

# Pango X lineage subgraphs

In this document we display subgraphs for all the main Pango X lineages that have samples present in the *sc2ts* ARG. Pango designations for both samples and internal nodes were assigned using [Pangolin 4.3.1](#) (see main text). For nodes with large numbers of descendants, only a selected sample of roughly 20–50 Pango X samples are shown in these subgraphs. Extra descendants of a node are shown with dotted lines indicating additional immediate children of a node (note that this is not the same as the number of descendant samples). In some cases, additional descendant nodes of different Pango designations (e.g. BA.2) are shown for context.

Sample nodes are shown as squares; internal inferred nodes as circles. Recombination nodes are presented as larger circular nodes, with a Pango designation followed by the breakpoint position(s) surrounded by slashes, e.g. a breakpoint at position 1234 bp is indicated as **/1234/** (but note that Pango X lineages that are not of recombinant origin in *sc2ts* will not have a clear recombination node). Nodes of the focal pango type are plotted in pink, or as a set of alternative colours if multiple Pango designations are plotted in a single subgraph. Mutations within each subgraph (tickmarks along edges) are coloured pink if they are flagged as consensus mutations the focal Pango lineage(s): often such mutations occur in lineages above the Pango X origination node. Alternatively, if there are multiple mutations at the same site within a subgraph (indicating problematic reversion or recurrent mutations) they are plotted in a unique colour. For example, two green mutation tickmarks will represent mutations at the same site. If one is a reversion of a previous mutation (often indicating an unparsimonious reconstruction of topology), then the mutation is emphasised with a solid black outline. Deletion mutations are filled in black, and insertions are given strong emphasis using a magenta fill; where a site experiences multiple deletions or insertions at the same site, the outline is given a site-specific colour: note that reinsertions of a previous large deletion are biologically implausible, and are likely to represent ARG reconstruction artefacts.

In the PDF version of this document, hovering over node names will reveal the `sample_id` of a node, and hovering over a mutation will reveal the position of the mutation and the inherited vs derived state. E.g. a mouseover label of `mut:A1234T` denotes a mutation from an A to a T at position 1234 in the genome. Technially this is implemented by faking a URL (this leads to the slightly annoying behaviour that actually clicking on the hover-over text will attempt to open a non-existent URL).

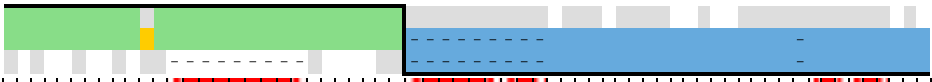
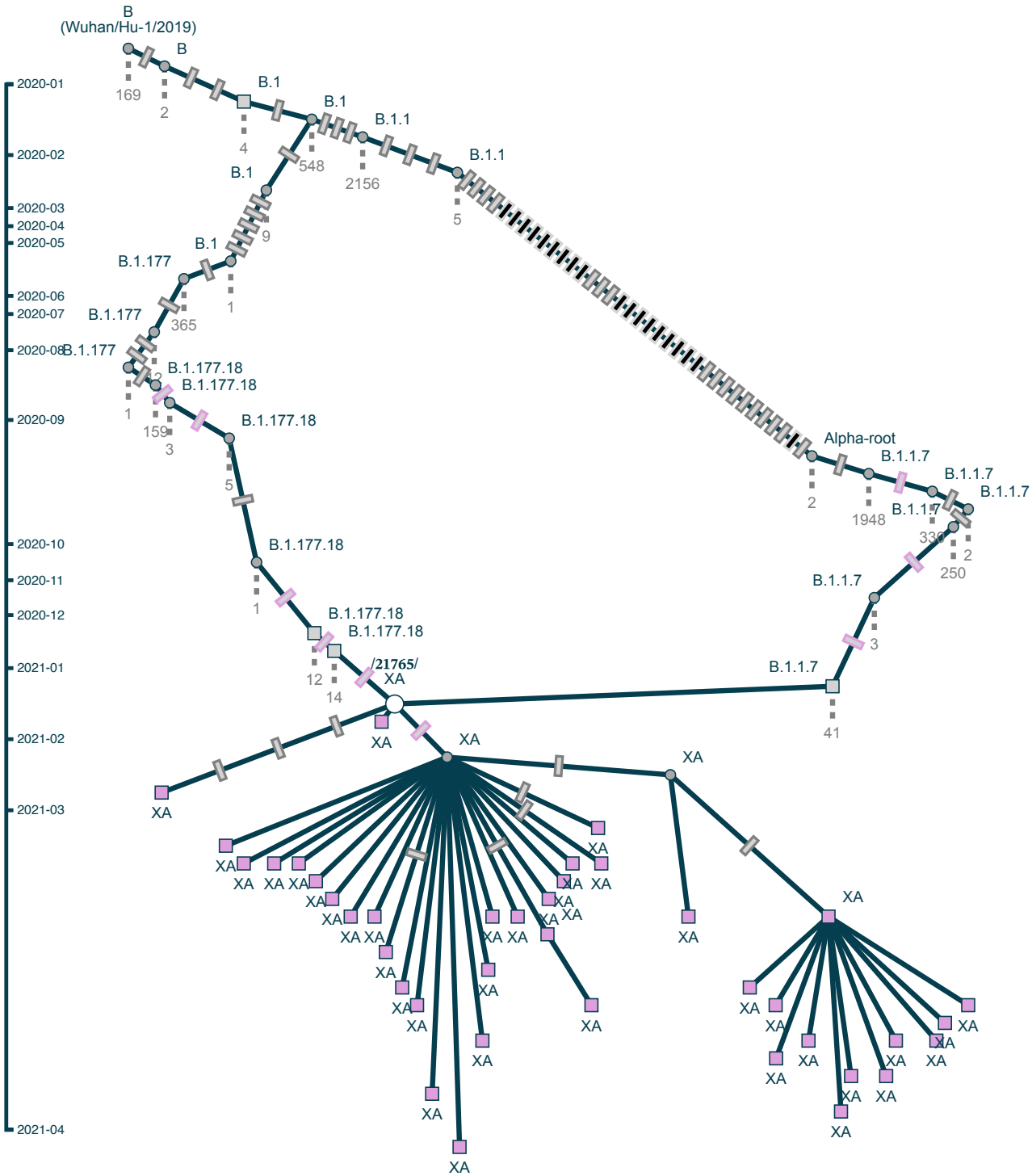
For Pango X lineages that have a recombinant origin in the ARG, the summary copying pattern is also displayed below the subgraph.

