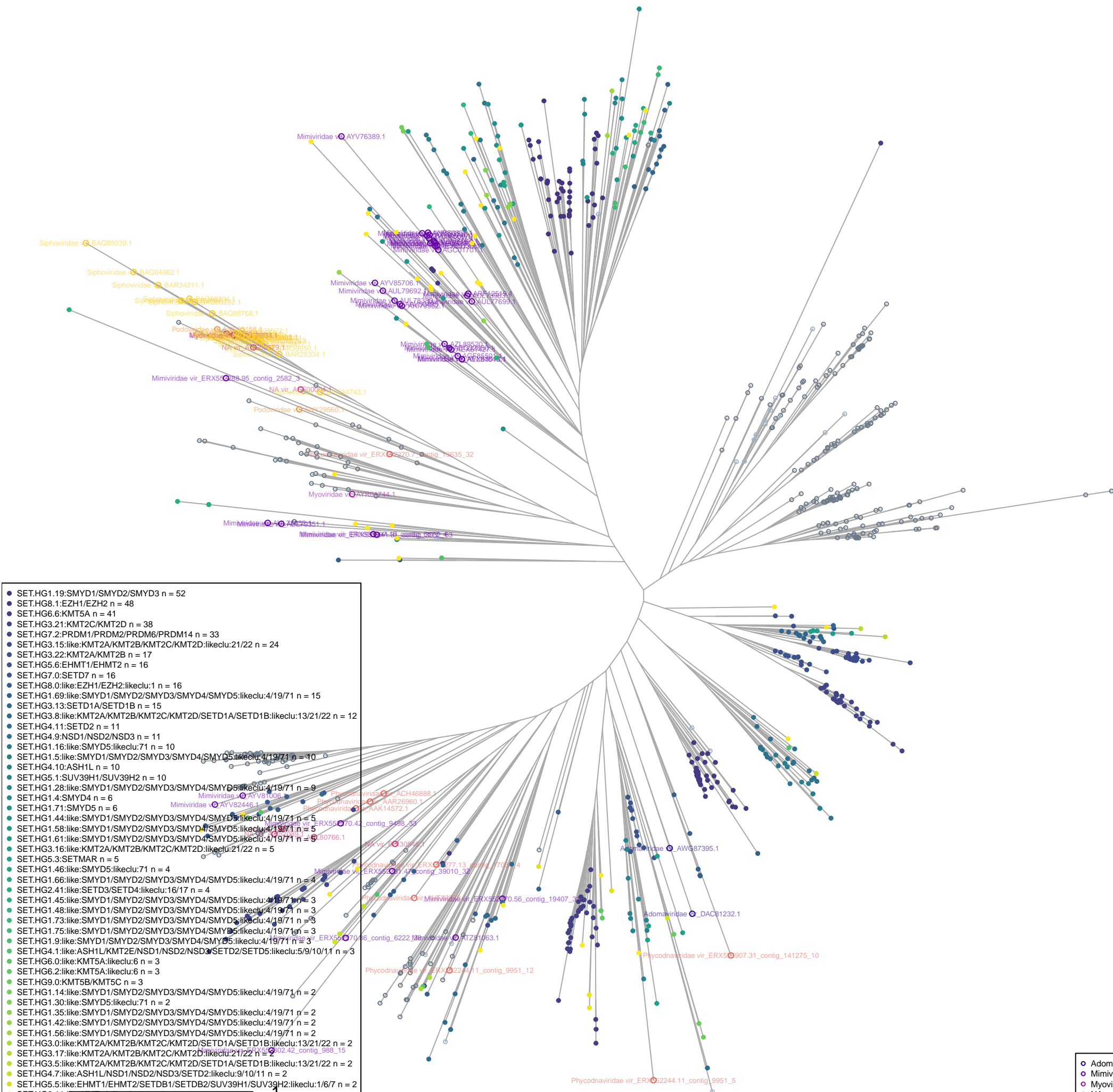


vir.SET.phy.HG1.seqs.iqtree.treefile
n=967 sequences

- eukaryotes
- archaea
- bacteria
- viruses

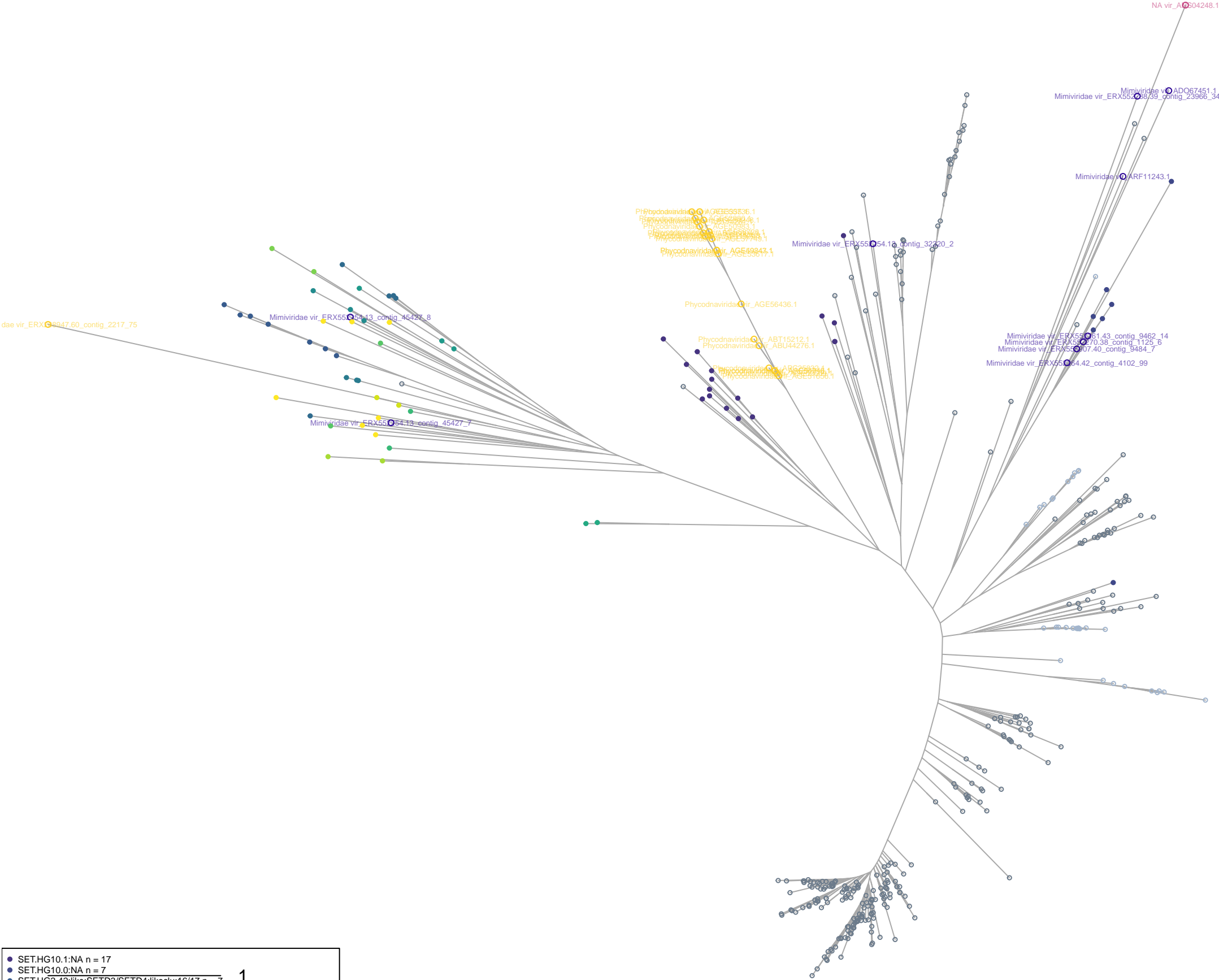
- SET.HG1.19:SMYD1/SMYD2/SMYD3 n = 52
- SET.HG8.1:EZH1/EZH2 n = 48
- SET.HG6.6:KMT5A n = 41
- SET.HG3.21:KMT2C/KMT2D n = 38
- SET.HG7.2:PRDM1/PRDM2/PRDM6/PRDM14 n = 33
- SET.HG3.15:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22 n = 24
- SET.HG3.22:KMT2A/KMT2B n = 17
- SET.HG5.6:EHMT1/EHMT2 n = 16
- SET.HG7.0:SETD7 n = 16
- SET.HG8.0:like:EZH1/EZH2:likeclu:1 n = 16
- SET.HG1.69:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 15
- SET.HG3.13:SETD1A/SETD1B n = 15
- SET.HG3.8:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 12
- SET.HG4.11:SETD2 n = 11
- SET.HG4.9:NSD1/NSD2/NSD3 n = 11
- SET.HG1.16:like:SMYD5:likeclu:71 n = 10
- SET.HG1.5:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 10
- SET.HG4.10:ASH1L n = 10
- SET.HG5.1:SUV39H1/SUV39H2 n = 10
- SET.HG1.28:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 9
- SET.HG1.4:SMYD4 n = 6
- SET.HG1.71:SMYD5 n = 6
- SET.HG1.44:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 5
- SET.HG1.58:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 5
- SET.HG1.61:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 5
- SET.HG3.16:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22 n = 5
- SET.HG5.3:SETMAR n = 5
- SET.HG1.46:like:SMYD5:likeclu:71 n = 4
