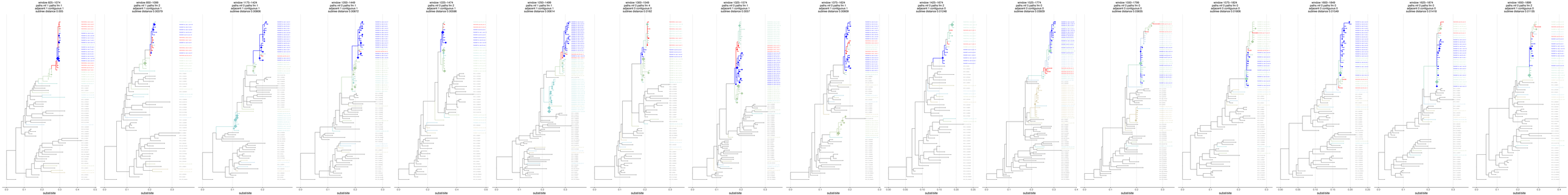
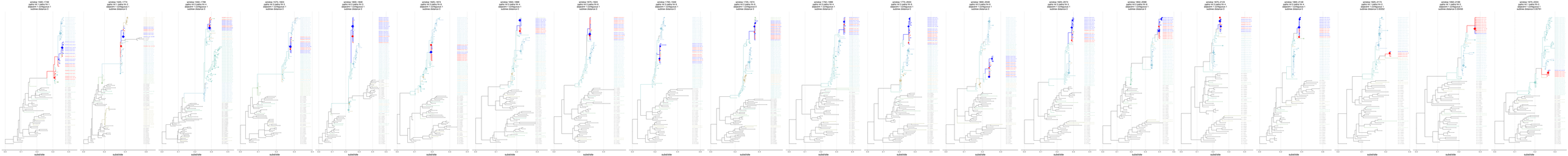
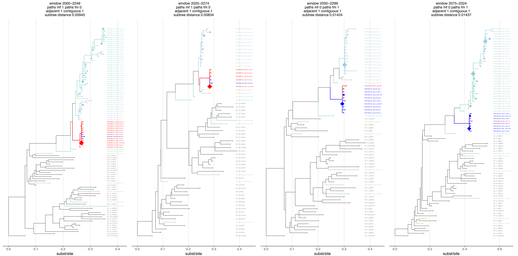
Deep sequence phylogenies
of male-female pair RkA05162M, RkA02020F (run 10)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.


window 825–1074
paths int 1 paths fm 1
adjacent 0 contiguous 1
subtree distance 0.0400
window 850–1099
paths int 0 paths fm 2
adjacent 1 contiguous 1
subtree distance 0.00079
window 1175–1424
paths int 0 paths fm 1
adjacent 1 contiguous 1
subtree distance 0.00606
window 1200–1449
paths int 0 paths fm 1
adjacent 1 contiguous 1
subtree distance 0.00612
window 1225–1474
paths int 0 paths fm 2
adjacent 1 contiguous 1
subtree distance 0.00598
window 1250–1499
paths int 0 paths fm 1
adjacent 1 contiguous 1
subtree distance 0.00614
window 1300–1549
paths int 0 paths fm 4
adjacent 0 contiguous 0
subtree distance 0.0142
window 1325–1574
paths int 0 paths fm 1
adjacent 1 contiguous 1
subtree distance 0.0027
window 1375–1624
paths int 0 paths fm 1
adjacent 1 contiguous 1
subtree distance 0.00609
window 1425–1674
paths int 0 paths fm 2
adjacent 0 contiguous 0
subtree distance 0.21248
window 1525–1774
paths int 0 paths fm 2
adjacent 0 contiguous 0
subtree distance 0.00629
window 1550–1799
paths int 0 paths fm 2
adjacent 0 contiguous 0
subtree distance 0.29608
window 1575–1824
paths int 0 paths fm 2
adjacent 0 contiguous 0
subtree distance 0.01806
window 1600–1849
paths int 0 paths fm 3
adjacent 0 contiguous 0
subtree distance 0.21549
window 1625–1874
paths int 0 paths fm 2
adjacent 0 contiguous 0
subtree distance 0.01418
window 1650–1899
paths int 0 paths fm 2
adjacent 1 contiguous 0
subtree distance 0.21136
subst/site

Deep sequence phylogenies
of male-female pair RkA00495M, RkA07422F (run 12)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.


window 1560–1766
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1570–1774
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1580–1788
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1575–1829
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1600–1840
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1625–1874
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1650–1898
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1675–1924
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1700–1949
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1725–1974
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1750–1999
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1775–2024
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1800–2049
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1825–2074
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1850–2099
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1875–2124
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1900–2149
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0
window 1925–2174
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0.00202
window 1950–2199
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0.00406
window 1975–2224
gamma-R = 0.000
alpha-R = 1.000
sulrate distance 0.00791
sulrate
sulrate

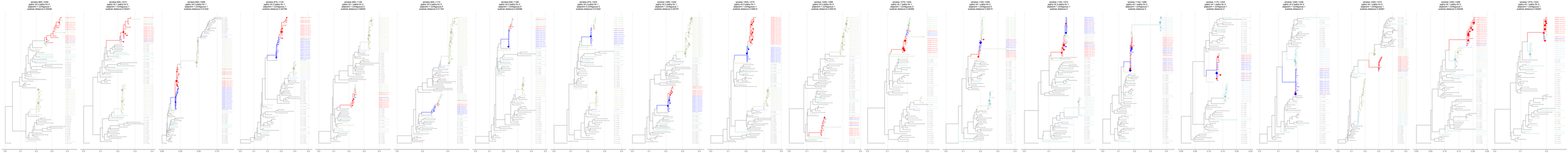

window 2560–2749
topology rank 1
adjacent 1 contiguous 1
subtree distance 0.00840
subst/site
-0.0
0.1
0.2
0.3
0.4

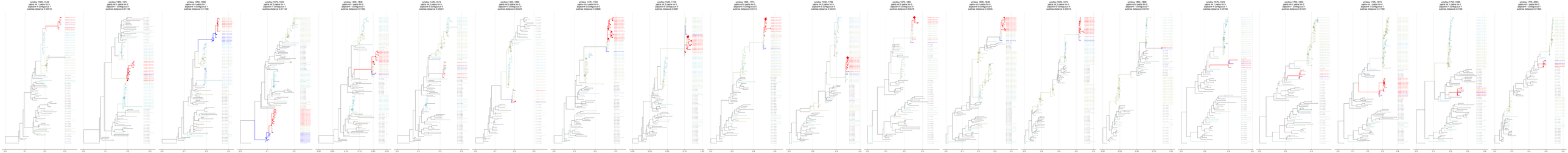
window 2625–2774
topology rank 1
adjacent 1 contiguous 1
subtree distance 0.00804
subst/site
-0.0
0.1
0.2
0.3
0.4

