N.phy.HG1.seqs.iqtree.treefile
n=1209 sequences





2

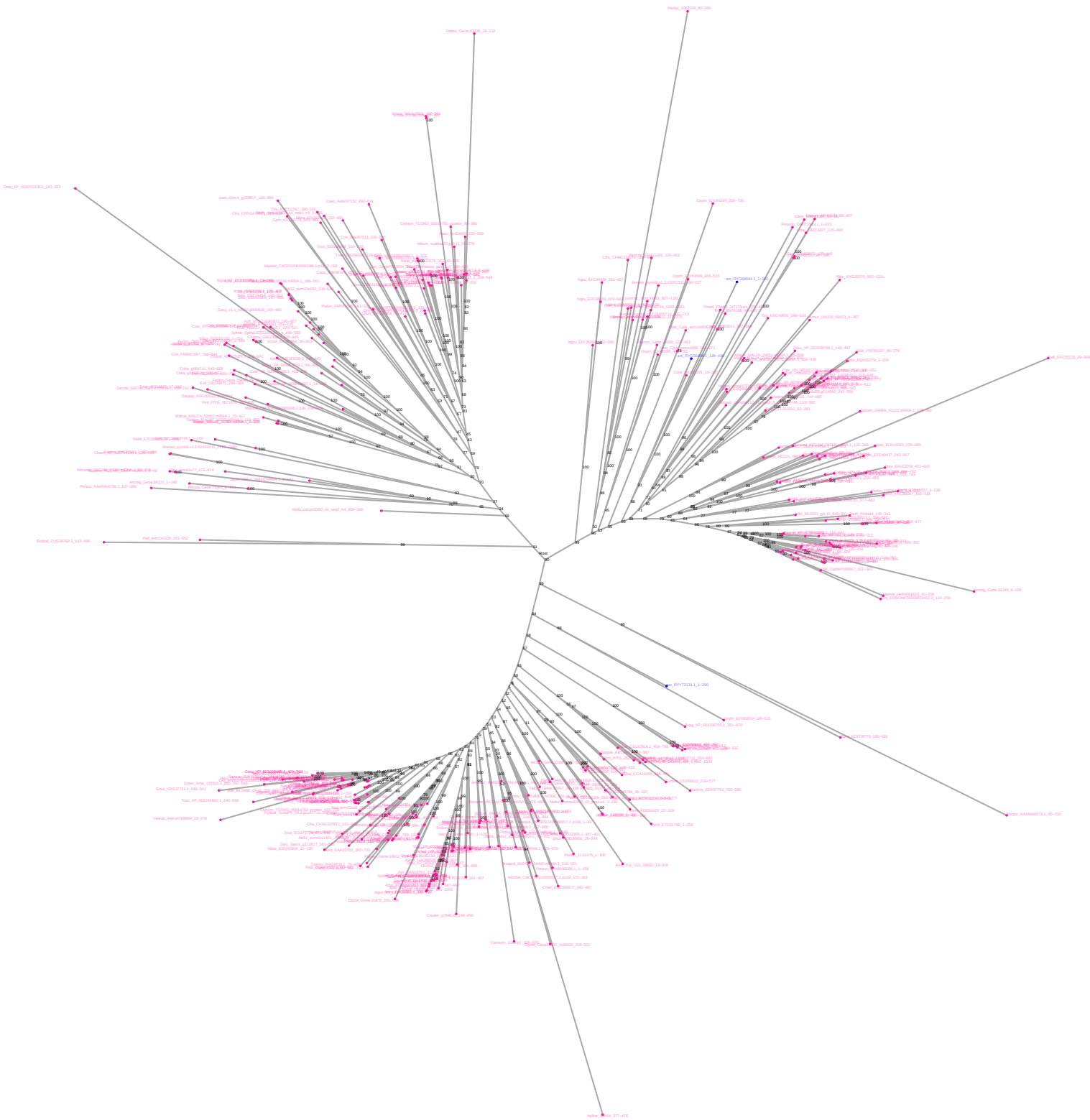
SNF2_N
euk.SNF2_N.phy.HG10.seqs.iqtree.treefile
n=397 sequences

eukaryotes
archaea
bacteria

SNF2_N.HG3.3:ERCC6 n = 166
SNF2_N.HG3.5:ERCC6L n = 104
SNF2_N.HG3.1:ERCC6L2 n = 98
SNF2_N.HG3.4:like:ERCC6L:likeclu:5 n = 15
other n = 11

1

NA n = 3



1

SNF2_N
euk.SNF2_N.phy.HG11.seqs.iqtree.treefile
n=395 sequences

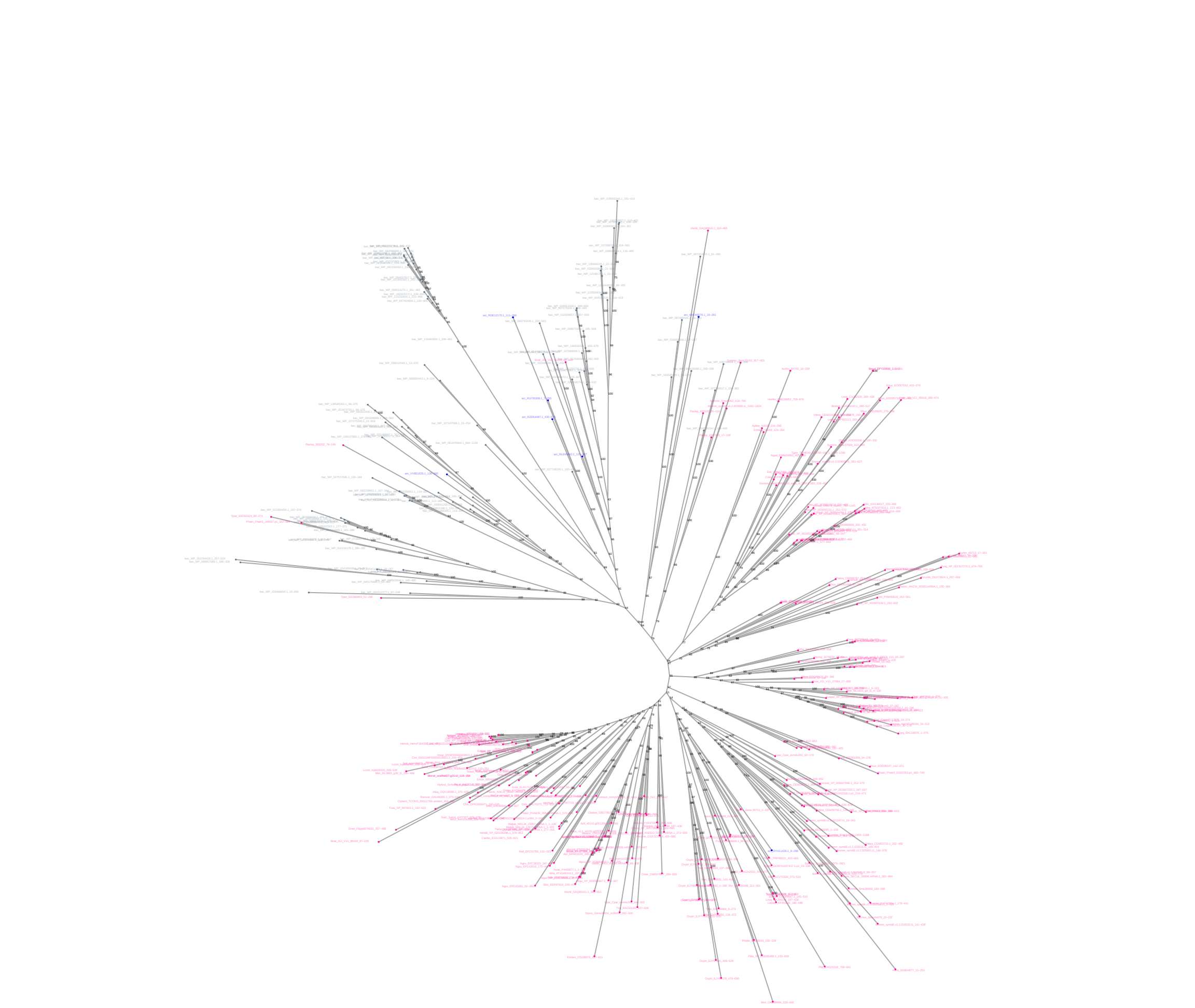
eukaryotes
archaea
bacteria

Thorarchaeota arc_RDE12170.1
NA arc_KKO49076.1
Euryarchaeota arc_RLF30308.1
Euryarchaeota arc_RZD64487.1
Woesearchaeota arc_RLE45243.1
NA arc_VOB51635.1

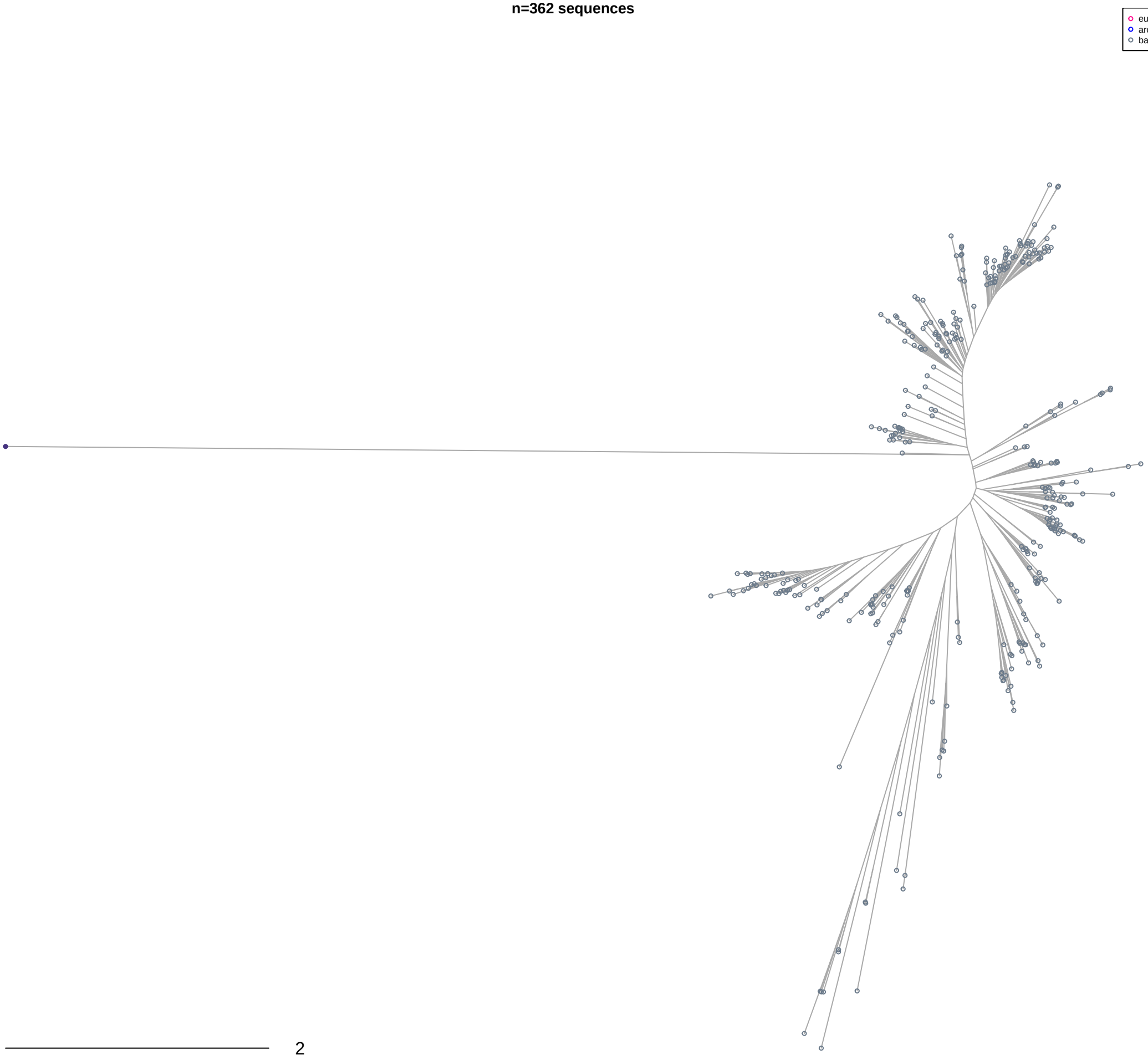
0.5

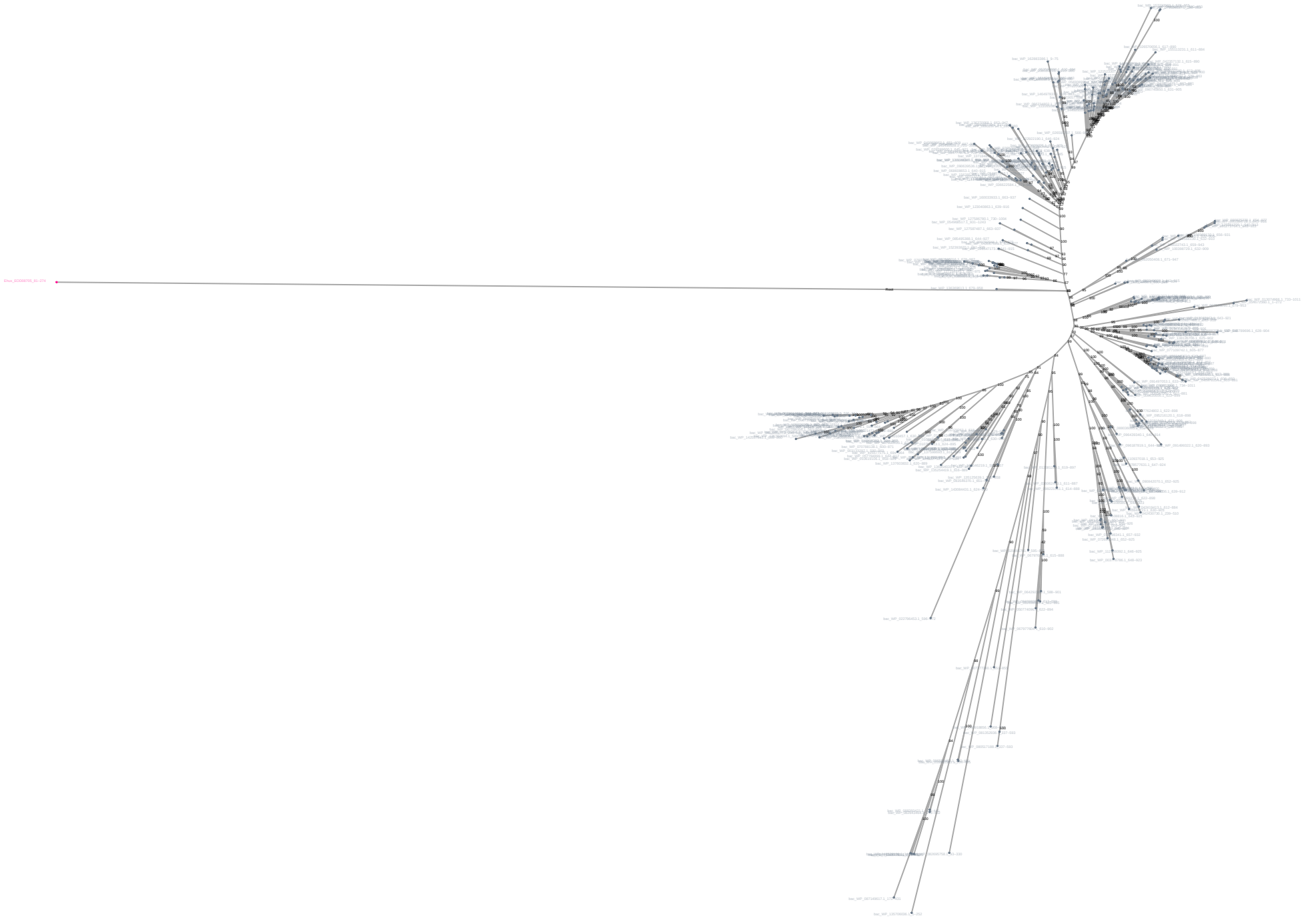
SNF2_N.HG9.2:SMARCAL1/ZRANB3 n = 266
other n = 19

Euryarchaeota n = 2
NA n = 3
Thorarchaeota n = 1
Woesearchaeota n = 1


0.5

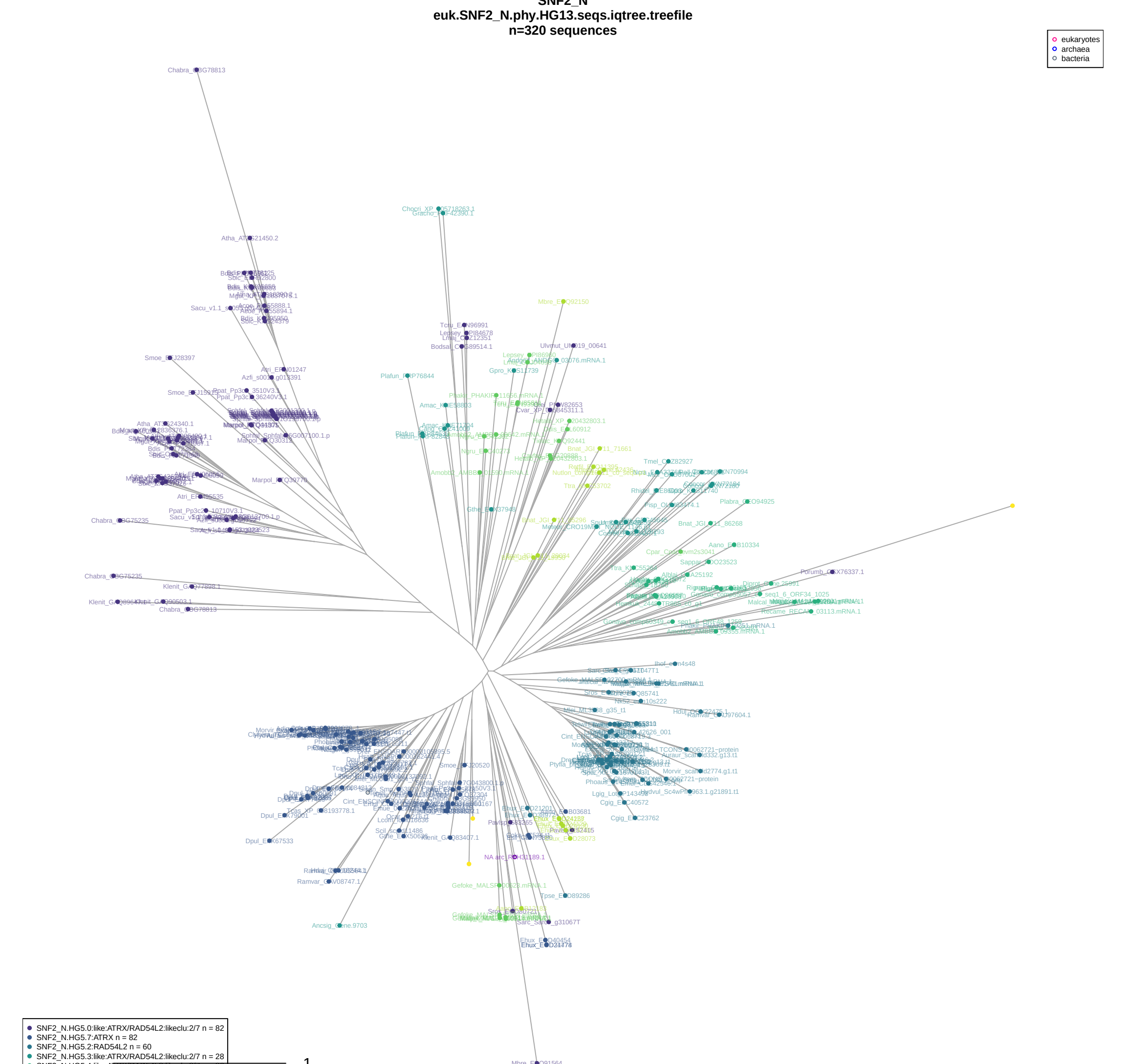
SNF2_N
euk.SNF2_N.phy.HG12.seqs.iqtree.treefile
n=362 sequences