## 45 pango-X lineages

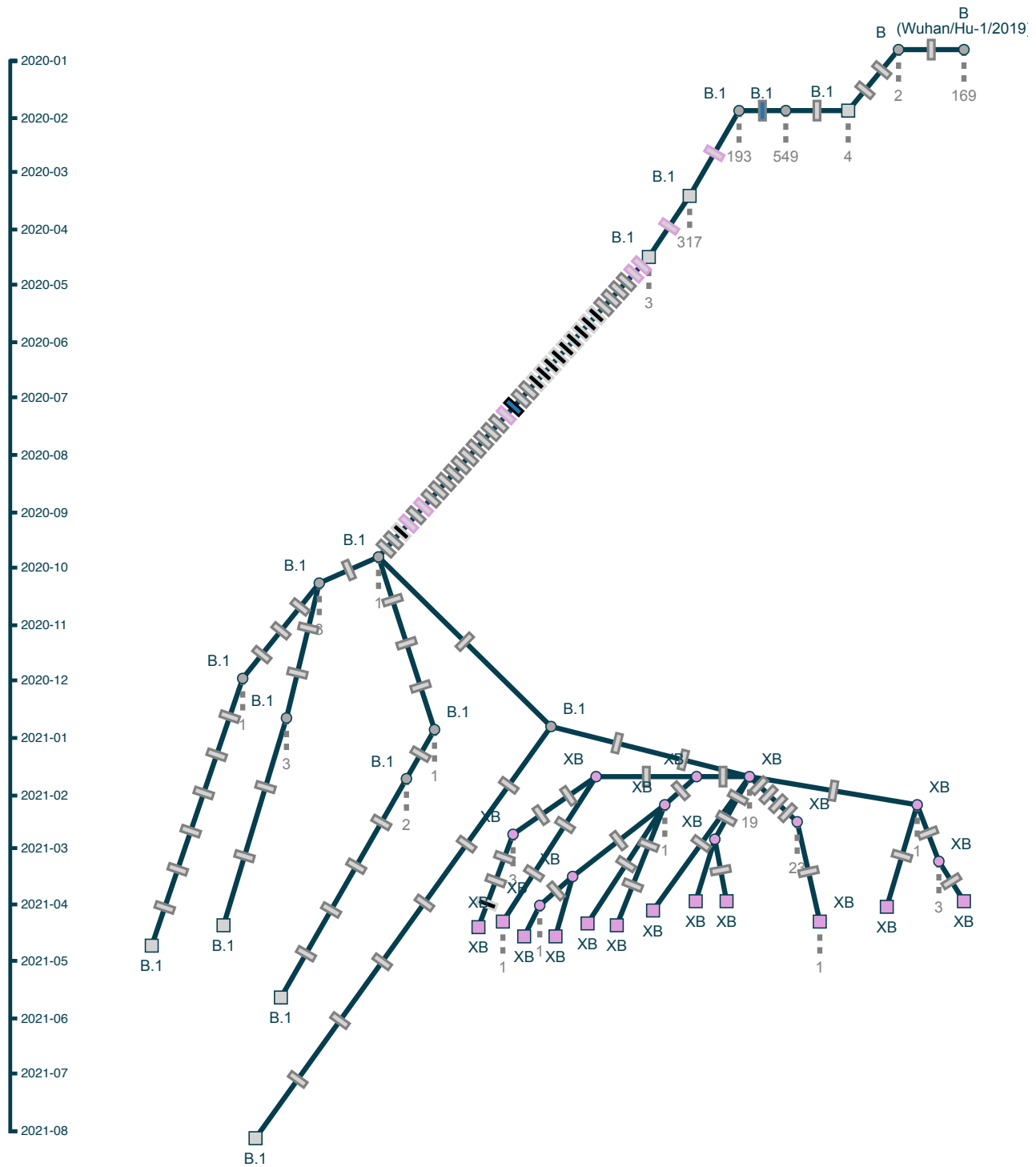
XA, XAA, XAC, XAD, XAE, XAF, XAG, XAJ, XAL, XAM, XAN, XAP, XAS, XAU, XAV, XAZ, XB, XBB, XBB.1, XBD, XBE, XBF, XBG, XBH, XBK, XBM, XBQ, XBR, XC, XE, XF, XG, XH, XJ, XL, XM, XN, XP, XQ, XR, XS, XU, XW, XY, XZ

Consensus mutations for each lineage taken from <https://covidcg.org>

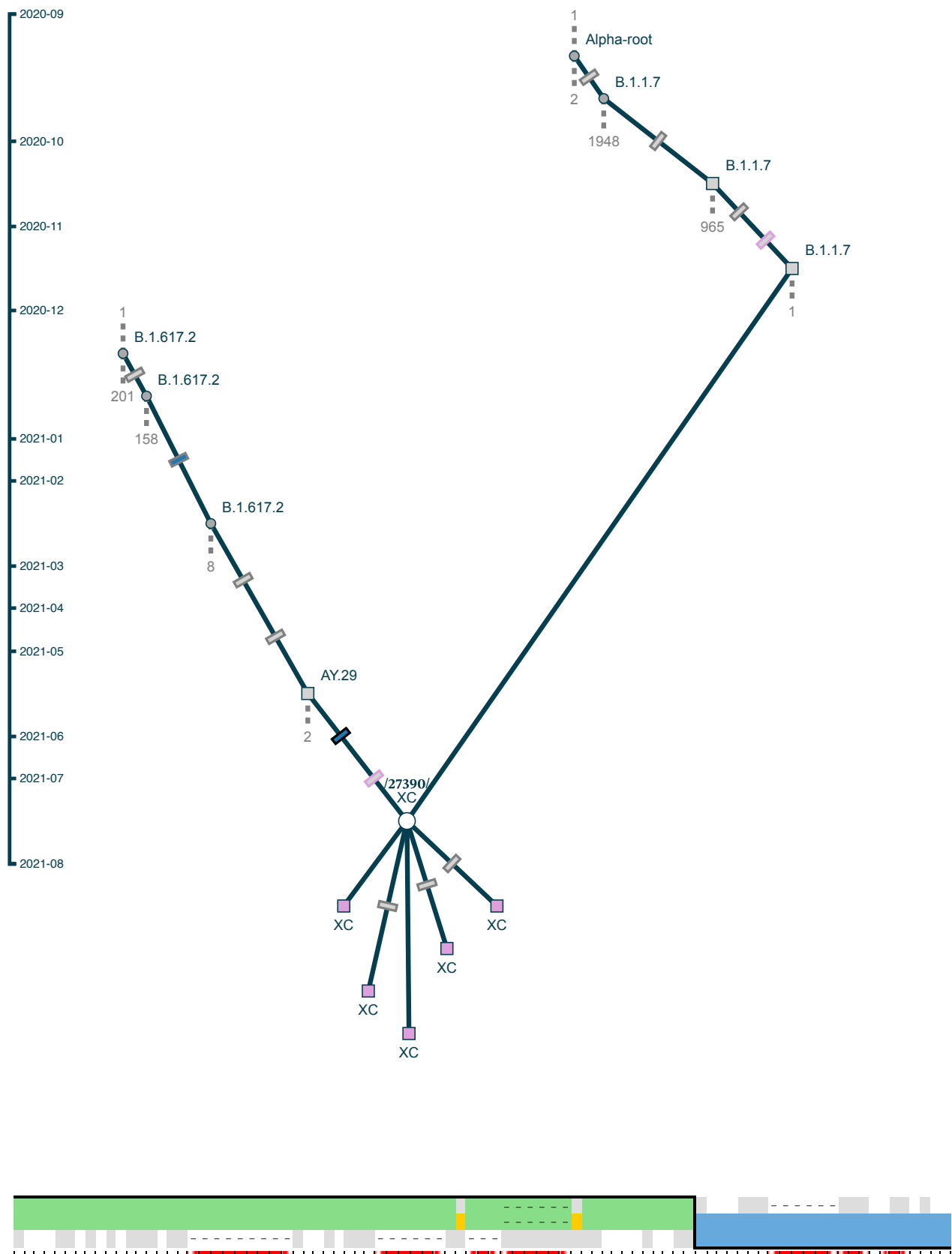
Subgraph of pango XA: (39 samples, 39 shown)



