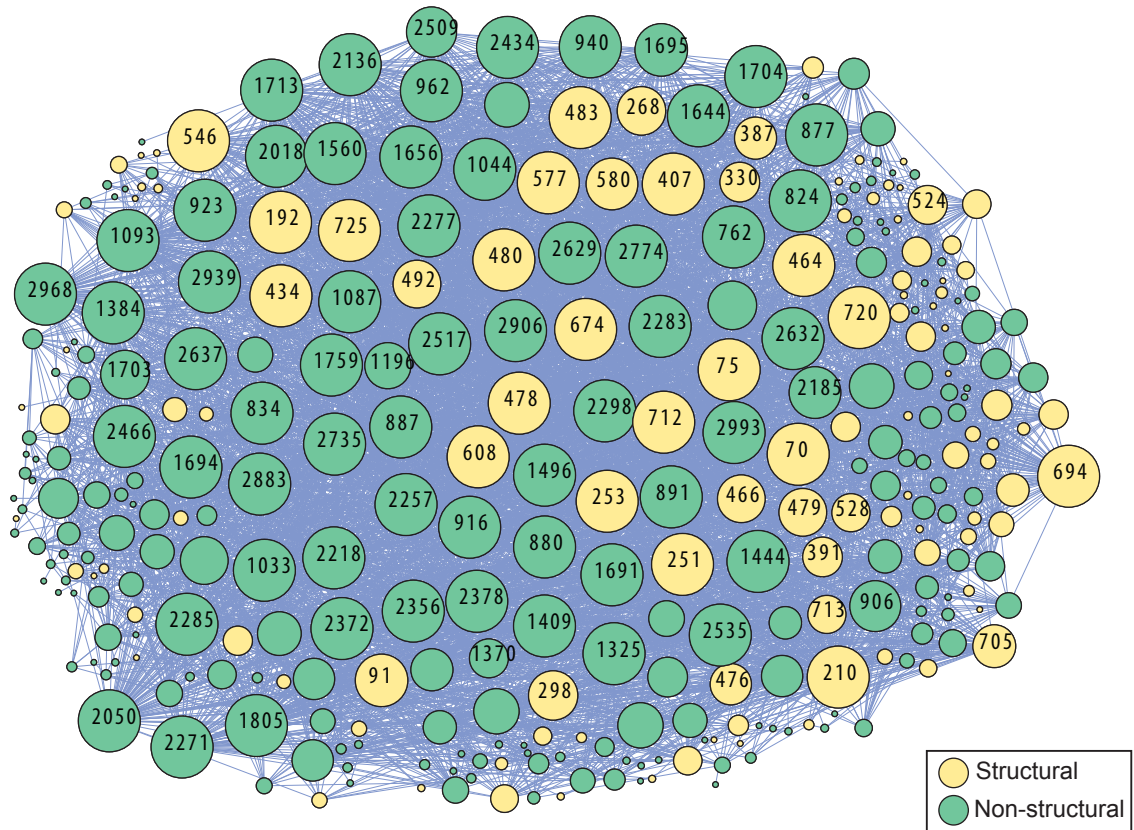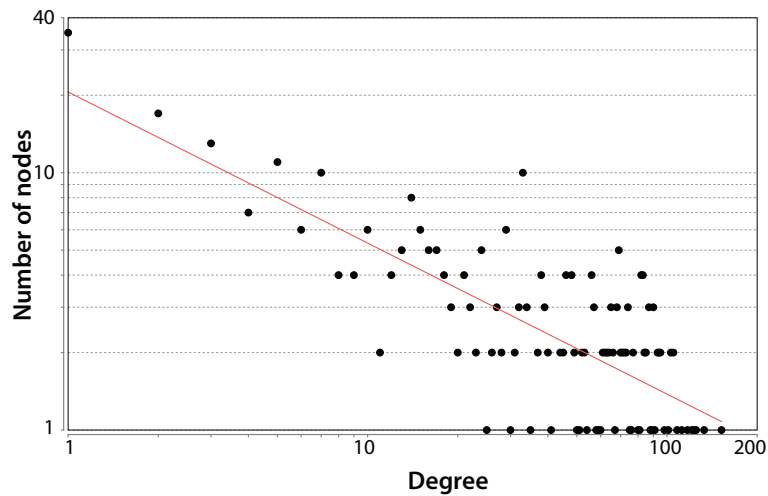# Hepatitis C virus genotype 1b covariance network



Distribution of nodes by degree of connectivity

**Supp. Fig 1a:** Network view of HCV 1b covariance network generated from 300 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
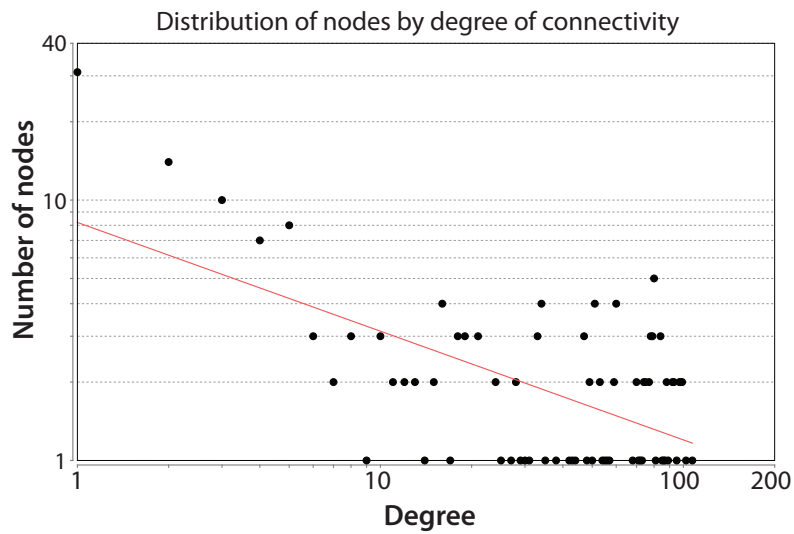
# Hepatitis C virus genotype 1a covariance network (100 sequences)



**Supp. Fig 1b:** Network view of HCV 1a covariance network generated from 100 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
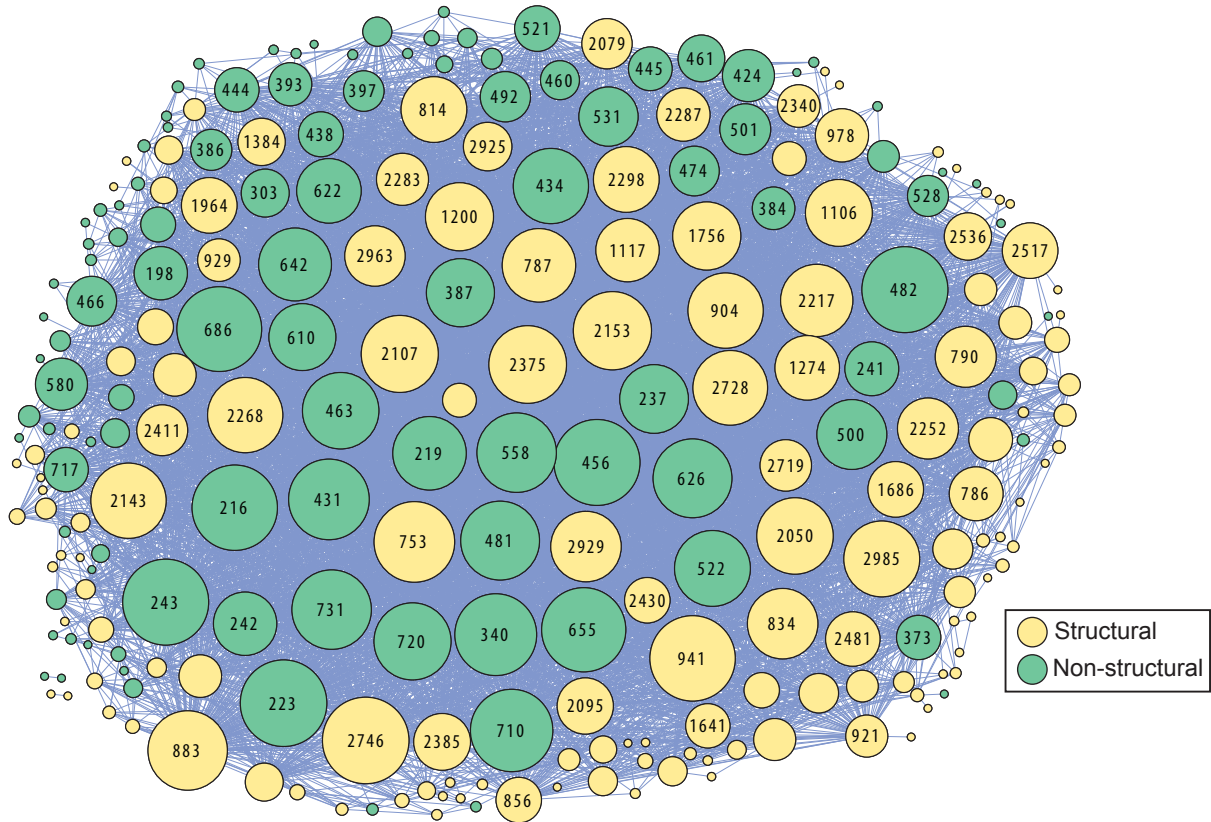
# Hepatitis C virus genotype 1a covariance network (47 sequences)



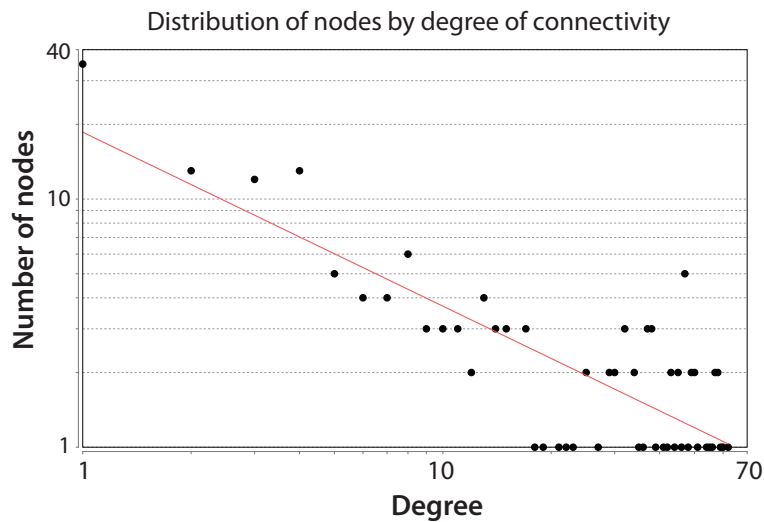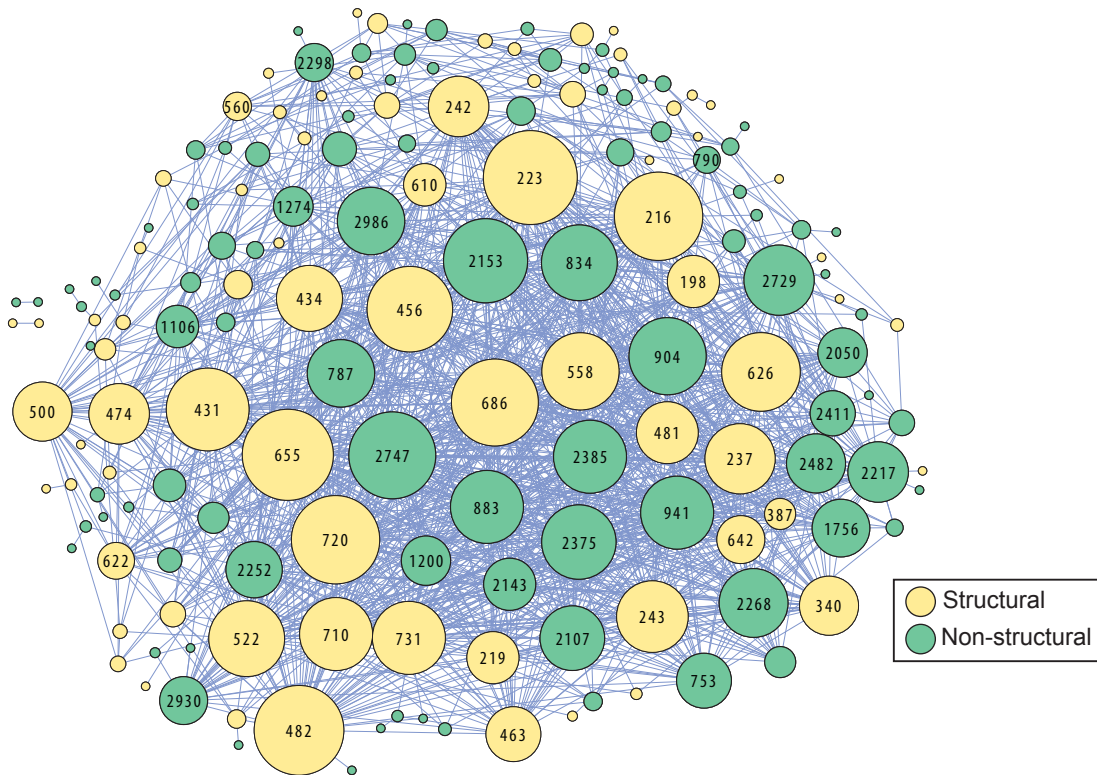Distribution of nodes by degree of connectivity

**Supp. Fig 1c:** Network view of HCV 1a covariance network generated from 47 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# Hepatitis C virus genotype 1a covariance network (32 sequences)



**Supp. Fig 1d:** Network view of HCV 1a covariance network generated from 32 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

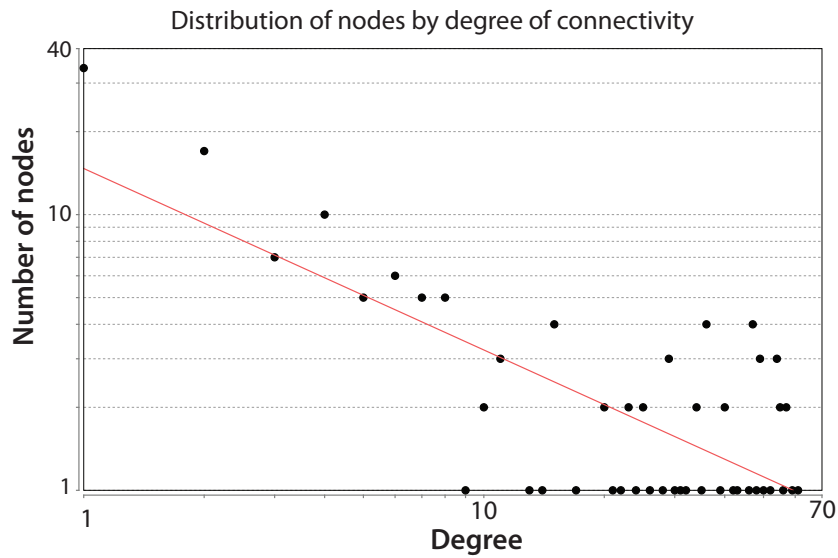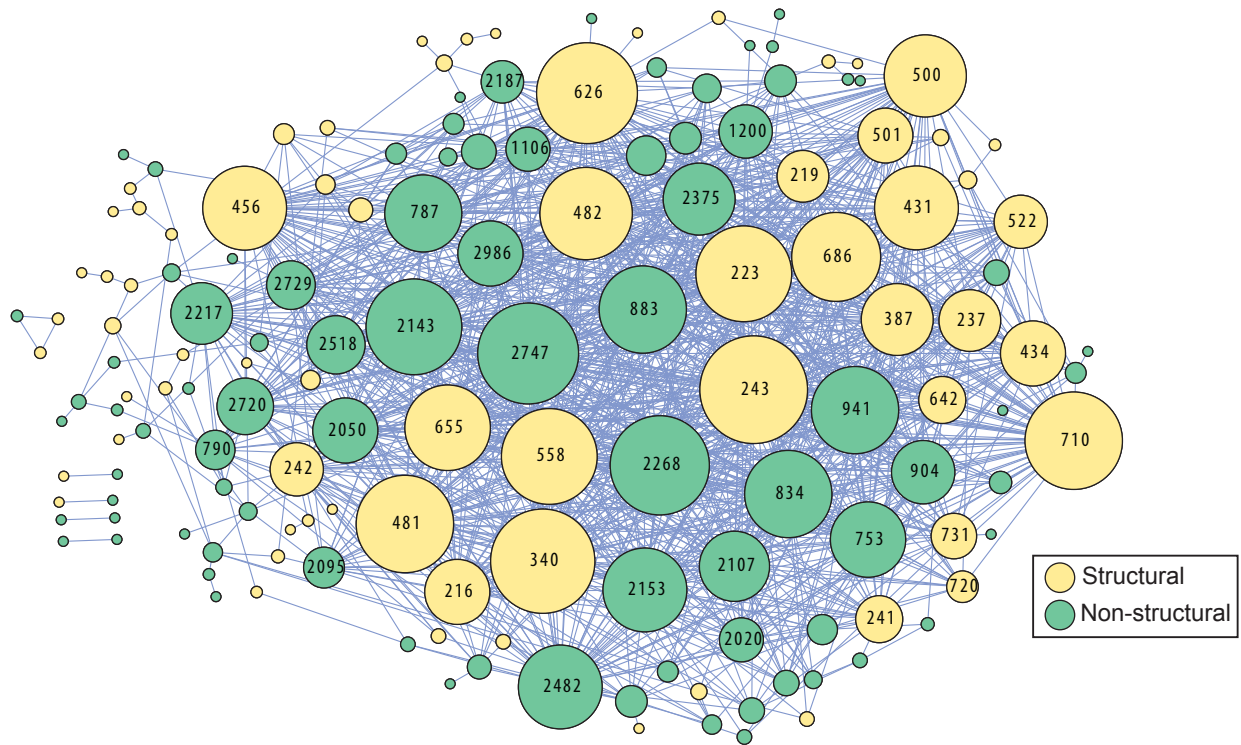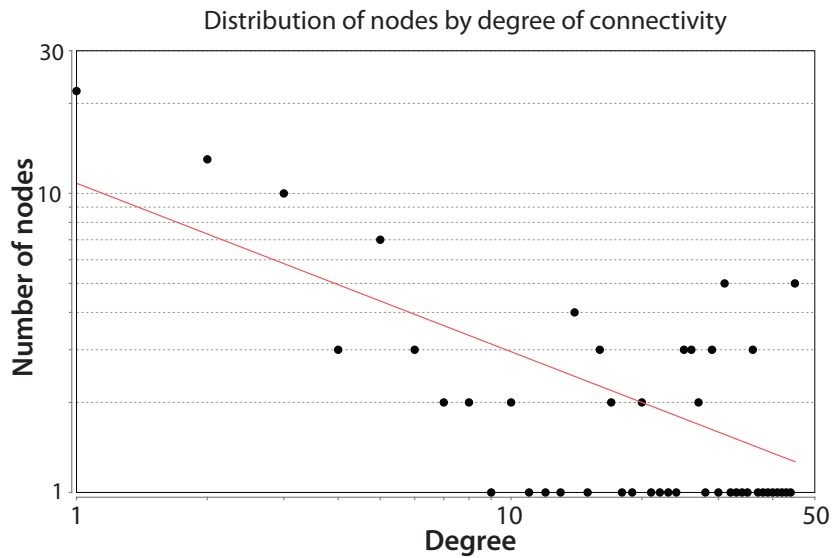# Hepatitis C virus genotype 1a covariance network (16 sequences)