2

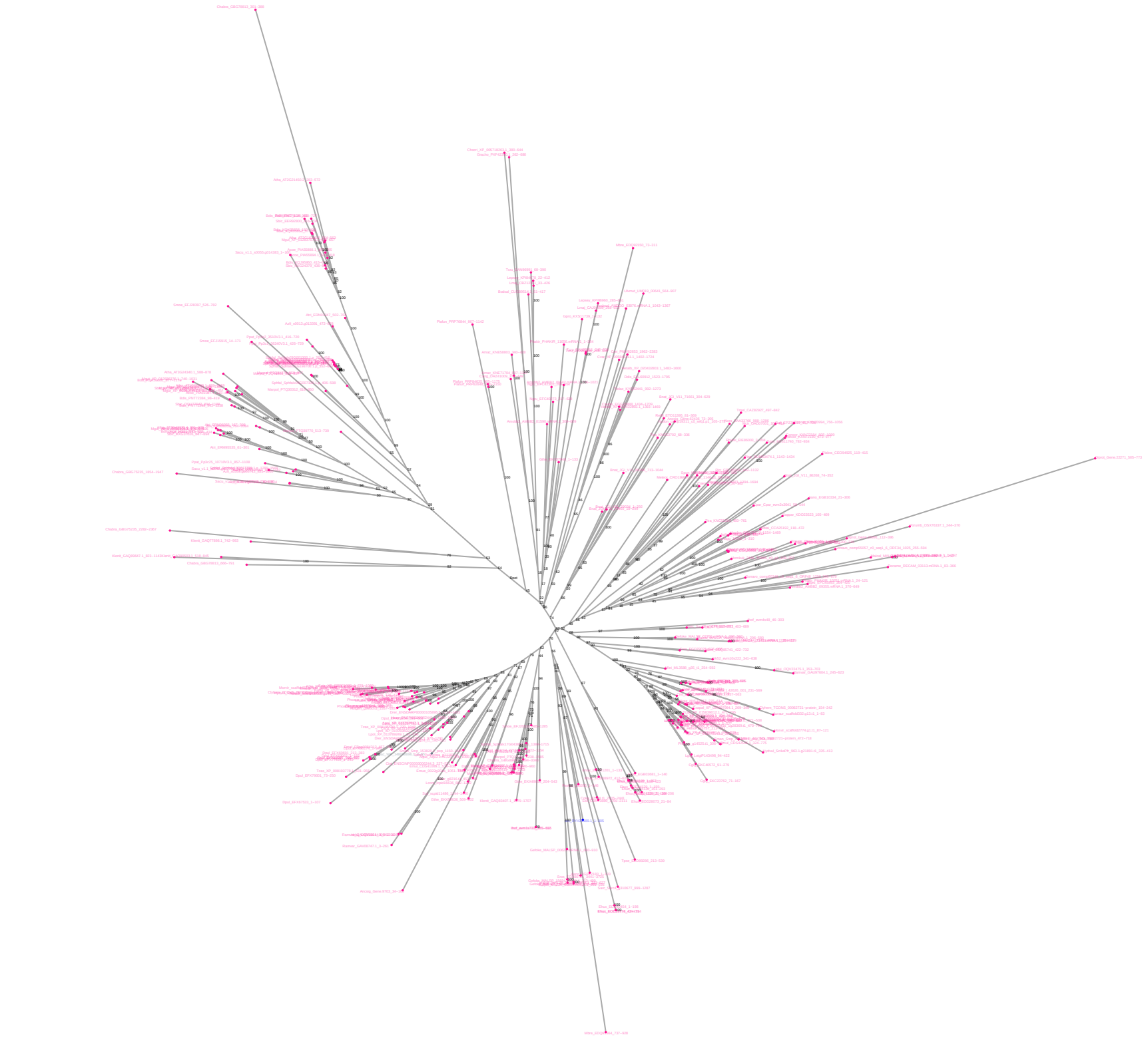
SNF2_N
euk.SNF2_N.phy.HG13.seqs.iqtree.treefile
n=320 sequences



SNF2_N.HG5.0:like:ATRX/RAD54L2:likeclu:2/7 n = 82
SNF2_N.HG5.7:ATRX n = 82
SNF2_N.HG5.2:RAD54L2 n = 60
SNF2_N.HG5.3:like:ATRX/RAD54L2:likeclu:2/7 n = 28
SNF2_N.HG5.4:like:ATRX/RAD54L2:likeclu:2/7 n = 26
SNF2_N.HG5.1:like:ATRX/RAD54L2:likeclu:2/7 n = 20
SNF2_N.HG5.5:like:ATRX:likeclu:7 n = 16
other n = 4

1

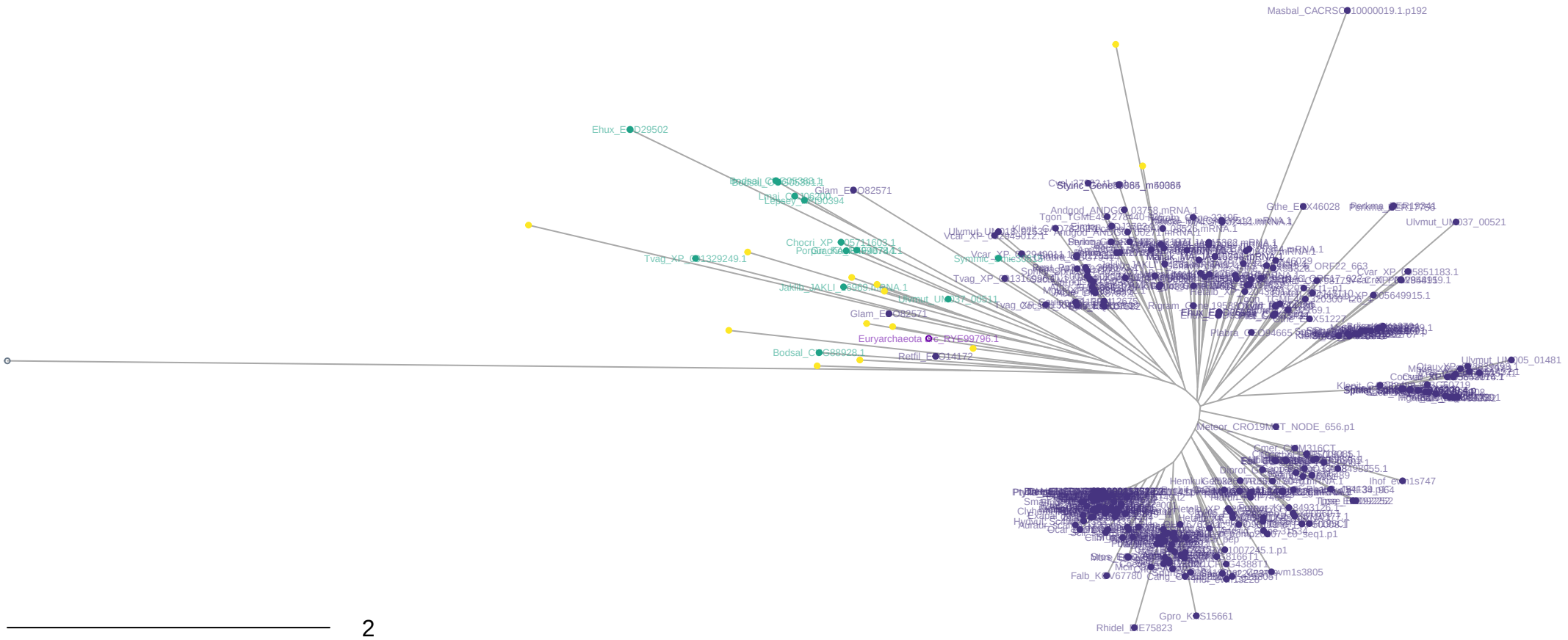
NA n = 1



1

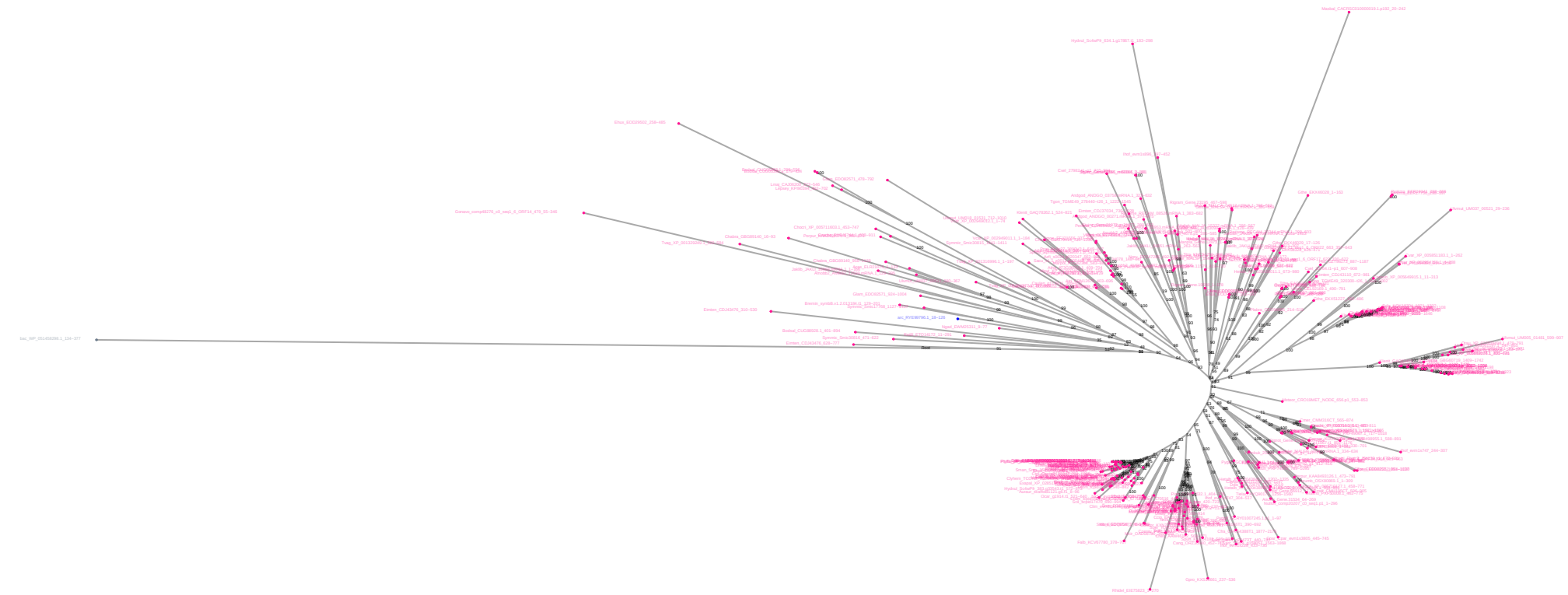
SNF2_N
euk.SNF2_N.phy.HG14.seqs.iqtree.treefile
n=314 sequences

eukaryotes
archaea
bacteria



SNF2_N.HG6.0:SMARCA2/SMARCA4 n = 286
SNF2_N.HG6.1:like:SMARCA2/SMARCA4:likeclu:0 n = 13
other n = 13

Euryarchaeota n = 1



2

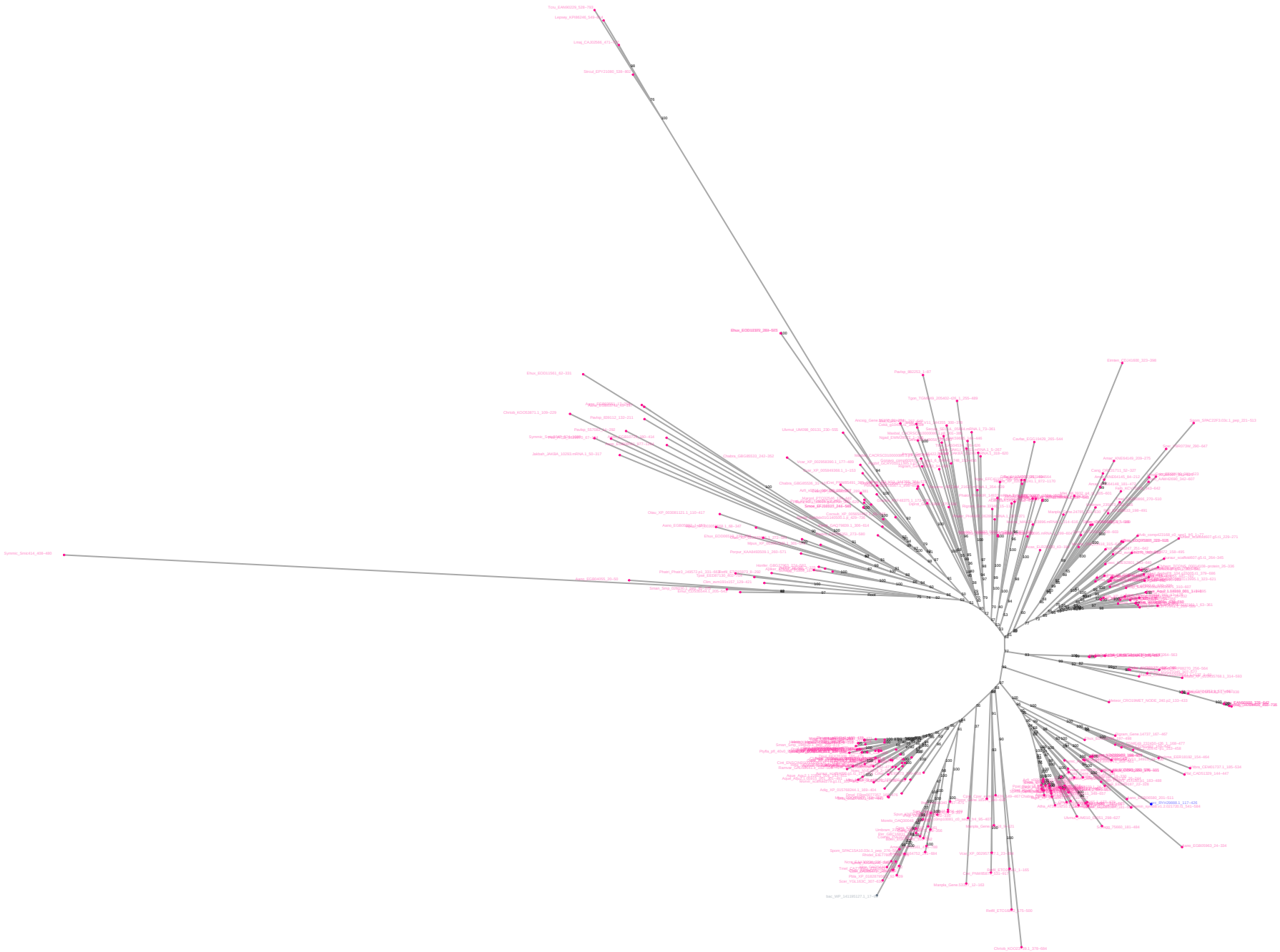
SNF2_N
euk.SNF2_N.phy.HG15.seqs.iqtree.treefile
n=313 sequences