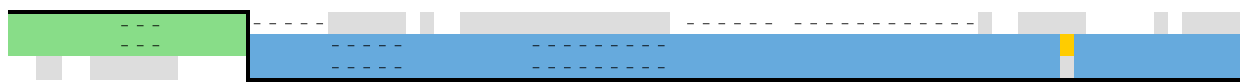
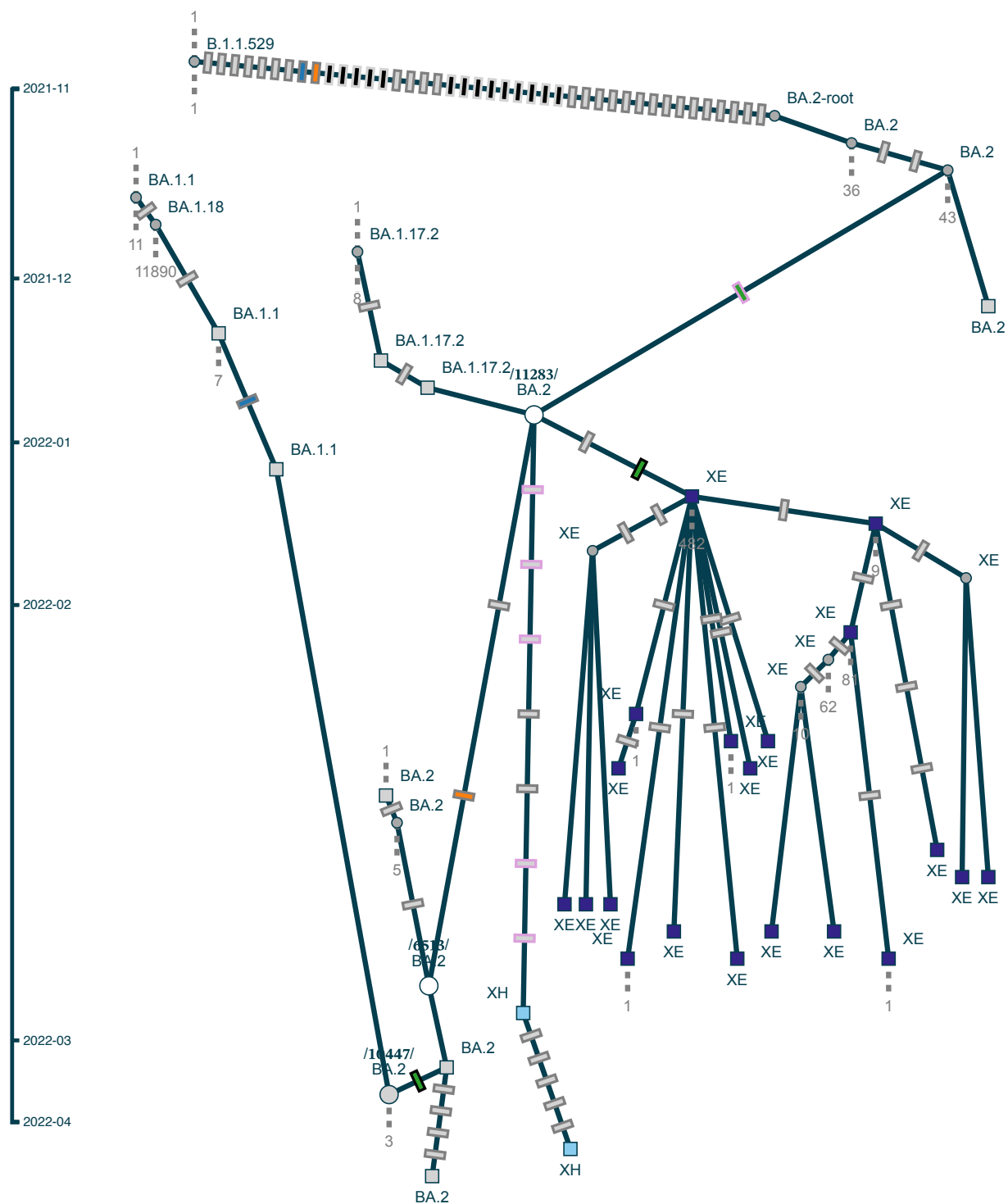
Subgraph of panglo XB: (192 samples, 12 shown)



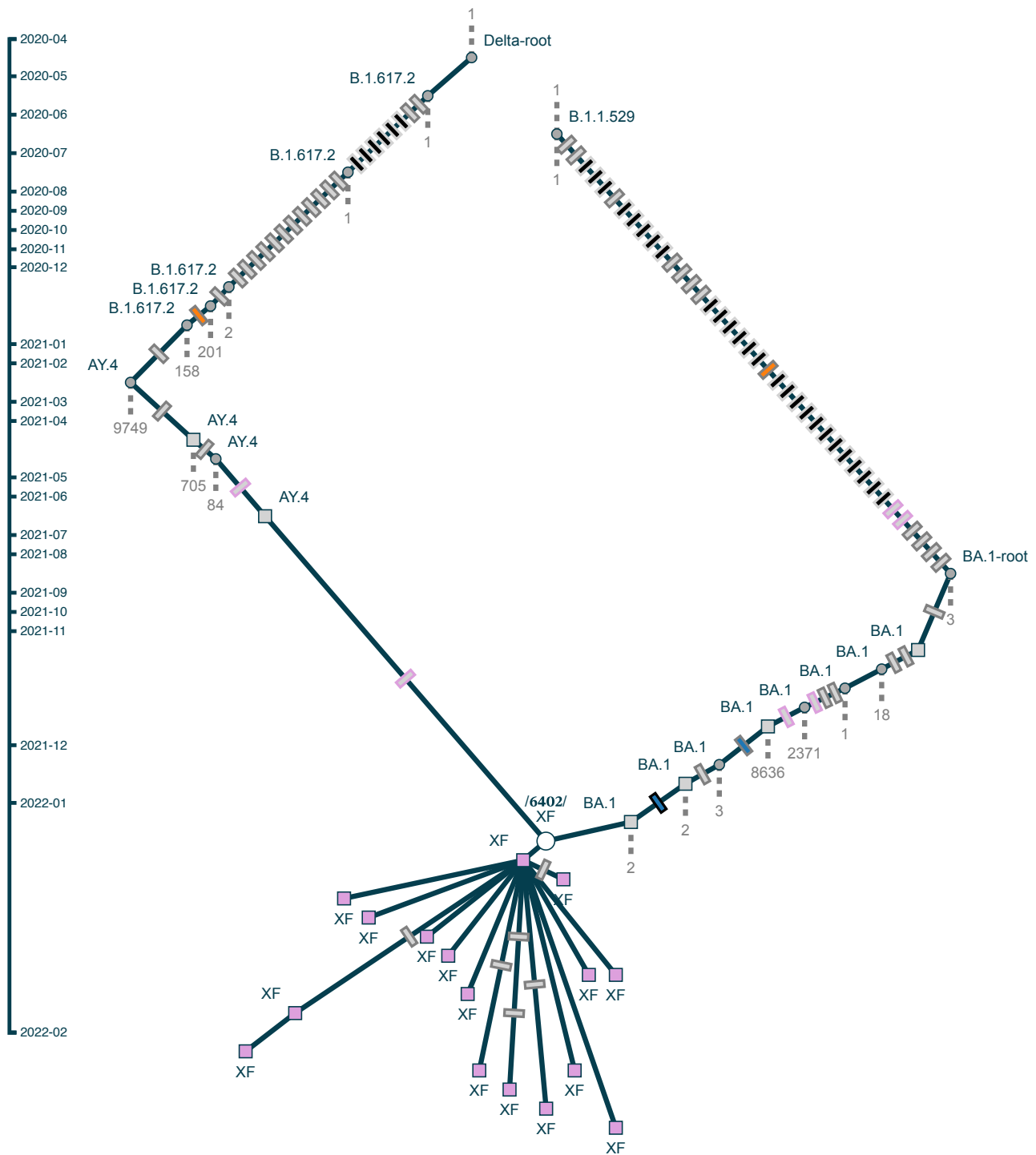
Subgraph of pango XC: (5 samples, 5 shown)