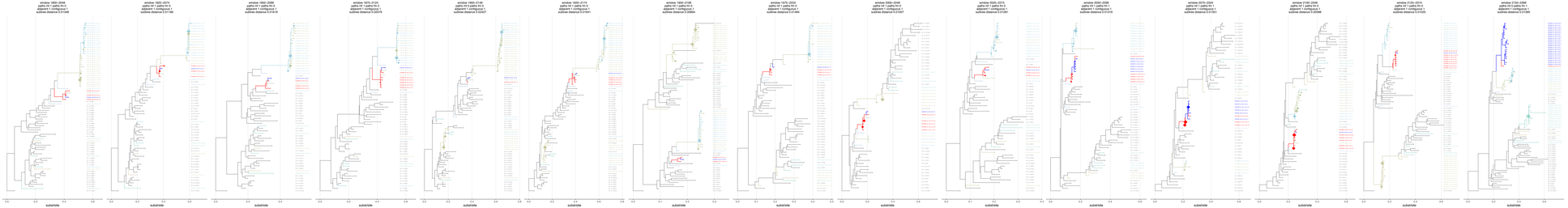
window 2930–3099
topology rank 1
adjacent 1 contiguous 1
subtree distance 0.01424
subst/site
-0.0
0.1
0.2
0.3
0.4

window 3575–3924
topology rank 1
adjacent 1 contiguous 1
subtree distance 0.01437
subst/site
-0.0
0.2
0.4
0.6

Deep sequence phylogenies
of male-female pair RkA02808M, RkA00505F (run 17)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.

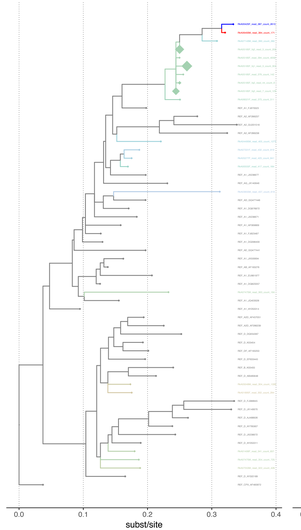

window 850–1049
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.03540
window 925–1074
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00441
window 950–1099
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.01540
window 975–1124
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00709
window 900–1149
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00633
window 925–1174
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.01704
window 950–1199
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00546
window 975–1224
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.01054
window 1000–1249
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00791
window 1025–1274
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00813
window 1050–1299
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00519
window 1075–1324
maximum 1 recombinant
allpairwise 1 contiguous 0
sublinee distance 0.00265
window 1100–1349
maximum 1 recombinant
allpairwise 1 contiguous 0
sublinee distance 0.00274
window 1125–1374
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0
window 1150–1399
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0
window 1175–1424
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0
window 1200–1449
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0
window 1225–1474
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00391
window 1250–1499
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00408
window 1275–1524
maximum 1 recombinant
allpairwise 1 contiguous 1
sublinee distance 0.00461
sublinEle


window 1360–1549
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.000510
window 1525–1574
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.011169
window 1350–1399
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.011186
window 1375–1424
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.011532
window 1400–1449
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.012404
window 1425–1474
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.030251
window 1450–1499
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.044425
window 1475–1724
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.050806
window 1500–1749
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.06871
window 1525–1774
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.091141
window 1550–1799
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.094251
window 1575–1824
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.102576
window 1600–1849
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.102505
window 1625–1874
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.102574
window 1650–1899
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.107177
window 1675–1924
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.107795
window 1700–1949
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.119427
window 1725–1974
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.121189
window 1750–1999
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.12126
window 1775–2024
gapped-codons=1
aligned=1 contiguous=1
sulrline distance:0.131476
subsitute
subsitute

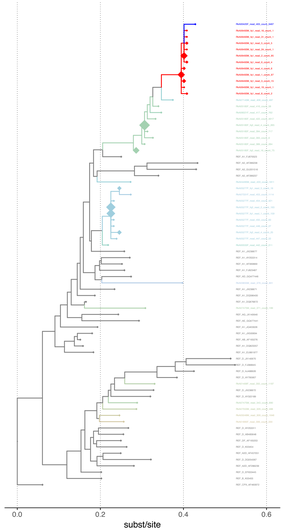

window 1860-2049
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1348
window 1925-2074
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1106
window 1992-2088
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:919
window 1973-2129
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:979
window 1900-2140
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:947
window 1925-2174
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:941
window 1900-2198
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:994
window 1975-2224
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1484
window 2000-2248
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1067
window 2025-2274
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1261
window 2050-2299
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1010
window 2075-2324
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:1301
window 2100-2349
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:998
window 2125-2374
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:925
window 2150-2399
gapseed.1.1.unitigs.fasta.1
alignment 1 unitigs.mm.1
sublime distance 0:0:0:995
0.0
0.2
0.4
0.6
0.8
1.0
sublime

Deep sequence phylogenies
of male-female pair RkA06493M, RkA00425F (run 34)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.

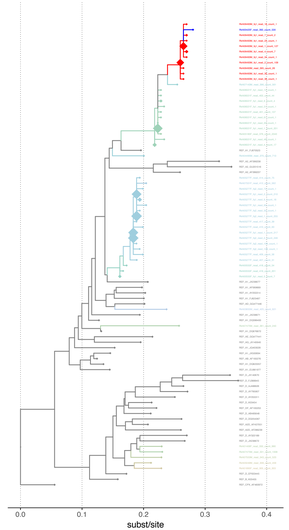
window 800–1049
paths mf 0 paths fm 0
adjacent 1 contiguous 1
subtree distance 0.02073



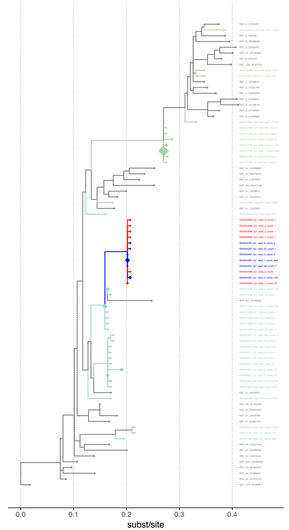
window 825–1074
paths mf 1 paths fm 0
adjacent 1 contiguous 1
subtree distance 0.02245



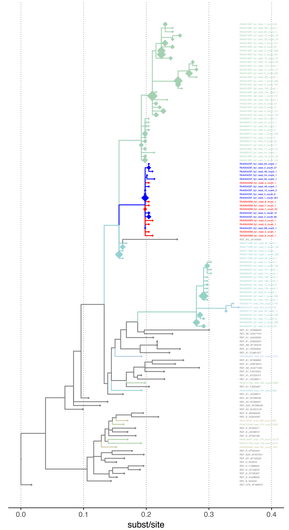
window 850–1099
paths mf 1 paths fm 0
adjacent 1 contiguous 1
subtree distance 0.01198