Legend:
- Structural
- Non-structural

## Distribution of nodes by degree of connectivity



Number of nodes vs. Degree

**Supp. Fig 1e:** Network view of HCV 1a covariance network generated from 16 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
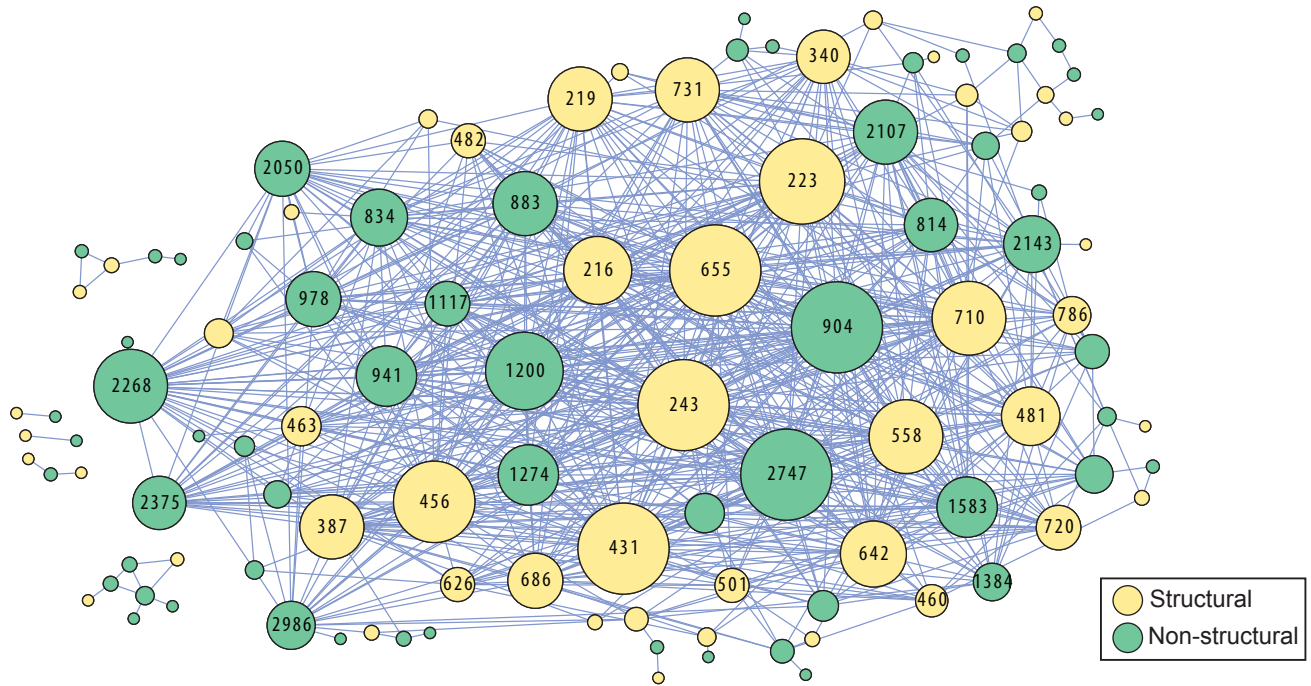
# GBV-C virus covariance network



**Supp. Fig 1f:** Network view of GBV-C covariance network generated from 40 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# Dengue virus 2 covariance network



Supp. Fig 1g: Network view of DV-2 covariance network generated from 100 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

**West Nile virus covariance network**

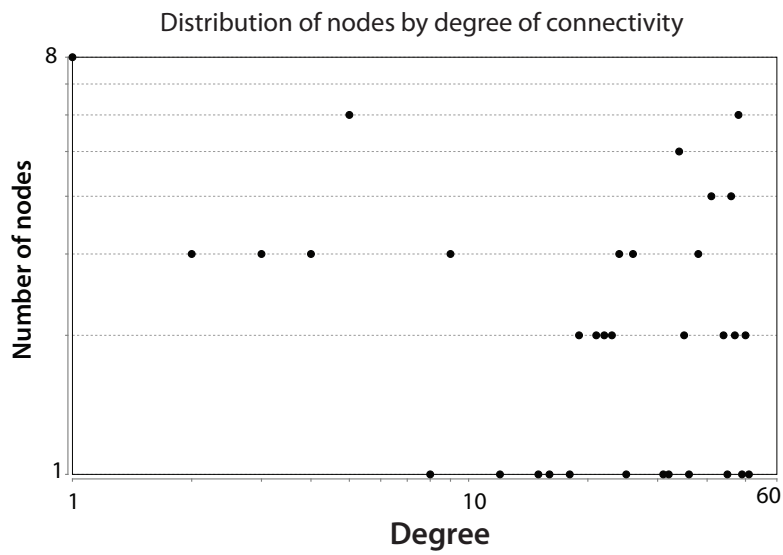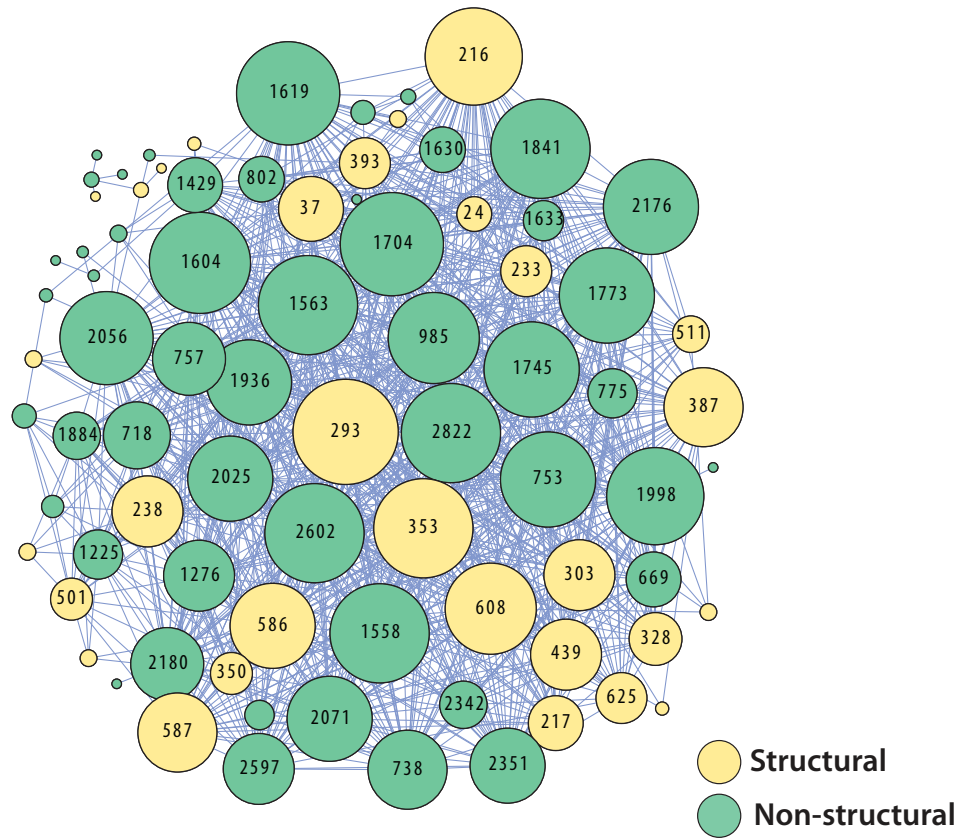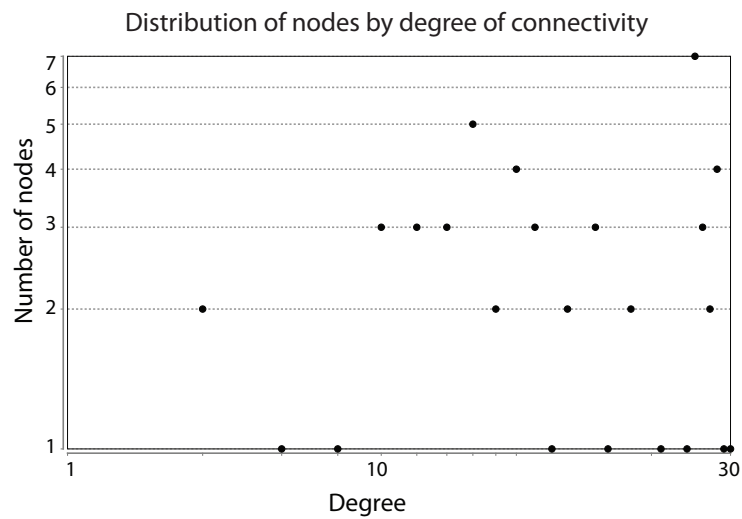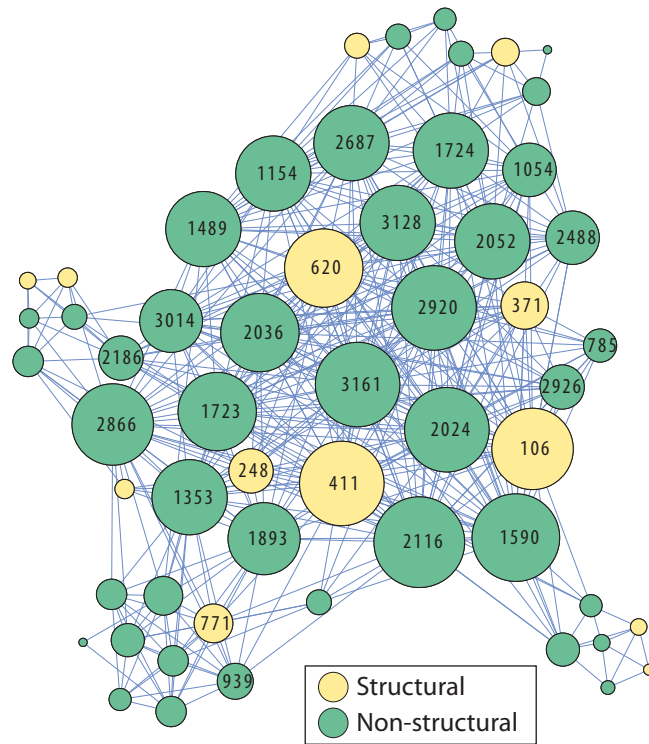Distribution of nodes by degree of connectivity

**Supp. Fig 1h:** Network view of WNV covariance network generated from 64 full-length poly-protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# Hepatitis A virus covariance network





**Supp. Fig 1i:** Network view of Hepatitis A virus covariance network generated from 33 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
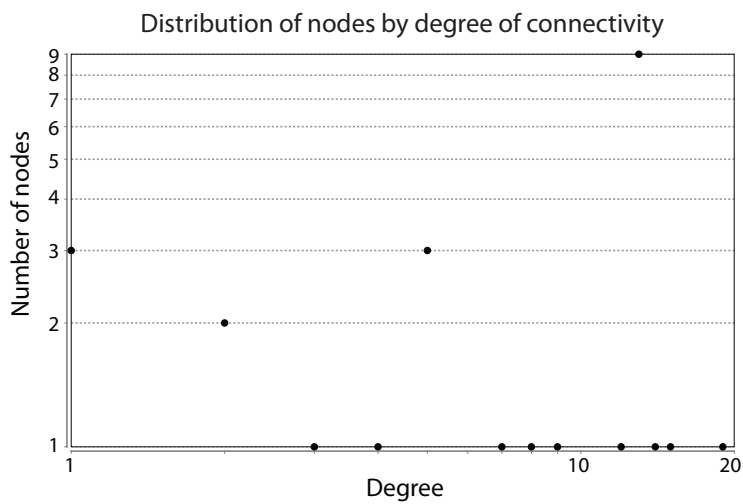
# Polio virus type 1 covariance network



Distribution of nodes by degree of connectivity

**Supp. Fig 1j:** Network view of Poliovirus type 1 covariance network generated from 63 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
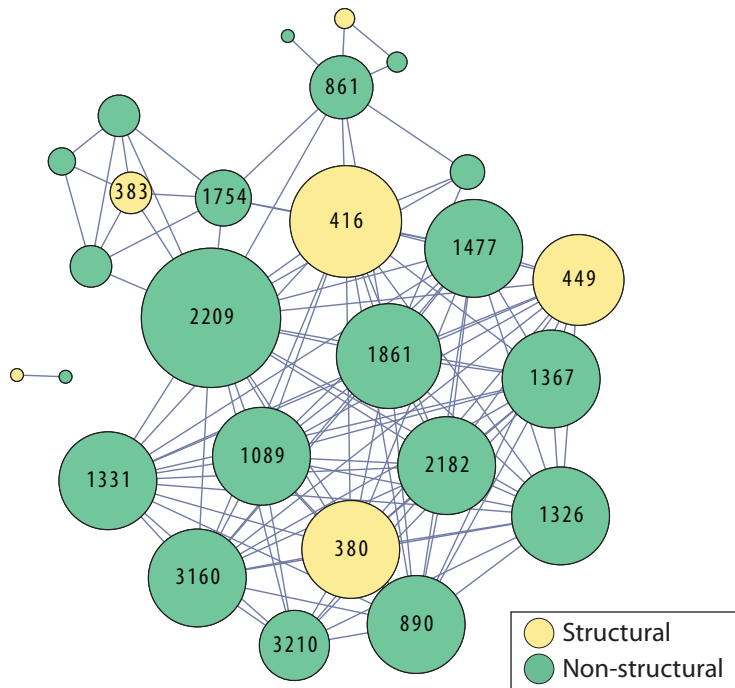
# Hepatitis E virus (genotype 3) covariance network



**Supp. Fig 1k:** Network view of Hepatitis E virus covariance network generated from 41 full-length concatenated protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