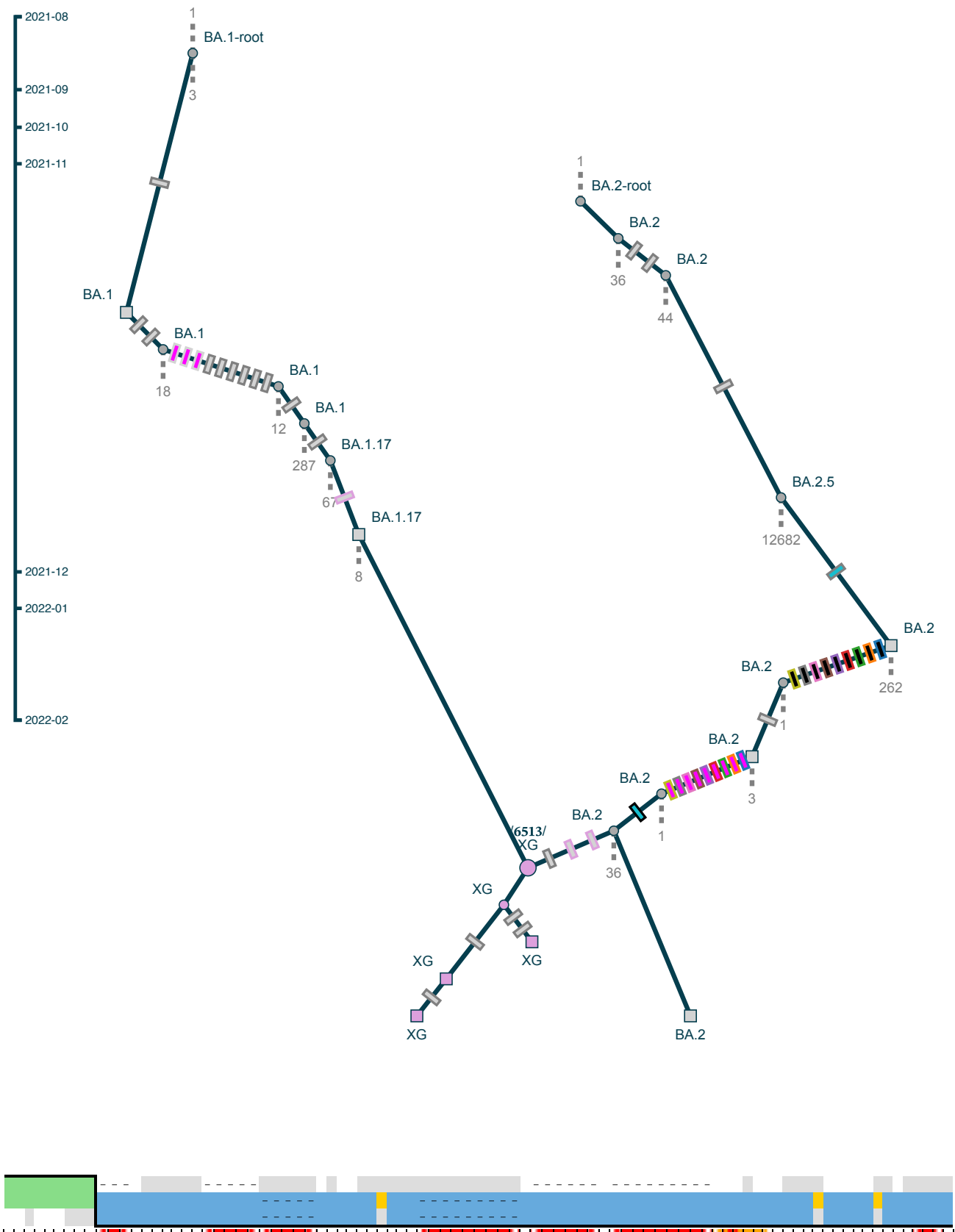
Subgraph of pango XE/XH: (1118 samples, 22 shown)



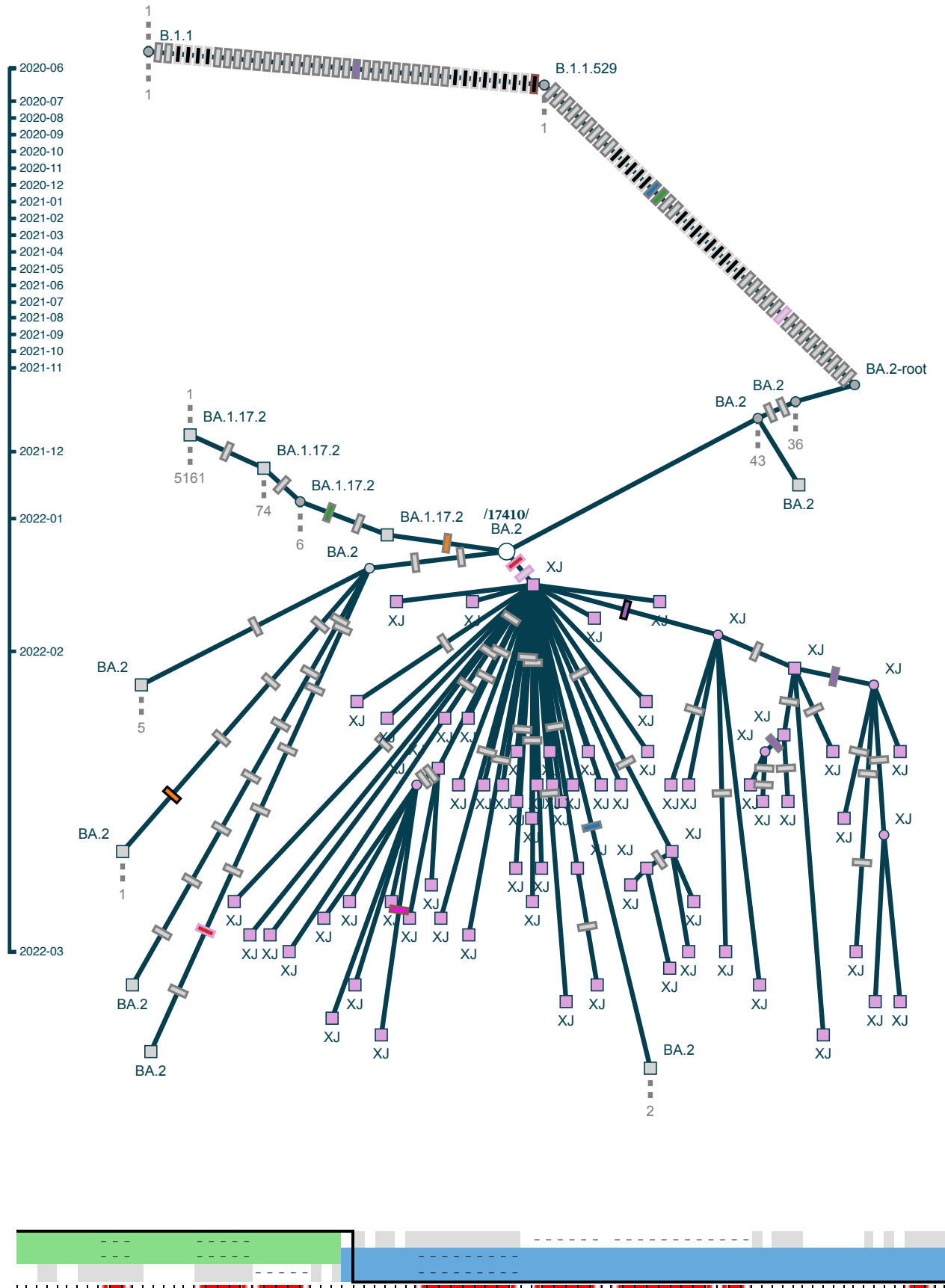
Subgraph of pango XF: (16 samples, 16 shown)