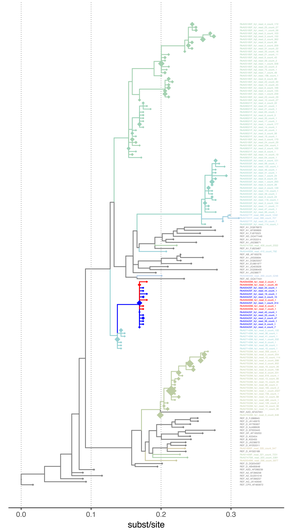
window 1525–1774
paths mf 0 paths fm 6
adjacent 1 contiguous 1
subtree distance 0



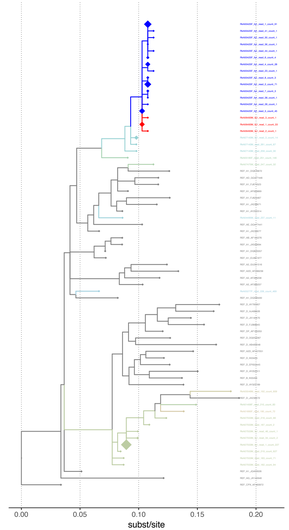
window 1550–1799
paths mf 0 paths fm 8
adjacent 1 contiguous 1
subtree distance 0



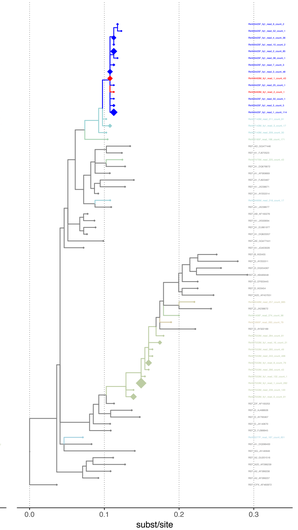
window 1575–1824
paths mf 0 paths fm 5
adjacent 1 contiguous 1
subtree distance 0



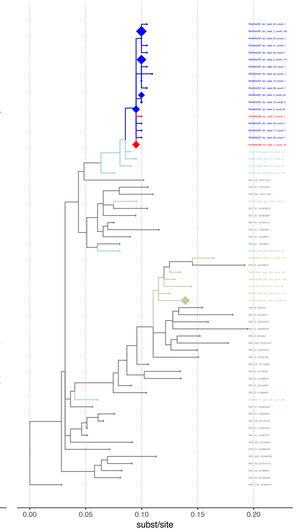
window 2325–2574
paths mf 0 paths fm 3
adjacent 1 contiguous 1
subtree distance 0



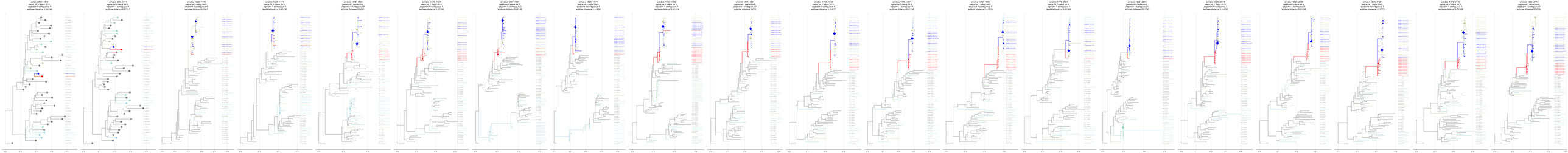
window 2350–2599
paths mf 0 paths fm 2
adjacent 1 contiguous 1
subtree distance 0

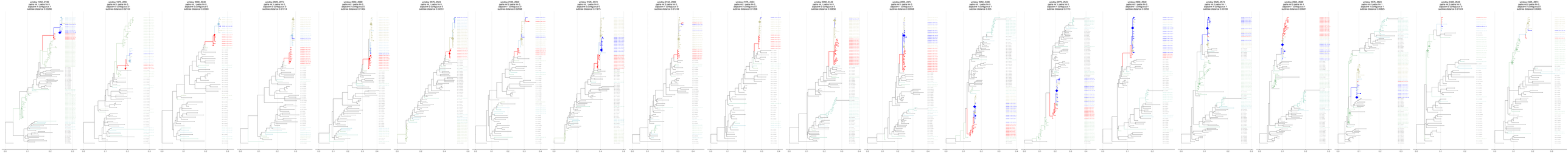


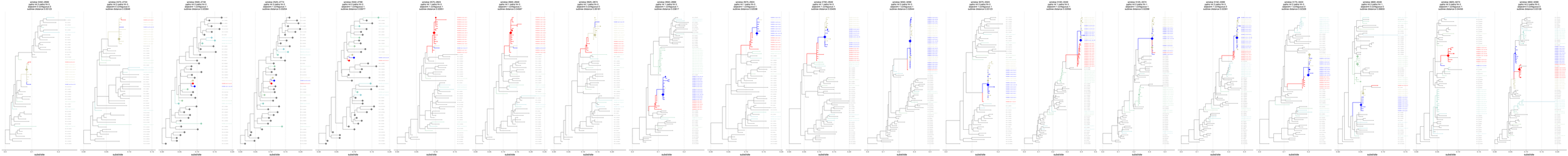
window 2375–2624
paths mf 0 paths fm 2
adjacent 1 contiguous 1
subtree distance 0

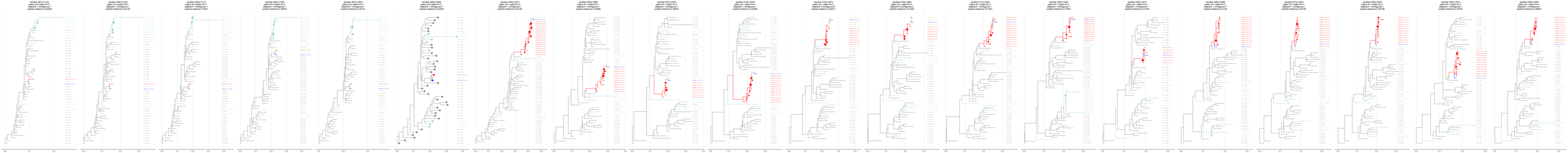


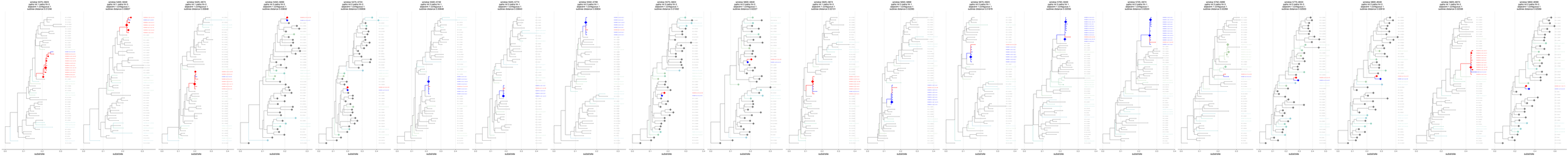
Deep sequence phylogenies
of male-female pair RkA02803M, RkA00868F (run 42)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.