**Supp. Fig 1l:** Network view of Rabies virus covariance network generated from 26 full-length concatenated protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.
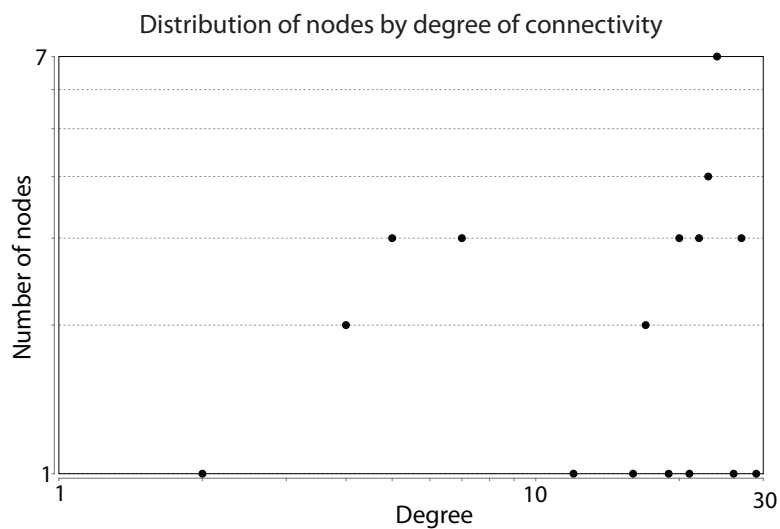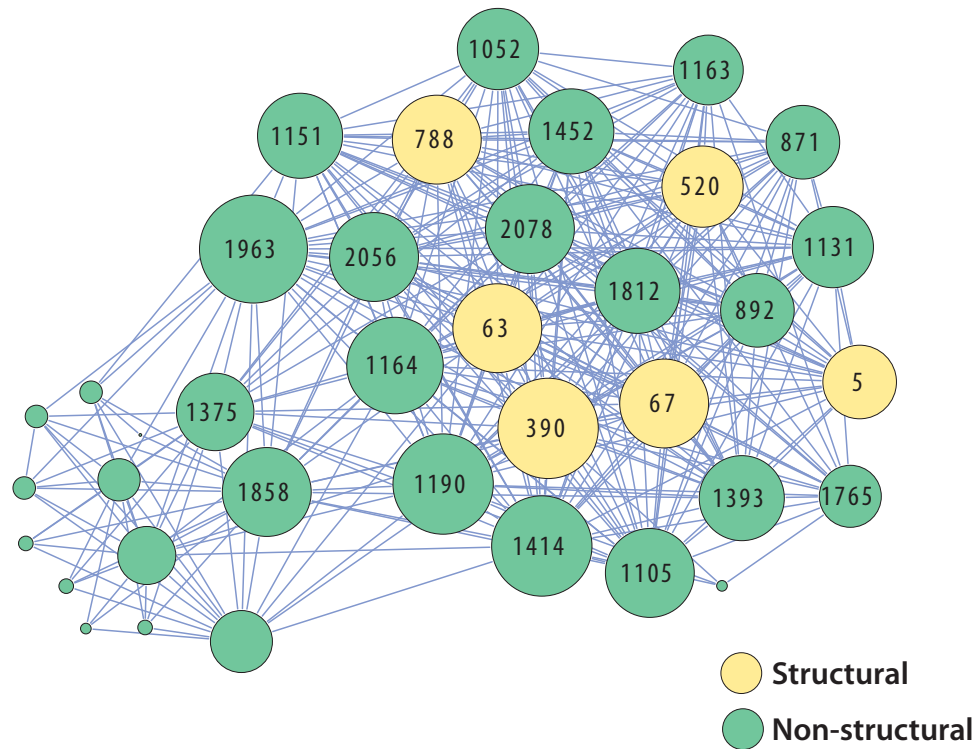
# Hepatitis Delta virus covariance network
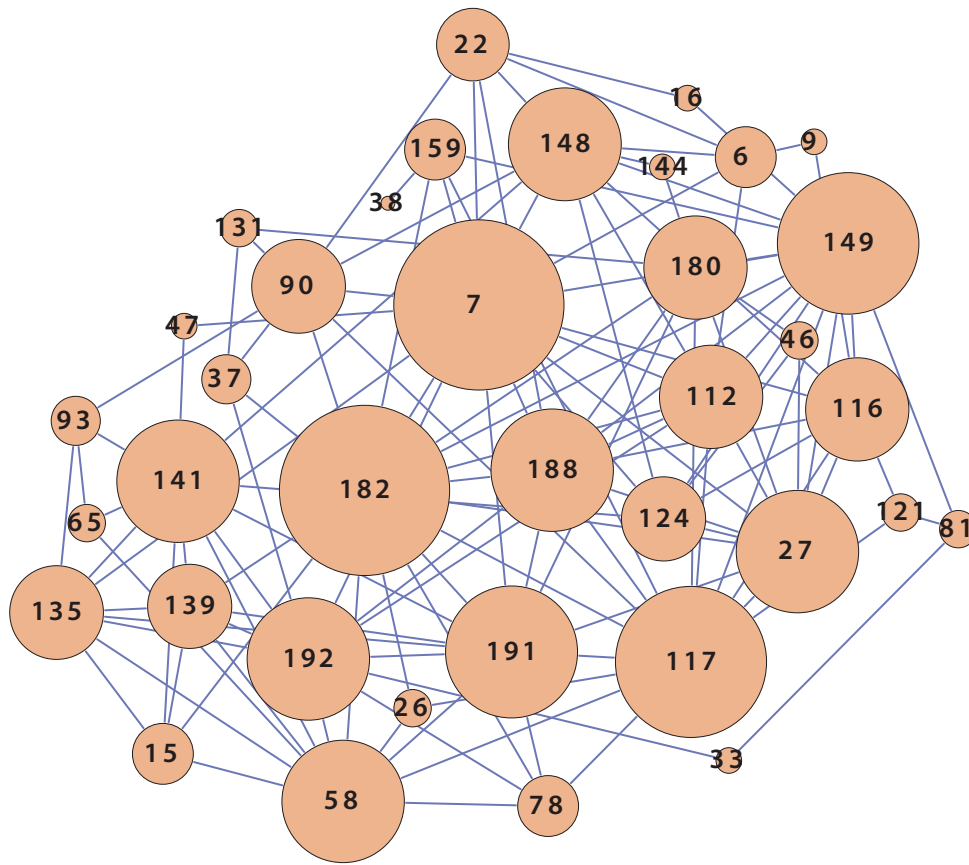


Distribution of nodes by degree of connectivity
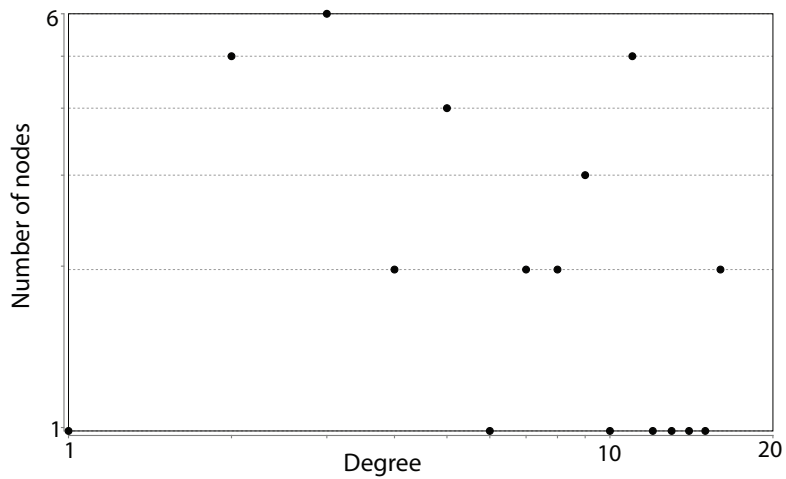
**Supp. Fig 1m:** Network view of Hepatitis Delta virus covariance network generated from 75 small antigen protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# Parvovirus B19 virus genotype 2 covariance network



Distribution of nodes by degree of connectivity
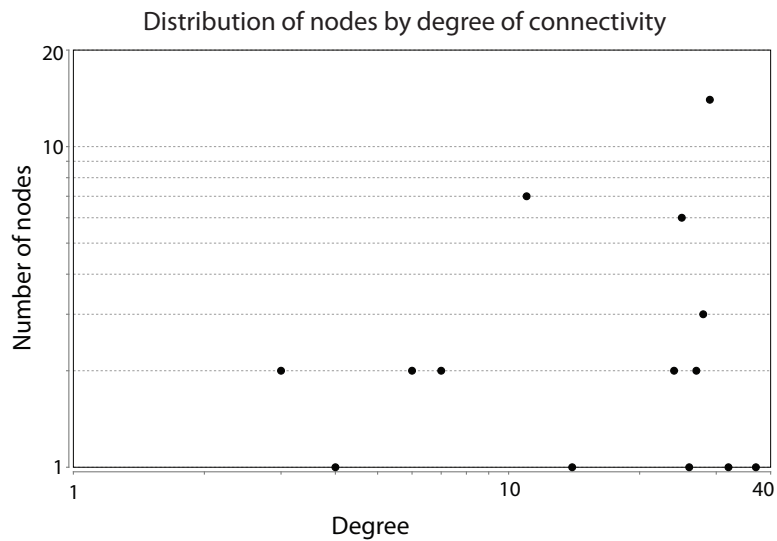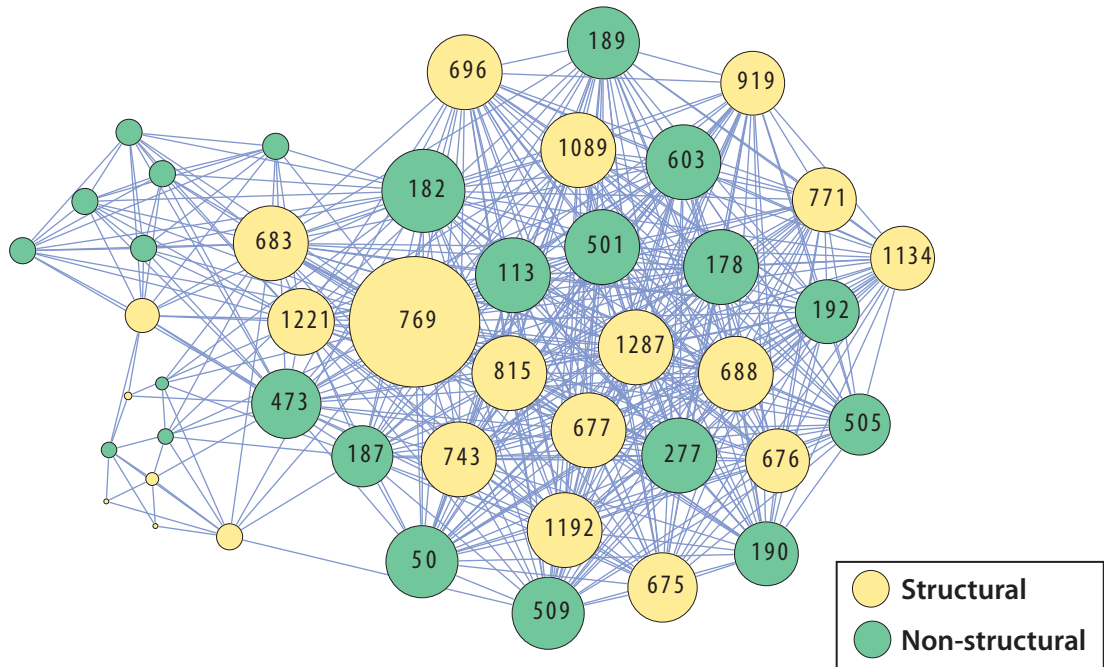
**Supp. Fig 1n:** Network view of Parvo B19 virus covariance network generated from 20 full-length polyprotein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# Hepatitis B virus genotype C covariance network
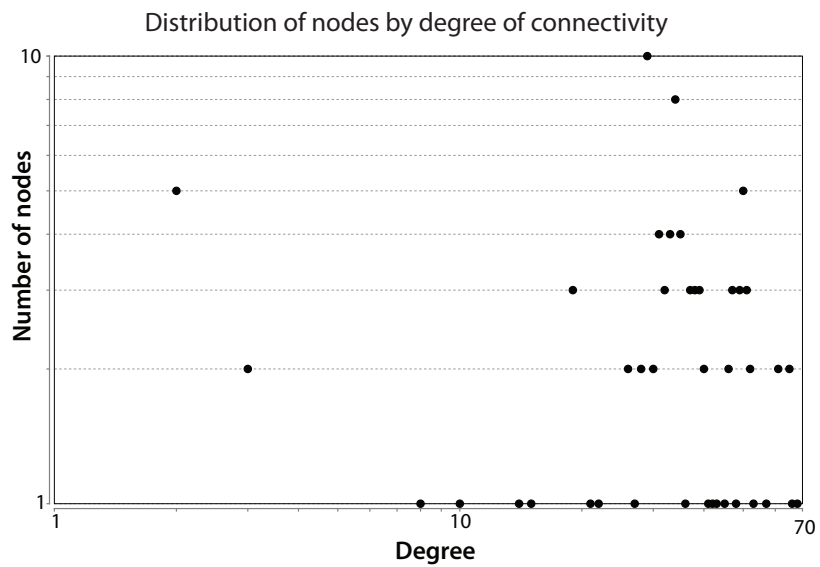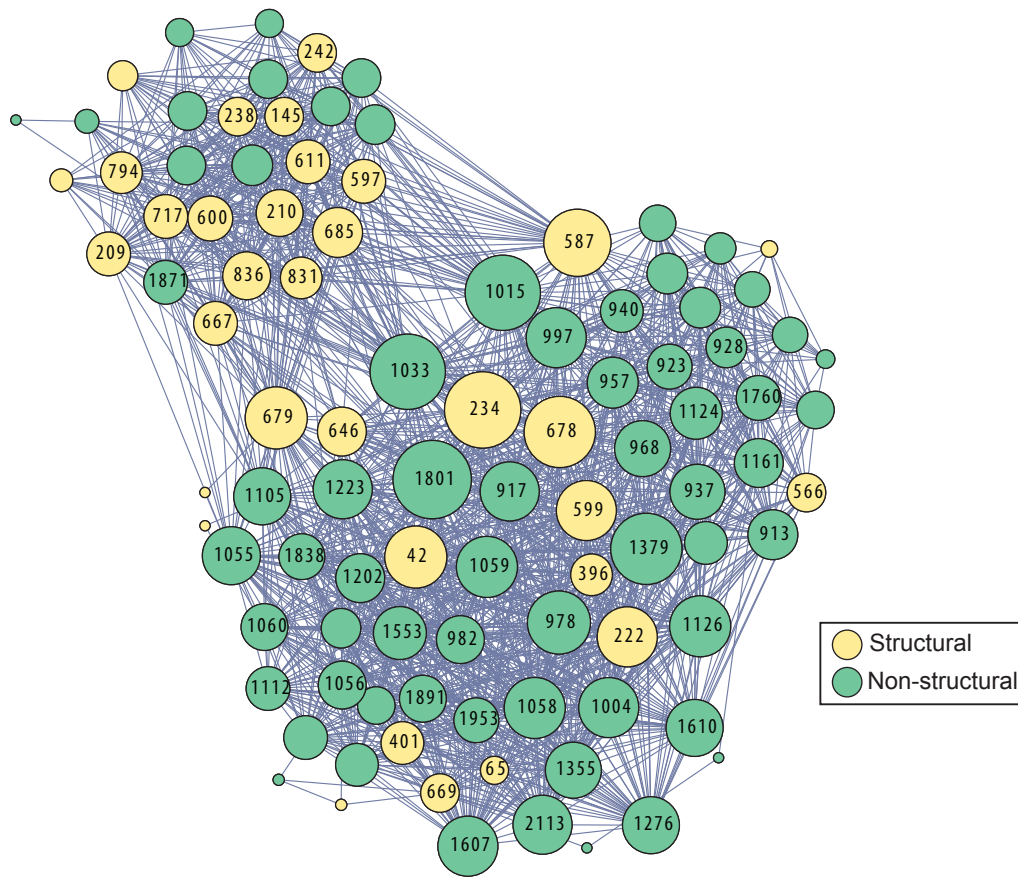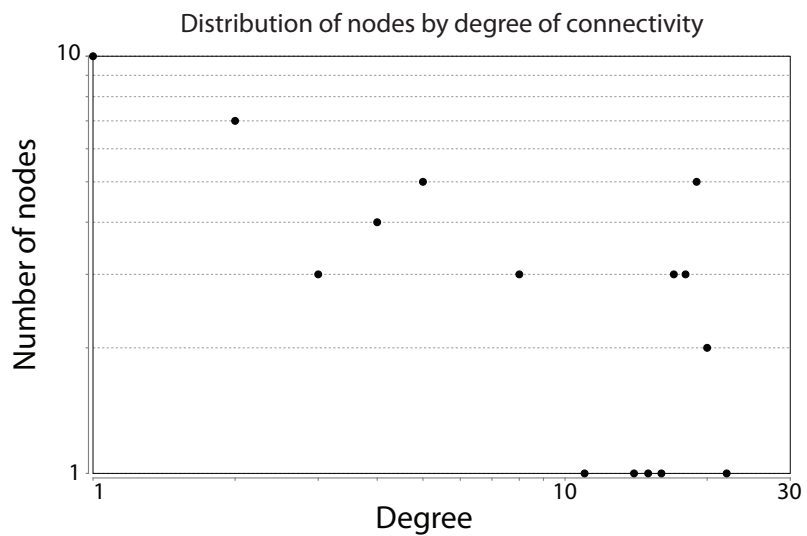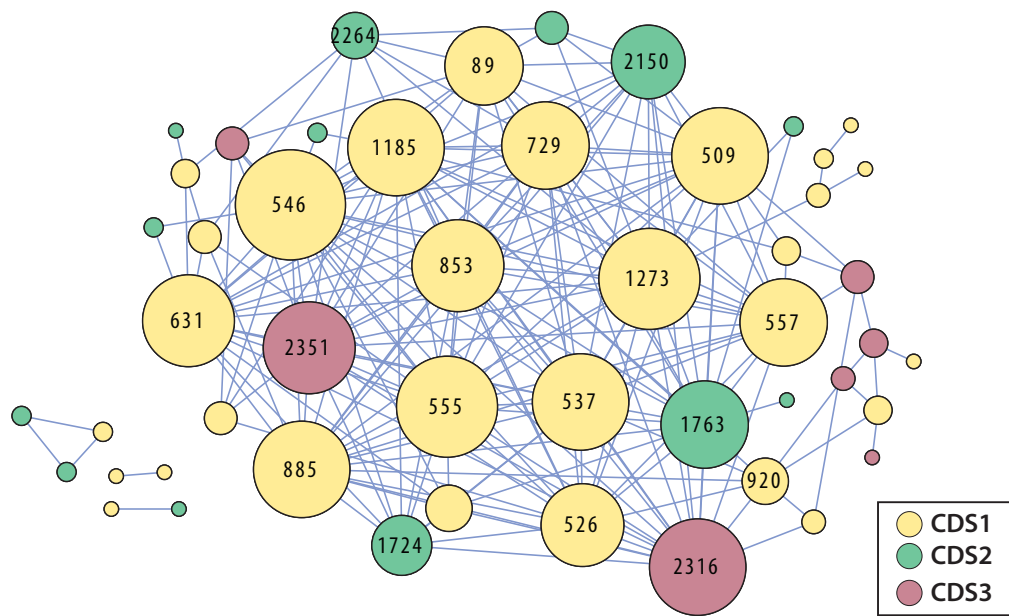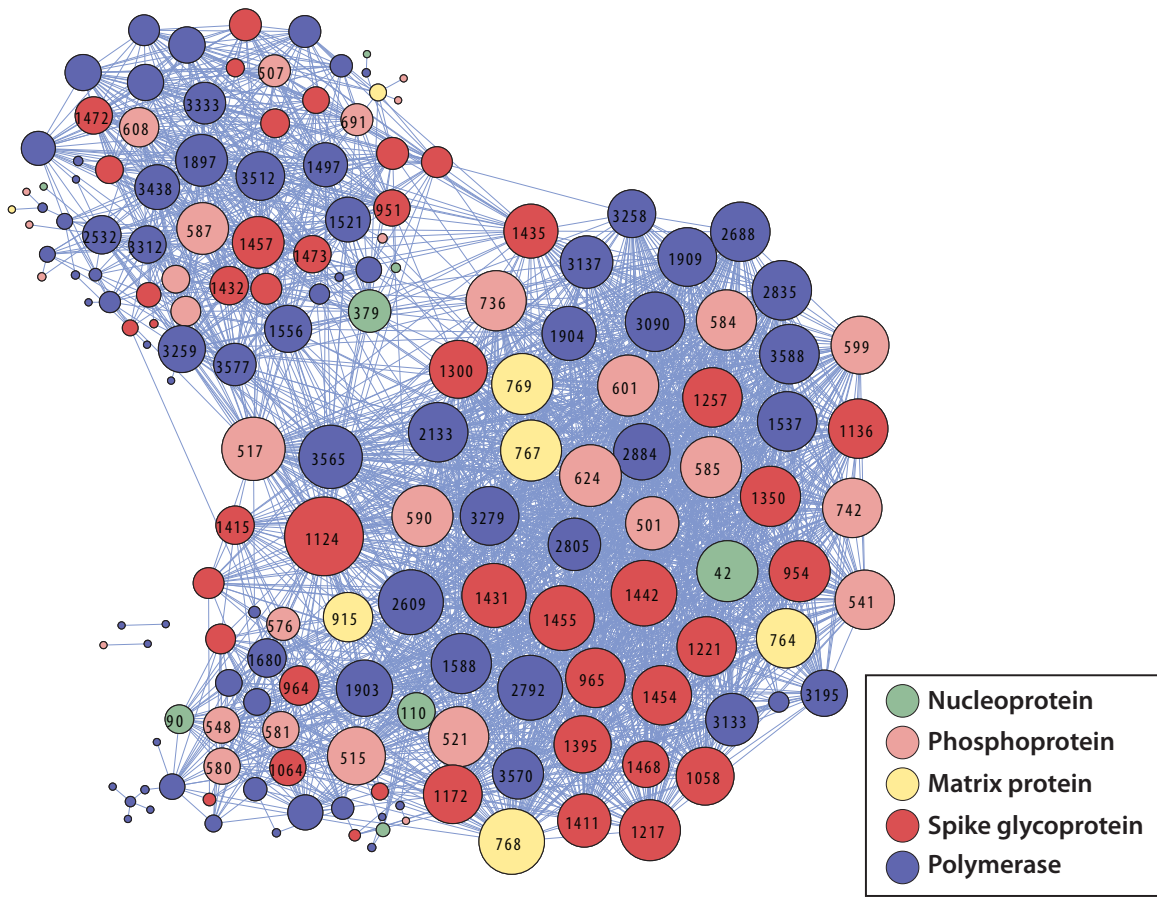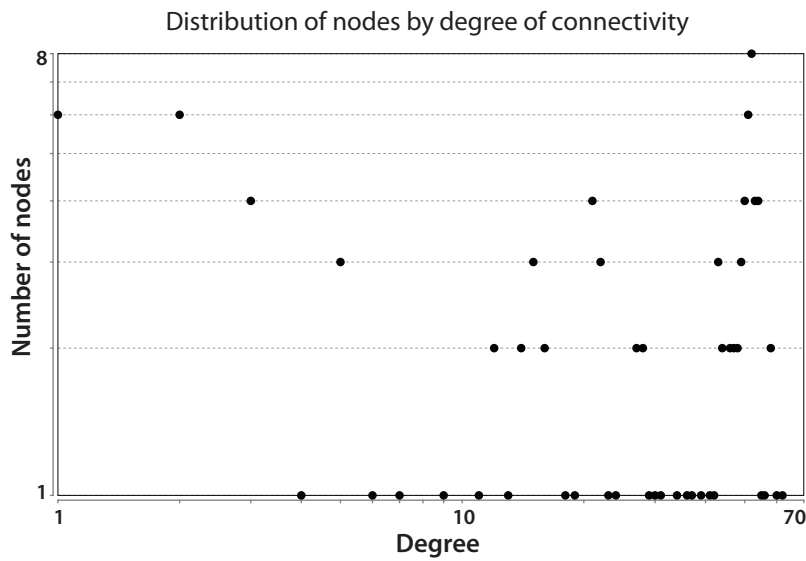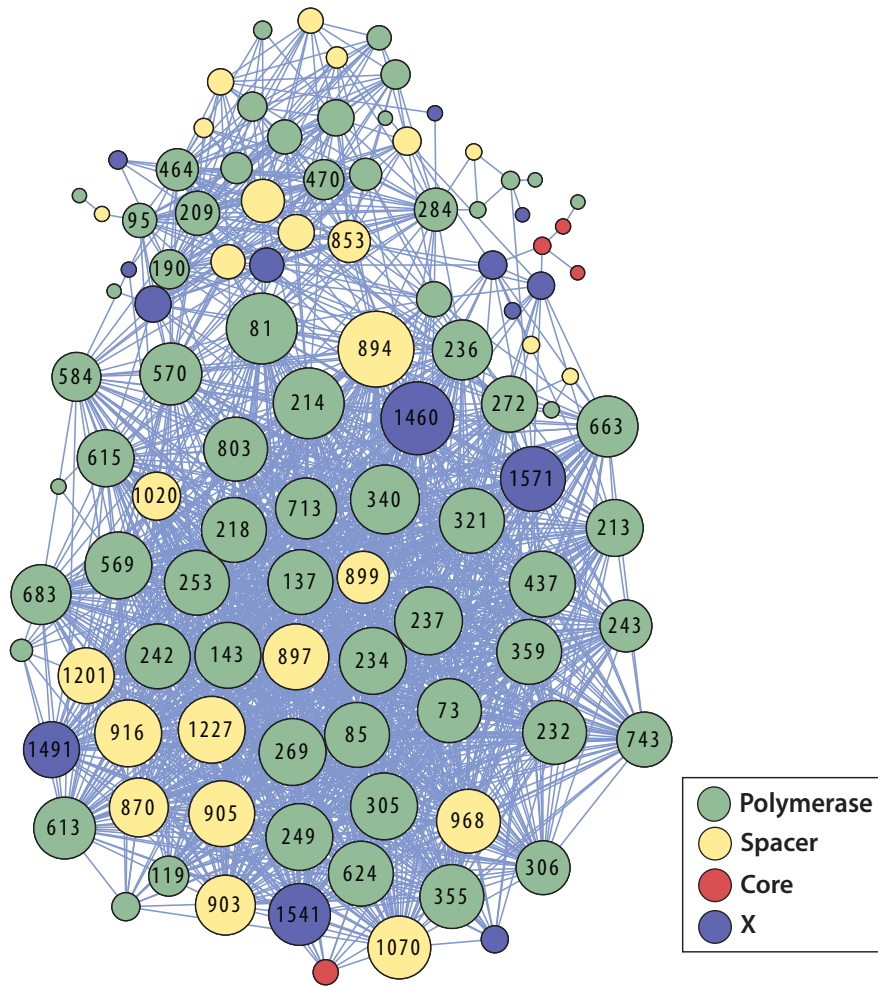