Subgraph of pango XG: (3 samples, 3 shown)

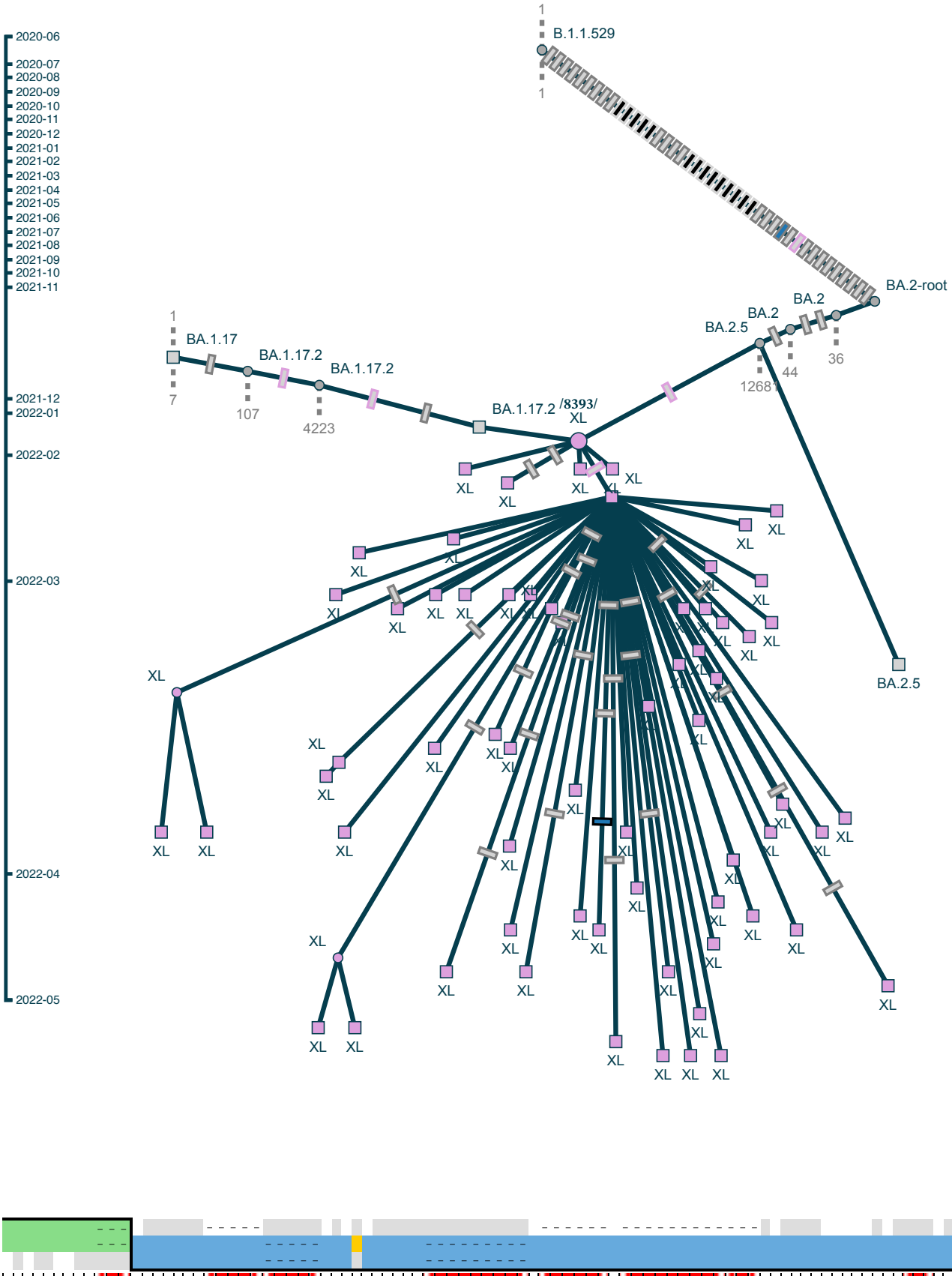


Subgraph of pango XJ: (68 samples, 68 shown)