- SET.HG1.66:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 4
- SET.HG2.41:like:SETD3/SETD4:likeclu:16/17 n = 4
- SET.HG1.45:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 3
- SET.HG1.48:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 3
- SET.HG1.73:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 3
- SET.HG1.75:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 3
- SET.HG1.9:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 3
- SET.HG4.1:like:ASH1L/KMT2E/NSD1/NSD2/NSD3/SETD2/SETD5:likeclu:5/9/10/11 n = 3
- SET.HG6.0:like:KMT5A:likeclu:6 n = 3
- SET.HG6.2:like:KMT5A:likeclu:6 n = 3
- SET.HG9.0:KMT5B/KMT5C n = 3
- SET.HG1.14:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 2
- SET.HG1.30:like:SMYD5:likeclu:71 n = 2
- SET.HG1.35:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 2
- SET.HG1.42:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 2
- SET.HG1.56:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 2
- SET.HG3.0:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 2
- SET.HG3.17:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22 n = 2
- SET.HG3.5:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22 n = 2
- SET.HG4.7:like:ASH1L/NSD1/NSD2/NSD3/SETD2:likeclu:9/10/11 n = 2
- SET.HG5.5:like:EHMT1/EHMT2/SETDB1/SETDB2/SUV39H1/SUV39H2:likeclu:1/6/7 n = 2
- SET.HG6.11:like:KMT5A:likeclu:6 n = 2
- SET.HG6.3:like:KMT5A:likeclu:6 n = 2
- SET.HG7.1:like:PRDM1/PRDM2/PRDM6/PRDM14:likeclu:2 n = 2
- other n = 36