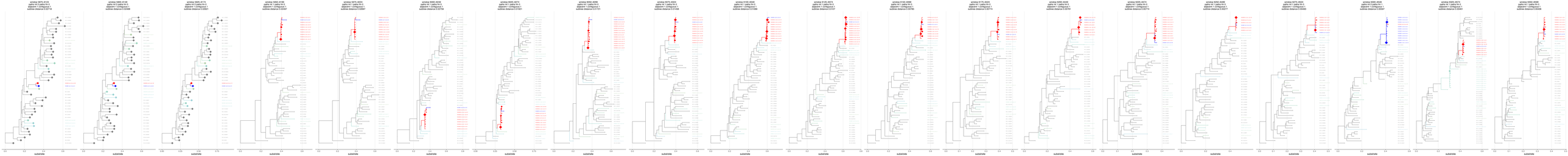

window 880–1049
gene 1–1049 bp
aligned 1 contiguous 1
sublime distance 0.06740
window 925–1074
gene 1–1074 bp
aligned 1 contiguous 1
sublime distance 0.07617
window 1020–1169
gene 1–1169 bp
aligned 1 contiguous 1
sublime distance 0.0581
window 1325–1774
gene 1–1774 bp
aligned 1 contiguous 1
sublime distance 0.02196
window 1350–1799
gene 1–1799 bp
aligned 1 contiguous 1
sublime distance 0.03917
window 1375–1824
gene 1–1824 bp
aligned 1 contiguous 1
sublime distance 0.02146
window 1600–1849
gene 1–1849 bp
aligned 1 contiguous 1
sublime distance 0.02143
window 1625–1874
gene 1–1874 bp
aligned 1 contiguous 1
sublime distance 0.01808
window 1650–1899
gene 1–1899 bp
aligned 1 contiguous 1
sublime distance 0.01574
window 1675–1924
gene 1–1924 bp
aligned 1 contiguous 1
sublime distance 0.0112
window 1700–1949
gene 1–1949 bp
aligned 1 contiguous 1
sublime distance 0.01457
window 1725–1974
gene 1–1974 bp
aligned 1 contiguous 1
sublime distance 0.01706
window 1750–1999
gene 1–1999 bp
aligned 1 contiguous 1
sublime distance 0.01518
window 1775–2024
gene 1–2024 bp
aligned 1 contiguous 1
sublime distance 0.01982
window 1800–2049
gene 1–2049 bp
aligned 1 contiguous 1
sublime distance 0.01763
window 1825–2074
gene 1–2074 bp
aligned 1 contiguous 1
sublime distance 0.01052
window 1850–2099
gene 1–2099 bp
aligned 1 contiguous 1
sublime distance 0.01086
window 1875–2124
gene 1–2124 bp
aligned 1 contiguous 1
sublime distance 0.01772
window 1900–2149
gene 1–2149 bp
aligned 1 contiguous 1
sublime distance 0.02528
window 1925–2174
gene 1–2174 bp
aligned 1 contiguous 1
sublime distance 0.02143
substitute

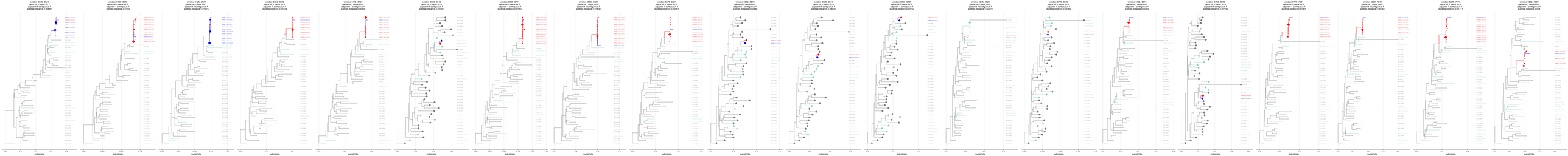

window 1860–2198
gapseq.fr | ambiguous 1
alignment 1 (ambiguous 1)
sulfitree distance 0.02266
window 1875–2234
gapseq.fr | ambiguous 2
alignment 1 (ambiguous 2)
sulfitree distance 0.02124
window 2000–2340
gapseq.fr | ambiguous 3
alignment 1 (ambiguous 3)
sulfitree distance 0.02260
window 2025–2374
gapseq.fr | ambiguous 4
alignment 1 (ambiguous 4)
sulfitree distance 0.01914
window 2050–2399
gapseq.fr | ambiguous 5
alignment 1 (ambiguous 5)
sulfitree distance 0.01454
window 2075–2424
gapseq.fr | ambiguous 6
alignment 1 (ambiguous 6)
sulfitree distance 0.00631
window 2100–2449
gapseq.fr | ambiguous 7
alignment 1 (ambiguous 7)
sulfitree distance 0.00808
window 2125–2474
gapseq.fr | ambiguous 8
alignment 1 (ambiguous 8)
sulfitree distance 0.01875
window 2150–2499
gapseq.fr | ambiguous 9
alignment 1 (ambiguous 9)
sulfitree distance 0.01249
window 2175–2524
gapseq.fr | ambiguous 10
alignment 1 (ambiguous 10)
sulfitree distance 0.01308
window 2200–2548
gapseq.fr | ambiguous 11
alignment 1 (ambiguous 11)
sulfitree distance 0.00808
window 2225–2574
gapseq.fr | ambiguous 12
alignment 1 (ambiguous 12)
sulfitree distance 0.00808
window 2250–2599
gapseq.fr | ambiguous 13
alignment 1 (ambiguous 13)
sulfitree distance 0.000
window 2275–2624
gapseq.fr | ambiguous 14
alignment 1 (ambiguous 14)
sulfitree distance 0.00113
window 2300–2649
gapseq.fr | ambiguous 15
alignment 1 (ambiguous 15)
sulfitree distance 0.00808
window 2325–2674
gapseq.fr | ambiguous 16
alignment 1 (ambiguous 16)
sulfitree distance 0.00730
window 2350–2699
gapseq.fr | ambiguous 17
alignment 1 (ambiguous 17)
sulfitree distance 0.00861
window 2375–2724
gapseq.fr | ambiguous 18
alignment 1 (ambiguous 18)
sulfitree distance 0.00825
window 2400–2749
gapseq.fr | ambiguous 19
alignment 1 (ambiguous 19)
sulfitree distance 0.01824
window 2425–2774
gapseq.fr | ambiguous 20
alignment 1 (ambiguous 20)
sulfitree distance 0.00835
subtitle