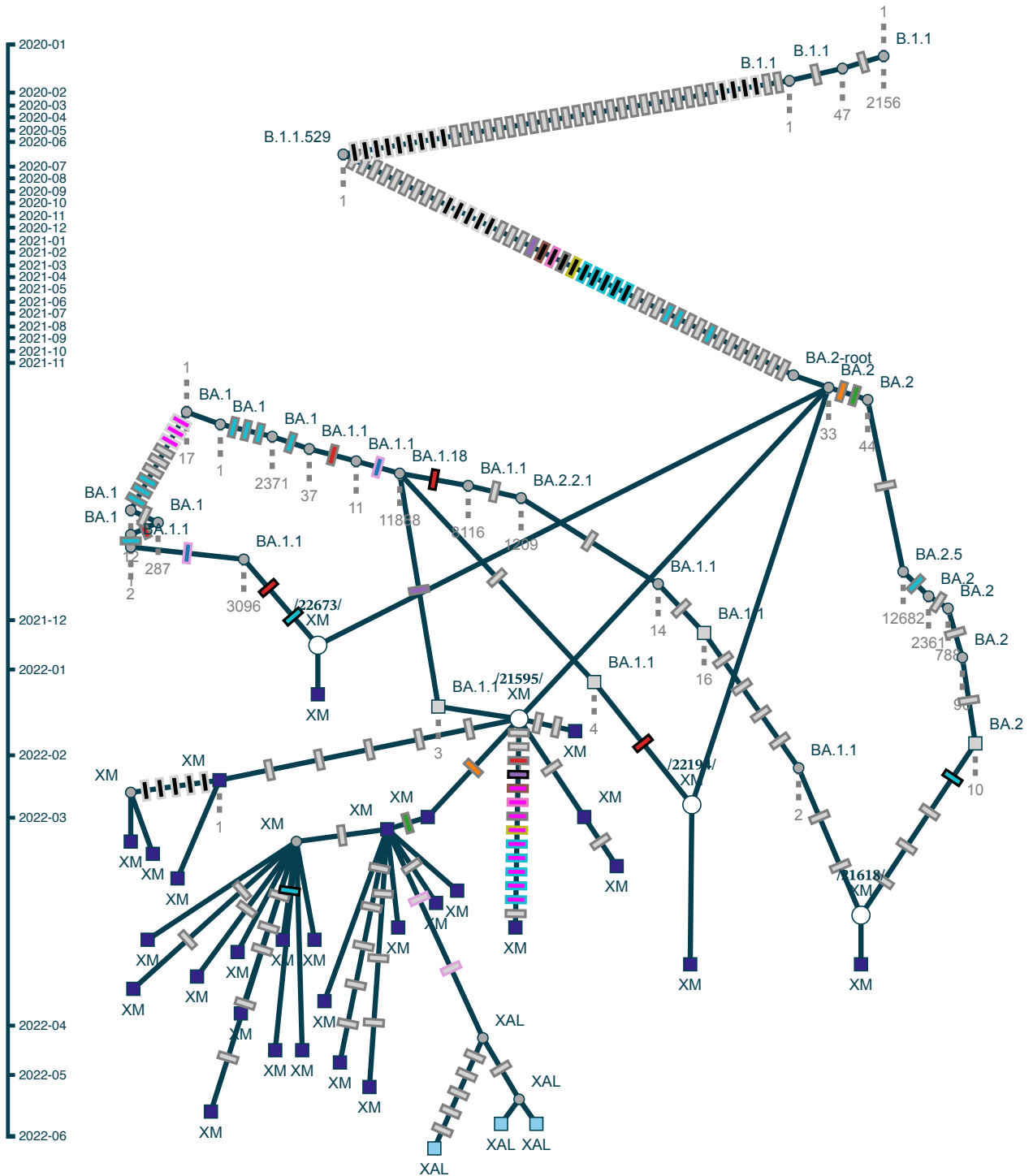




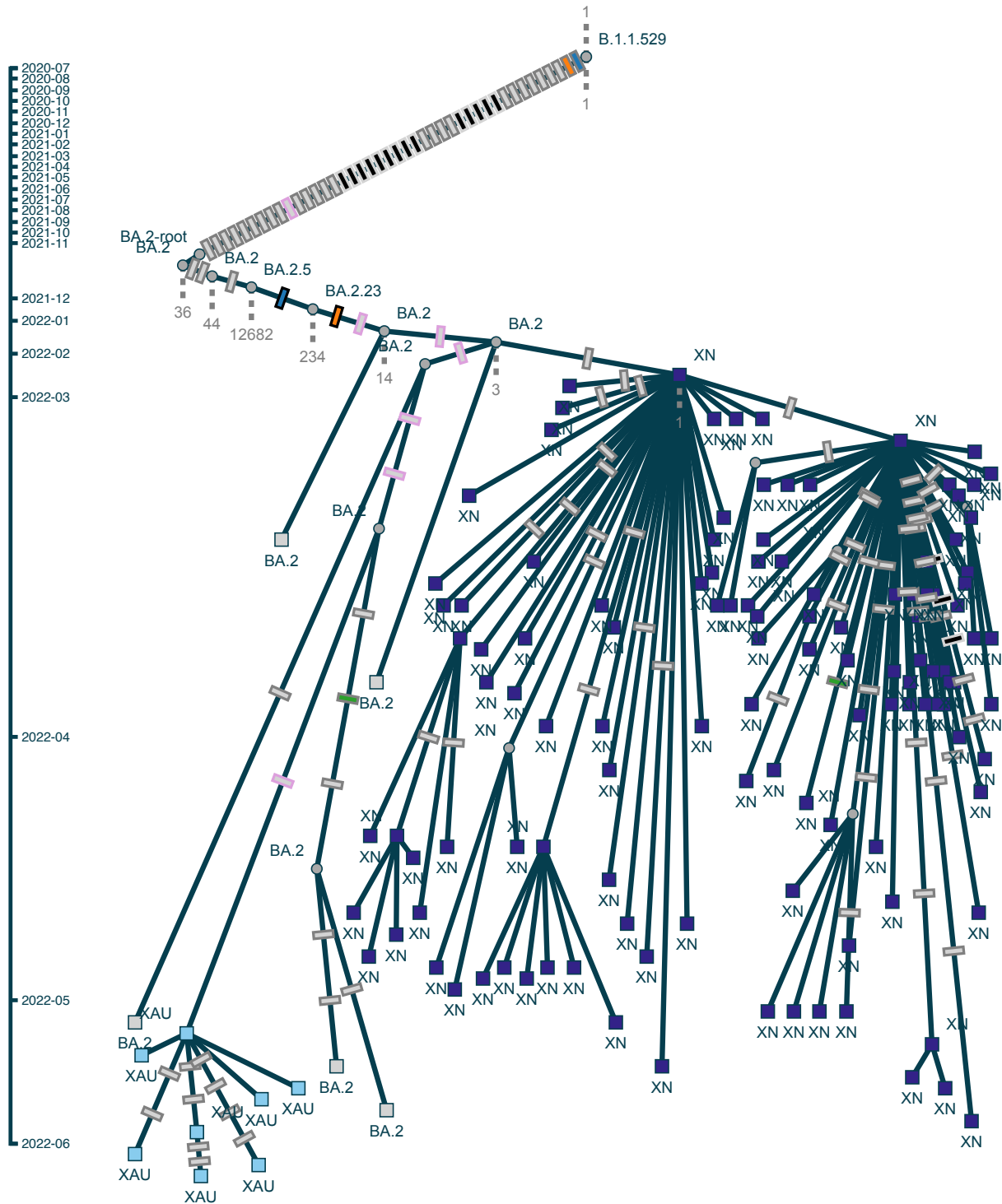
Subgraph of pango XL: (64 samples, 64 shown)



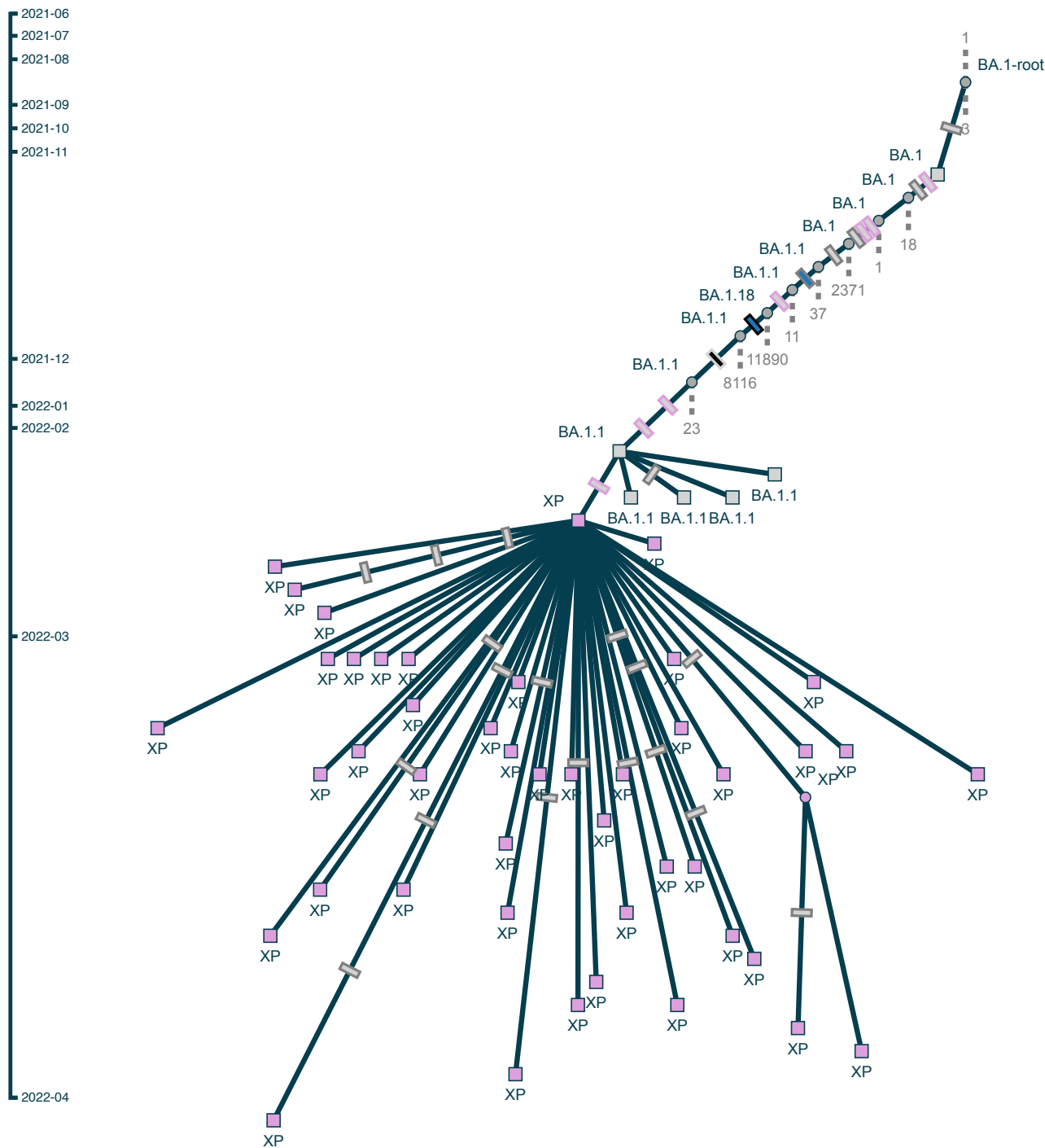
Subgraph of pango XM/XAL: (32 samples, 32 shown)