**Supp. Fig 1o:** Network view of Hepatitis B genotype C virus covariance network generated from 100 full-length concatenated protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

# HBV Genotype D network



## Distribution of nodes by degree of connectivity
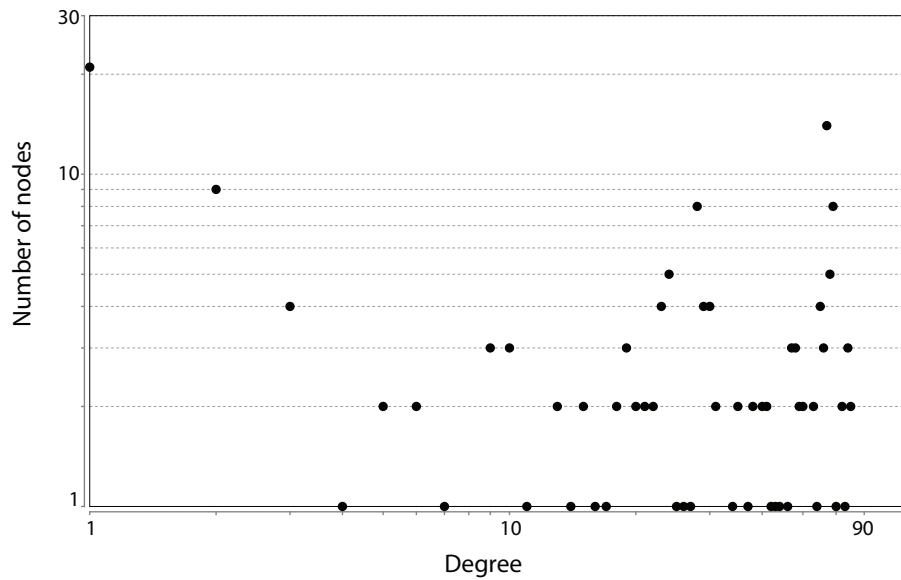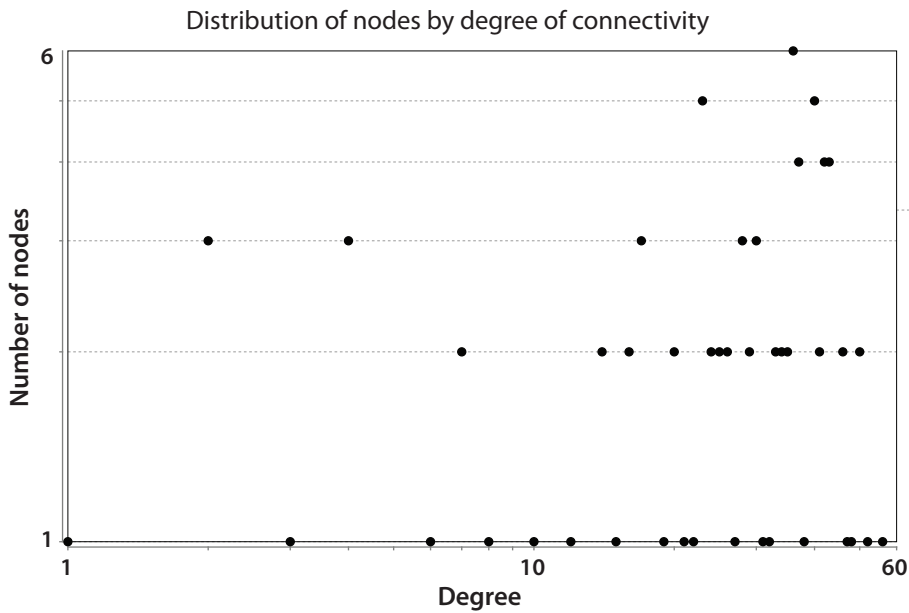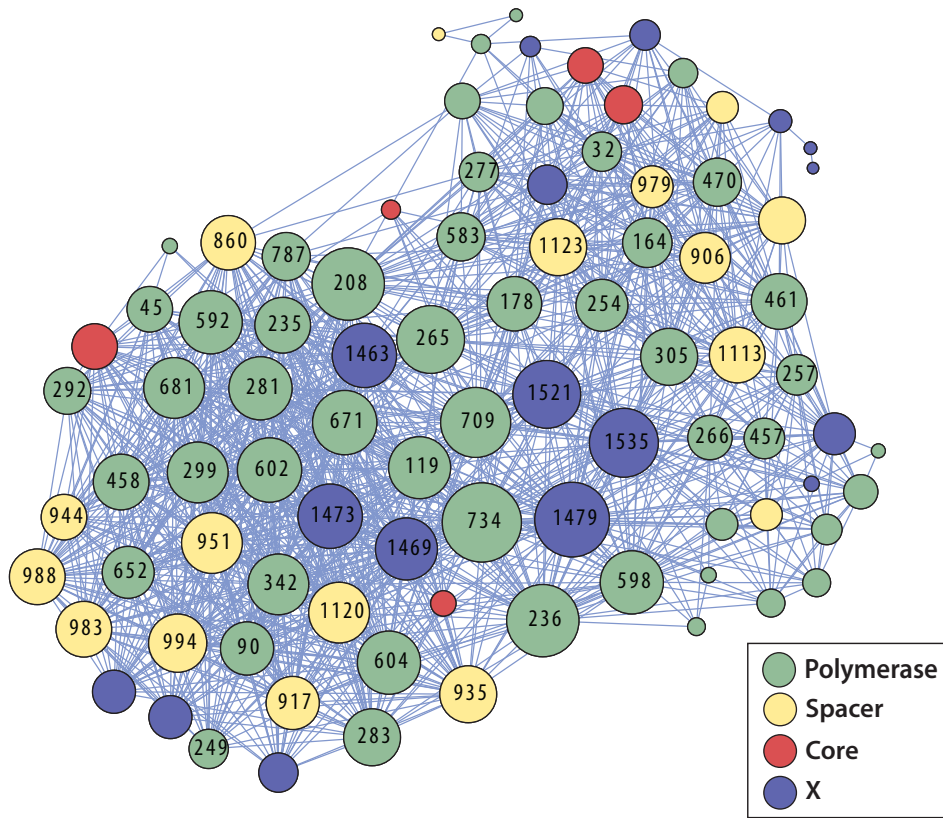
**Supp. Fig 1p:** Network view of Hepatitis B genotype C virus covariance network generated from 100 full-length concatenated protein sequences. The distribution of nodes by degree of connectivity is shown in the bottom panel.

HCV genotype 1b (300 sequences)

0.001
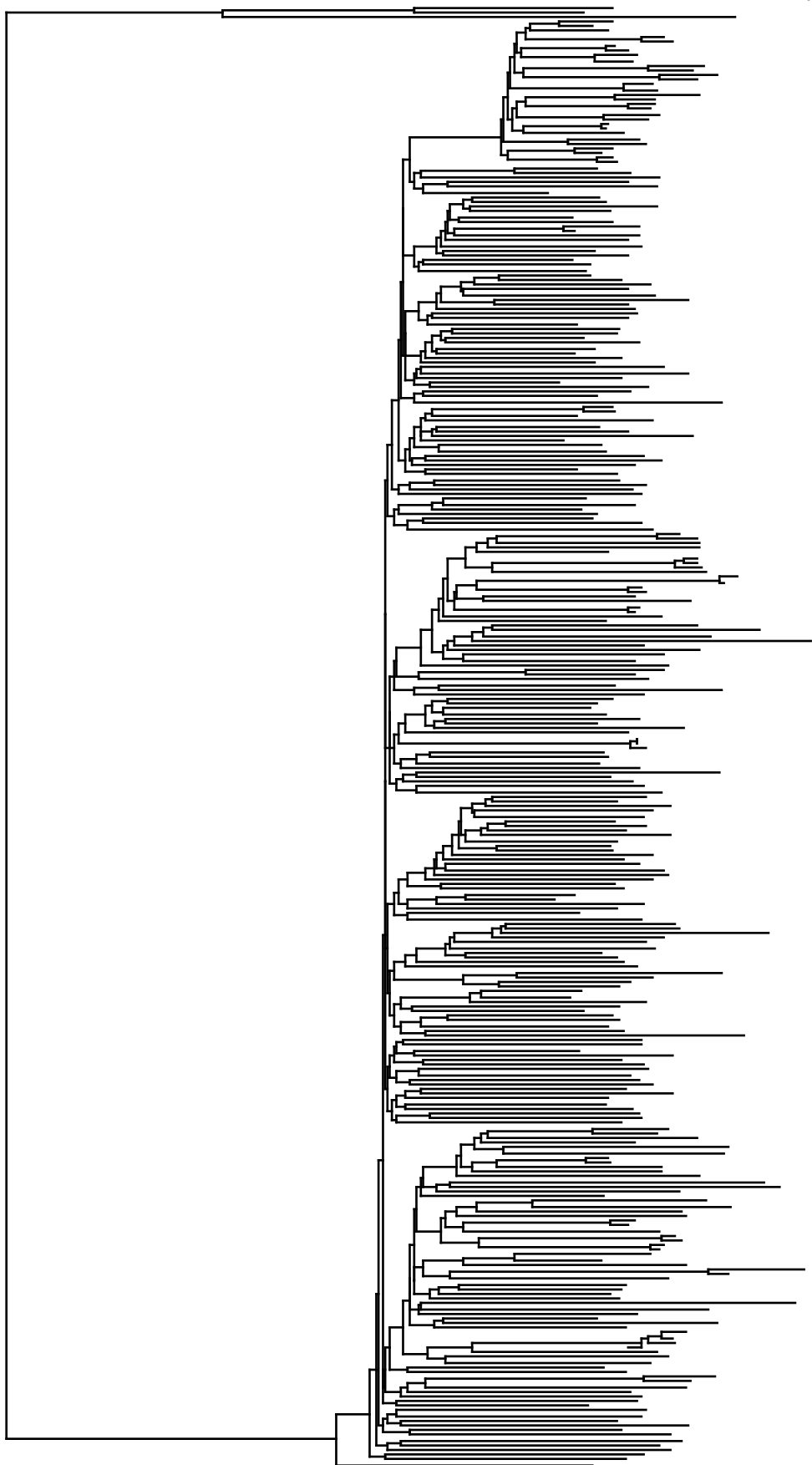
**Supp. Fig 1q:** Phylogenetic tree of 300 HCV 1b polyprotein sequences used to generate the corresponding covariance network.