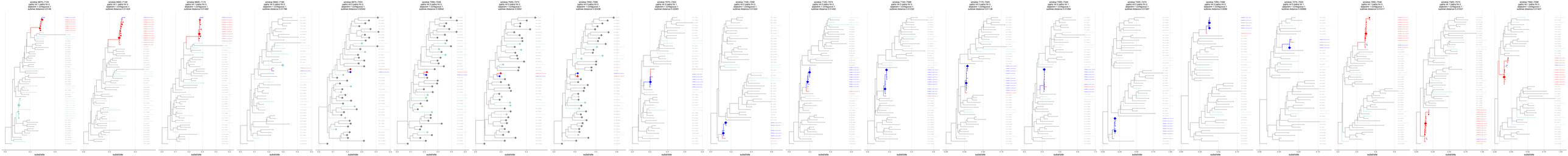

window 2460-2999
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.001123
window 2475-2774
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.000446
window 2500-2749
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.01054
window 2525-2774
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.01024
window 2550-2799
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.01877
window 2575-2824
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.00061
window 2600-2849
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.04047
window 2625-2874
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.00149
window 2650-2899
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02817
window 2675-2924
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02838
window 2700-2949
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.00435
window 2725-2974
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02604
window 2750-2999
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.01123
window 2775-3024
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.01123
window 2800-3049
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02968
window 2825-3074
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02708
window 2850-3099
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02038
window 2875-3124
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02298
window 2900-3149
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02291
window 2925-3174
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.02026
window 2950-3199
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.04630
window 2975-3224
gapseq.fasttree.tree
alignment 1 contiguous 1
subtree distance 0.03139
subtree distance

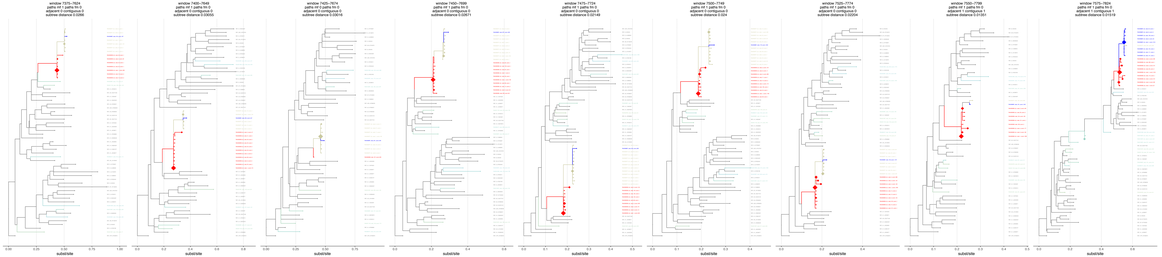

window 4475-5124
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.03363
window 4900-5149
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.03142
window 4925-5174
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.0351
window 4950-5199
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02937
window 4975-5224
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02741
window 5000-5249
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.03205
window 5025-5274
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02134
window 5050-5299
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02068
window 5075-5324
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02007
window 5100-5349
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02063
window 5125-5374
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02011
window 5150-5399
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.01933
window 5175-5424
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.01961
window 5200-5449
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.01927
window 5225-5474
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.01945
window 5250-5499
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.01935
window 5275-5524
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02129
window 5300-5549
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02138
window 5325-5574
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.02161
window 5350-5599
MN908947.3 / chr1
alignment 1 / contig:node 1
sublime distance 0.03863
sublimeTile


window 5375-5924
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.01040
window 5400-5949
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00807
window 5425-5974
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00848
window 5450-5999
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00833
window 5475-6024
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00836
window 5500-6049
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00840
window 5525-6074
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00843
window 5550-6099
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00834
window 5575-6124
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.01920
window 5600-6149
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00577
window 5625-6174
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.01101
window 5650-6199
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.02295
window 5675-6224
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.01878
window 5700-6249
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00599
window 5725-6274
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00824
window 5750-6299
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.01250
window 5775-6324
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.00653
window 5800-6349
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.02618
window 5825-6374
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.02338
window 5850-6399
gapseq 1 unitigcov 1
alignment 1 unitigcov 1
sublime distance 0.02049
sublime

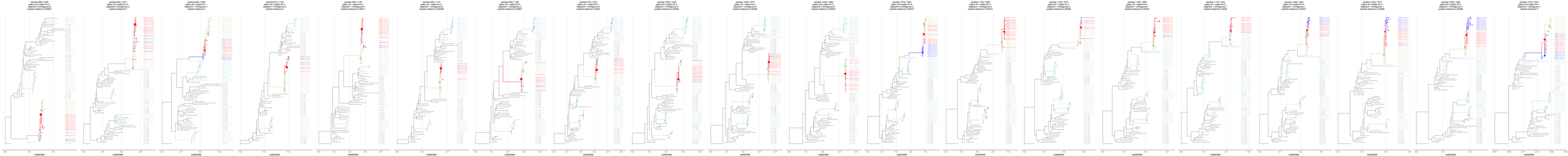

subtitle

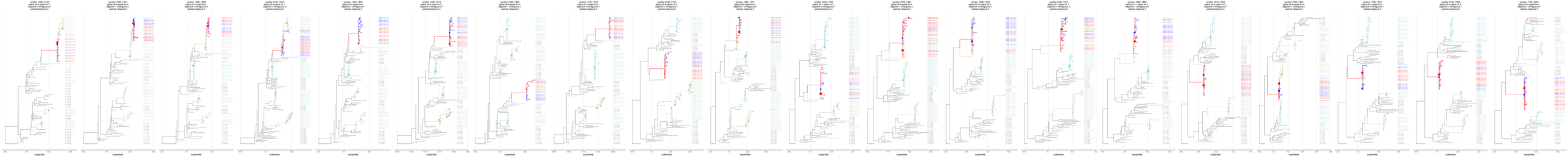

window 6375–6624
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.09867
window 6400–6649
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01420
window 6425–6674
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01275
window 6450–6699
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01549
window 6475–6724
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.00859
window 6500–6749
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01051
window 6525–6774
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01067
window 6550–6799
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01808
window 6575–6824
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02081
window 6600–6849
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02446
window 6625–6874
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.00631
window 6650–6899
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02753
window 6675–6924
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02079
window 6700–6949
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02820
window 6725–6974
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02204
window 6750–6999
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.02138
window 6775–7024
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01961
window 6800–7049
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.00764
window 6825–7074
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.01111
window 6850–7099
gene 2 / ORF2ab
alignment 1 / contiguous 1
sublime distance 0.0114
sublime