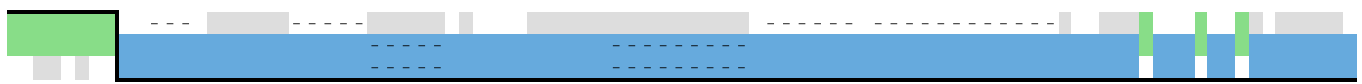
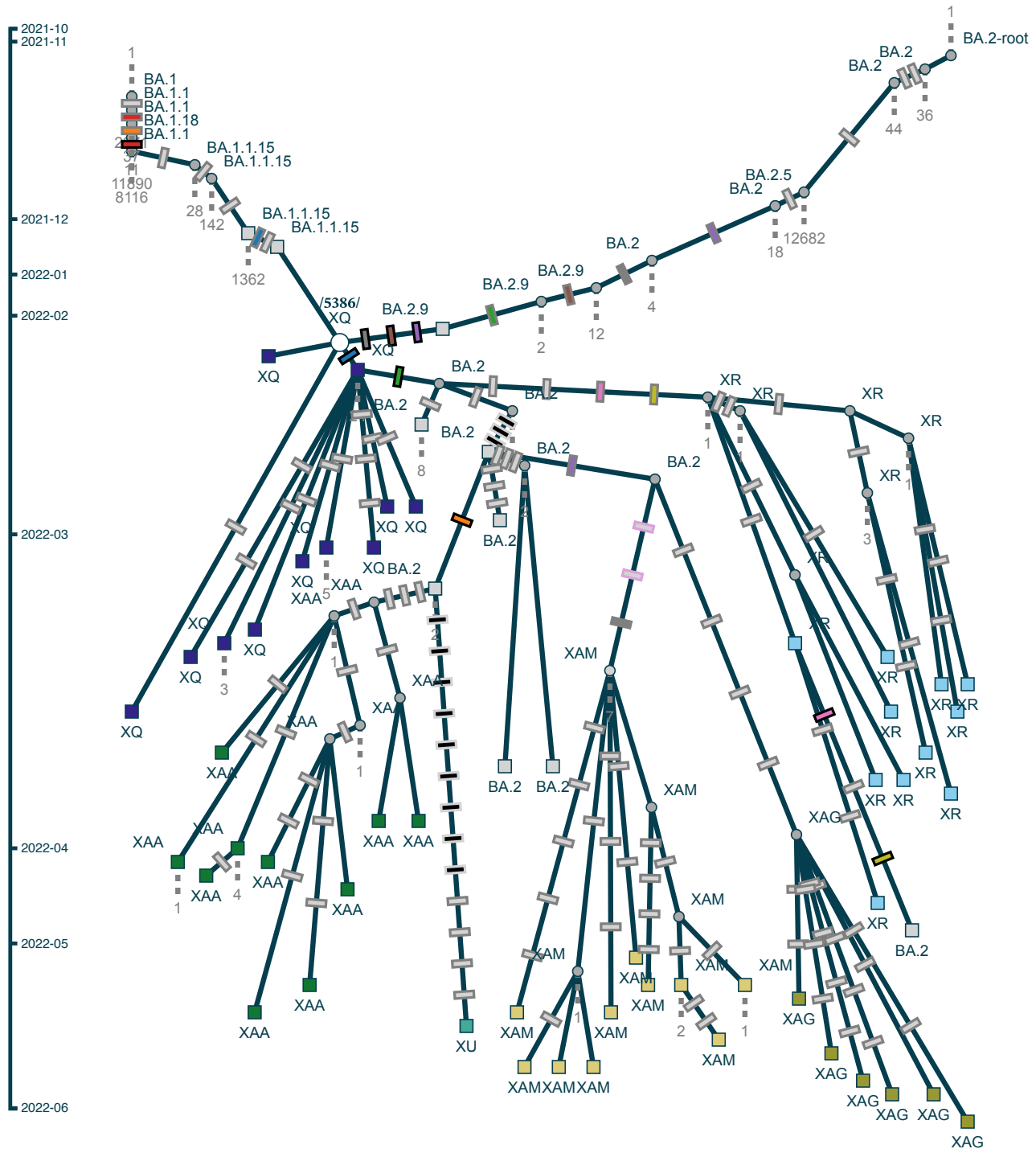
Subgraph of pango XN/XAU: (128 samples, 128 shown)



