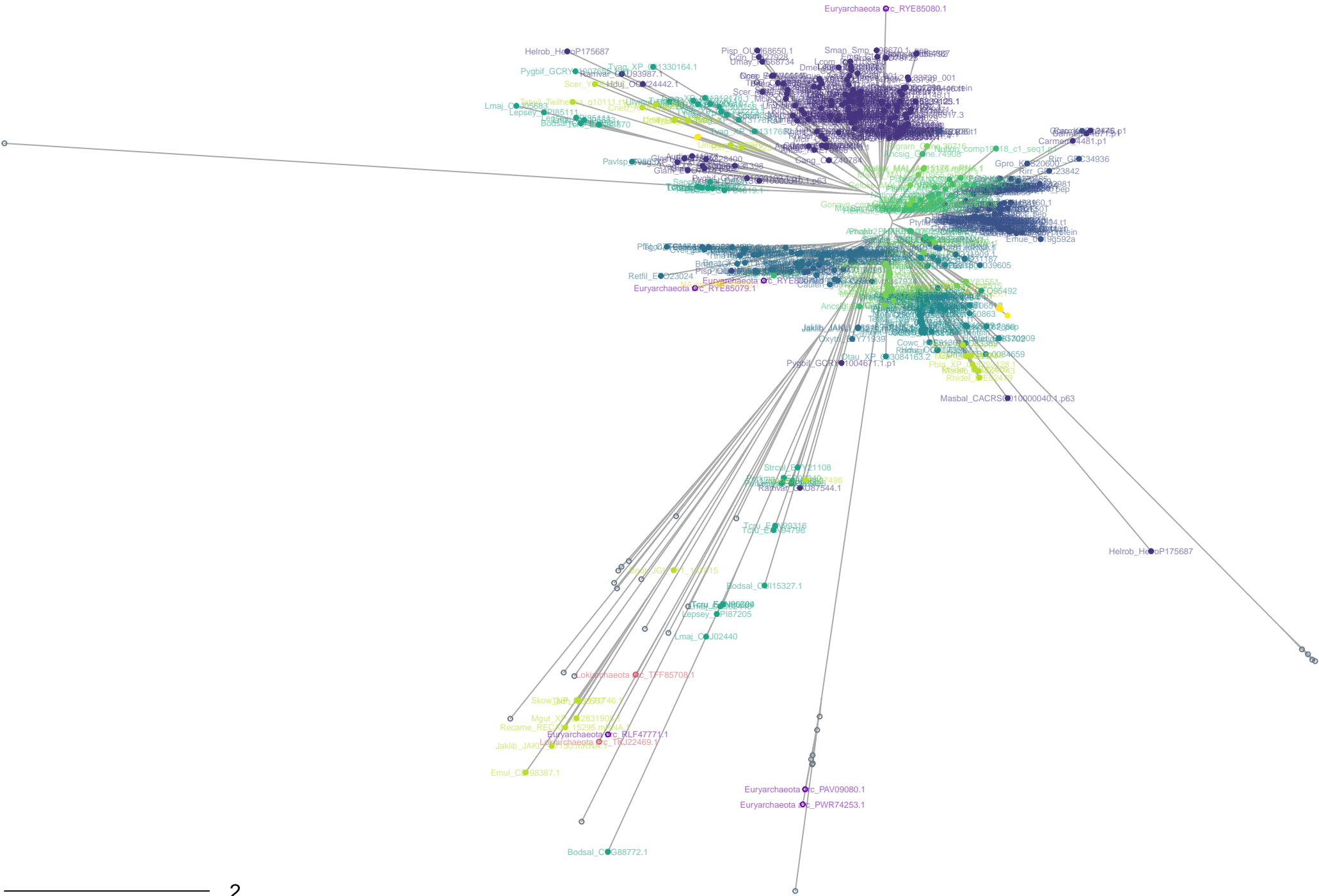


MOZ_SAS
euk.MOZ_SAS.phy.HG1.seqs.iqtree.treefile
n=553 sequences

- eukaryotes
- archaea
- bacteria



- MOZ_SAS.HG1.2:KAT6A/KAT6B/KAT7 n = 156
- MOZ_SAS.HG1.4:KAT5 n = 85
- MOZ_SAS.HG1.6:like:KAT5/KAT8:likeclu:4/5 n = 75
- MOZ_SAS.HG1.5:KAT8 n = 64
- MOZ_SAS.HG1.3:like:KAT5/KAT8:likeclu:4/5 n = 40
- MOZ_SAS.HG1.8:like:KAT5/KAT8:likeclu:4/5 n = 34
- MOZ_SAS.HG1.7:like:KAT5/KAT8:likeclu:4/5 n = 26
- MOZ_SAS.HG1.0:like:KAT5/KAT6A/KAT6B/KAT7/KAT8:likeclu:2/4/5 n = 24
- other n = 6

- Euryarchaeota n = 6
- Lokiarchaeota n = 2
- NA n = 4