**HCV genotype 1a**
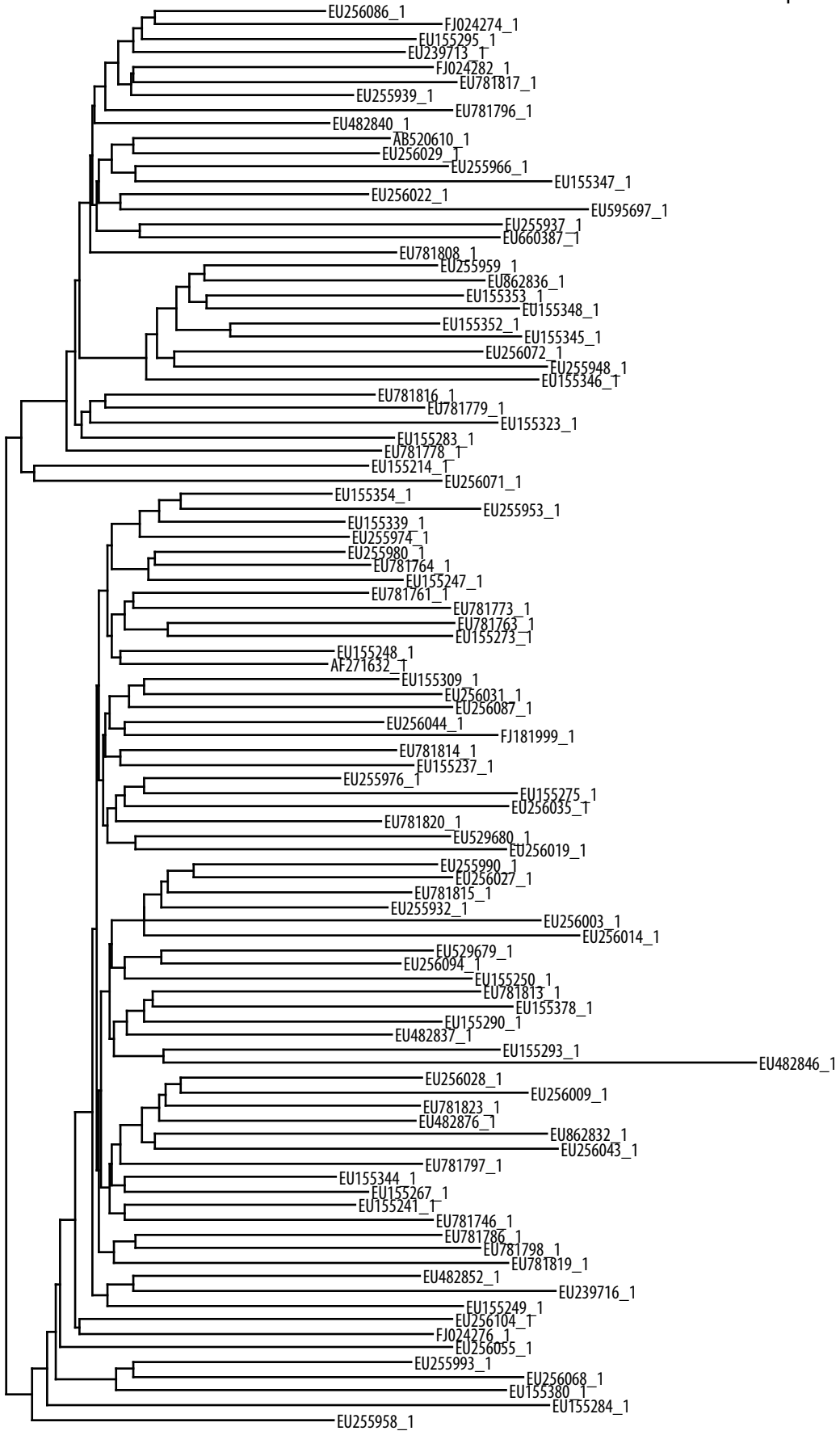


**Supp. Fig 1r:** Phylogenetic tree of 100 HCV 1a polyprotein sequences used to generate the corresponding covariance network.
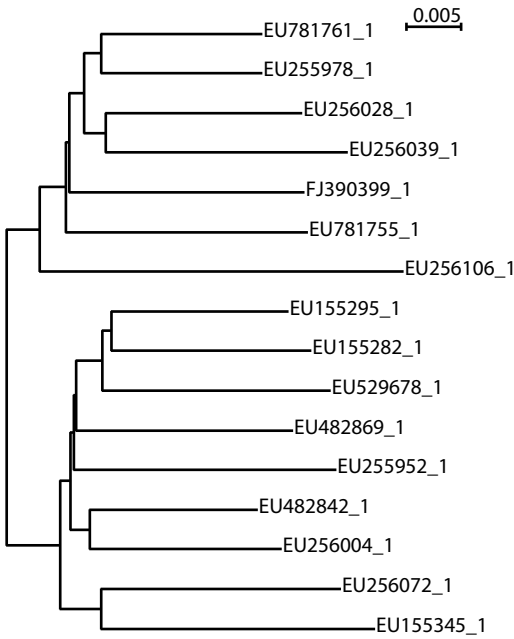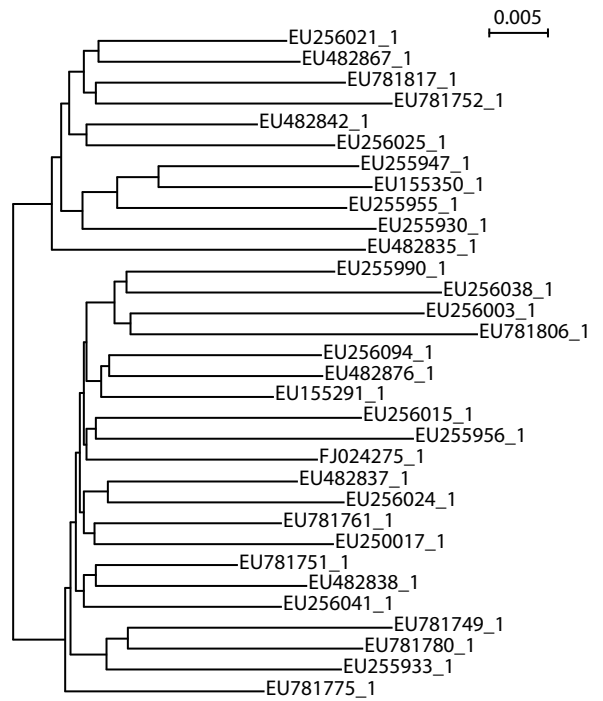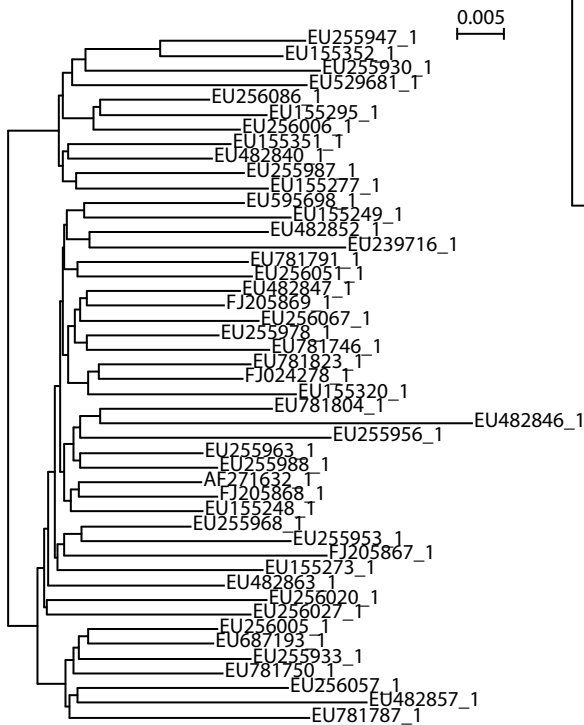
**Supp. Fig 1s:** Phylogenetic trees of 16, 32 and 47 HCV 1a polyprotein sequences used to generate the corresponding covariance networks.
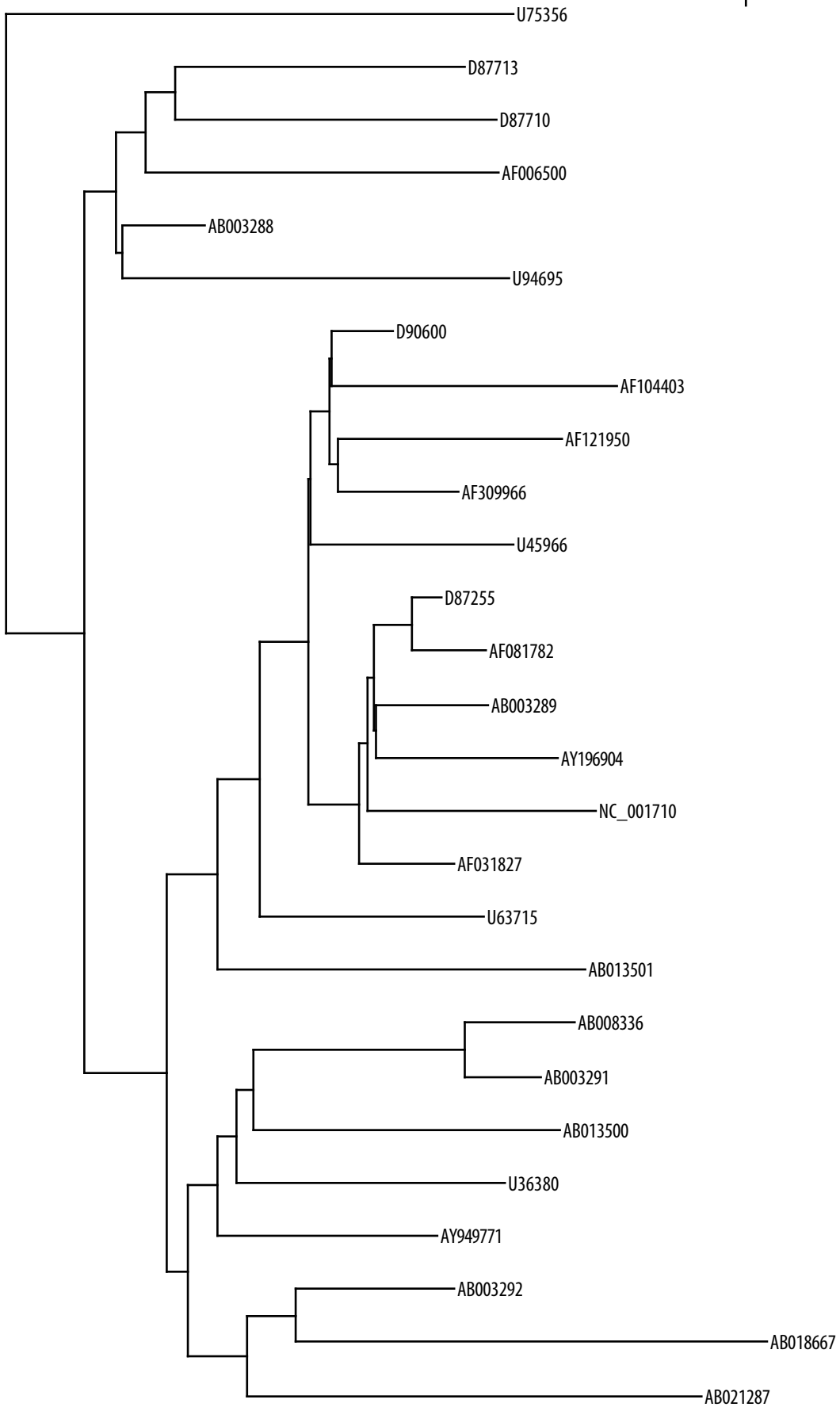
**Supp. Fig 1t:** Phylogenetic tree of 27 GBV-C polyprotein sequences used to generate the corresponding covariance network.