eukaryotes
archaea
bacteria

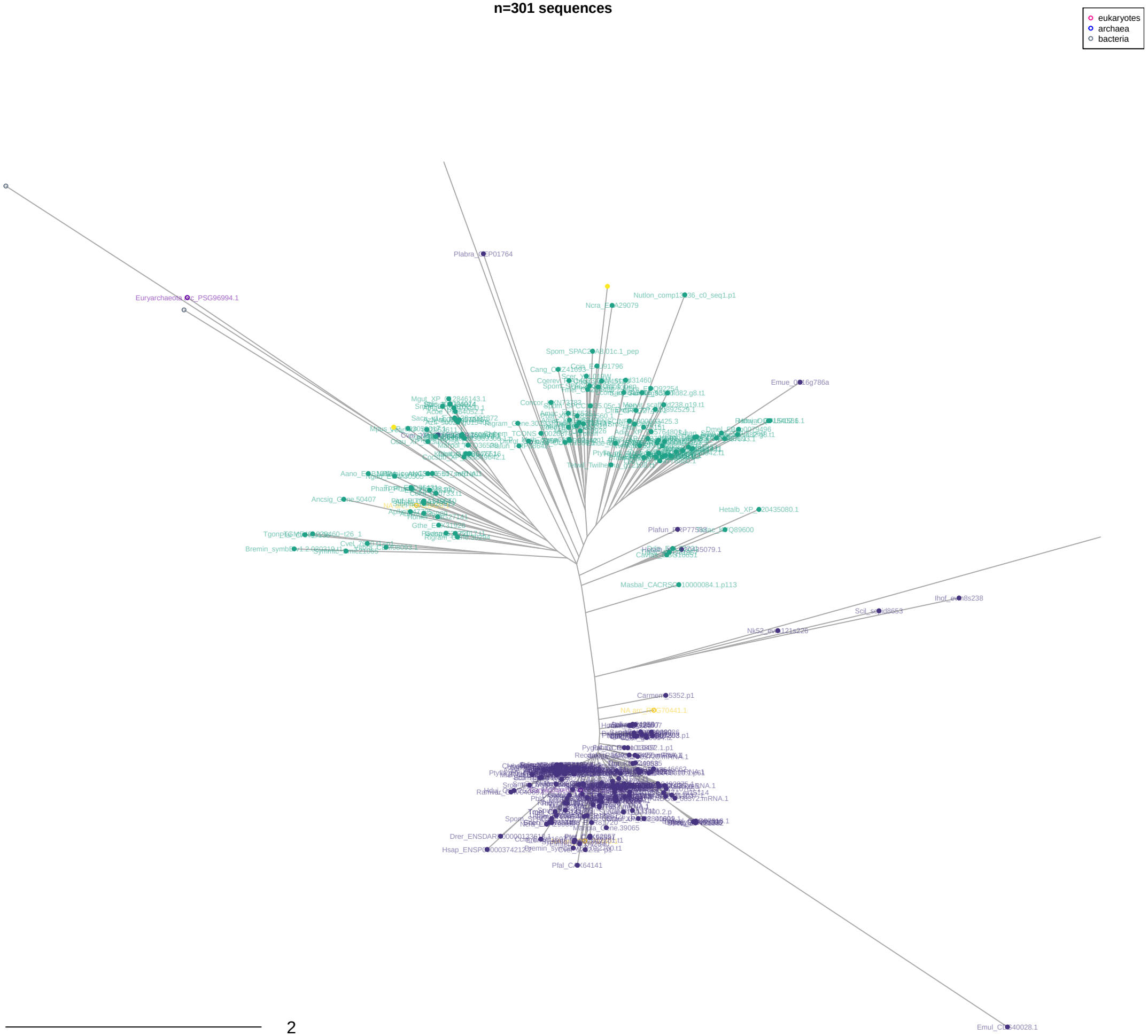
1

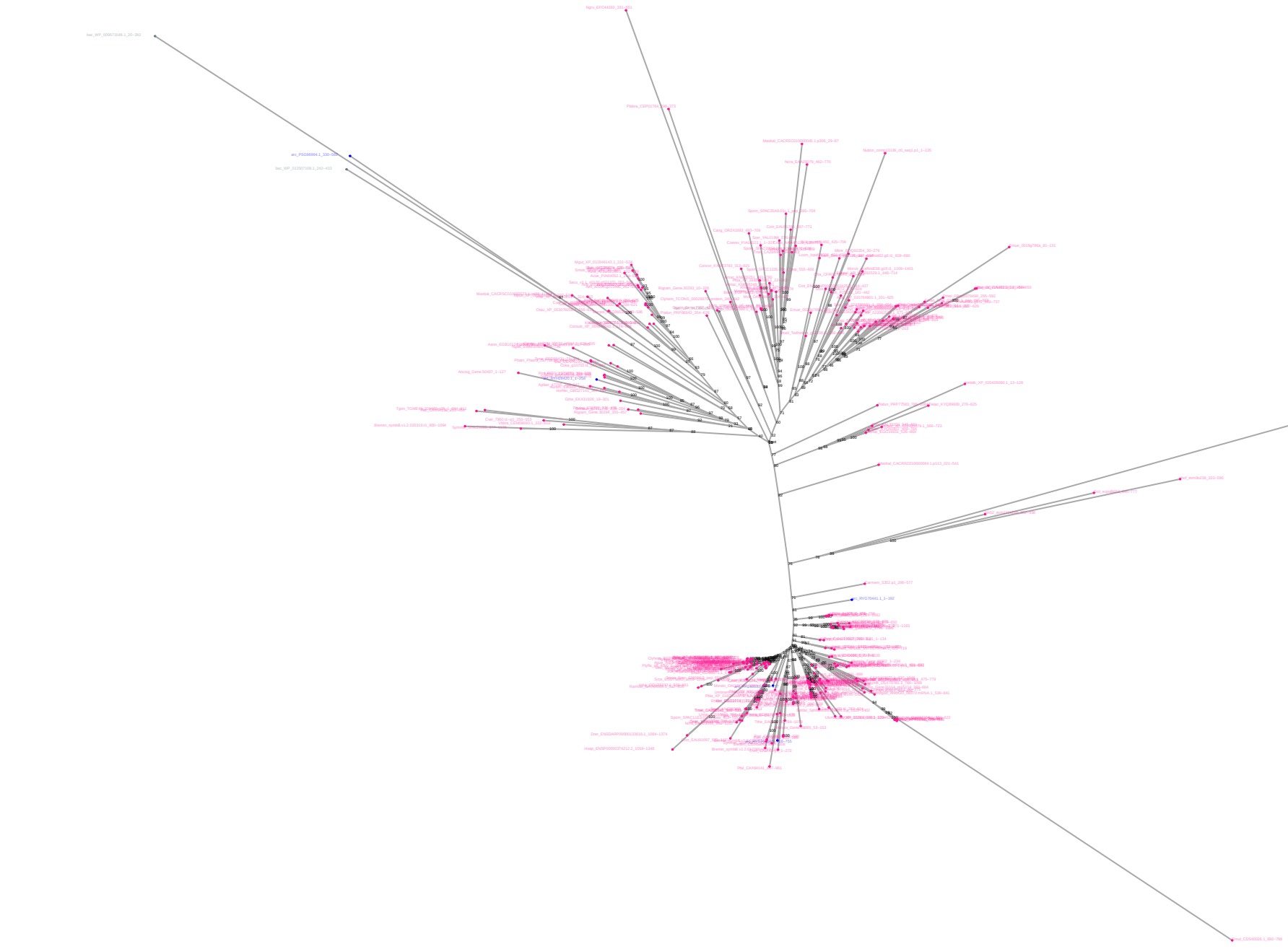
SNF2_N.HG7.8:RAD54B/RAD54L n = 241
SNF2_N.HG7.7:like:RAD54B/RAD54L:likeclu:8 n = 30
other n = 40

NA n = 1


1

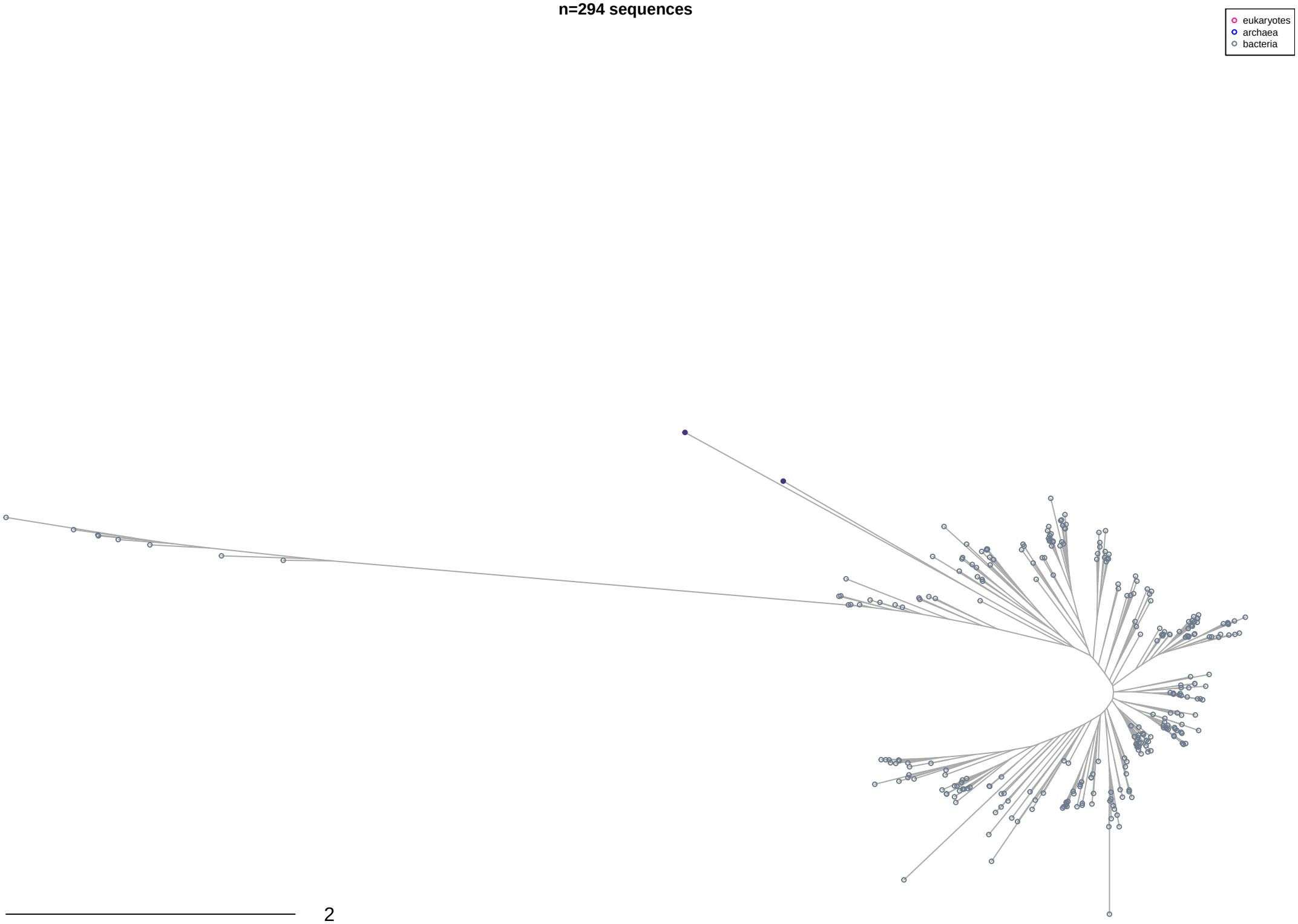
SNF2_N
euk.SNF2_N.phy.HG16.seqs.iqtree.treefile
n=301 sequences

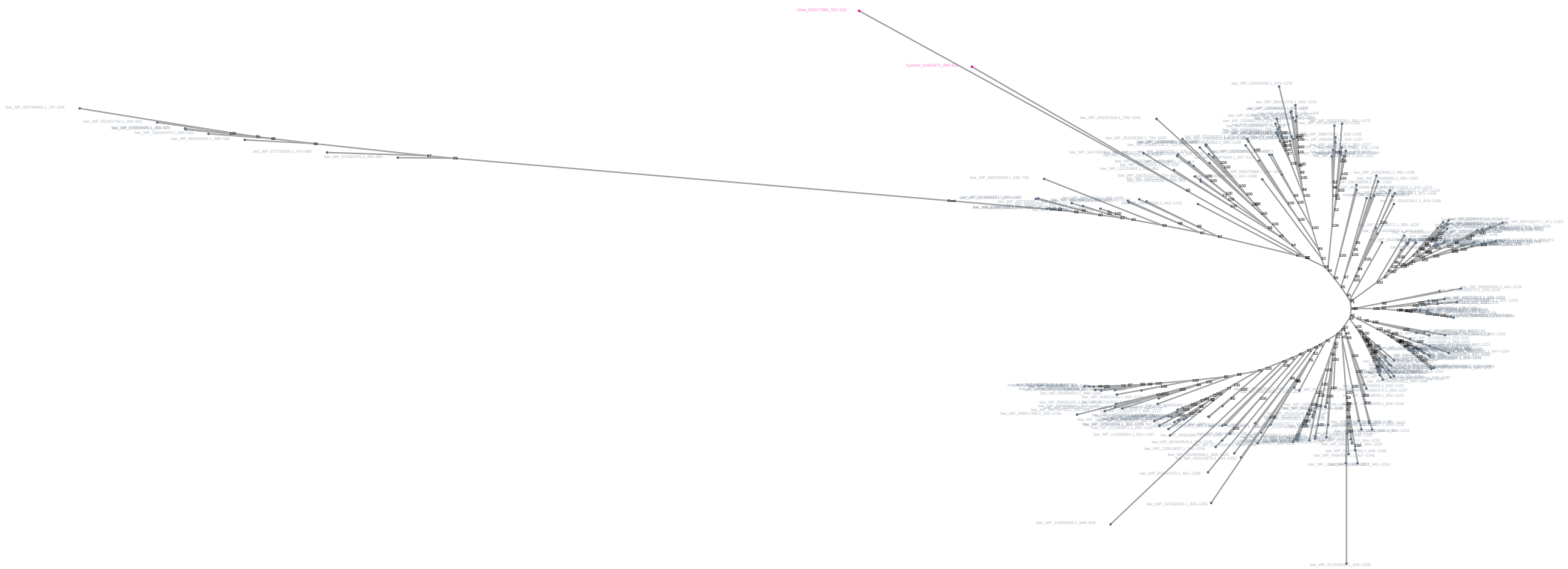




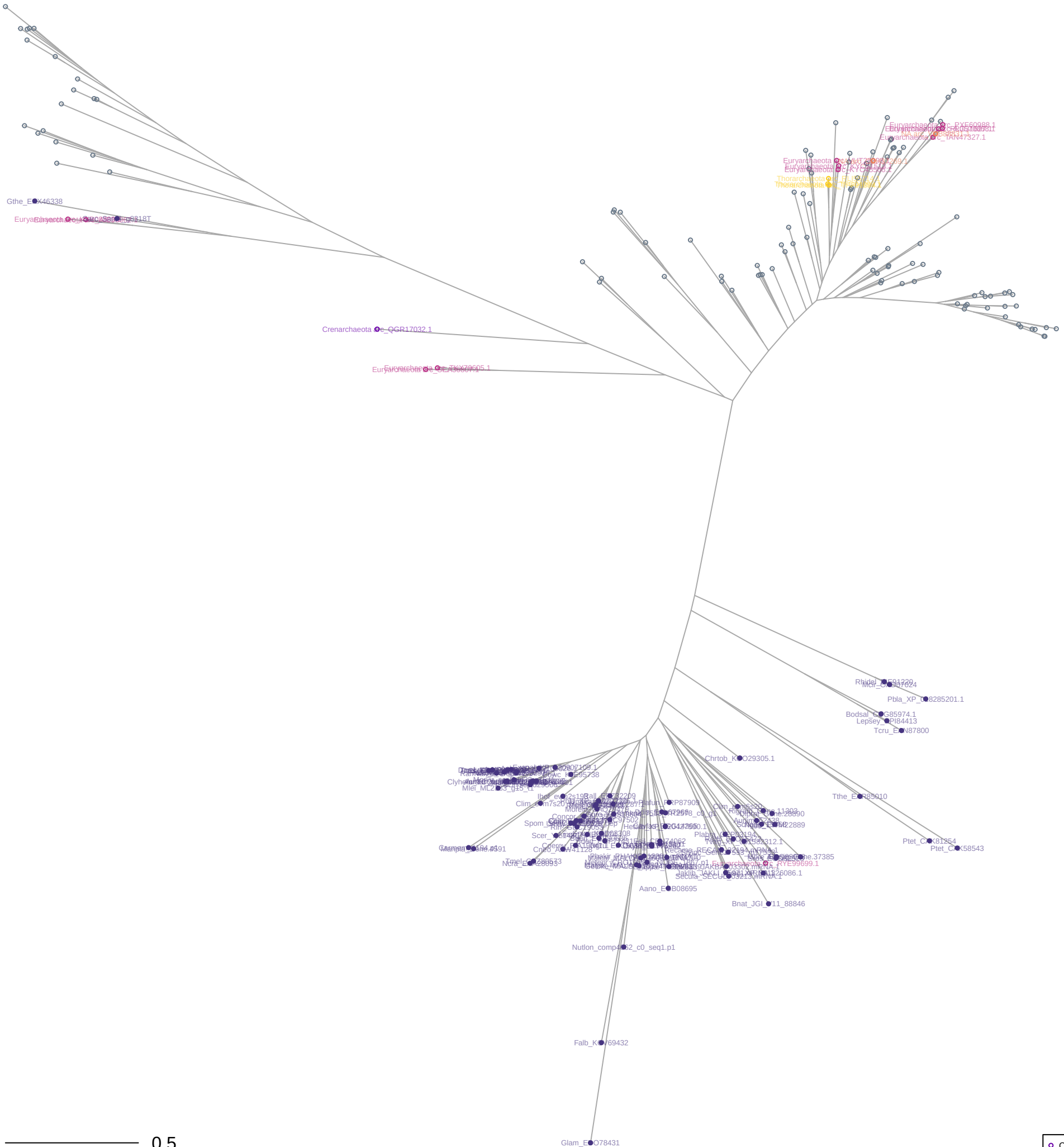
2

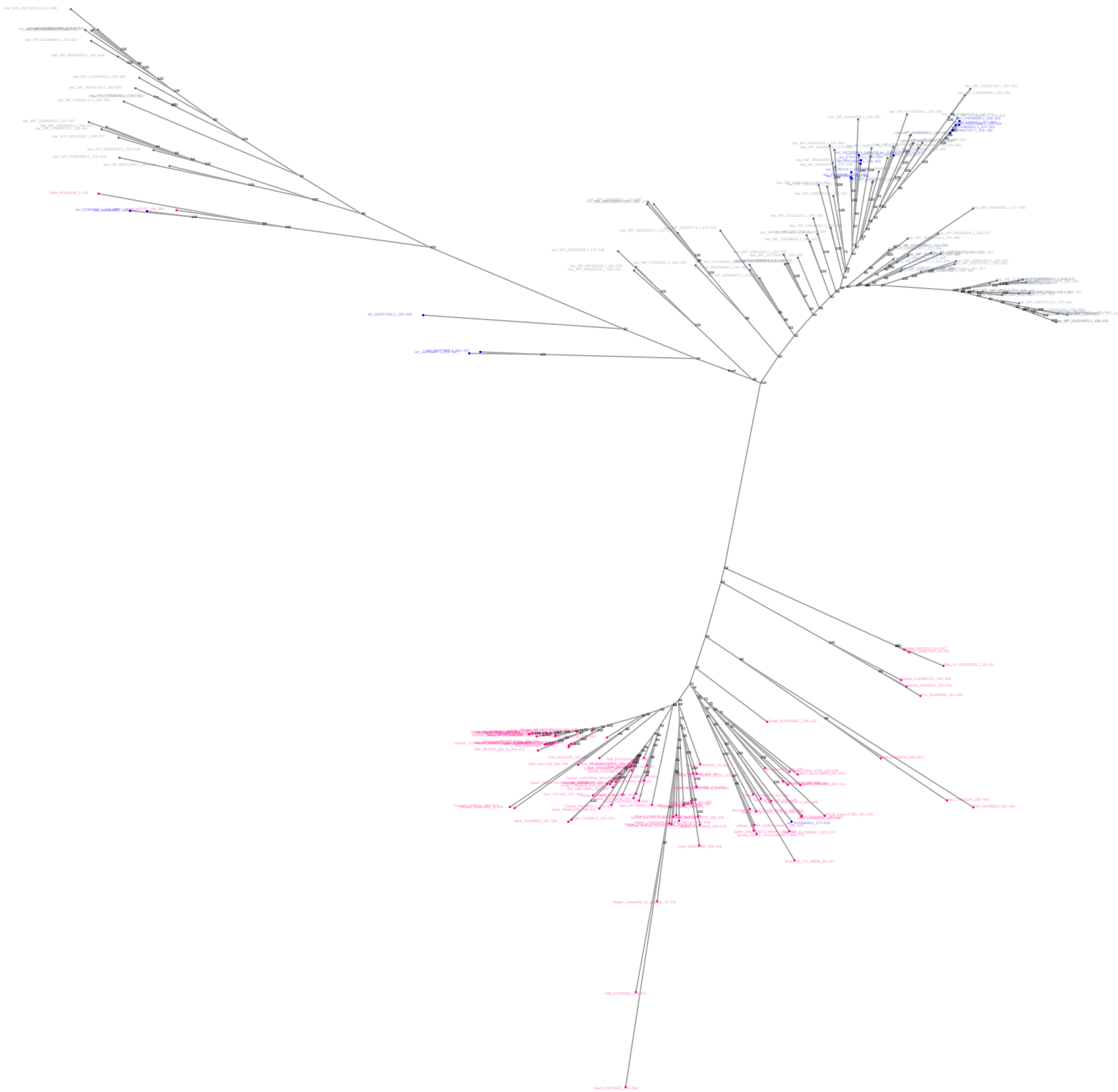
SNF2_N
euk.SNF2_N.phy.HG17.seqs.iqtree.treefile
n=294 sequences