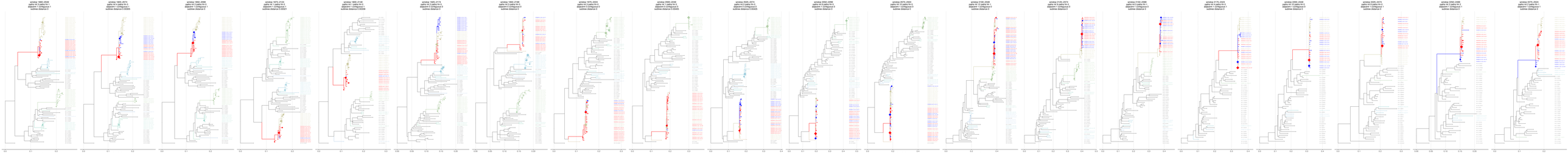

window 6875–7174
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01146
window 6900–7149
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01424
window 6925–7174
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01482
window 6950–7199
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01786
window 6975–7224
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.02042
window 7000–7249
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.02063
window 7025–7274
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.02602
window 7050–7299
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.02638
window 7075–7324
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.02581
window 7100–7349
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01553
window 7125–7374
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01442
window 7150–7399
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01232
window 7175–7424
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01136
window 7200–7449
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01084
window 7225–7474
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01067
window 7250–7499
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.0088
window 7275–7524
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.00890
window 7300–7549
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01017
window 7325–7574
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01057
window 7350–7599
maximum RF distance 0
alignment 1 (ambiguous 1)
subtree distance 0.01047
subtree/site

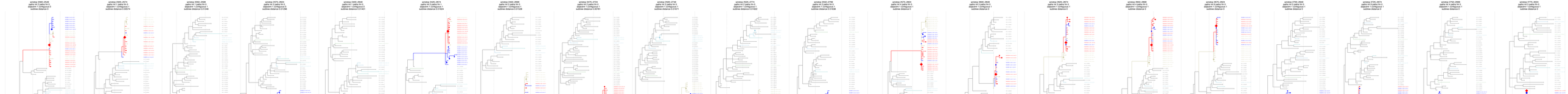

window 7375–7624
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.0266
window 7400–7649
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.00600
window 7425–7674
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.00616
window 7450–7699
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.00671
window 7475–7724
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.00749
window 7500–7749
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.0204
window 7525–7774
maximum 1 recombinant
alignment 1 contiguous 0
subtree distance 0.00204
window 7550–7799
maximum 1 recombinant
alignment 1 contiguous 1
subtree distance 0.01351
window 7575–7824
maximum 1 recombinant
alignment 1 contiguous 1
subtree distance 0.01319
subst/site

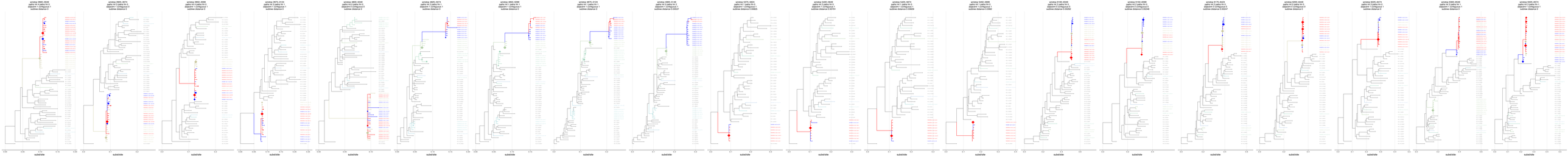
Deep sequence phylogenies
of male-female pair RkA02918M, RkA02908F (run 83)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.

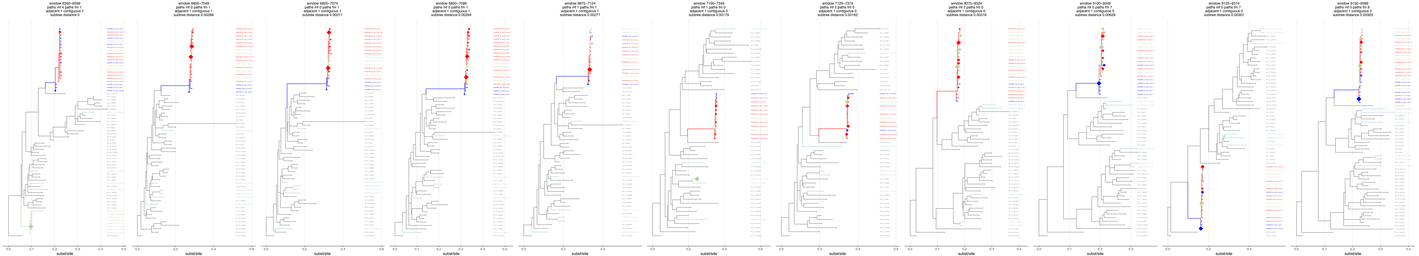

window 850–1049
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09857
window 925–1074
gamma-MRCA = 1
adjacent 1 contiguous 1
subtree distance 0
window 950–1099
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0
window 975–1124
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0
window 900–1149
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09911
window 925–1174
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09298
window 950–1199
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09067
window 975–1224
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.0955
window 1000–1249
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09262
window 1025–1274
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09543
window 1050–1299
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09561
window 1075–1324
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09547
window 1100–1349
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09373
window 1125–1374
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09365
window 1150–1399
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09530
window 1175–1424
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.0952
window 1200–1449
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09307
window 1225–1474
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09380
window 1250–1499
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0.09486
window 1275–1524
gamma-MRCA = 1
adjacent 1 contiguous 0
subtree distance 0
subtreeAge


window 1360–1548
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1325–1574
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1330–1588
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1375–1624
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1400–1649
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1425–1674
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1450–1698
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1475–1724
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1500–1748
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1525–1774
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1550–1798
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1575–1824
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1600–1848
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1625–1874
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1650–1899
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1675–1924
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1700–1949
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1725–1974
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1750–1999
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
window 1775–2024
gapwin 1 contiguous 1
adjacent 1 contiguous 0
subtree distance 0
subtreWe

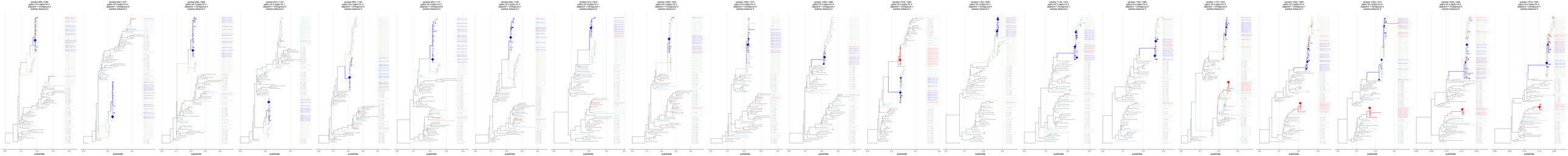

window 1860-2049
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 1825-2014
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0.00305
window 1860-2088
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 1875-2129
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0.00321
window 1900-2140
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0.00339
window 1925-2174
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 1950-2198
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 1975-2224
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2000-2249
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0.00405
window 2025-2274
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0.00425
window 2050-2299
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2075-2324
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2100-2349
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2125-2374
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2150-2399
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2175-2424
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2200-2449
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2225-2474
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2250-2499
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
window 2275-2524
gapseq.fasttree.tree
alignment 1 contiguous 1
sublime distance 0
sublimeTree