# Dengue virus type 2
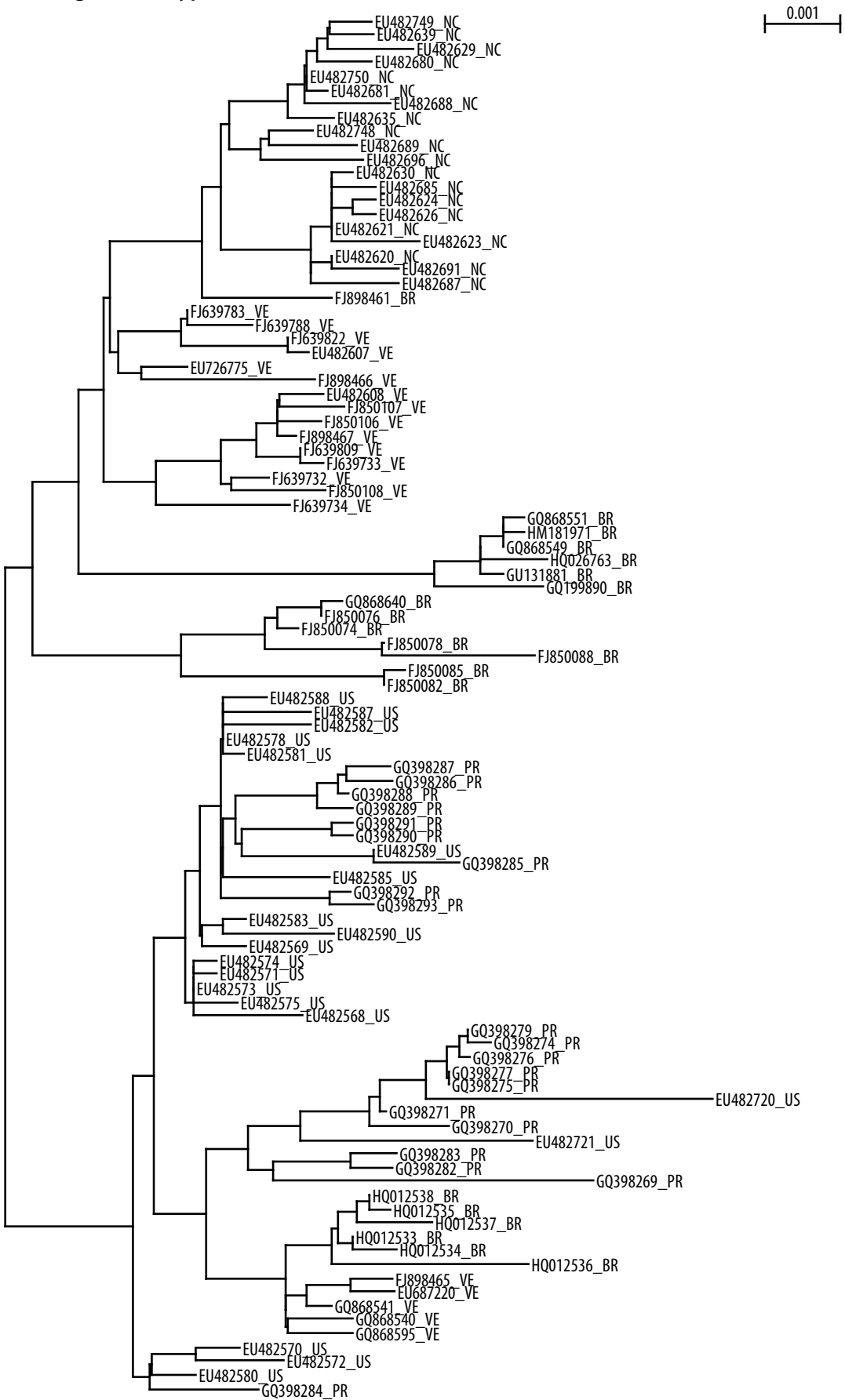


**Supp. Fig 1u:** Phylogenetic tree of 100 DV-2 polyprotein sequences used to generate the corresponding covariance network.
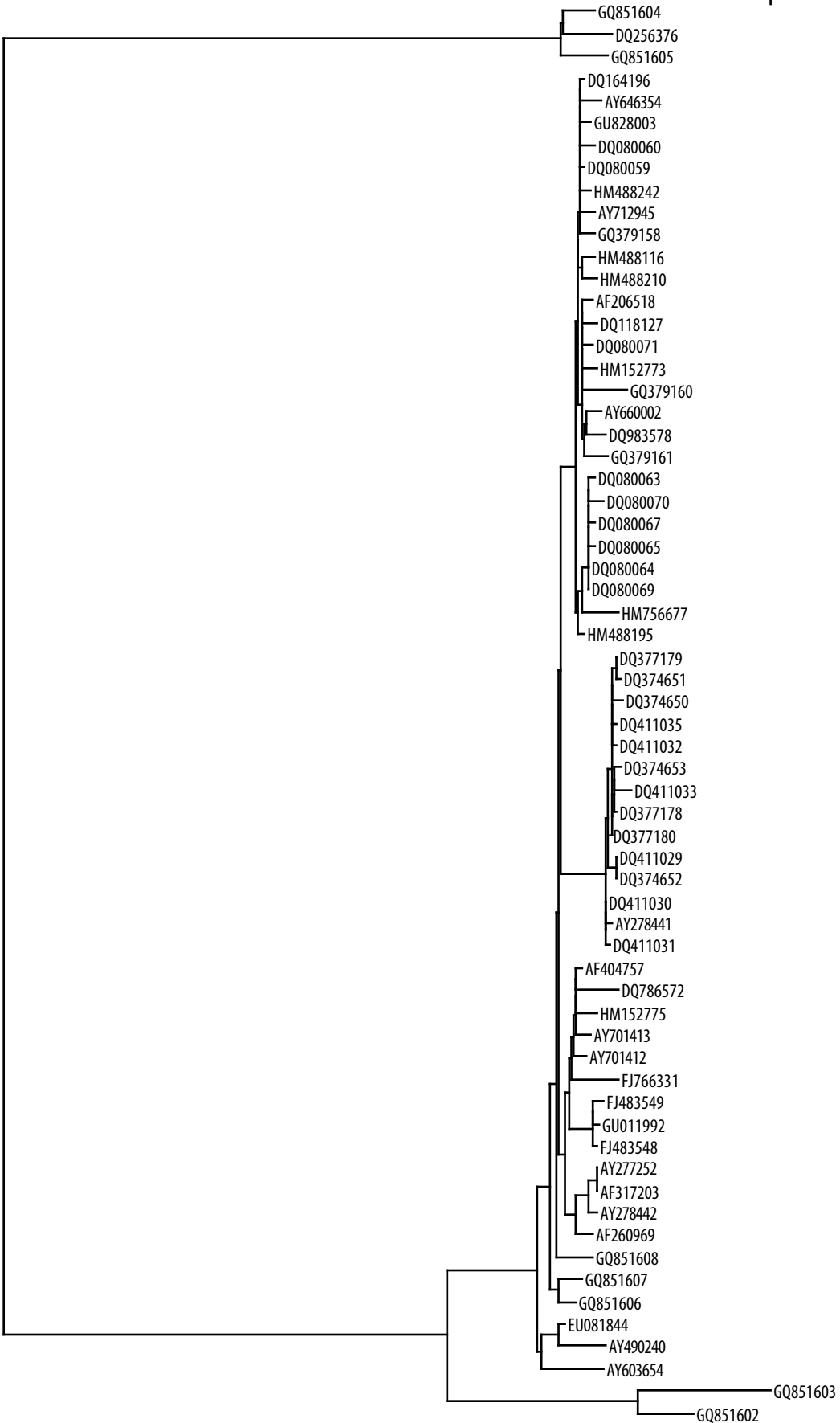
**Supp. Fig 1v:** Phylogenetic tree of 64 WNV polyprotein sequences used to generate the corresponding covariance network.

**Hepatitis A virus**

0.002

SLF88_1
CF53_Berne_1
H2K15_1
H2K20_1
H2K10_1
H2K5_1
L_A_1_1
UNK_M20273_1
UNK_M59810_1
UNK_M59809_1
UNK_M59808_1
IVA_1
HAF_203_1
UNK_M16632_1
UNK_FB746524_1
LP014_1
AH1_1
FH2_1
DL3_1
LY6_1
LU38_WT_1
H2_1
FH1_1
GBM_14_1
GBM_15_1
FG_1
GBM_16_1
AH2_1
AH3_1
FH3_1
UNK_K02990_1
M2_1
HAV5_1

**Supp. Fig 1w:** Phylogenetic tree of 33 HAV polyprotein sequences used to generate the corresponding covariancenetwork.

**Poliovirus type1**

0.005

AF111981_1
AF111953_1
AF111982_1
AF111961_1
AF111966_1
AF111983_1
AF111984_1
AY278553_1
AF405690_1
AF405670_1
AF405687_1
AF405688_1
AF405685_1
AF405681_1
AF405686_1
AF405689_1
AF405672_1
AF405671_1
AF405674_1
AF405677_1
AF405678_1
AF405676_1
AF405679_1
AF405682_1
AF405680_1
AF405684_1
AF405683_1
AF405665_1
AF405662_1
AF458333_1
AF416342_1
AF405664_1
AF405668_1
AF405667_1
AF405666_1
AF405669_1
FJ769380_1
FJ769381_1
FJ769379_1
FJ769378_1
FJ769383_1
GQ984141_1
AY184219_1
AF538843_1
AF538842_1
AF538840_1
AF538841_1
EF682357_1
EF682358_1
EF682356_1
EF682359_1
AJ132960_1
AJ132961_1
FJ859063_1
FJ859061_1
FJ859059_1
FJ859058_1
FJ859060_1
FJ859064_1
FJ859062_1
AF462419_1
AF462418_1
AY560657_1

**Supp. Fig 1x:** Phylogenetic tree of 63 Poliovirus type 1 polyprotein sequences used to generate the corresponding covariance network.

**Hepatitis E virus**

0.002

FJ998008
FJ705359
AB290312
AB369691
AP003430
AB091394
AB189073
AB189072
AB189070
AB222182
AB246676
AB291963
AB437318
AB301710
AB362843
AB425831
AB222183
AB236320
AB291962
AB481229
AB443623
AB291957
AB291956
AB291951
AB074920
AB074918
AB089824
AF060668
AB481228
AY575857
AF082843
AF060669
HQ709170
HQ389543
FJ426404
FJ426403
AY115488
AB073912
AB369689
FJ527832
AB222184

**Supp. Fig 1y:** Phylogenetic tree of 41 HEV type 3 concatenated protein sequences used to generate the corresponding covariance network.

**Crimean-Congo Hemorrhagic Fever virus**

0.005

- ChYL04057
- Ch79121M18
- Semunya
- Congo3010
- ArD8194
- ArD15786
- Matin
- Ch68031
- Oman
- Bagdad12
- TADJ_HU8966
- Afg09_2990
- Kashmanov
- Drosdov
- Kosovo_Hoti
- TurKelkit06
- Tur10849
- SudanAlFallah_3
- SPU128_81_7
- Sudan_AB1
- SPU103_87
- SPU97_85
- SPU415_85
- ArD39554
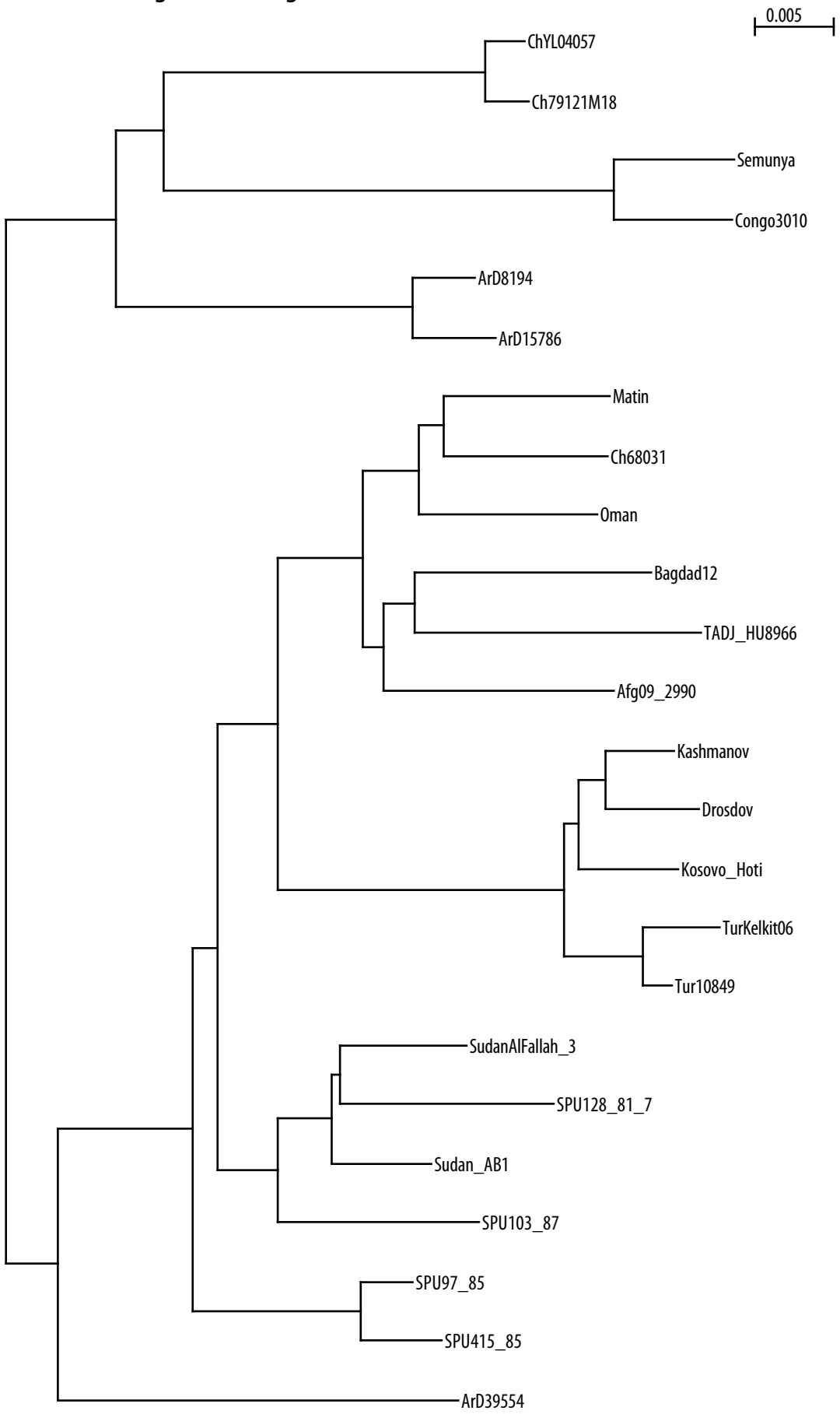
**Supp. Fig 1z:** Phylogenetic tree of 24 CCHV concatenated protein sequences used to generate the corresponding covariance network.
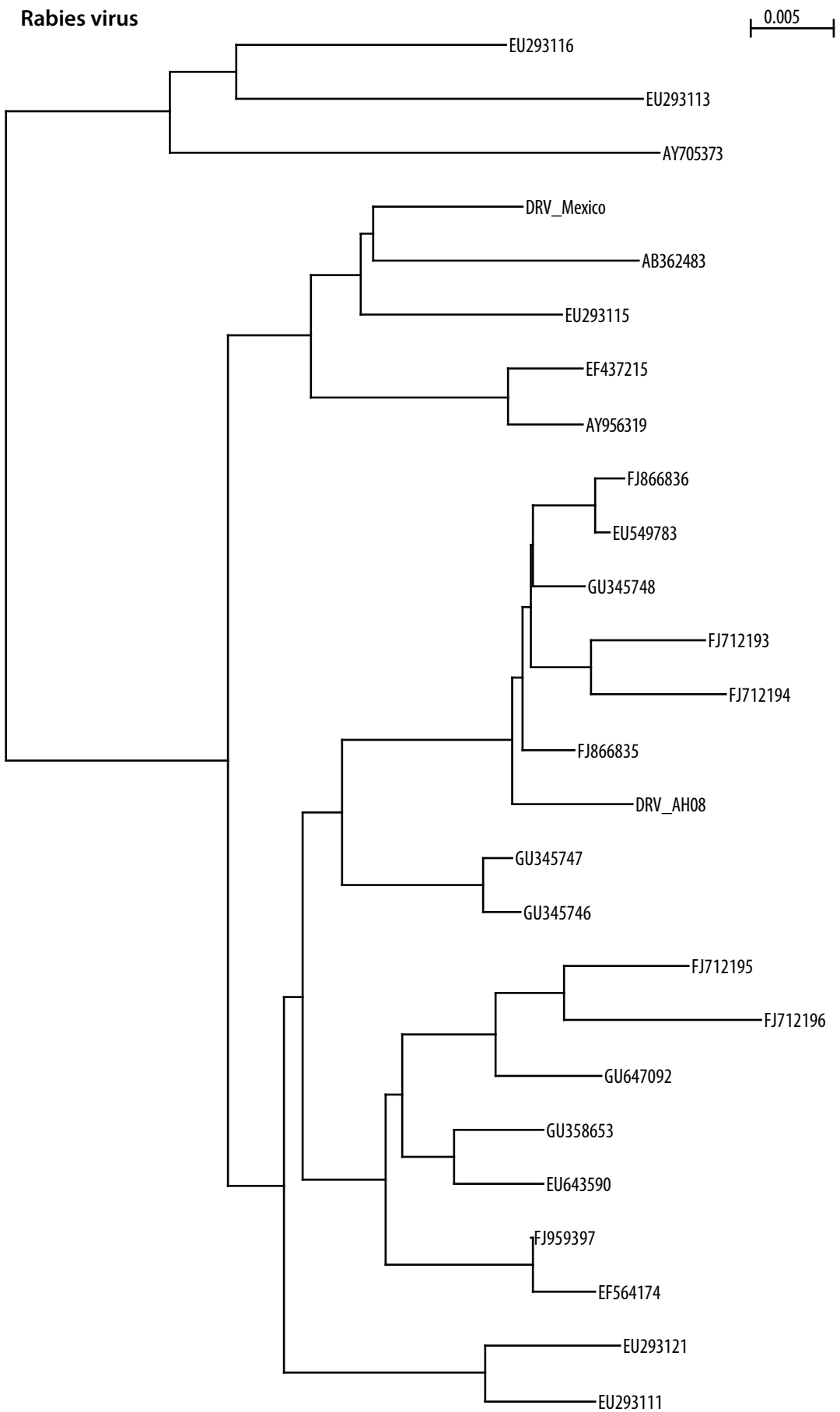
**Supp. Fig 1aa:** Phylogenetic tree of 26 rabies virus protein sequences used to generate the corresponding covariance network.
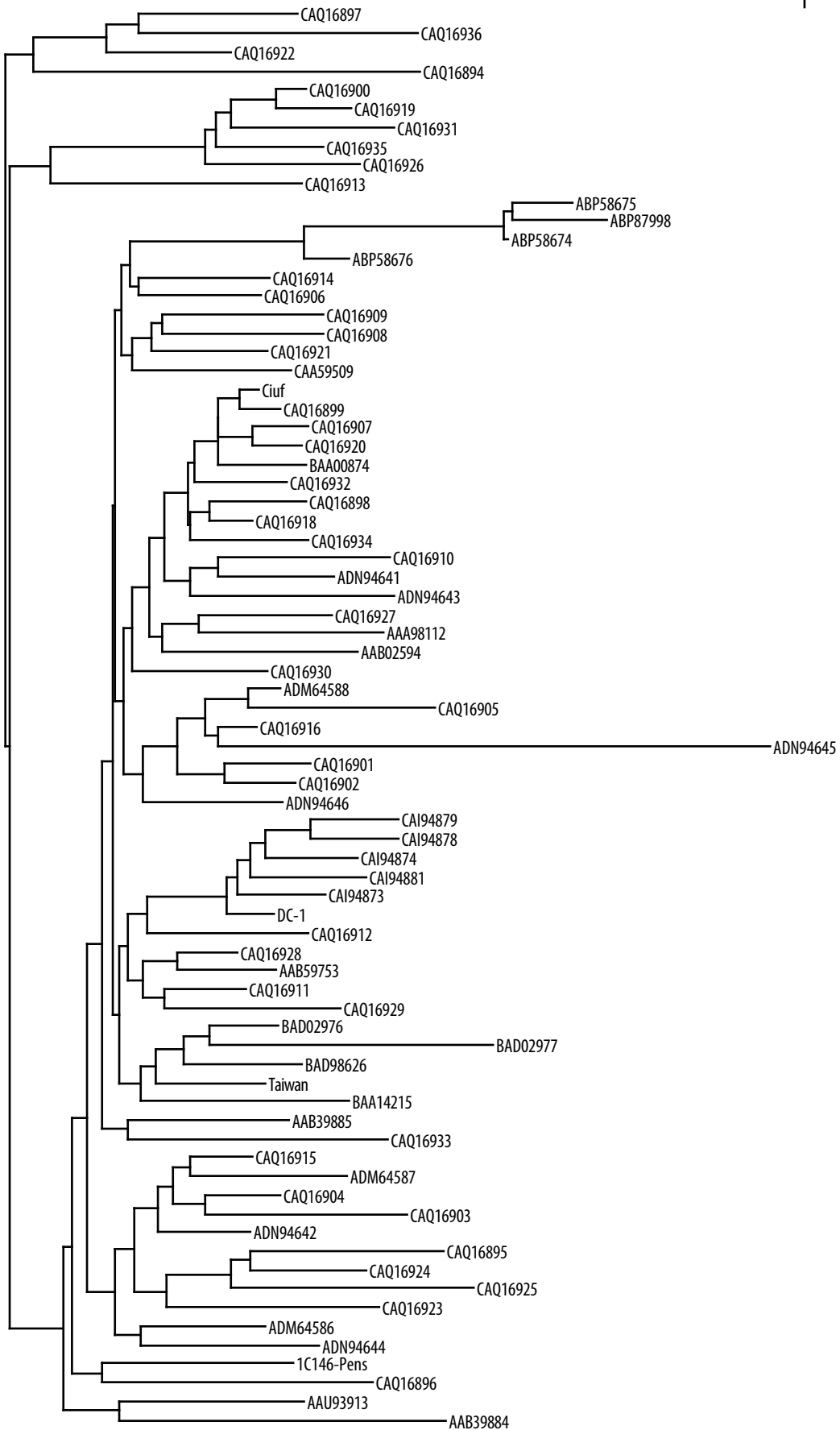
**Supp. Fig 1ab:** Phylogenetic tree of 75 Hepatitis delta protein sequences used to generate the corresponding covariance network.