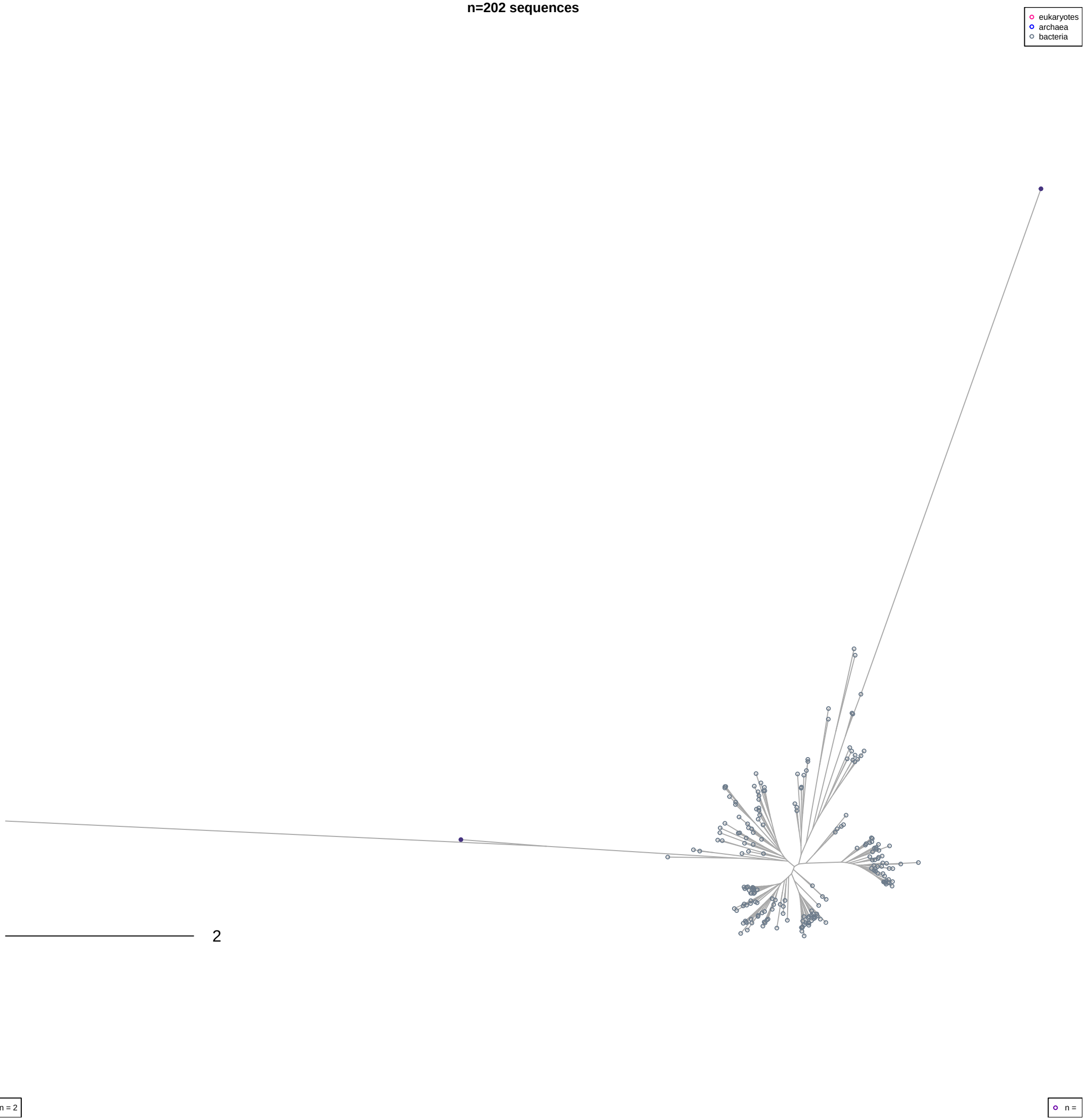


SNF2_N
euk.SNF2_N.phy.HG18.seqs.iqtree.treefile
n=228 sequences



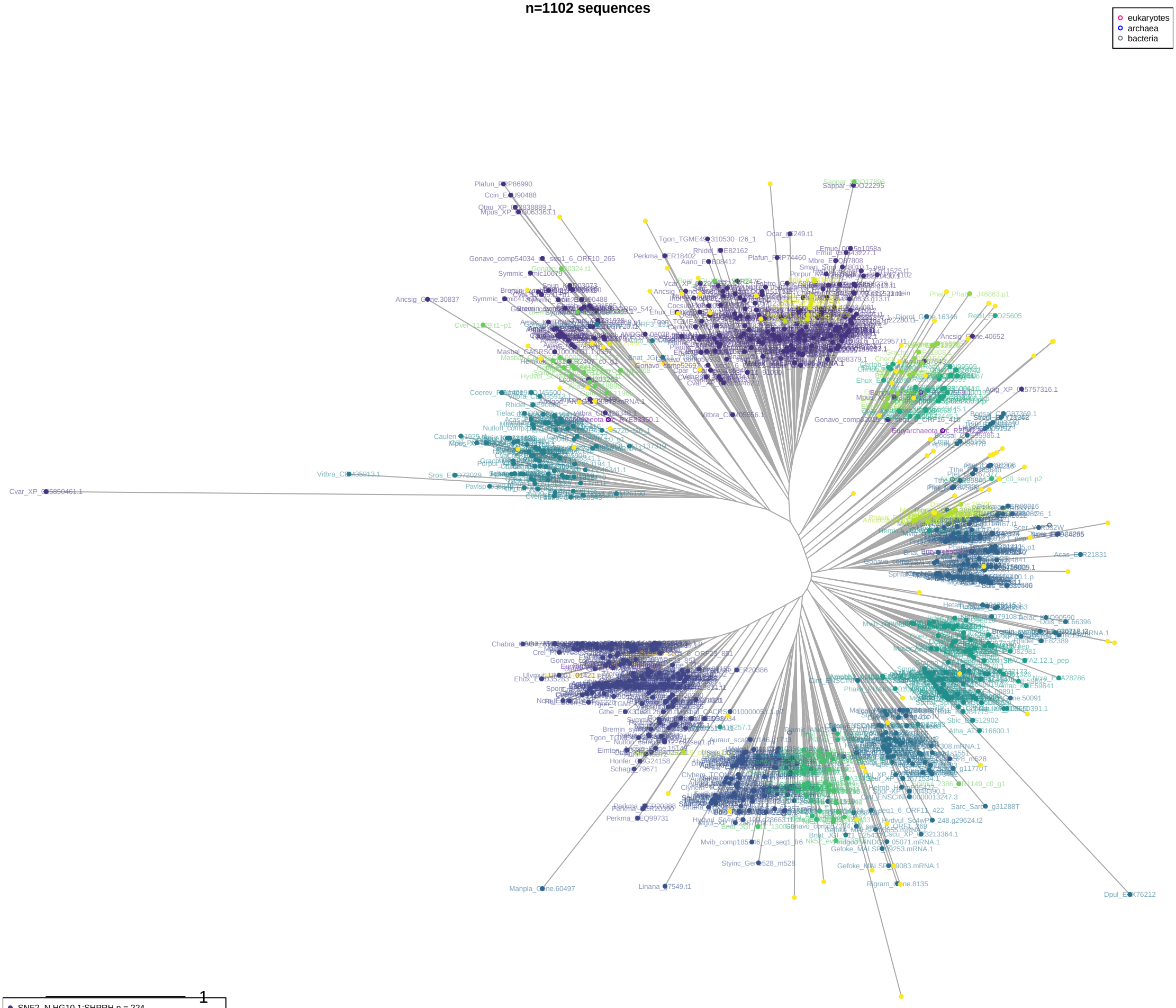

0.5

SNF2_N
euk.SNF2_N.phy.HG19.seqs.iqtree.treefile
n=202 sequences



2

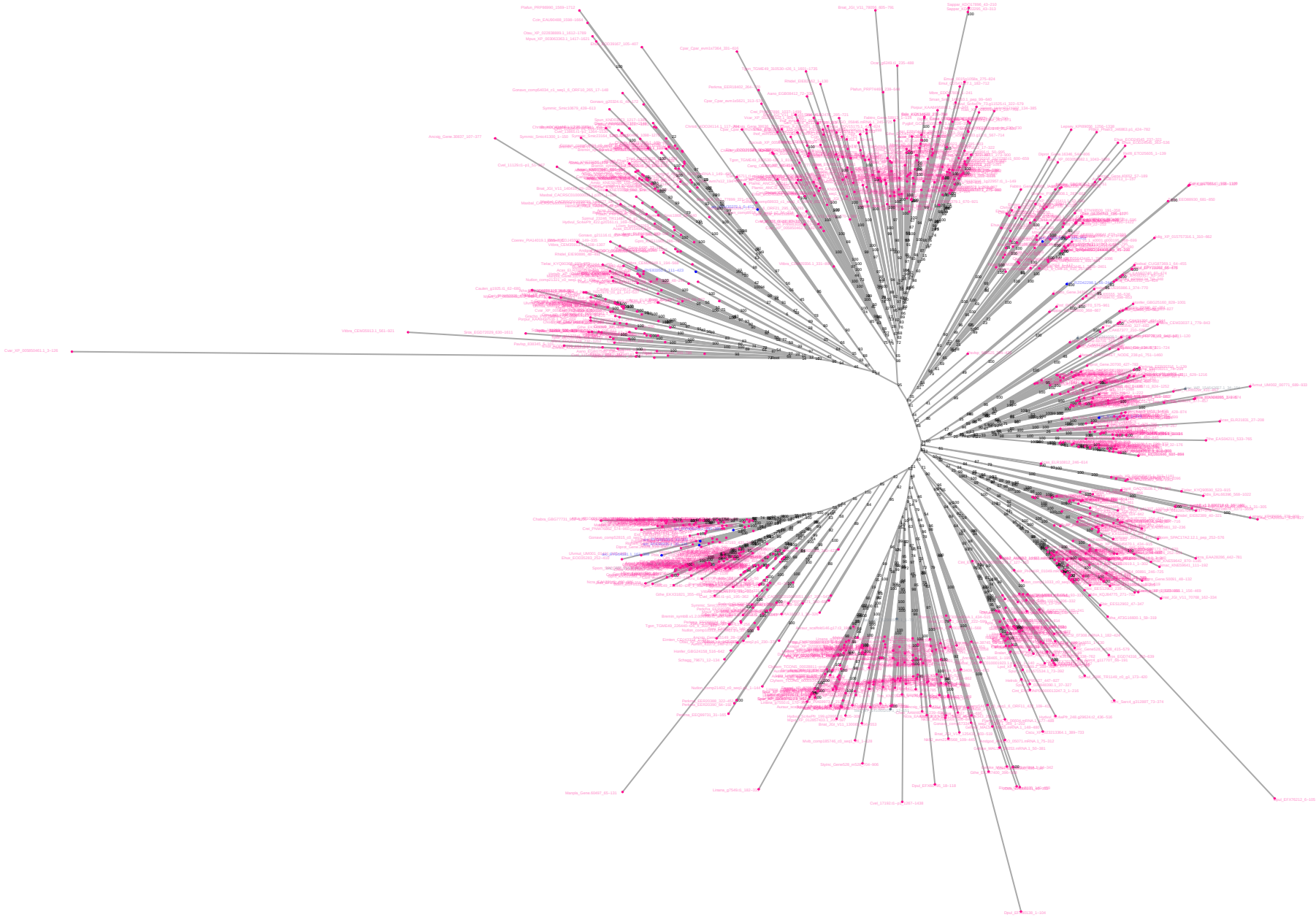
SNF2_N
euk.SNF2_N.phy.HG2.seqs.iqtree.treefile
n=1102 sequences



1

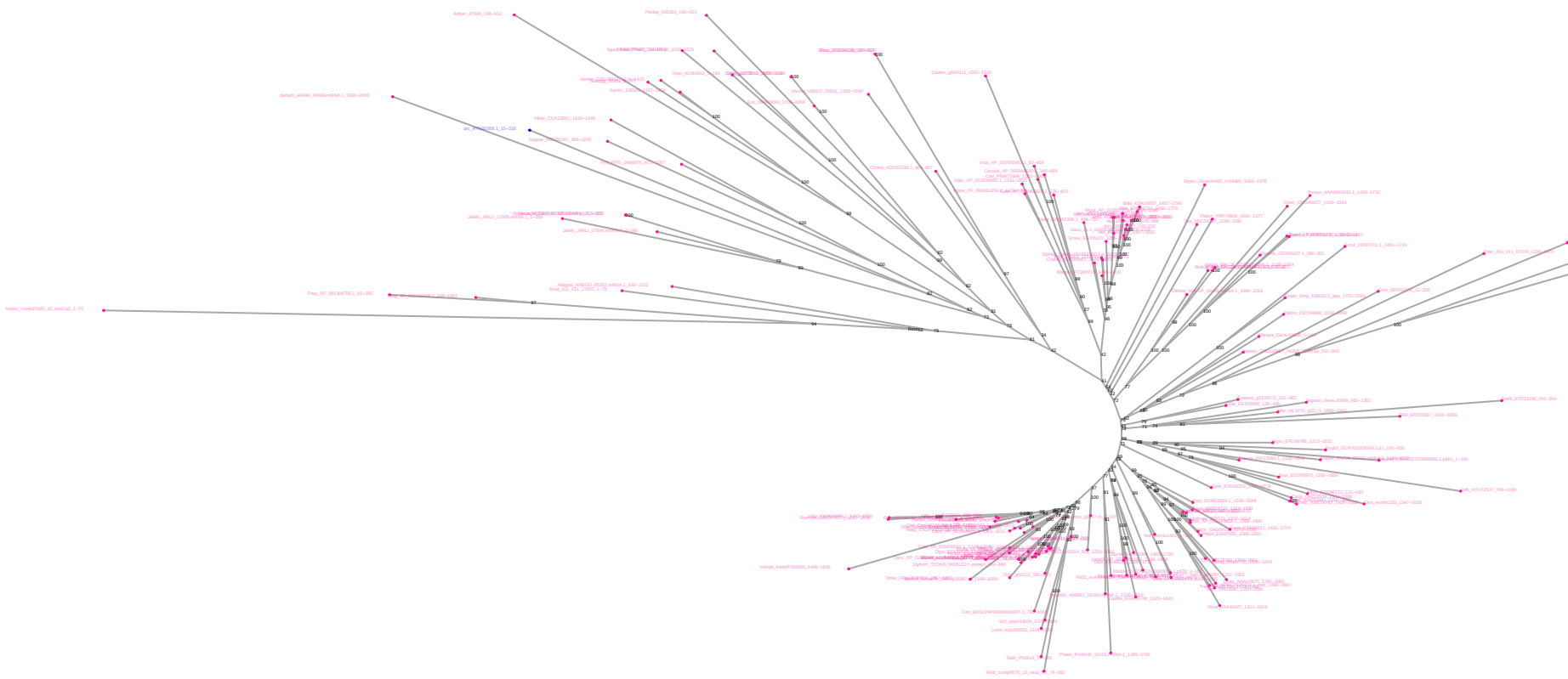
- SNF2_N.HG10.1:SHPRH n = 224
- SNF2_N.HG1.17:like:HLTF/TTF2:likeclu:18/26 n = 169
- SNF2_N.HG1.26:HLTF n = 98
- SNF2_N.HG1.16:like:HLTF/TTF2:likeclu:18/26 n = 96
- SNF2_N.HG1.18:TTF2 n = 93
- SNF2_N.HG1.4:like:HLTF/TTF2:likeclu:18/26 n = 87
- SNF2_N.HG1.29:like:TTF2:likeclu:18 n = 58
- SNF2_N.HG1.27:like:TTF2:likeclu:18 n = 47
- SNF2_N.HG1.7:like:HLTF/TTF2:likeclu:18/26 n = 32
- SNF2_N.HG1.25:like:HLTF:likeclu:26 n = 25
- SNF2_N.HG1.23:like:HLTF:likeclu:26 n = 19
- SNF2_N.HG1.12:like:HLTF/TTF2:likeclu:18/26 n = 17
- SNF2_N.HG1.1:like:HLTF/TTF2:likeclu:18/26 n = 15
- SNF2_N.HG1.20:like:HLTF/TTF2:likeclu:18/26 n = 15
- SNF2_N.HG10.0:like:SHPRH:likeclu:1 n = 10
- other n = 80