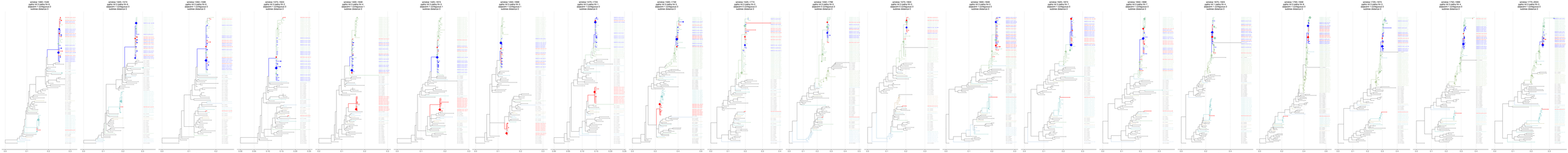

window 2360–2549
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2385–2574
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.00574
window 2390–2599
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01240
window 2375–2624
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01286
window 2405–2649
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01401
window 2425–2674
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01424
window 2455–2699
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01529
window 2475–2724
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.00781
window 2500–2749
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01671
window 2525–2774
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01652
window 2550–2798
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0.01638
window 2575–2824
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2600–2849
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2625–2874
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2650–2899
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2675–2924
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2700–2949
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2725–2974
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2750–2999
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
window 2775–3024
gamma 1 / contiguous 1
adjacent 1 / contiguous 1
sublime distance 0
sublime
sublime

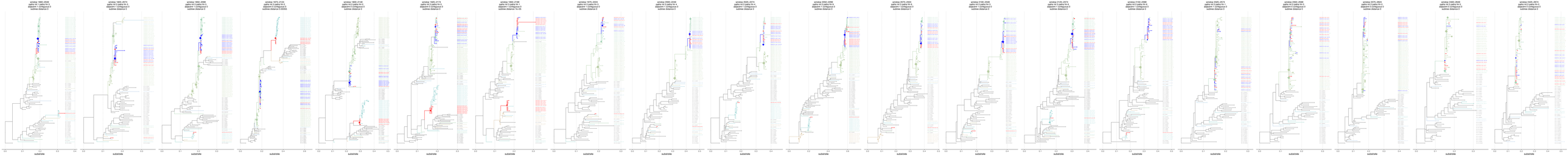

window 2860-3049
gapart-1 / ontiguous-1
subtree distance 0
window 2925-3074
gapart-1 / ontiguous-1
subtree distance 0
window 2950-3099
gapart-1 / ontiguous-1
subtree distance 0
window 3875-3124
gapart-1 / ontiguous-1
subtree distance 0
window 4050-3049
gapart-1 / ontiguous-1
subtree distance 0
window 4425-3074
gapart-1 / ontiguous-1
subtree distance 0
window 4650-3099
gapart-1 / ontiguous-1
subtree distance 0
window 4875-3124
gapart-1 / ontiguous-1
subtree distance 0
window 5000-3149
gapart-1 / ontiguous-1
subtree distance 0.00537
window 5375-3924
gapart-1 / ontiguous-1
subtree distance 0.00835
window 5400-3949
gapart-1 / ontiguous-1
subtree distance 0.00791
window 5425-3974
gapart-1 / ontiguous-1
subtree distance 0.00835
window 5450-3999
gapart-1 / ontiguous-1
subtree distance 0.0060
window 5100-4049
gapart-1 / ontiguous-1
subtree distance 0.00262
window 5150-4099
gapart-1 / ontiguous-1
subtree distance 0.00246
window 5175-4124
gapart-1 / ontiguous-1
subtree distance 0.00247
window 5200-4149
gapart-1 / ontiguous-1
subtree distance 0
window 5225-4174
gapart-1 / ontiguous-1
subtree distance 0
window 5300-4549
gapart-1 / ontiguous-1
subtree distance 0
window 5325-4574
gapart-1 / ontiguous-1
subtree distance 0
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale
subtreVale

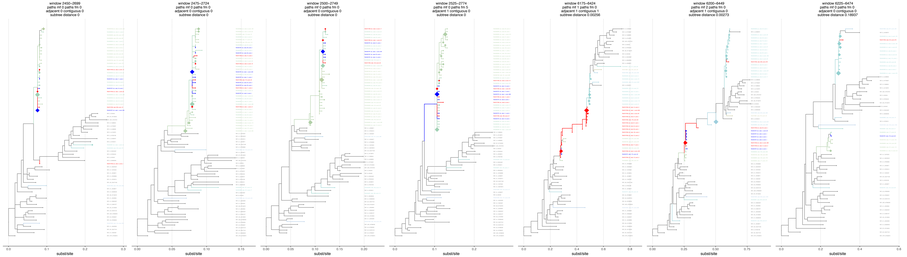

window 6350-6599
chromosome 1 : 6350 - 6599
alignment 1 contiguous 1
subtree distance 0
subtree distance 0.00266
subtree distance 0.00271
subtree distance 0.00284
subtree distance 0.00377
subtree distance 0.001179
subtree distance 0.001142
subtree distance 0.002419
subtree distance 0.00628
subtree distance 0.00567
subtree distance 0.00563
subtree
subtree

Deep sequence phylogenies
of male-female pair RkA07475M, RkA03573F (run 204)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.


window 850–1049
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 925–1074
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 950–1099
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 975–1124
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 990–1149
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 925–1174
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 950–1199
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 975–1224
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1000–1249
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1025–1274
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1050–1299
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1075–1324
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1100–1349
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1125–1374
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1150–1399
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1175–1424
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1200–1449
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1225–1474
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1250–1499
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
window 1275–1524
maximum likelihood tree
alignment 1 contiguous 0
sublime distance 0
sublimeTile