- Adomaviridae n = 2
- Mimiviridae n = 40
- Myoviridae n = 3
- NA n = 7
- Phycodnaviridae n = 9
- Podoviridae n = 3
- Siphoviridae n = 20

SET
vir.SET.phy.HG2.seqs.iqtree.treefile
n=414 sequences

- eukaryotes
- archaea
- bacteria
- viruses



- SET.HG10.1:NA n = 17
- SET.HG10.0:NA n = 7
- SET.HG2.42:like:SETD3/SETD4:likeclu:16/17 n = 7
- SET.HG2.17:SETD4 n = 5
- SET.HG2.14:like:SETD3/SETD4:likeclu:16/17 n = 3
- SET.HG2.31:like:SETD3/SETD4:likeclu:16/17 n = 3
- SET.HG2.34:like:SETD3/SETD4:likeclu:16/17 n = 3
- SET.HG1.58:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71 n = 2
- SET.HG2.11:like:SETD3/SETD4:likeclu:16/17 n = 2
- SET.HG2.12:like:SETD3/SETD4:likeclu:16/17 n = 2
- SET.HG2.18:like:SETD3/SETD4:likeclu:16/17 n = 2
- SET.HG2.41:like:SETD3/SETD4:likeclu:16/17 n = 2
- SET.HG2.8:SETD6 n = 2
- other n = 7

1

- Mimiviridae n = 10
- NA n = 1
- Phycodnaviridae n = 23