- Euryarchaeota n = 5
- NA n = 4

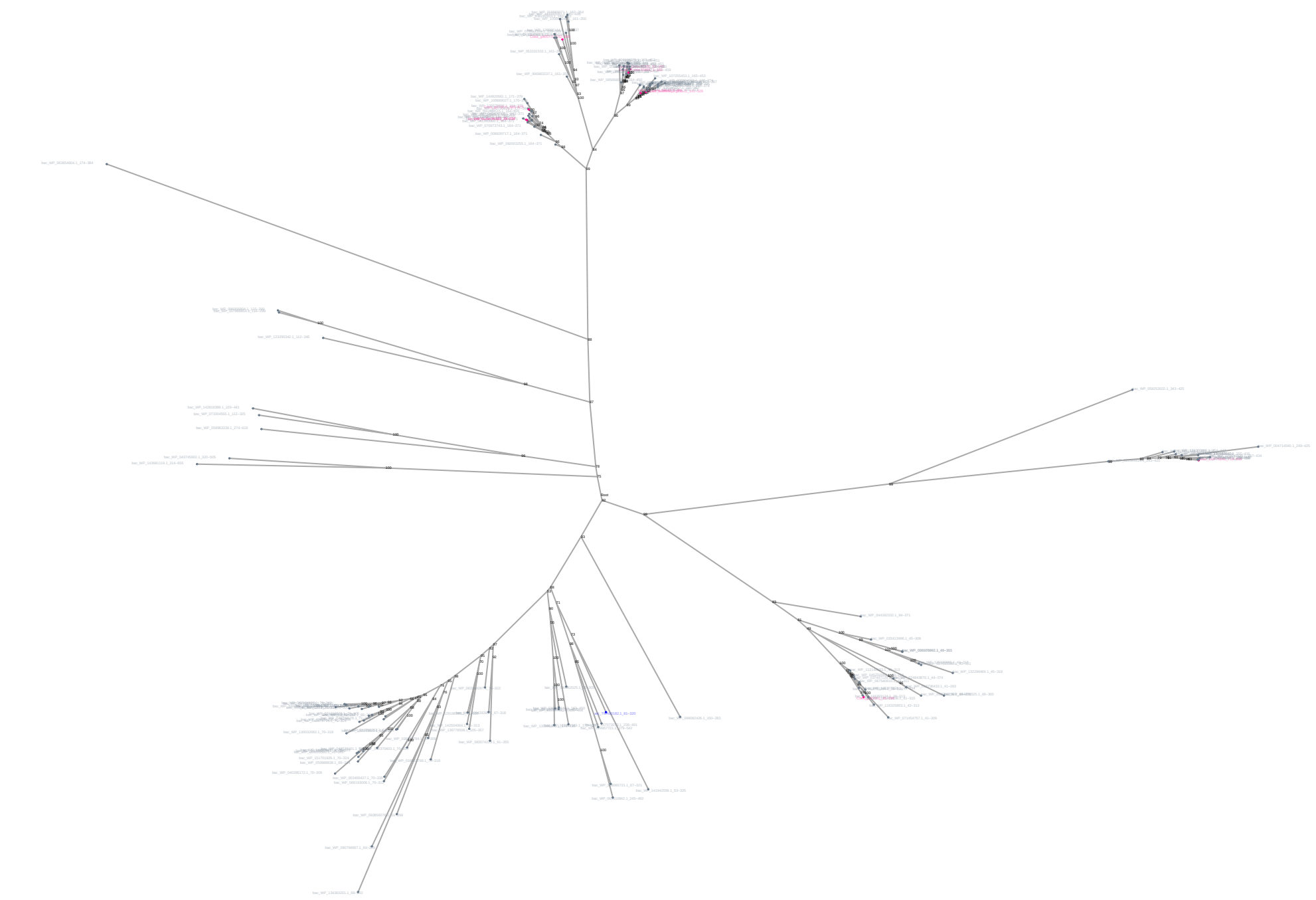


1

SNF2_N
euk.SNF2_N.phy.HG20.seqs.iqtree.treefile
n=169 sequences

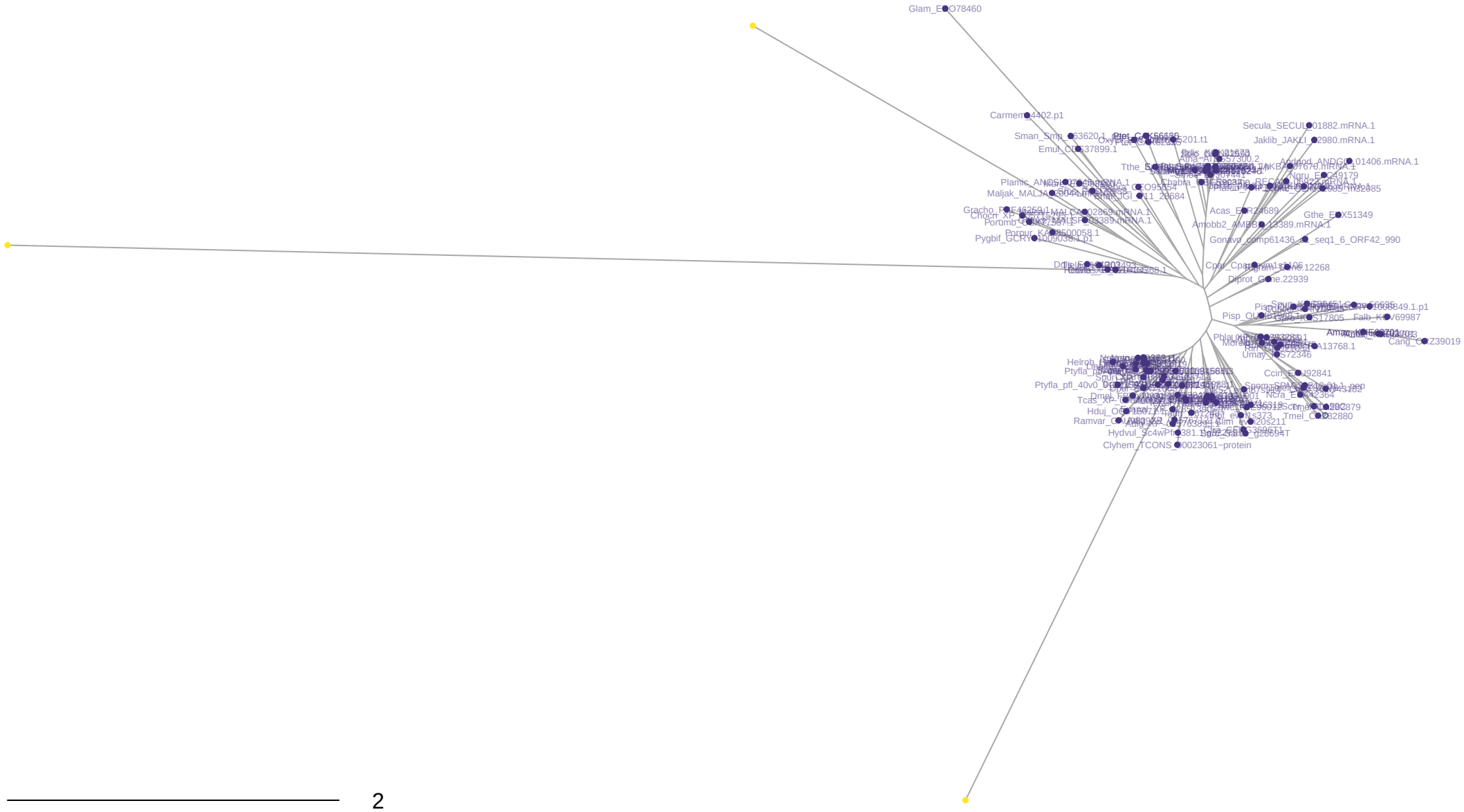

1

SNF2_N
euk.SNF2_N.phy.HG21.seqs.iqtree.treefile
n=153 sequences


bac_WP_063654604.1_274–384
bac_WP_123290343.1_112–345
bac_WP_142816388.1_103–441
bac_WP_073304655.1_112–325
bac_WP_058962239.1_274–416
bac_WP_043745932.1_305–505
bac_WP_143691119.1_314–455
bac_WP_144820660.1_271–370
bac_WP_005668627.1_170–371
bac_WP_086509717.1_164–371
bac_WP_092003255.1_164–371
bac_WP_044282332.1_94–371
bac_WP_032413966.1_45–308
bac_WP_132396469.1_45–318
bac_WP_057454757.1_41–309
bac_WP_058253932.1_343–425
bac_WP_004716540.1_249–425
bac_WP_141942568.1_53–325
bac_WP_130332082.1_70–316
bac_WP_086193006.1_70–312
bac_WP_040286172.1_70–309
bac_WP_086577…_91–355
bac_WP_134383201.1_69–…
bac_WP_099092436.1_100–283
Root
1

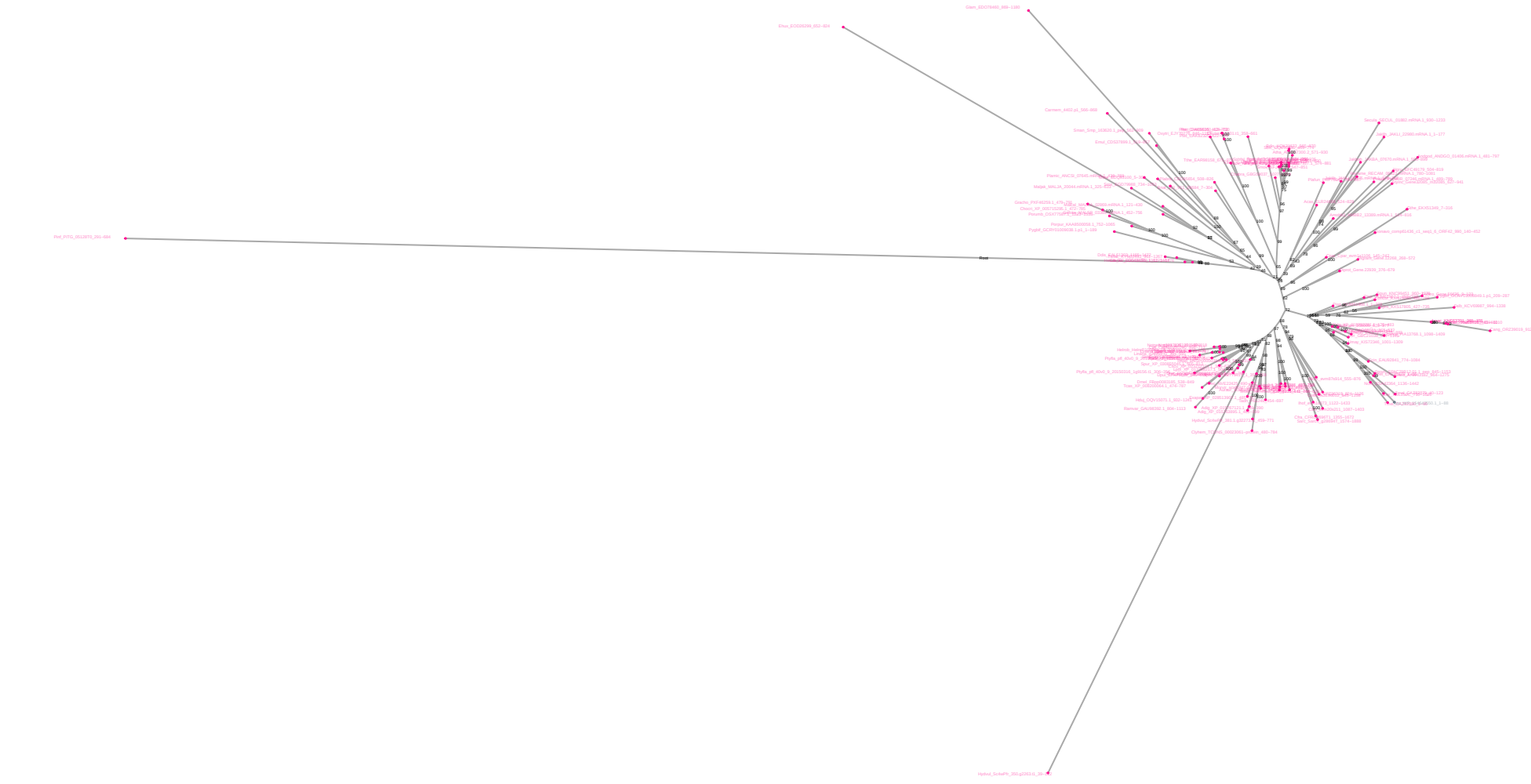
SNF2_N
euk.SNF2_N.phy.HG22.seqs.iqtree.treefile
n=138 sequences

eukaryotes
archaea
bacteria



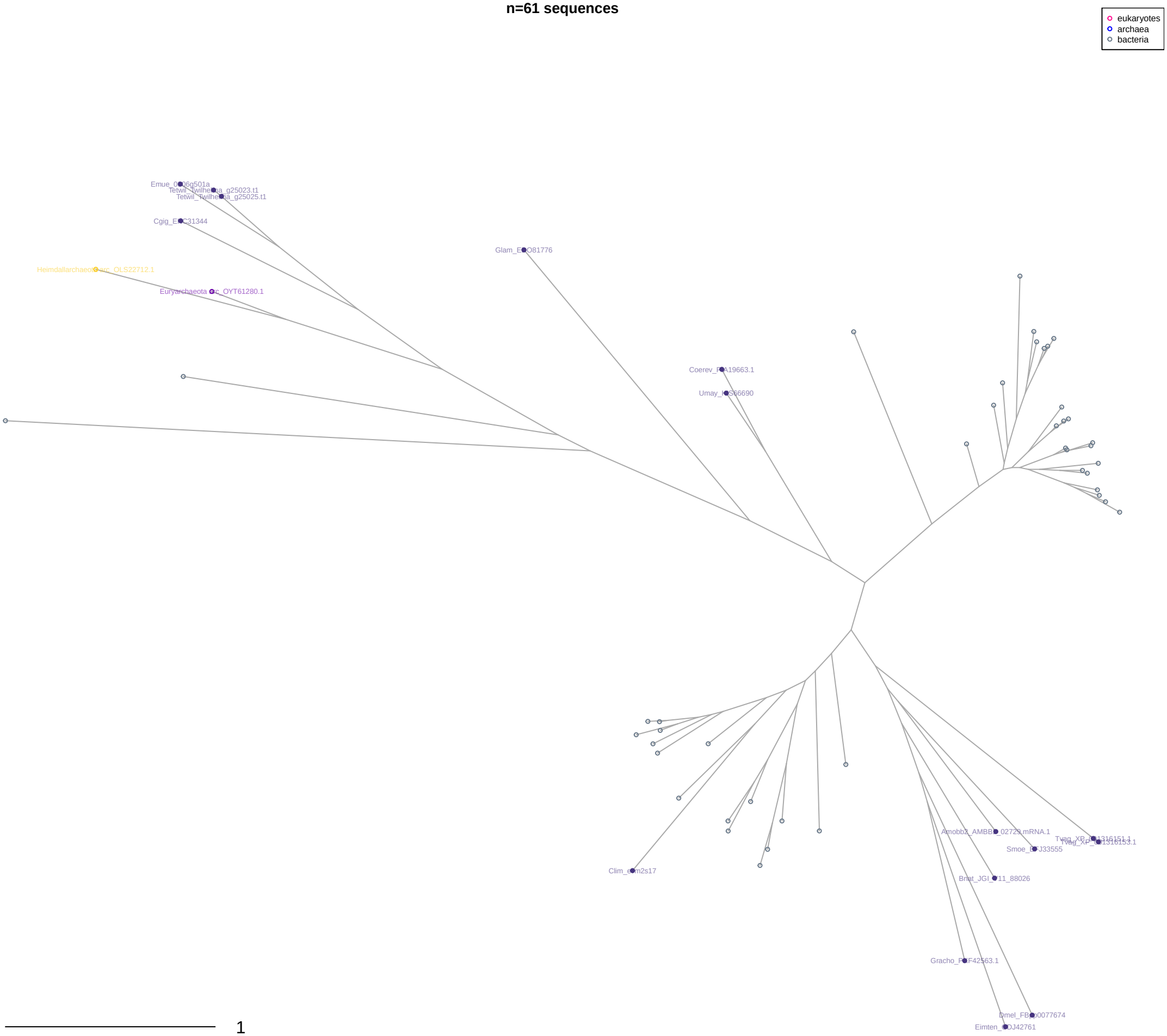
SNF2_N.HG13.0:INO80 n = 134
other n = 3

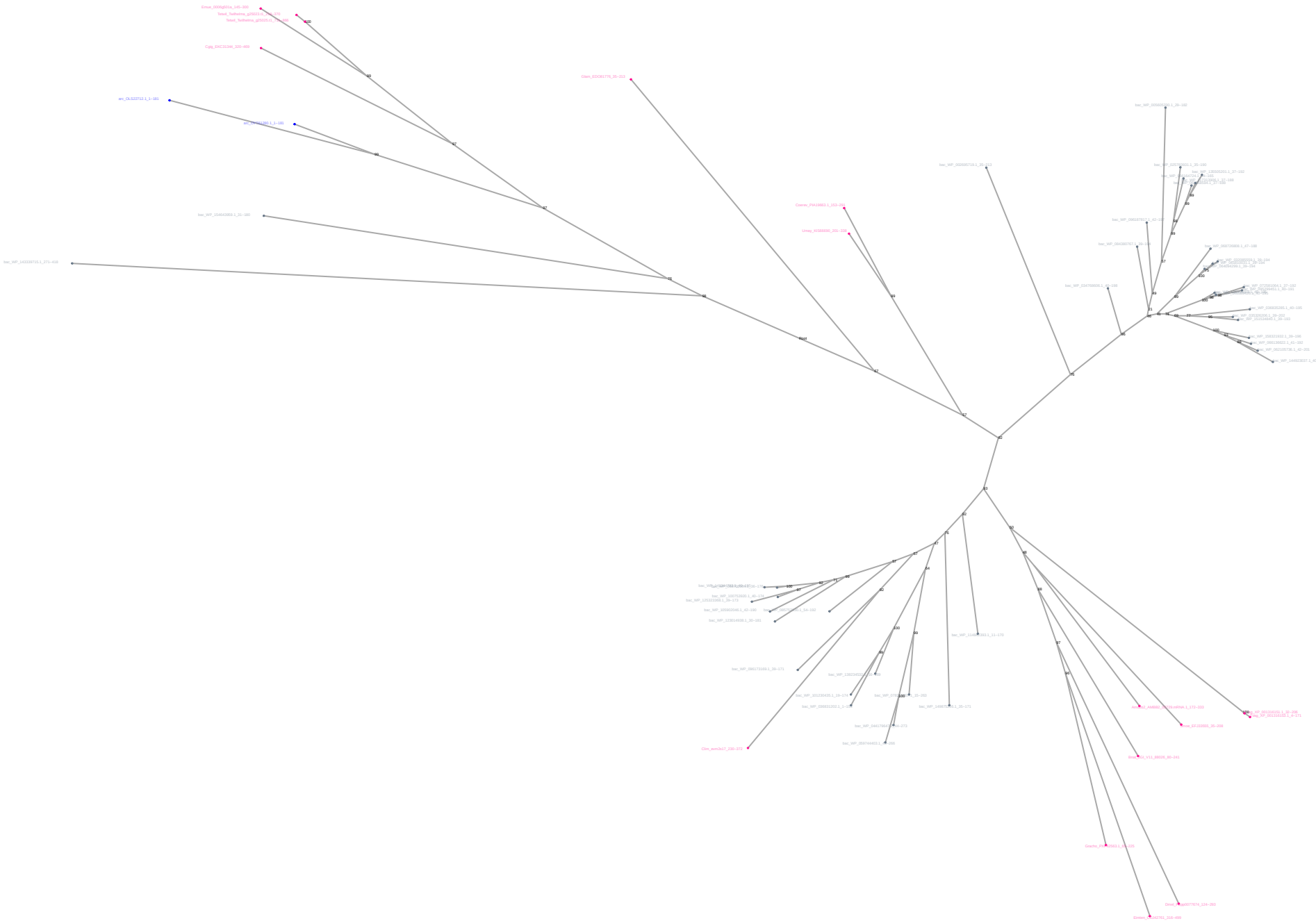
n =


Glam_EDO78460_869–1180
Ehux_EOD05299_652–824
Carmem_4402.p1_566–868
Smain_Snip_163835.1_p1_2–209
Emul_CDG37660.1_1–228
Tthe_EAR86100_870–1
Nadpl_MAL2A_20044.mRNA.1_325–632
Gracho_PRF46259.1_479–778
Chorri_XP_005715295.1_472–771
Pirspec_KAA8580658.1_752–1060
Pyglef_GCRY01009038.1.p1_1–189
Root
Pod_PITG_05128T0_291–684
Sinvem_comp91438_c1_seq1_6_ORF42_960_140–402
Sinvem_Gene.22939_376–679
Sinvem_Gene.22939_369–372
Sinvem_KIG72346_1051–1309
Sinvem_EAL80841_774–1084
Sinvem_KIG72346_1136–1442
Sinvem_KIG72346_1322–1433
Sinvem_KIG72346_1087–1403
Hyahyal_ScHaPh_350.g23631.t1_39–457