# Influenza A (H3N2) virus

├─ 0.001 ┤

- Wellington_52_2004
- Whanganui_417_2004
- Auckland_621_2005
- Canterbury_01_2005
- Canterbury_104_2004
- Tairawhiti_223_2004
- Christchurch_13_2004
- Waikato_10_2005
- Queensland_56_2005
- Otago_3_2005
- Yucatan_844_2003
- Western_Australia_79_2005
- Wisconsin_67_2005
- Hong_Kong_HKU49_2005
- Colorado_UR060023_2007
- Tokyo_UtSk1_2007
- Taiwan_70113_2007
- Illinois_UR060334_2007
- Managua_7_2007
- California_UR060347_2007
- Alabama_UR060482_2007
- Kansas_UR070129_2008
- Boston_10_2008
- New_York_3626_2009
- Dakar_WRAIR0011T_2009
- Florida_UR070146_2008
- Ohio_UR070043_2008
- Delware_WRAIR1240_2009
- Korea_AF05_2008
- Peru_WRAIR1508P_2007
- Iraq_WRAIR1157P_2009
- Qatar_AF02_2008

**Supp. Fig 1ac:** Phylogenetic tree of 32 IV-A concatenated protein sequences used to generate the corresponding covariance network.

**Parvovirus B19**

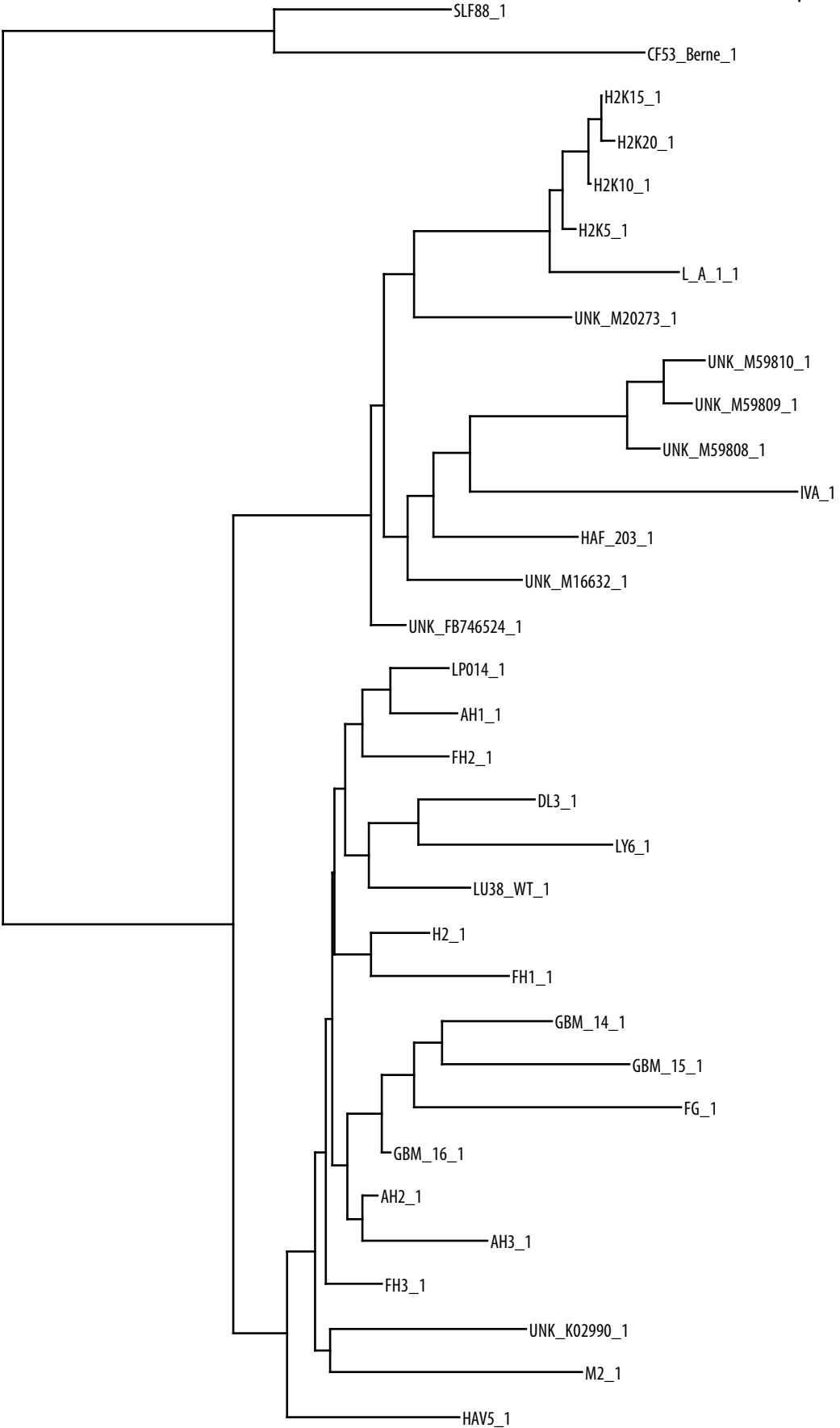**Supp. Fig 1ad:** Phylogenetic tree of 20 PvB19 protein sequences used to generate the corresponding covariance network.
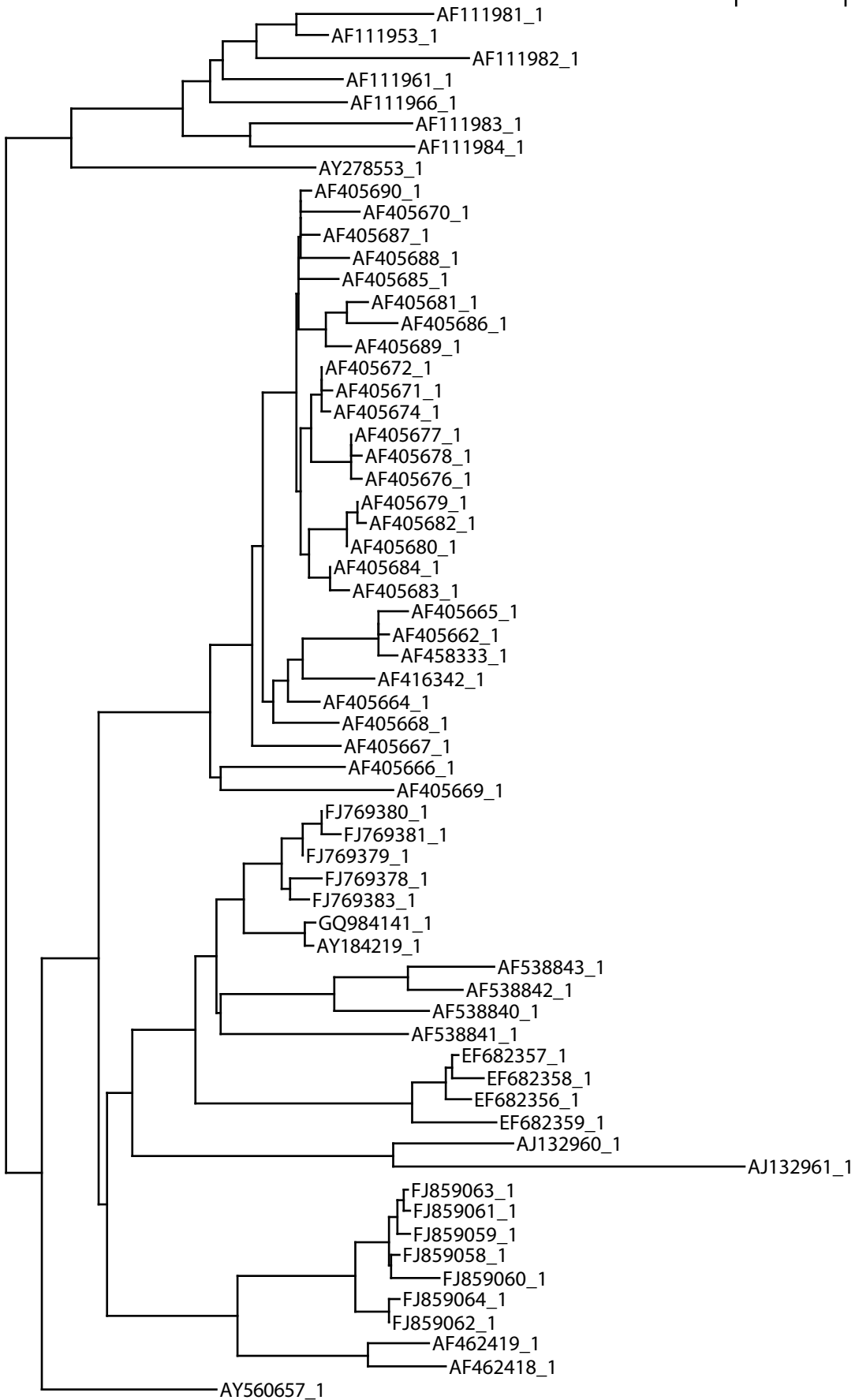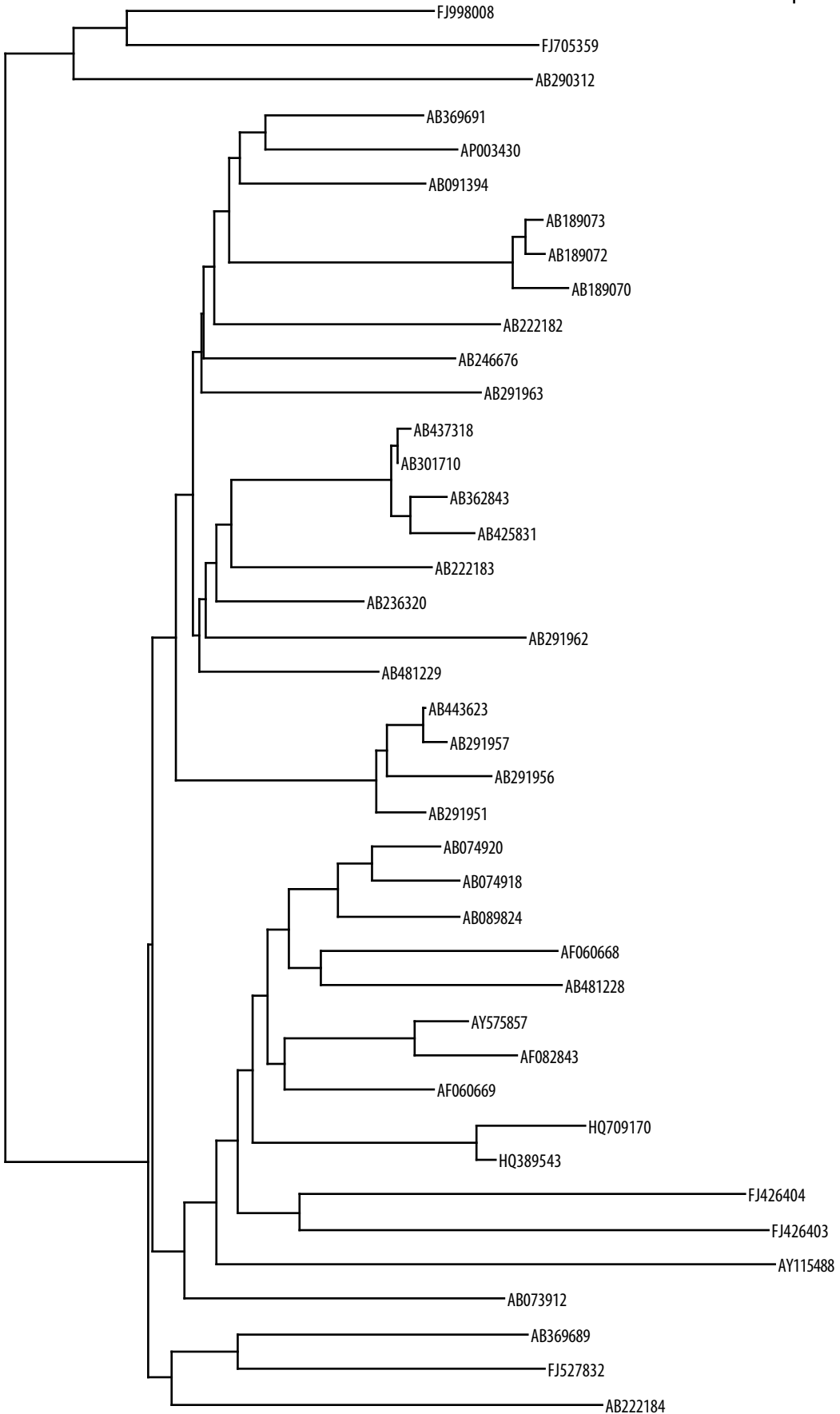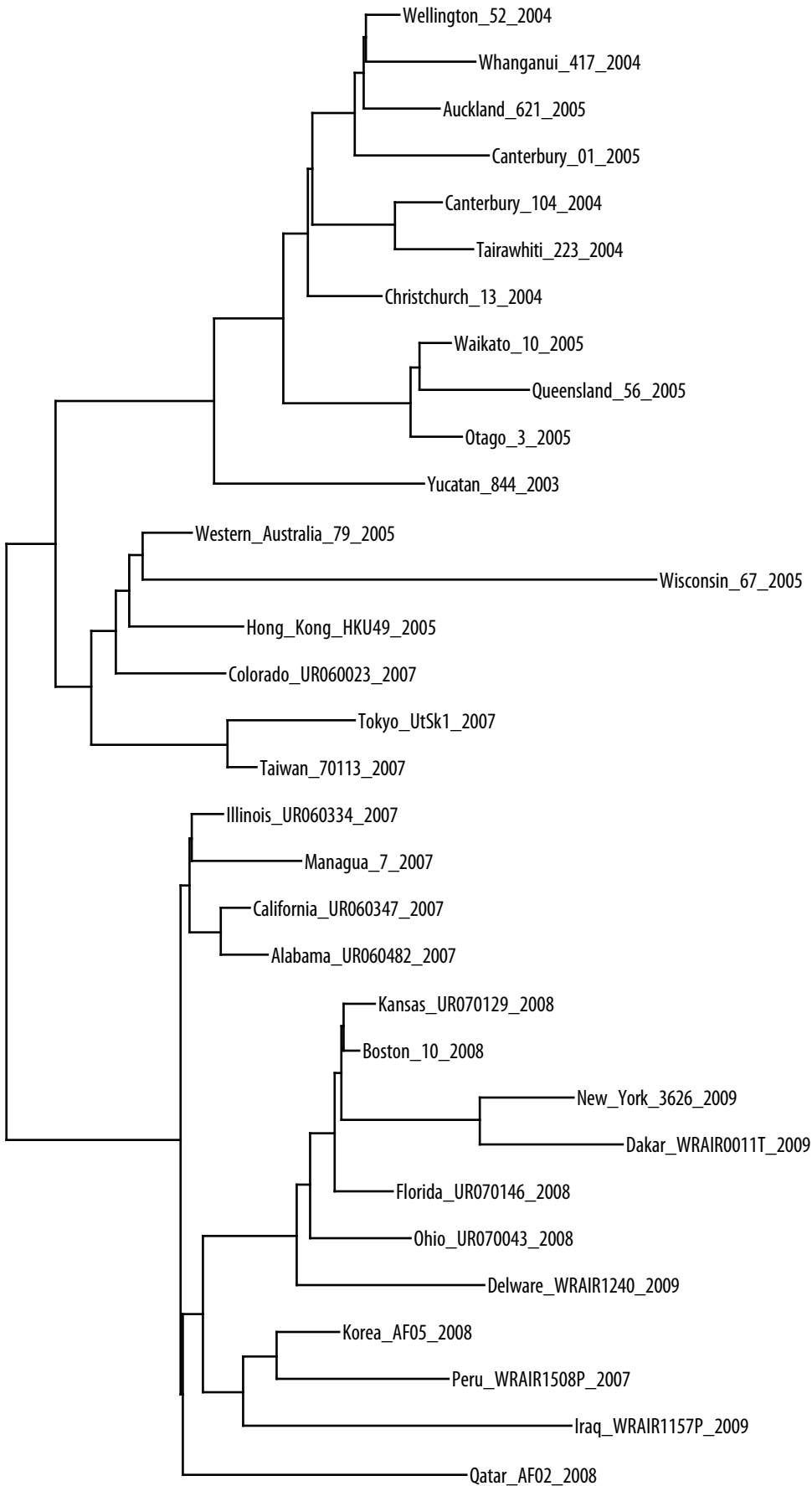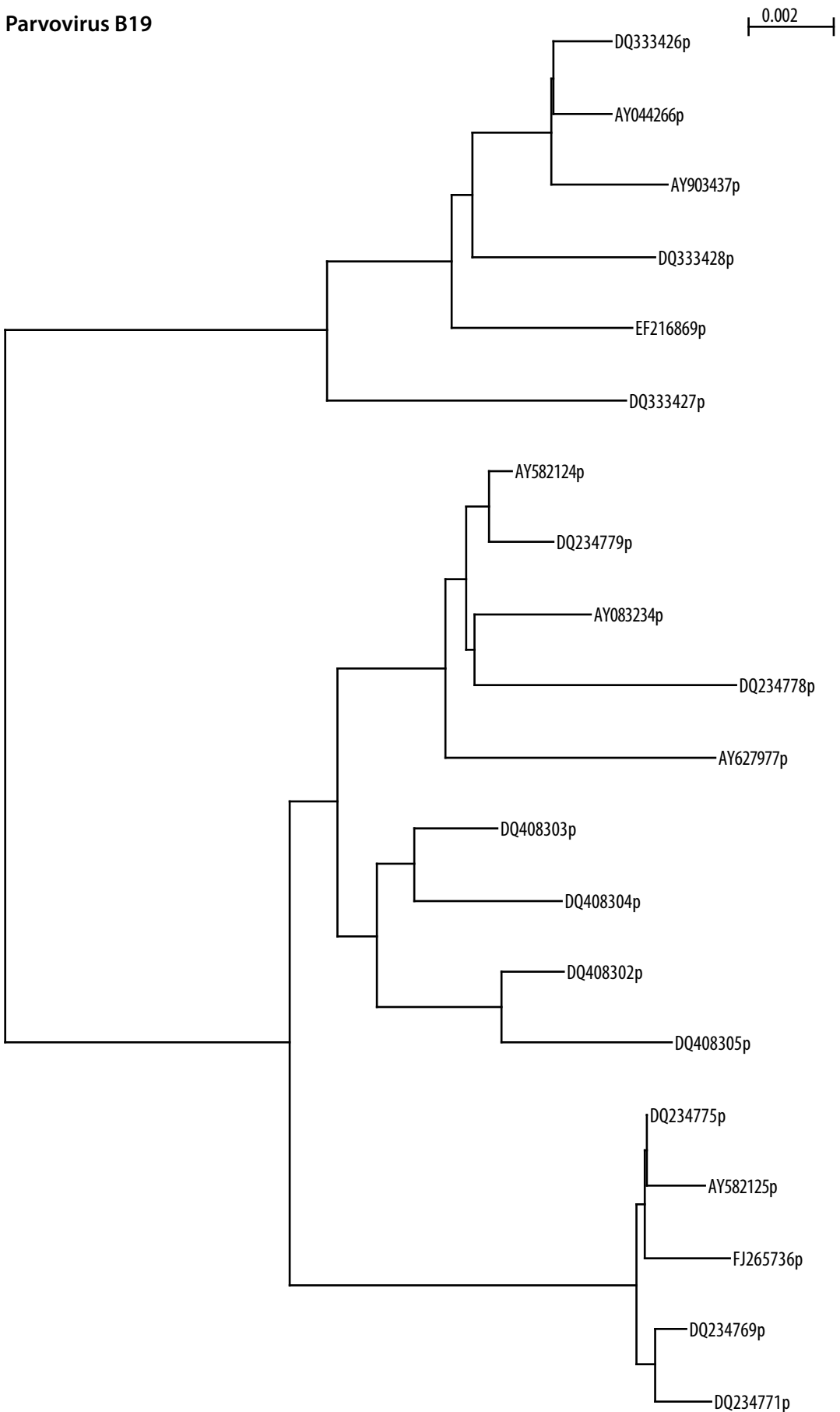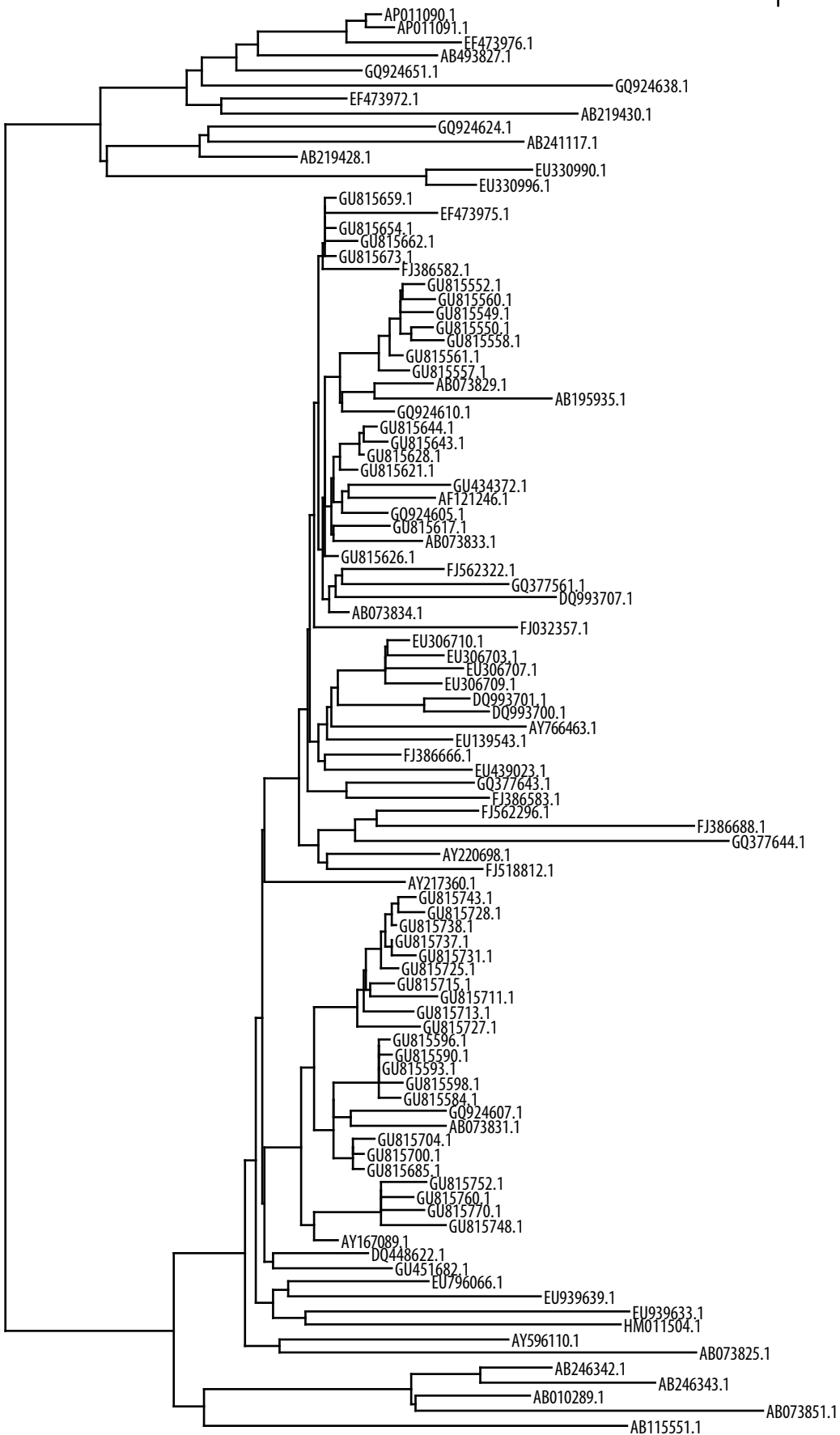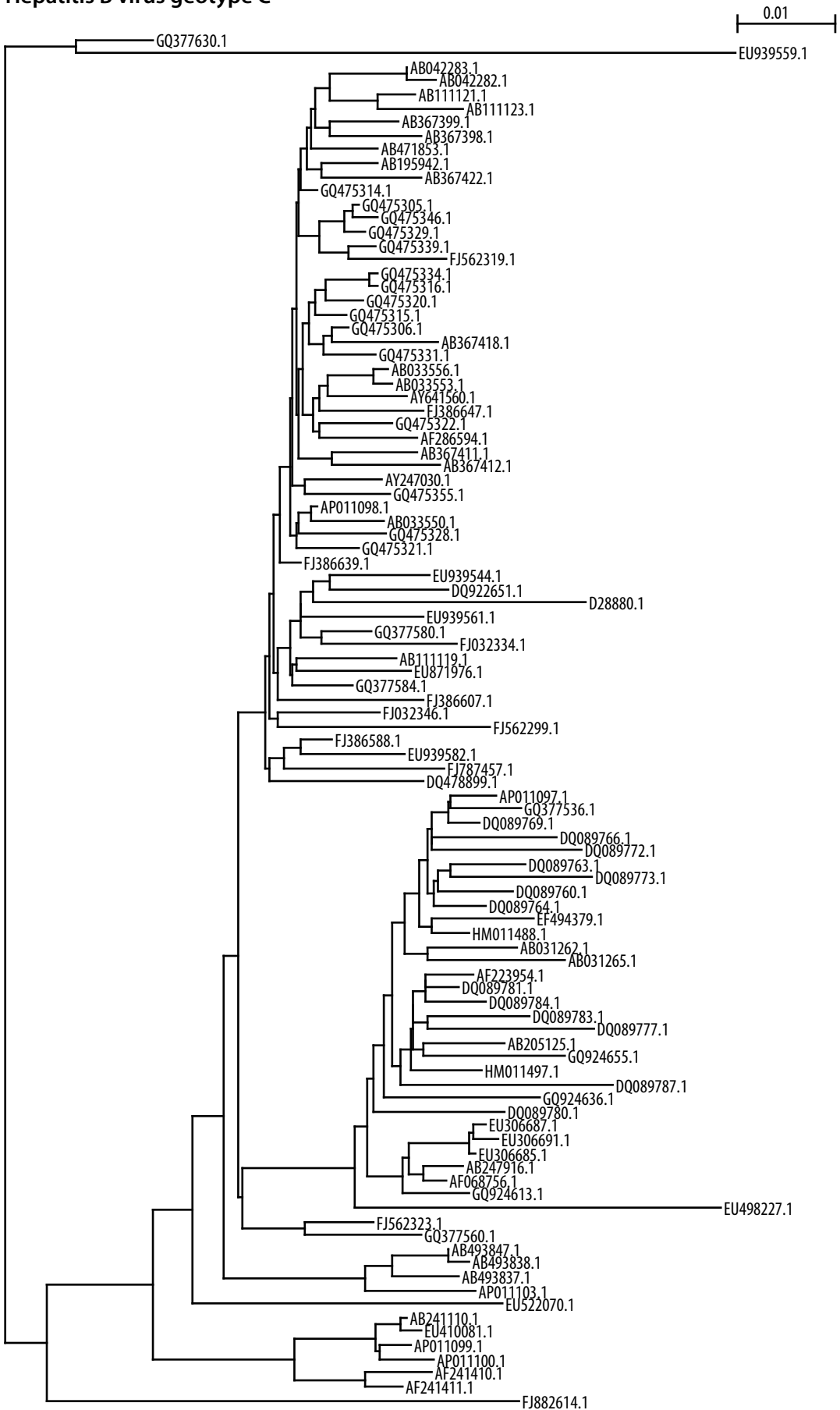
# Hepatitis B virus genotype B

