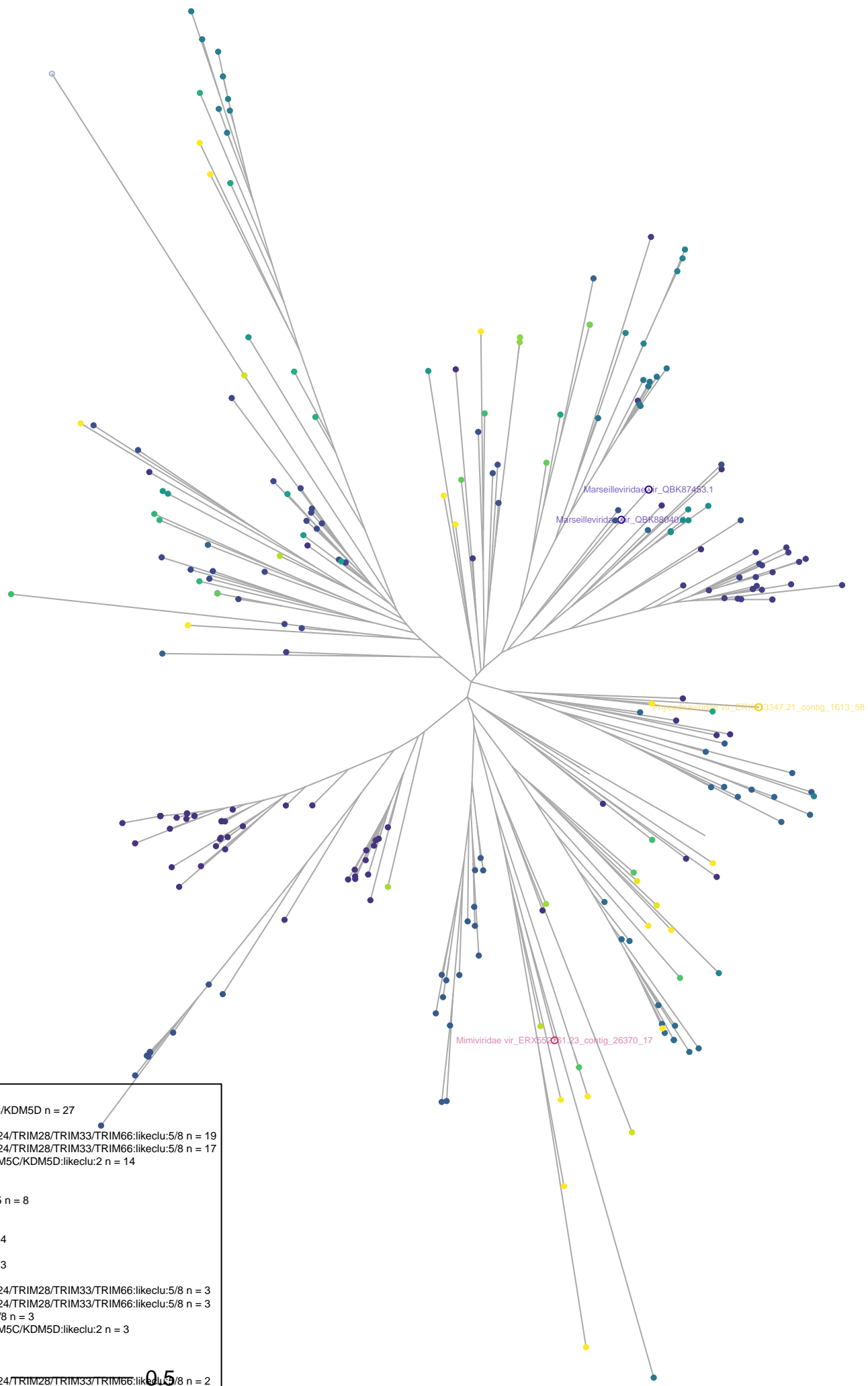


PHD  
vir.PHD.phy.HG1.seqs.iqtree.treefile  
n=260 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- PHD.HG4.5:BAZ1A/BAZ1B/BAZ2A/BAZ2B n = 60
- PHD.HG8.2:KDM4A/KDM4B/KDM4C/KDM5A/KDM5B/KDM5C/KDM5D n = 27
- PHD.HG4.0:PHRF1 n = 20
- PHD.HG4.2:like:BAZ1A/BAZ1B/BAZ2A/BAZ2B/SP140L/TRIM24/TRIM28/TRIM33/TRIM66:likeclu:5/8 n = 19
- PHD.HG4.4:like:BAZ1A/BAZ1B/BAZ2A/BAZ2B/SP140L/TRIM24/TRIM28/TRIM33/TRIM66:likeclu:5/8 n = 17
- PHD.HG8.1:like:KDM4A/KDM4B/KDM4C/KDM5A/KDM5B/KDM5C/KDM5D:likeclu:2 n = 14
- PHD.HG6.4:PHF10 n = 11
- PHD.HG15.1:like:RSF1:likeclu:0 n = 9
- PHD.HG3.9:like:AIRE/PHF12/PHF21A/PHF21B:likeclu:8/12/15 n = 8
- PHD.HG14.1:UHRF1/UHRF2 n = 7
- PHD.HG24.0:NA n = 6
- PHD.HG3.1:like:AC006064.6/CHD3/CHD4/CHD5:likeclu:4 n = 4
- PHD.HG14.0:like:UHRF1/UHRF2:likeclu:1 n = 3
- PHD.HG3.2:like:AC006064.6/CHD3/CHD4/CHD5:likeclu:4 n = 3
- PHD.HG3.21:like:PHF12/PHF21A/PHF21B:likeclu:12/15 n = 3
- PHD.HG4.1:like:BAZ1A/BAZ1B/BAZ2A/BAZ2B/SP140L/TRIM24/TRIM28/TRIM33/TRIM66:likeclu:5/8 n = 3
- PHD.HG4.3:like:BAZ1A/BAZ1B/BAZ2A/BAZ2B/SP140L/TRIM24/TRIM28/TRIM33/TRIM66:likeclu:5/8 n = 3
- PHD.HG6.0:like:DPF1/DPF2/KAT6A/KAT6B/PHF10:likeclu:4/6/8 n = 3
- PHD.HG8.0:like:KDM4A/KDM4B/KDM4C/KDM5A/KDM5B/KDM5C/KDM5D:likeclu:2 n = 3
- PHD.HG9.1:NA n = 3
- PHD.HG1.1:CXXC1/DIDO1/PHF3 n = 2
- PHD.HG19.0:NA n = 2
- PHD.HG4.6:like:BAZ1A/BAZ1B/BAZ2A/BAZ2B/SP140L/TRIM24/TRIM28/TRIM33/TRIM66:likeclu:5/8 n = 2
- PHD.HG6.2:like:DPF1/DPF2/KAT6A/KAT6B/PHF10:likeclu:4/6/8 n = 2
- PHD.HG6.7:like:KAT6A/KAT6B:likeclu:8 n = 2
- other n = 16

- Marseilleviridae n = 2
- Mimiviridae n = 1
- Phycodnaviridae n = 1