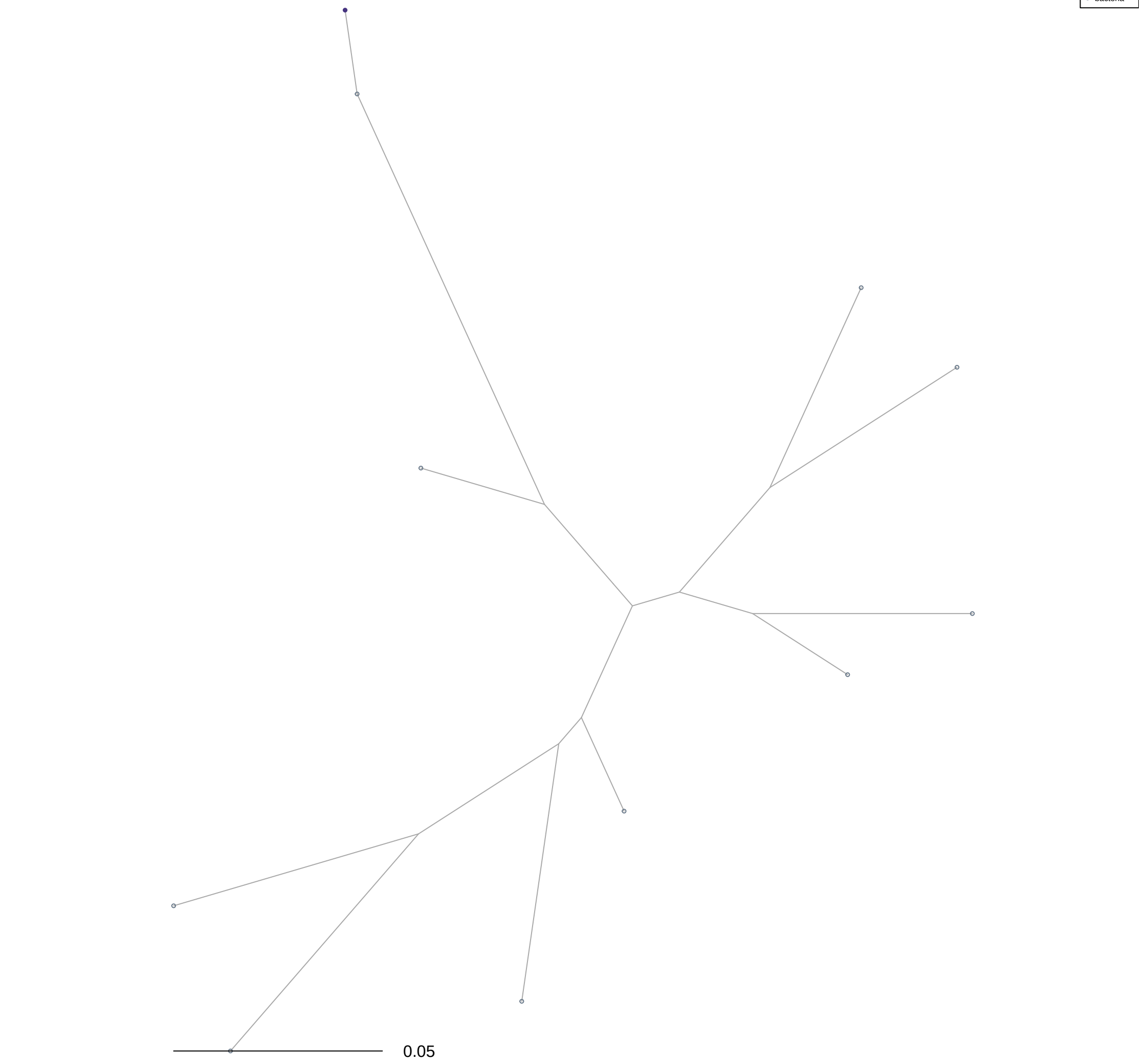
2

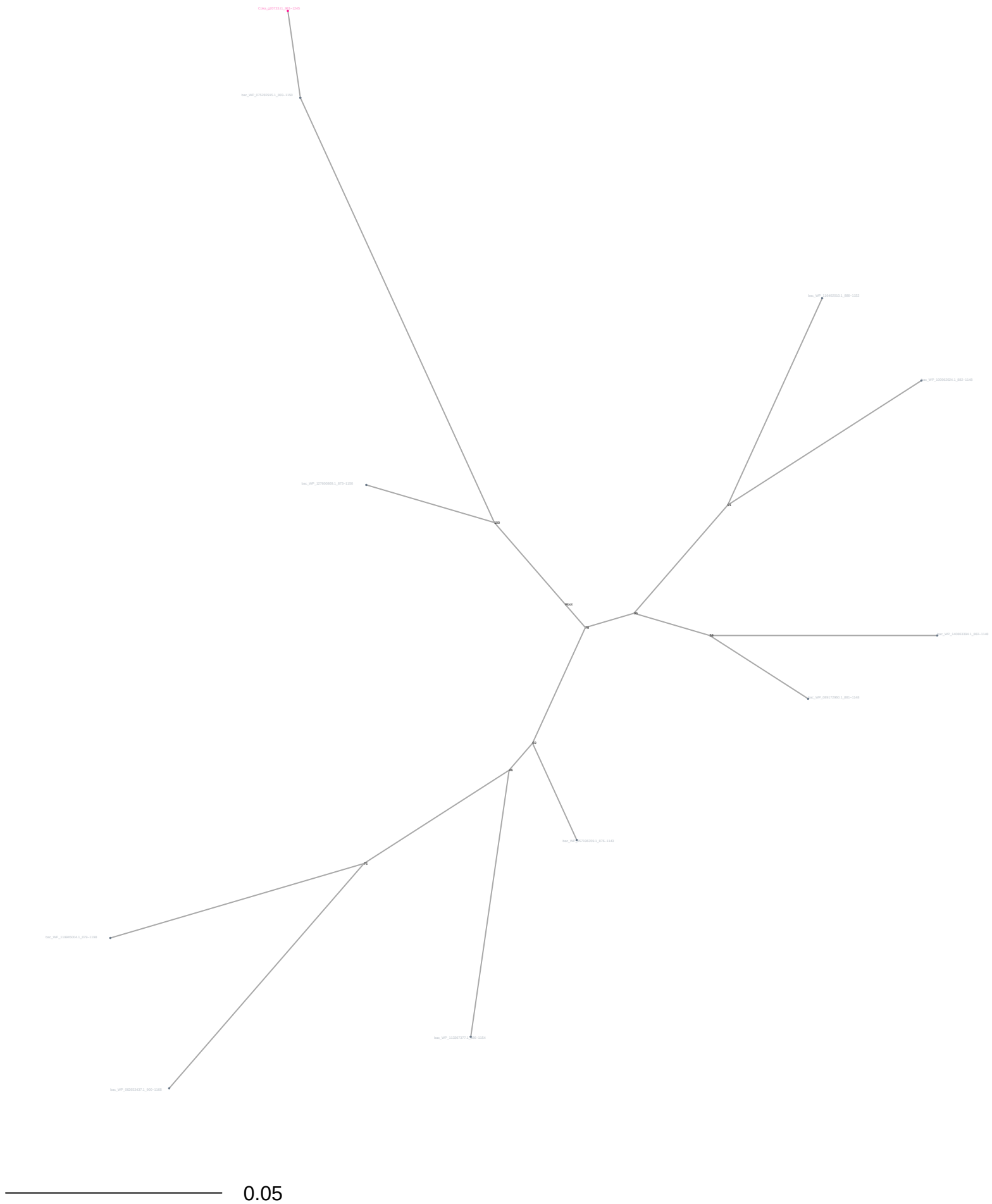
SNF2_N
euk.SNF2_N.phy.HG23.seqs.iqtree.treefile
n=61 sequences




Ecrue_G000gd00a_145–305
Tetwd_Tedhelma_g05023.t1_1–150
Tetwd_Tedhelma_g05025.t1_1–150
Cpig_EXC31344_320–469
arc_OLS27712.1_1–181
arc_OLS41280.1_1–181
bac_WP_154643959.1_31–180
bac_WP_143339715.1_271–419
Glam_EDO81776_35–203
Cseney_PIA19683.1_152–302
Umay_KIS66680_203–333
bac_WP_002695719.1_32–183
bac_WP_005503230.1_39–192
bac_WP_005503231.1_35–190
bac_WP_135365354.1_37–192
bac_WP_013119063.1_33–188
bac_WP_066187817.1_42–197
bac_WP_054350797.1_36–190
bac_WP_068726858.1_47–188
bac_WP_034769506.1_35–190
bac_WP_075951064.1_37–192
bac_WP_005239463.1_95–242
bac_WP_036835265.1_40–195
bac_WP_013302456.1_39–202
bac_WP_151534840.1_39–193
bac_WP_158121932.1_39–196
bac_WP_066136622.1_41–192
bac_WP_062165736.1_42–201
bac_WP_144603537.1_40–199
bac_WP_005503233.1_32–206
Aeq_WP_005316333.1_8–174
Aae_XP_015955_35–208
Bmal_V11_68026_80–241
Gracho_PIA12563.1_41–225
Dmel_NP_001077674_124–283
Elmtem_TCA02761_316–499
1

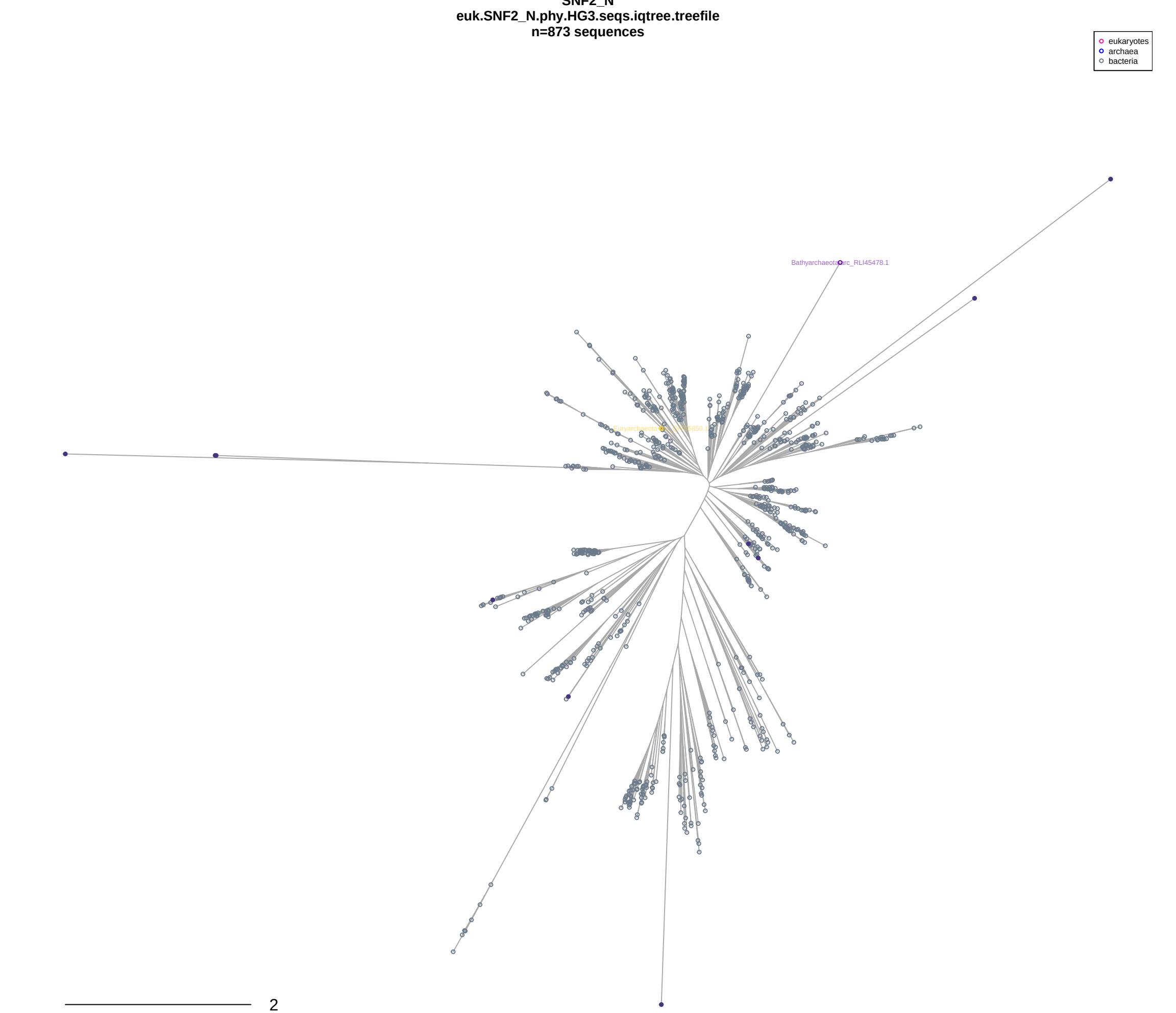
SNF2_N
euk.SNF2_N.phy.HG24.seqs.iqtree.treefile
n=11 sequences

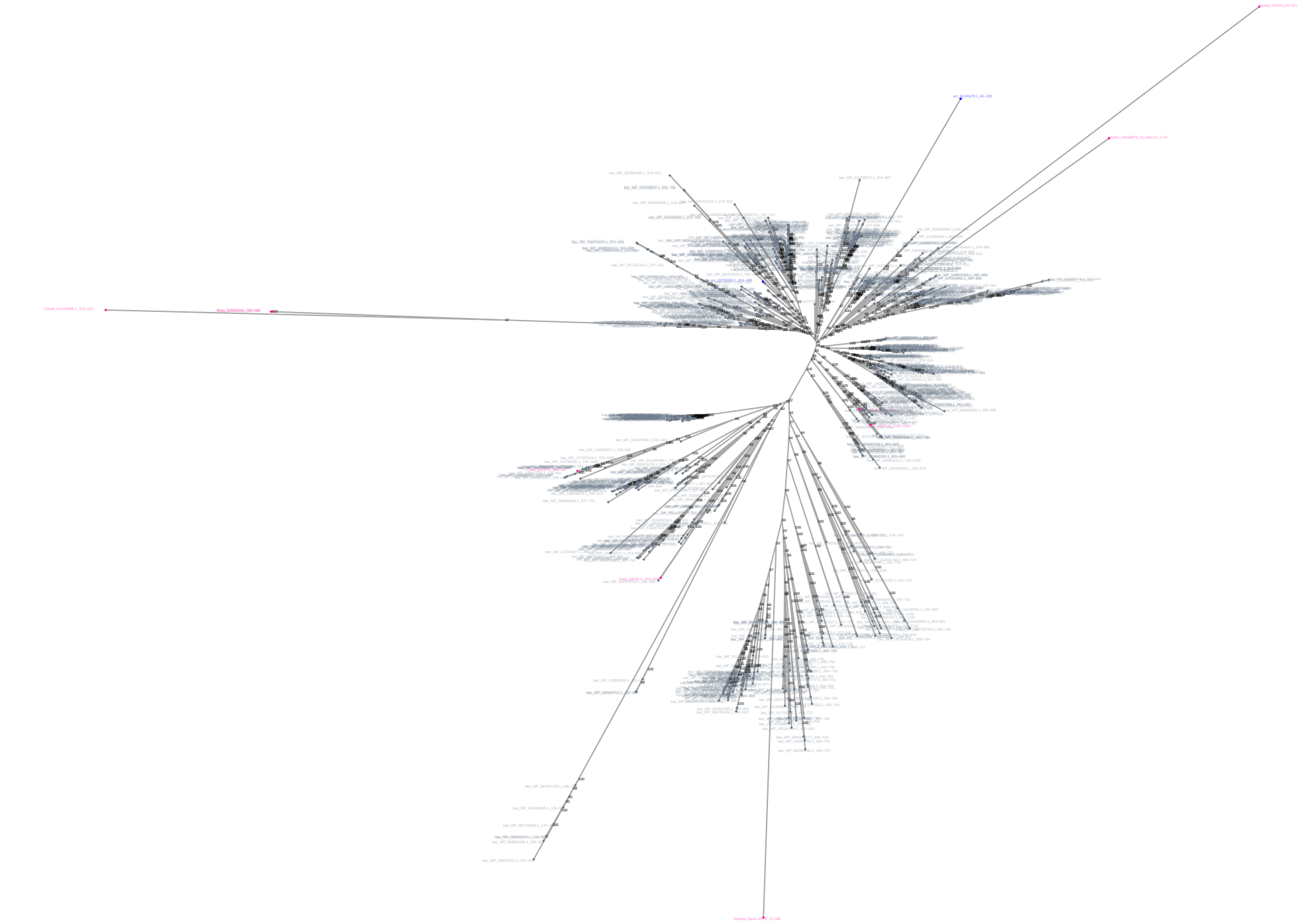



Coka_g2073141_881-1245
bac_WP_075282915.1_883-1150
bac_WP_116402010.1_886-1152
bac_WP_100962024.1_882-1148
bac_WP_127600869.1_873-1150
100
81
Root
79
56
53
bac_WP_140863394.1_882-1148
bac_WP_089172960.1_881-1148
69
61
bac_WP_057196359.1_876-1143
76
bac_WP_119845004.1_879-1198
bac_WP_112367377.1_886-1154
bac_WP_062653437.1_900-1168