0.005

```
AP011090.1
AP011091.1
EF473976.1
AB493827.1
GQ924651.1
                                    GQ924638.1
    EF473972.1
                        AB219430.1
        GQ924624.1
            AB241117.1
    AB219428.1
                    EU330990.1
                EU330996.1
GU815659.1
    EF473975.1
GU815654.1
GU815662.1
GU815673.1
    FJ386582.1
    GU815552.1
    GU815560.1
    GU815549.1
    GU815550.1
        GU815558.1
GU815561.1
    GU815557.1
        AB073829.1
                    AB195935.1
        GQ924610.1
    GU815644.1
    GU815643.1
    GU815628.1
    GU815621.1
            GU434372.1
            AF121246.1
        GQ924605.1
        GU815617.1
            AB073833.1
GU815626.1
        FJ562322.1
            GQ377561.1
                DQ993707.1
    AB073834.1
            FJ032357.1
        EU306710.1
        EU306703.1
            EU306707.1
        EU306709.1
            DQ993701.1
            DQ993700.1
                AY766463.1
            EU139543.1
        FJ386666.1
            EU439023.1
            GQ377643.1
            FJ386583.1
        FJ562296.1
                            FJ386688.1
                                GQ377644.1
        AY220698.1
            FJ518812.1
AY217360.1
    GU815743.1
    GU815728.1
    GU815738.1
    GU815737.1
    GU815731.1
    GU815725.1
    GU815715.1
        GU815711.1
    GU815713.1
        GU815727.1
    GU815596.1
    GU815590.1
    GU815593.1
        GU815598.1
        GU815584.1
            GQ924607.1
            AB073831.1
    GU815704.1
    GU815700.1
    GU815685.1
        GU815752.1
        GU815760.1
        GU815770.1
            GU815748.1
    AY167089.1
    DQ448622.1
    GU451682.1
        EU796066.1
            EU939639.1
                EU939633.1
                HM011504.1
            AY596110.1
                AB073825.1
            AB246342.1
                AB246343.1
        AB010289.1
                AB073851.1
        AB115551.1
```

**Supp. Fig 1ae:** Phylogenetic tree of 100 HBV-B concatenated protein sequences used to generate the corresponding covariance network.

**Supp. Fig 1af:** Phylogenetic tree of 100 HBV-C concatenated protein sequences used to generate the corresponding covariance network.
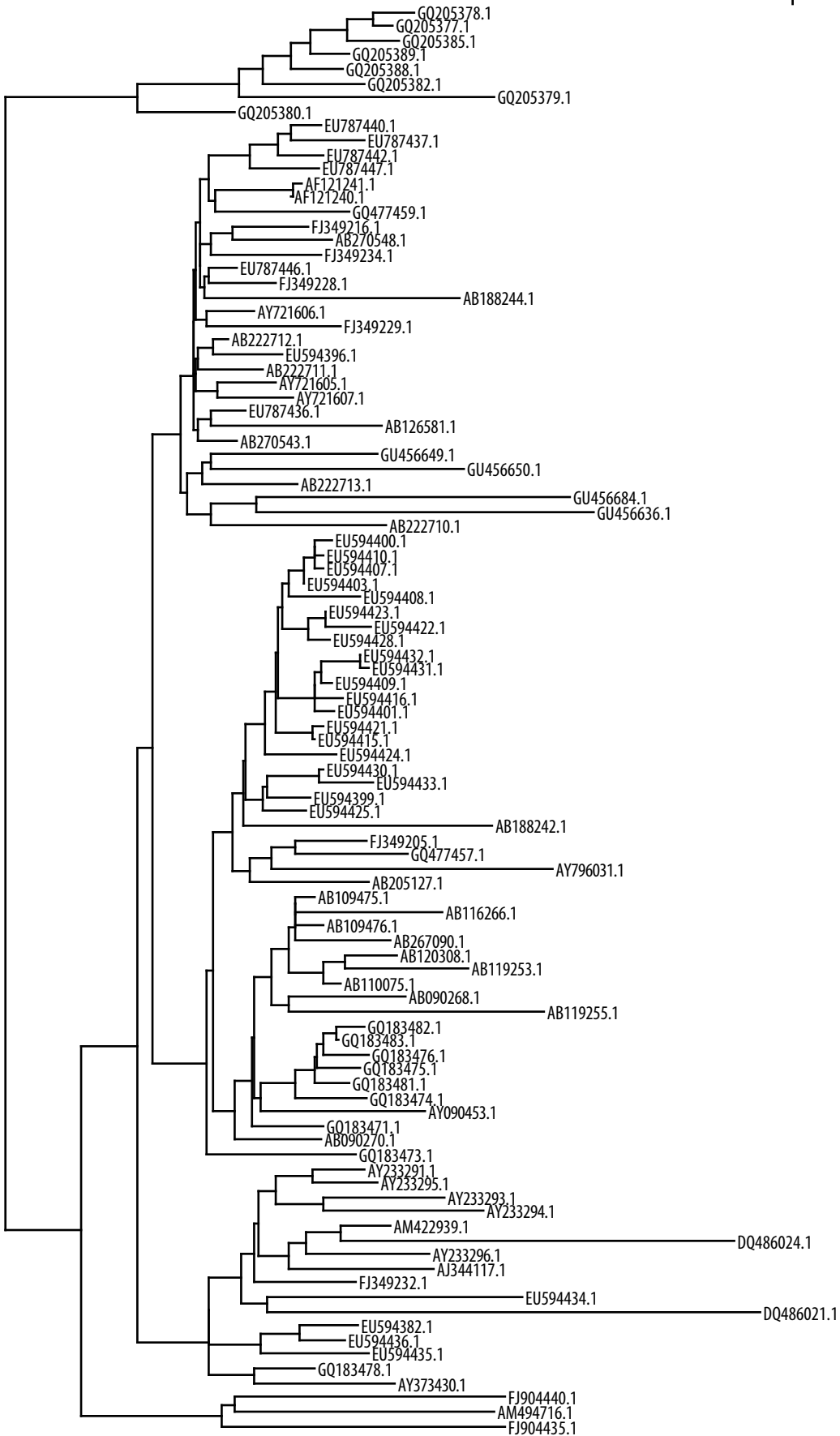
# Hepatitis B virus genotype D



**Supp. Fig 1ag:** Phylogenetic tree of 100 HBV-D concatenated protein sequences used to generate the corresponding covariance network.