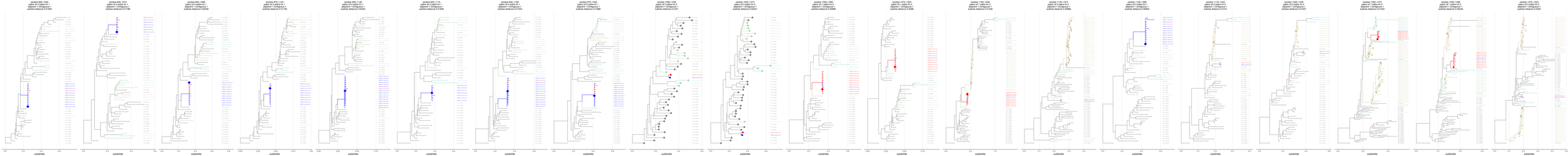

window 1360–1548
alignment 1 contiguous 0
subline distance 0
window 1525–1574
alignment 1 contiguous 0
subline distance 0
window 1350–1398
alignment 1 contiguous 0
subline distance 0
window 1375–1424
alignment 1 contiguous 0
subline distance 0
window 1400–1649
alignment 1 contiguous 0
subline distance 0
window 1425–1674
alignment 1 contiguous 0
subline distance 0
window 1450–1699
alignment 1 contiguous 0
subline distance 0
window 1475–1724
alignment 1 contiguous 0
subline distance 0
window 1500–1749
alignment 1 contiguous 0
subline distance 0
window 1525–1774
alignment 1 contiguous 0
subline distance 0
window 1550–1799
alignment 1 contiguous 0
subline distance 0
window 1575–1824
alignment 1 contiguous 0
subline distance 0
window 1600–1849
alignment 1 contiguous 0
subline distance 0
window 1625–1874
alignment 1 contiguous 0
subline distance 0
window 1650–1899
alignment 1 contiguous 0
subline distance 0
window 1675–1924
alignment 1 contiguous 0
subline distance 0
window 1700–1949
alignment 1 contiguous 0
subline distance 0
window 1725–1974
alignment 1 contiguous 0
subline distance 0
window 1750–1999
alignment 1 contiguous 0
subline distance 0
window 1775–2024
alignment 1 contiguous 0
subline distance 0
subtitle

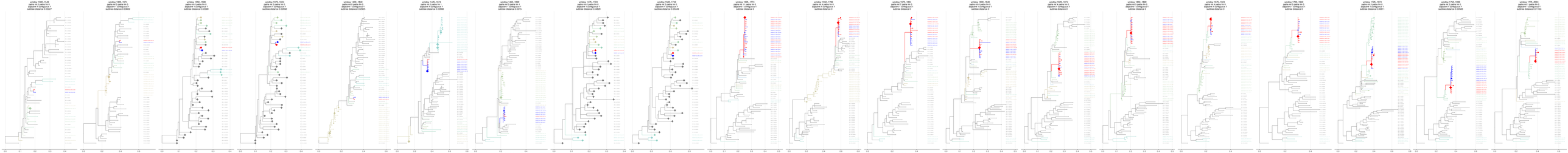

window 1840-2040
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 1825-2074
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 1800-2099
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 1875-2124
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0.00000
window 1900-2149
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 1925-2174
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 1950-2199
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 7e-05
window 1975-2224
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2000-2249
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2025-2274
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2050-2299
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2075-2324
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2100-2349
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2125-2374
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2150-2399
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2175-2424
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2200-2449
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2225-2474
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2250-2499
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2275-2524
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2300-2549
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
window 2325-2574
gapwidth 1 collapsed 0
adjacent 1 collapsed 0
subtree distance 0
subtreeVale

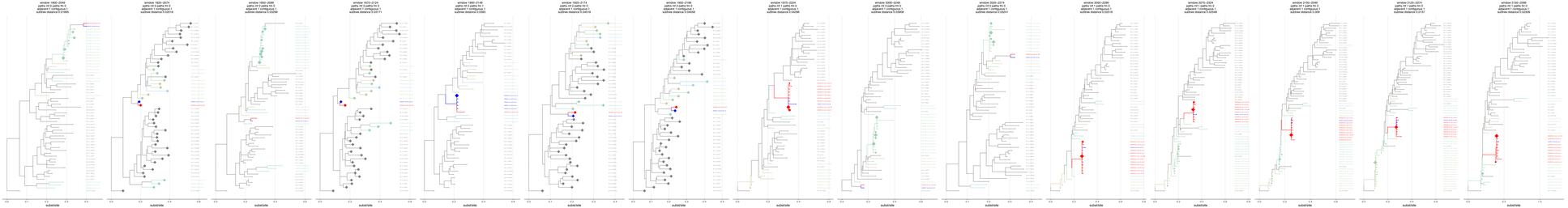

window 2400-2999
chromosome 1 contig_1
adjacent 0 contig_1
subtree distance 0
subtreeSize
window 2475-2774
chromosome 1 contig_1
adjacent 0 contig_1
subtree distance 0
subtreeSize
window 2500-2749
chromosome 1 contig_1
adjacent 0 contig_1
subtree distance 0
subtreeSize
window 2525-2774
chromosome 1 contig_1
adjacent 0 contig_1
subtree distance 0
subtreeSize

window 9175-9424
chromosome 1 contig_1
adjacent 1 contig_1
subtree distance 0.00256
subtreeSize
window 9200-9449
chromosome 1 contig_1
adjacent 1 contig_1
subtree distance 0.00273
subtreeSize
window 9225-9474
chromosome 1 contig_1
adjacent 1 contig_1
subtree distance 0.18607
subtreeSize

Deep sequence phylogenies
of male-female pair RkA00507M, RkA05021F (run 273)
for whom the phylogenetically inferred direction of transmission was inconsistent with clinical data.


window 850–1049
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01463
window 825–1074
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01798
window 850–1099
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.00526
window 875–1124
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01139
window 900–1149
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.02254
window 925–1174
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01468
window 950–1199
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01204
window 975–1224
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01868
window 1000–1249
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.0181
window 1025–1274
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.03541
window 1050–1299
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01660
window 1075–1324
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.0506
window 1100–1349
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01246
window 1125–1374
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.00669
window 1150–1399
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.00805
window 1175–1424
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.0141
window 1200–1449
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01607
window 1225–1474
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.01522
window 1250–1499
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.00549
window 1275–1524
maximum 1 recombinant
alignment 1 contiguous 1
sublime distance 0.02054
sublime


window 1361-1545
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.00207
window 1525-1674
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.00960
window 1630-1788
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.02099
window 1673-1824
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.02860
window 1400-1640
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.02825
window 1425-1674
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.03968
window 1400-1588
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.0210
window 1475-1724
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.04629
window 1530-1740
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.05249
window 1525-1774
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1530-1798
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1575-1824
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1580-1849
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1625-1874
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1650-1899
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1675-1924
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1700-1949
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0
window 1725-1974
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.00611
window 1750-1999
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.00585
window 1775-2024
gapseq1 1 contigs1
alignment 1 contigs1
sublime distance 0.01153
sublime


window 1860-2048
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.01865
window 1925-2074
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02018
window 1992-2088
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02090
window 1975-2129
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02011
window 1990-2140
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02083
window 1925-2174
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.01910
window 1990-2198
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.01909
window 1975-2204
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.01956
window 2000-2246
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02068
window 2025-2274
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02041
window 2050-2298
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02010
window 2075-2324
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02040
window 2100-2348
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.000
window 2125-2374
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02127
window 2150-2398
maximum likelihood tree
alignment 1 contiguous 1
sublime distance 0.02059
0.0
0.1
0.2
0.3
0.4
0.5
sublime