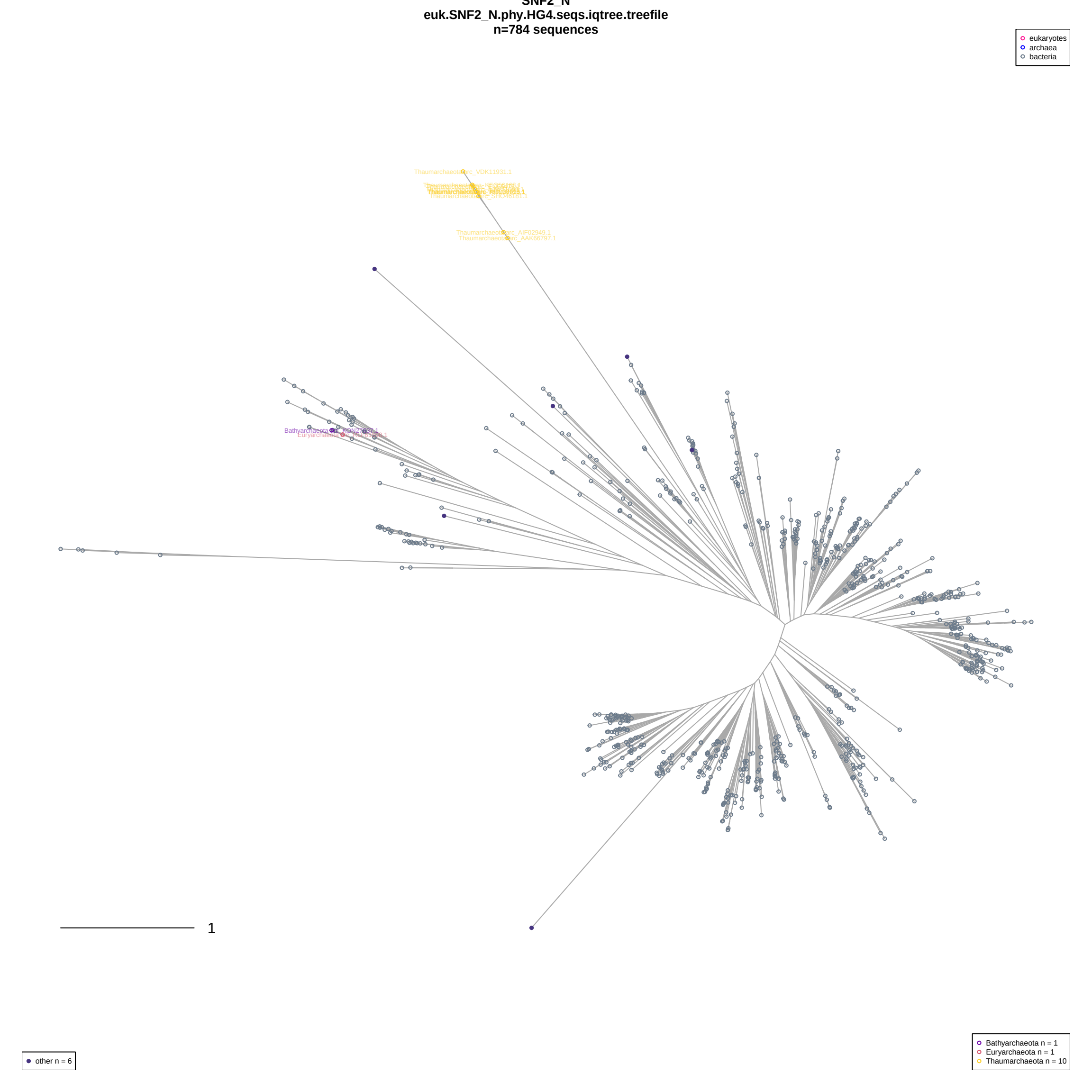
0.05

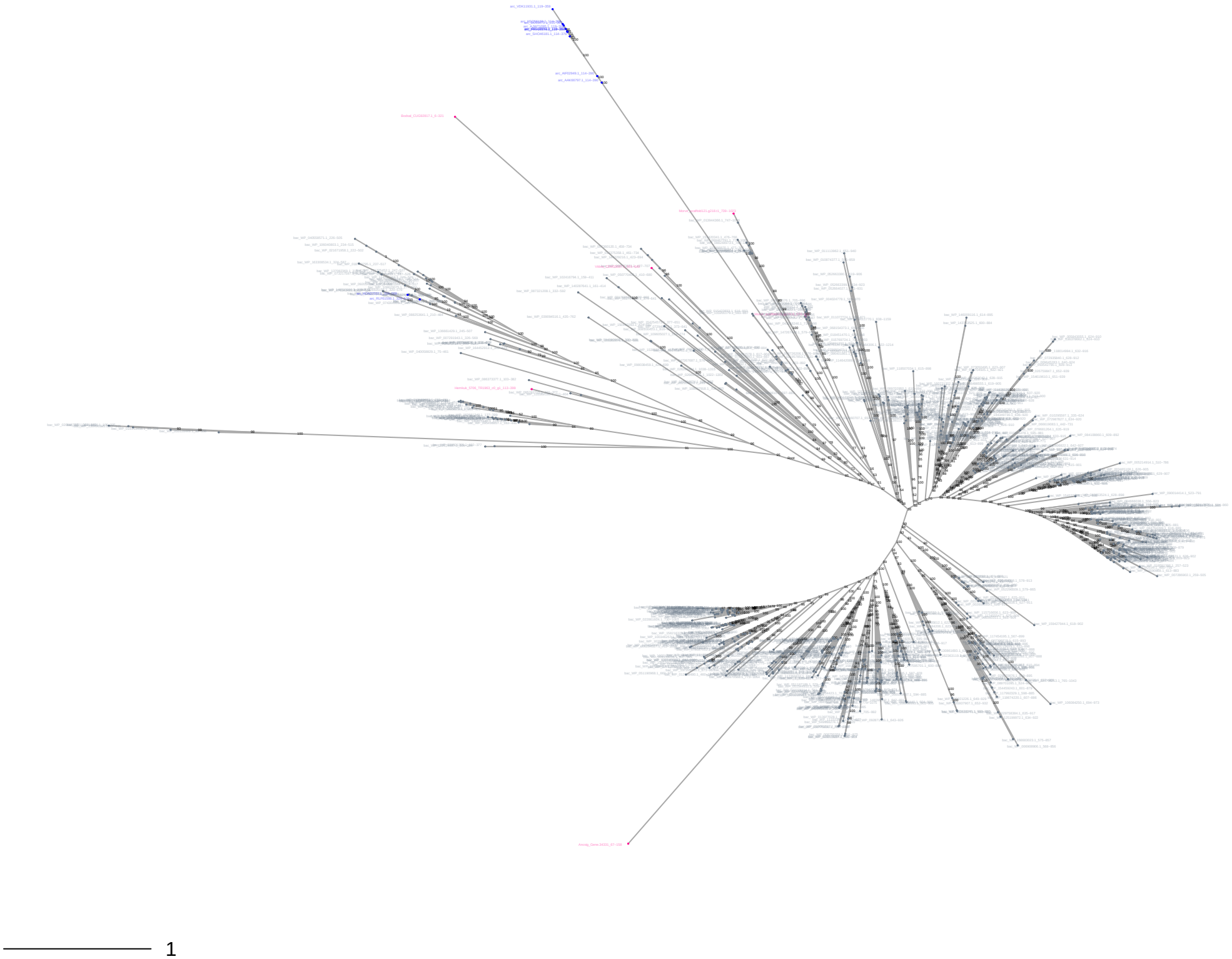
SNF2_N
euk.SNF2_N.phy.HG3.seqs.iqtree.treefile
n=873 sequences



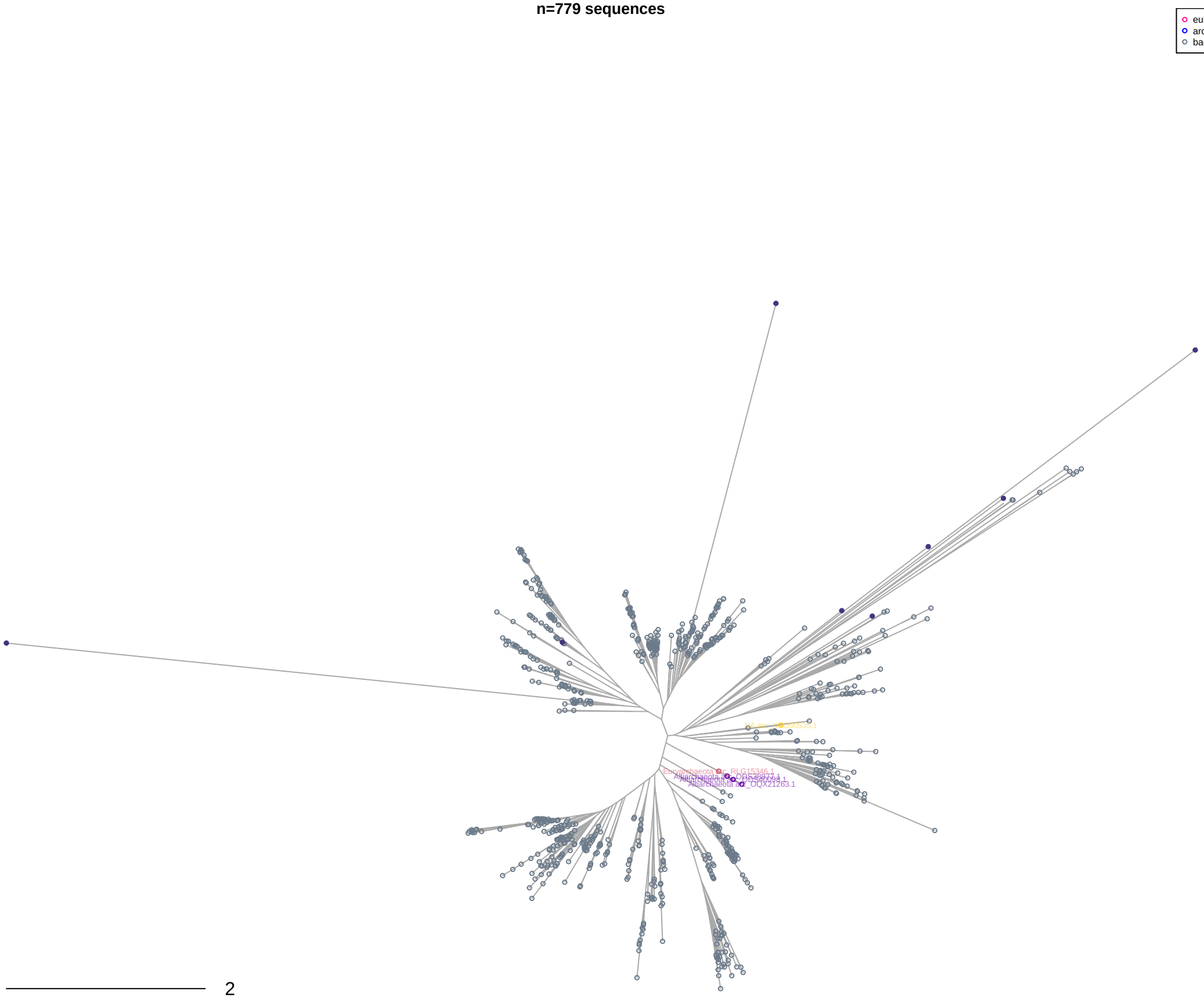


2


SNF2_N
euk.SNF2_N.phy.HG4.seqs.iqtree.treefile
n=784 sequences
eukaryotes
archaea
bacteria
Thaumarchaeota_arc_VDK11931.1
Thaumarchaeota_arc_AIF02949.1
Thaumarchaeota_arc_AAK66797.1
Bathyarchaeota_arc_KON27037.1
Euryarchaeota_arc_KEE61698.1
1
other n = 6
Bathyarchaeota n = 1
Euryarchaeota n = 1
Thaumarchaeota n = 10

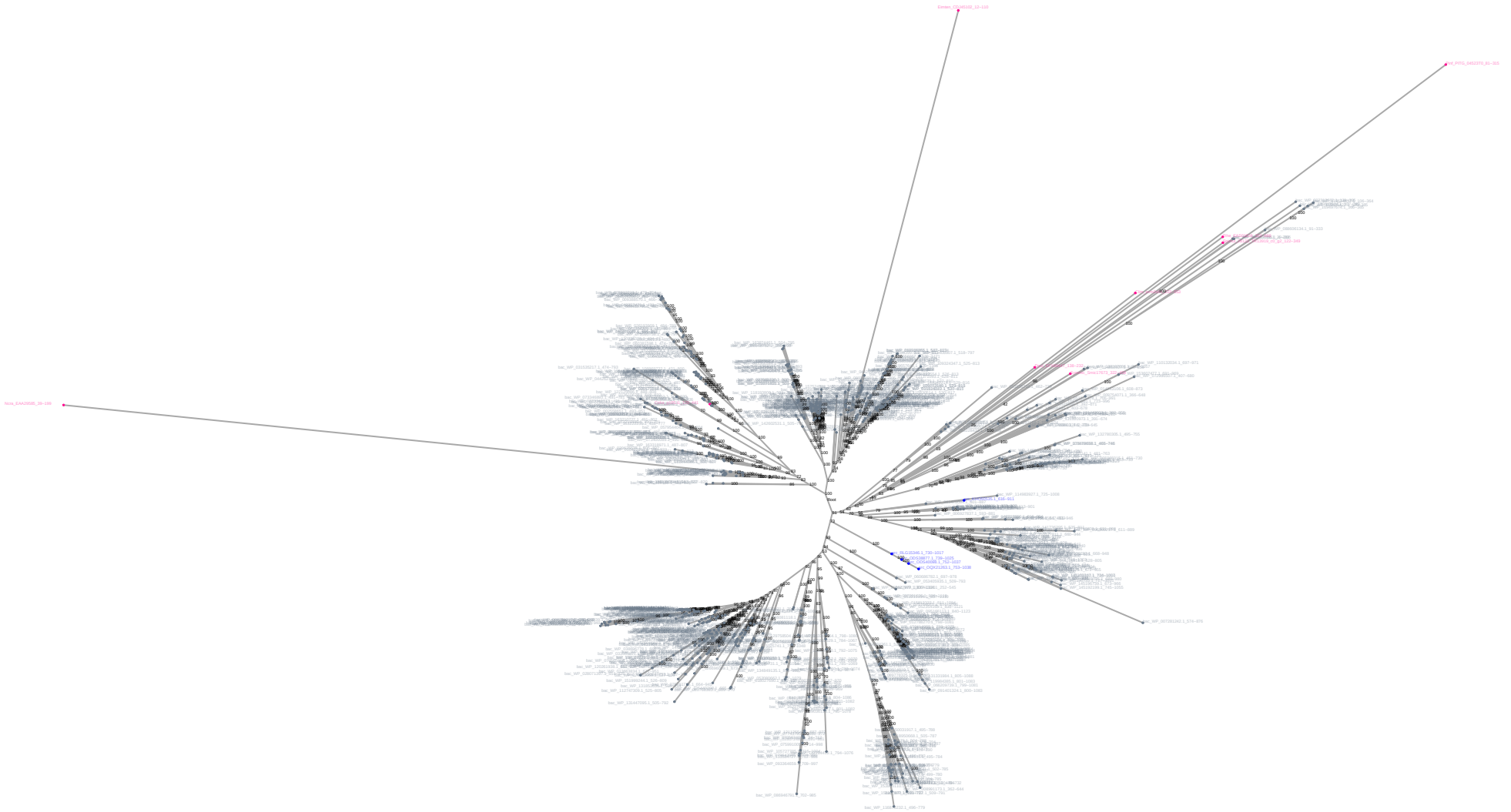

1

SNF2_N
euk.SNF2_N.phy.HG5.seqs.iqtree.treefile
n=779 sequences



other n = 8

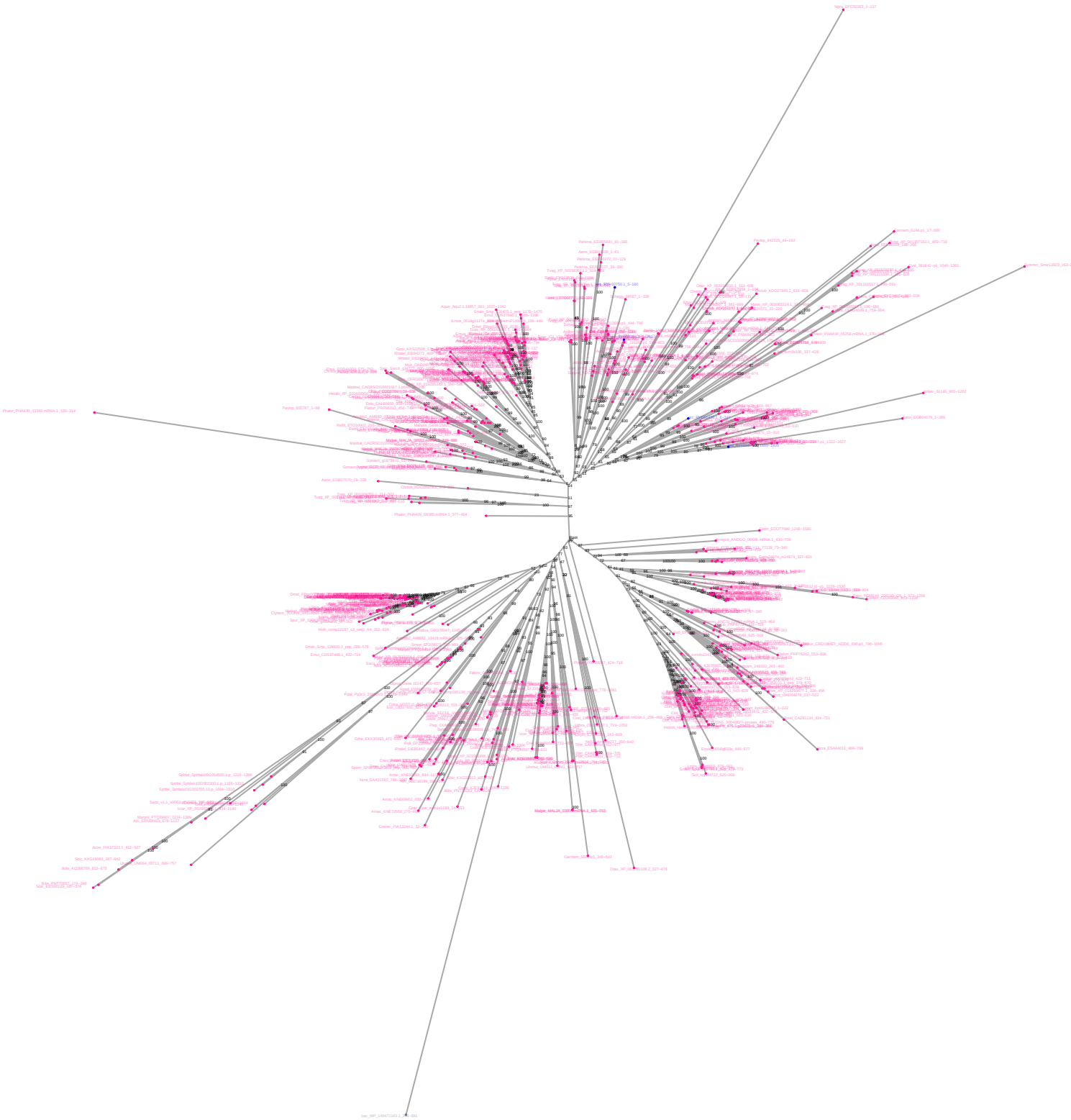
Altiarchaeota n = 3
Euryarchaeota n = 1
NA n = 1



2

SNF2_N
euk.SNF2_N.phy.HG6.seqs.iqtree.treefile
n=613 sequences

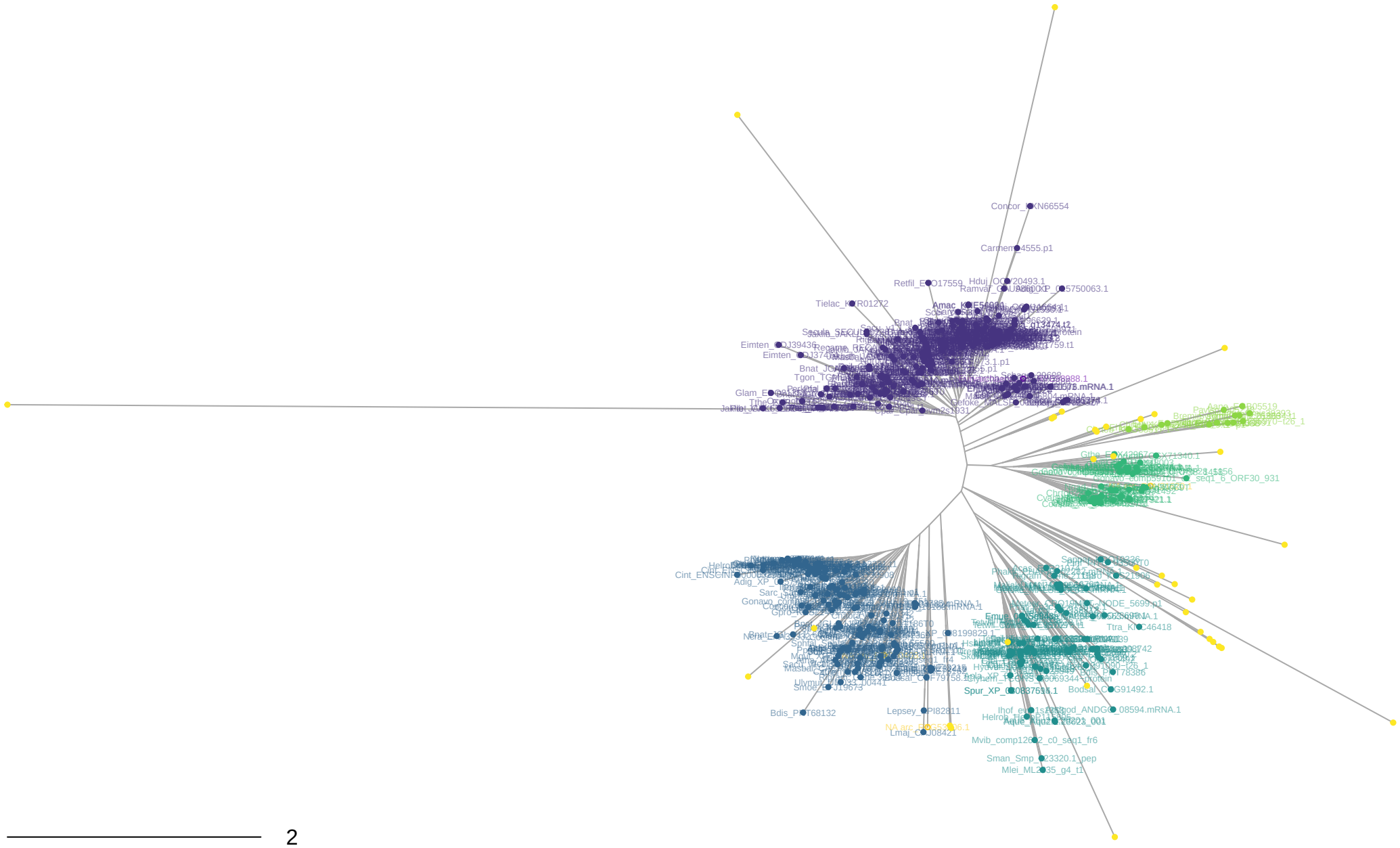
eukaryotes
archaea
bacteria
Phakir_PHAKIP_13392.mRNA.1
Aano_EOB03126
Pavlsp_042225
Tvag_XP_001307162.1
Ngru_EOC38554
Tvag_XP_001321894.1
Tvag_XP_001315517.1
Ngru_EOC44174
Otau_XP_003074615.1
Chrtob_KOO27945.1
Tvag_XP_001326267.1
Chrtob_KOO31071
Chrtob_KOO24267.1
Schag_98587
Retfil_EOO6771
Aque_Aqu2_18657_001
Smar_Smp_090770.1.pep
Emue_Emue_P14739
Dmel_FBpp0289115
Chrtob_KOO31956
Chrtob_KOO27454
Chrtob_KOO31956
Chrtob_KOO27454
Chrtob_KOO31956
Chrtob_KOO27454



1

SNF2_N
euk.SNF2_N.phy.HG7.seqs.iqtree.treefile
n=536 sequences

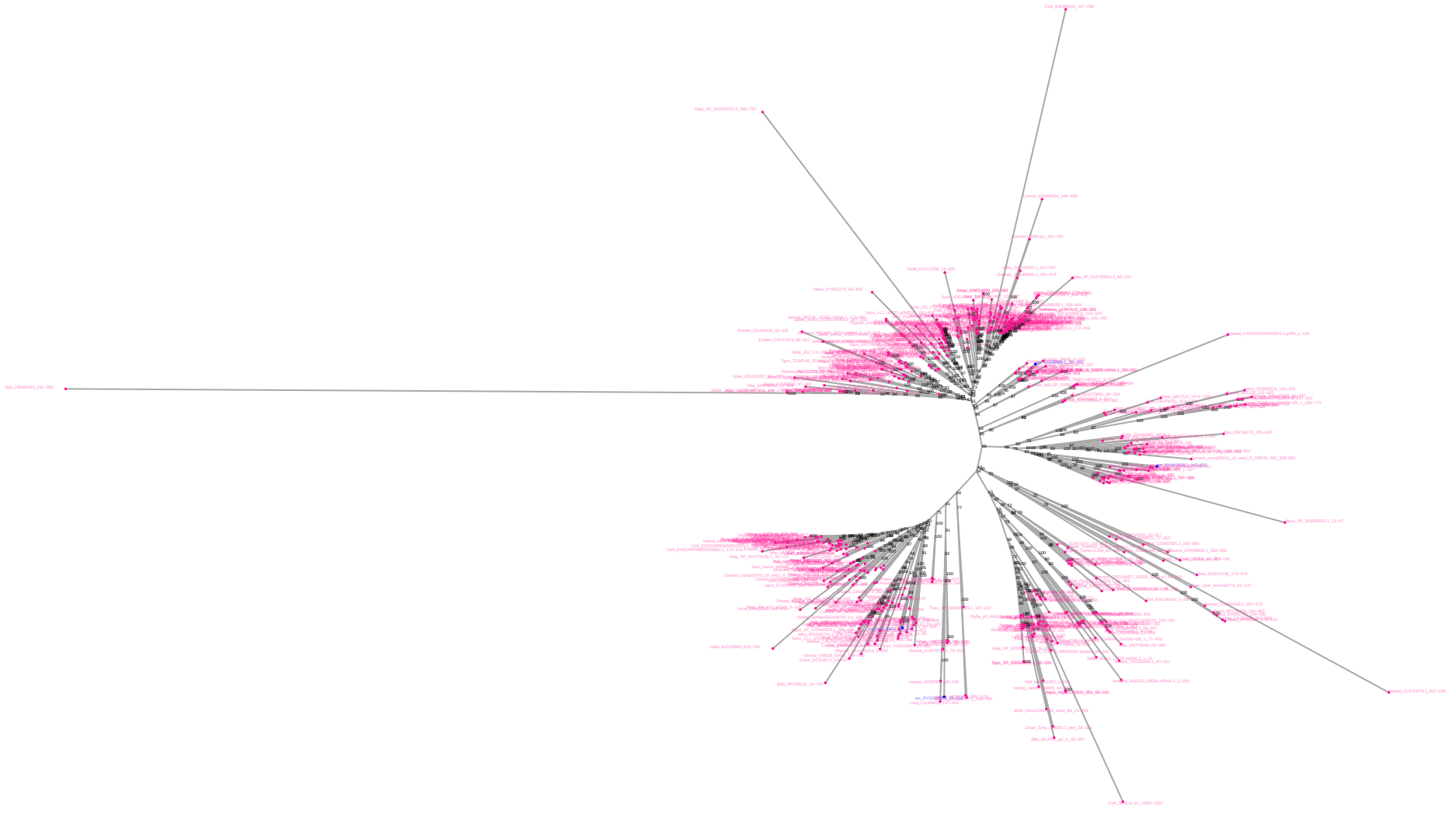
eukaryotes
archaea
bacteria



2

SNF2_N.HG2.10:SMARCA1/SMARCA5 n = 230
SNF2_N.HG2.3:HELLS n = 134
SNF2_N.HG2.0:CHD1L n = 78
SNF2_N.HG2.15:like:SMARCA1/SMARCA5:likeclu:10 n = 41
SNF2_N.HG2.12:like:SMARCA1/SMARCA5:likeclu:10 n = 14
other n = 35

Euryarchaeota n = 1
NA n = 3



2

SNF2_N
euk.SNF2_N.phy.HG8.seqs.iqtree.treefile
n=480 sequences

eukaryotes
archaea
bacteria

Bathyarchaeota arc_RLI41411.1

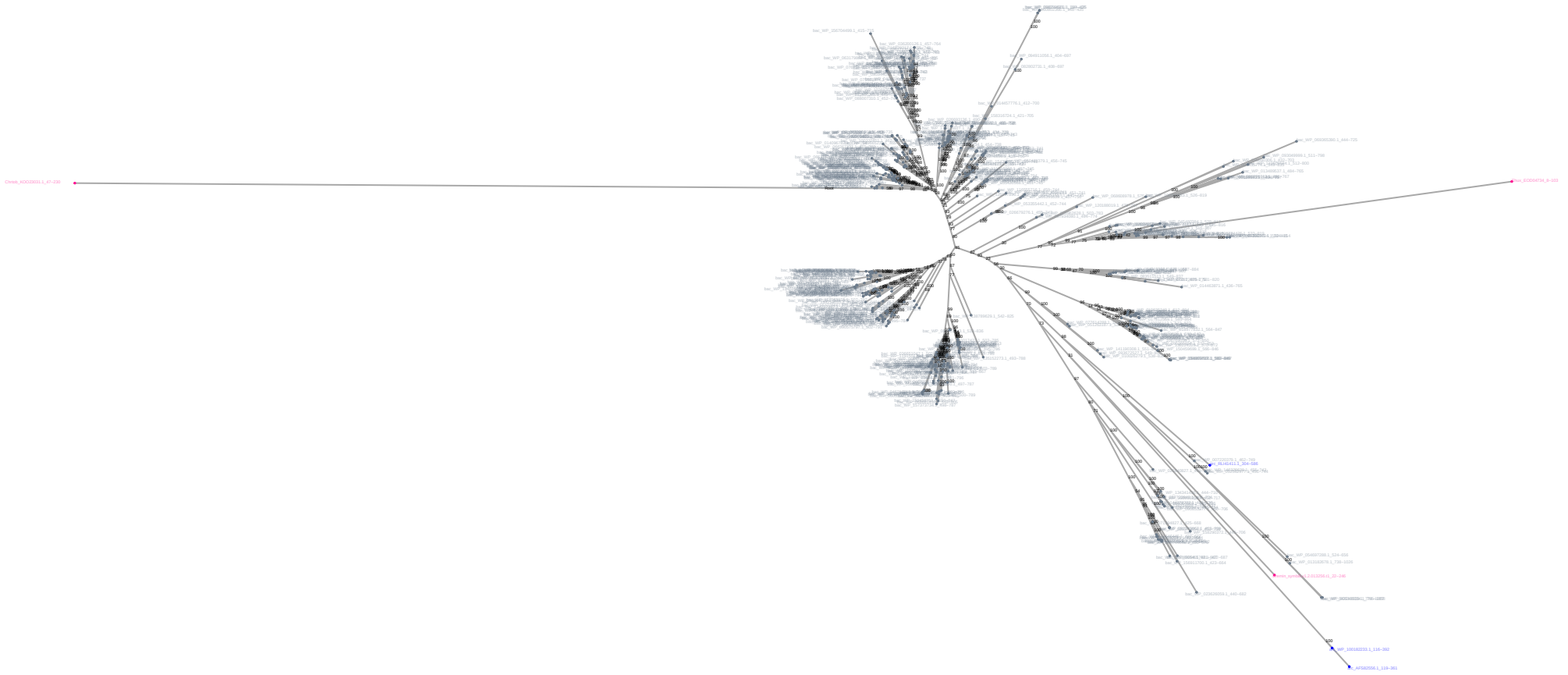
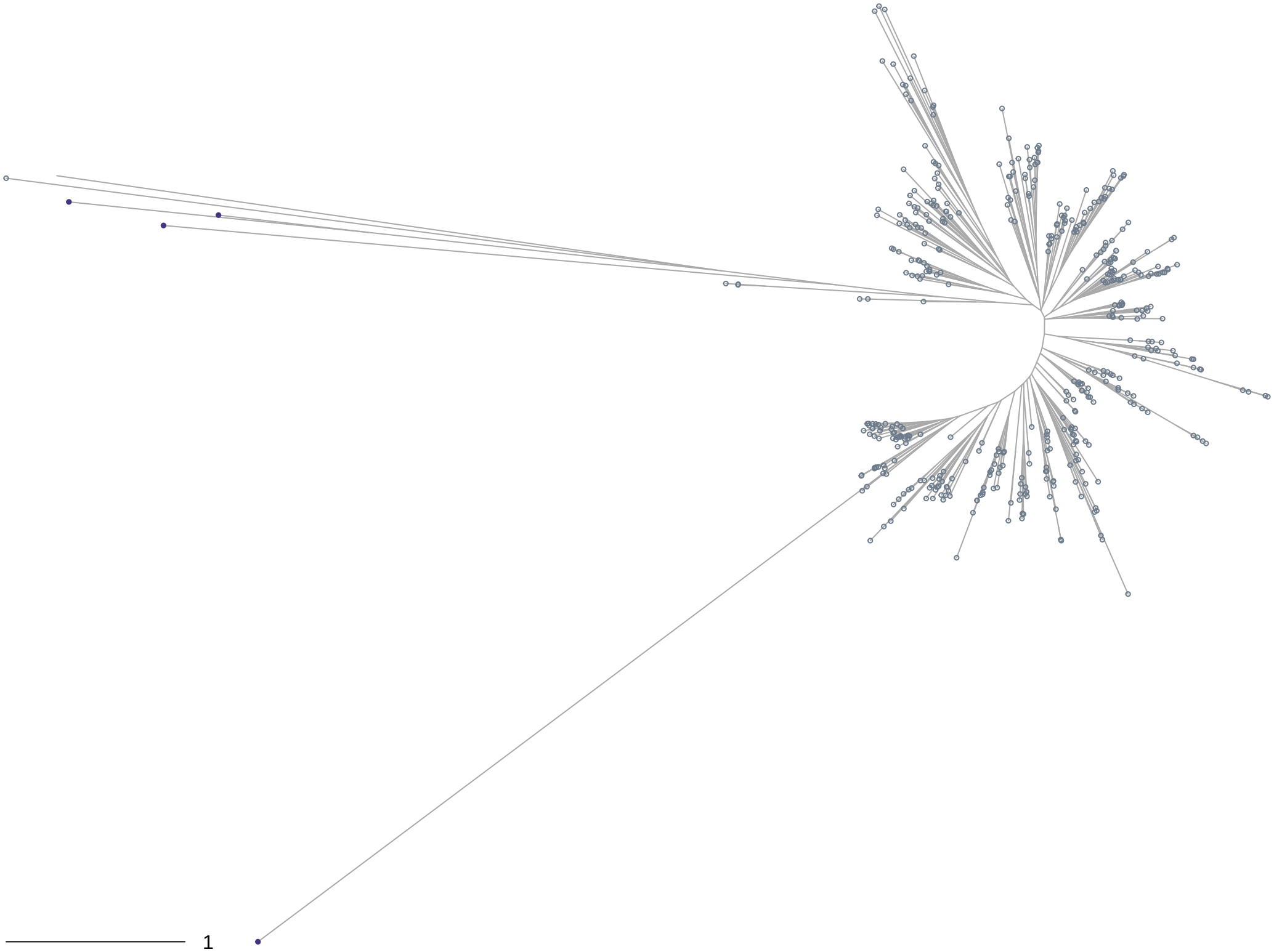
Thaumarchaeota arc_WP_100182233.1

Thaumarchaeota arc_AFS82556.1

5

other n = 3

Bathyarchaeota n = 1
Thaumarchaeota n = 2



SNF2_N
euk.SNF2_N.phy.HG9.seqs.iqtree.treefile
n=464 sequences