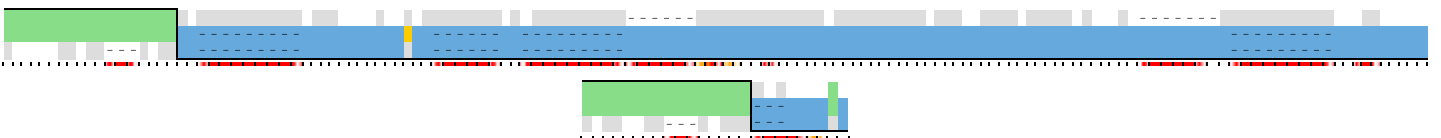
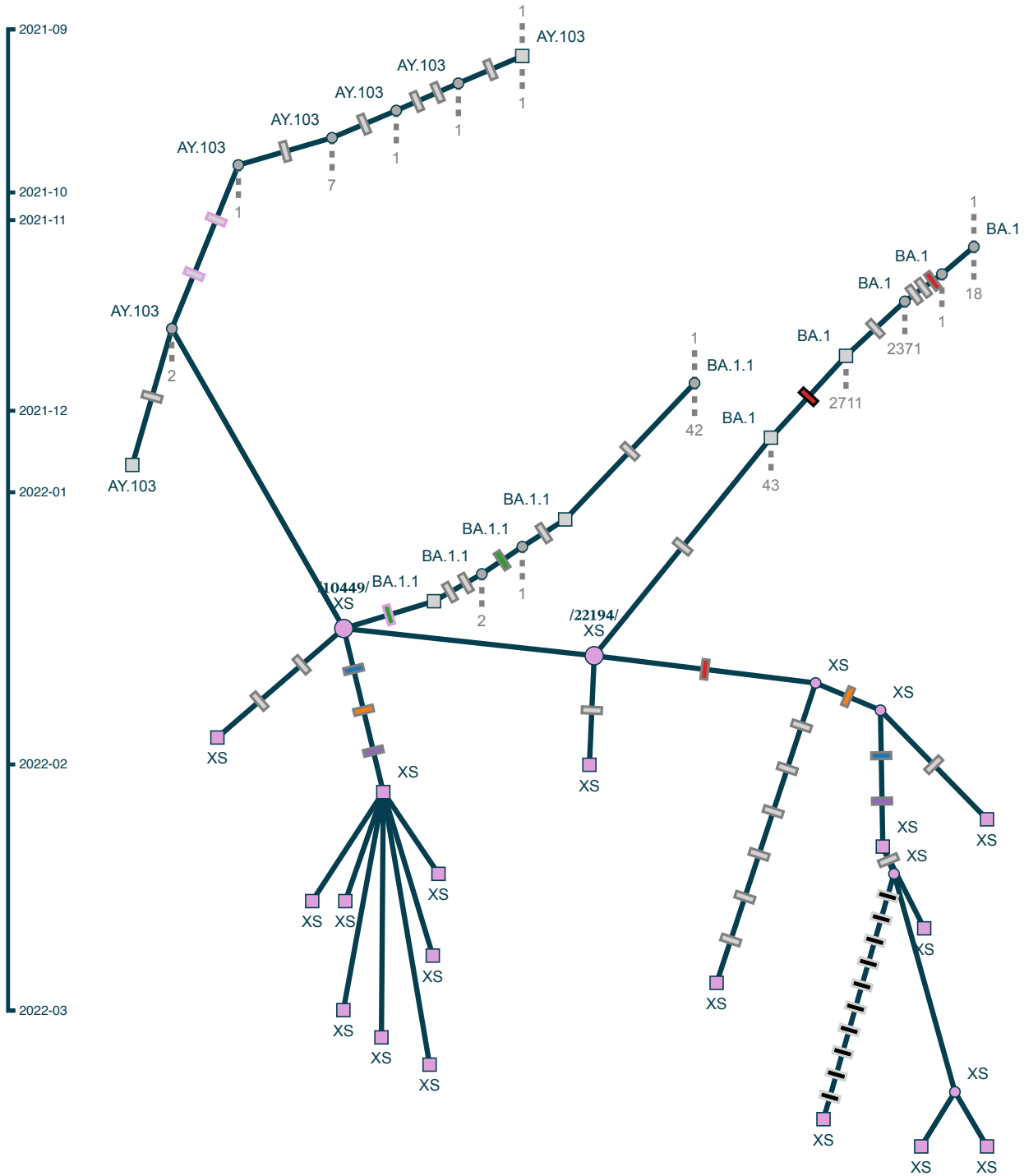
Subgraph of pango XP: (45 samples, 45 shown)



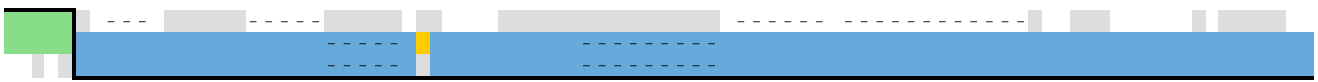
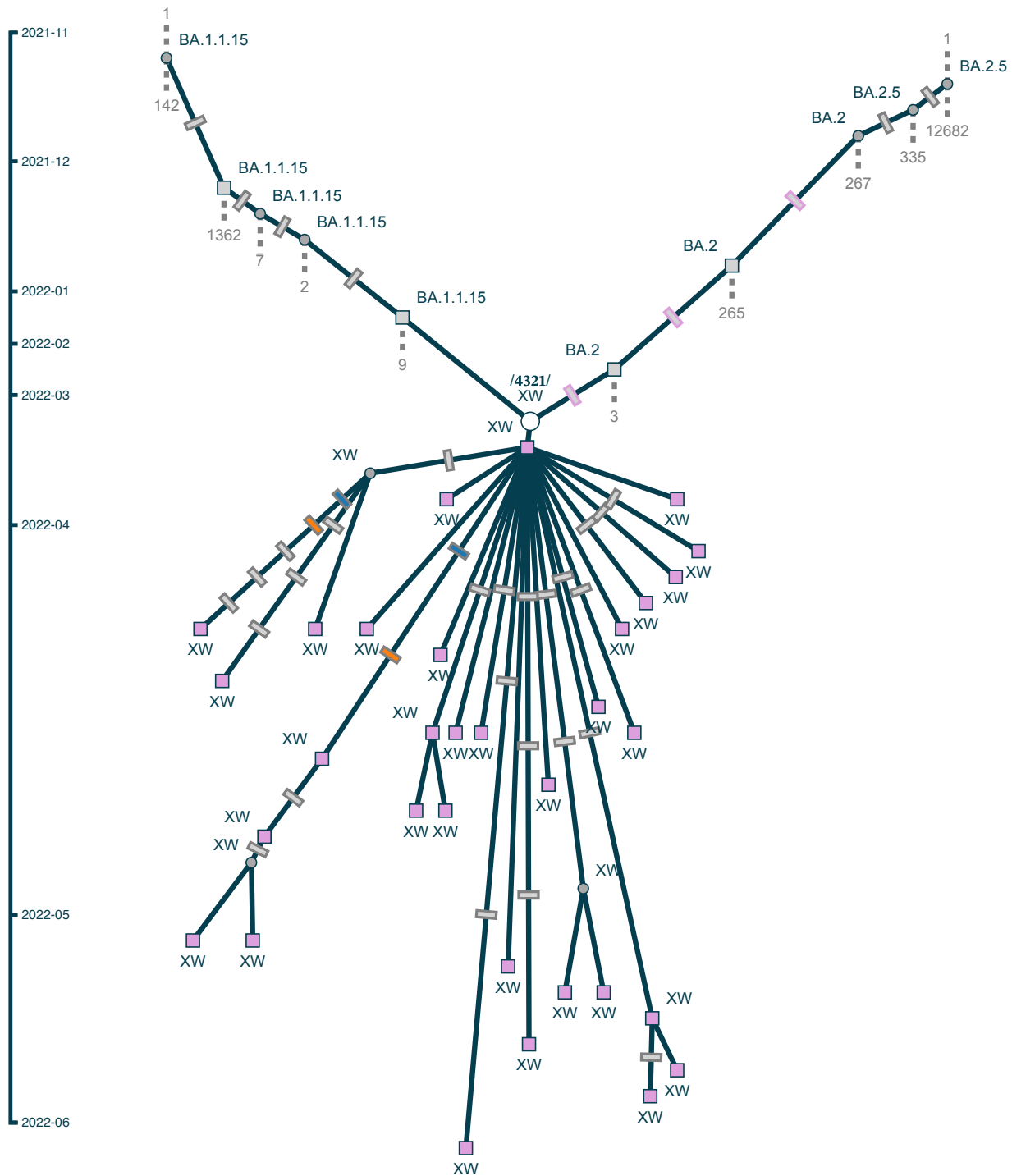
Subgraph of pango XQ/XR/XU/XAA/XAG/XAM: (117 samples, 49 shown)



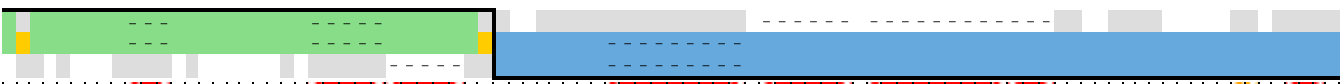
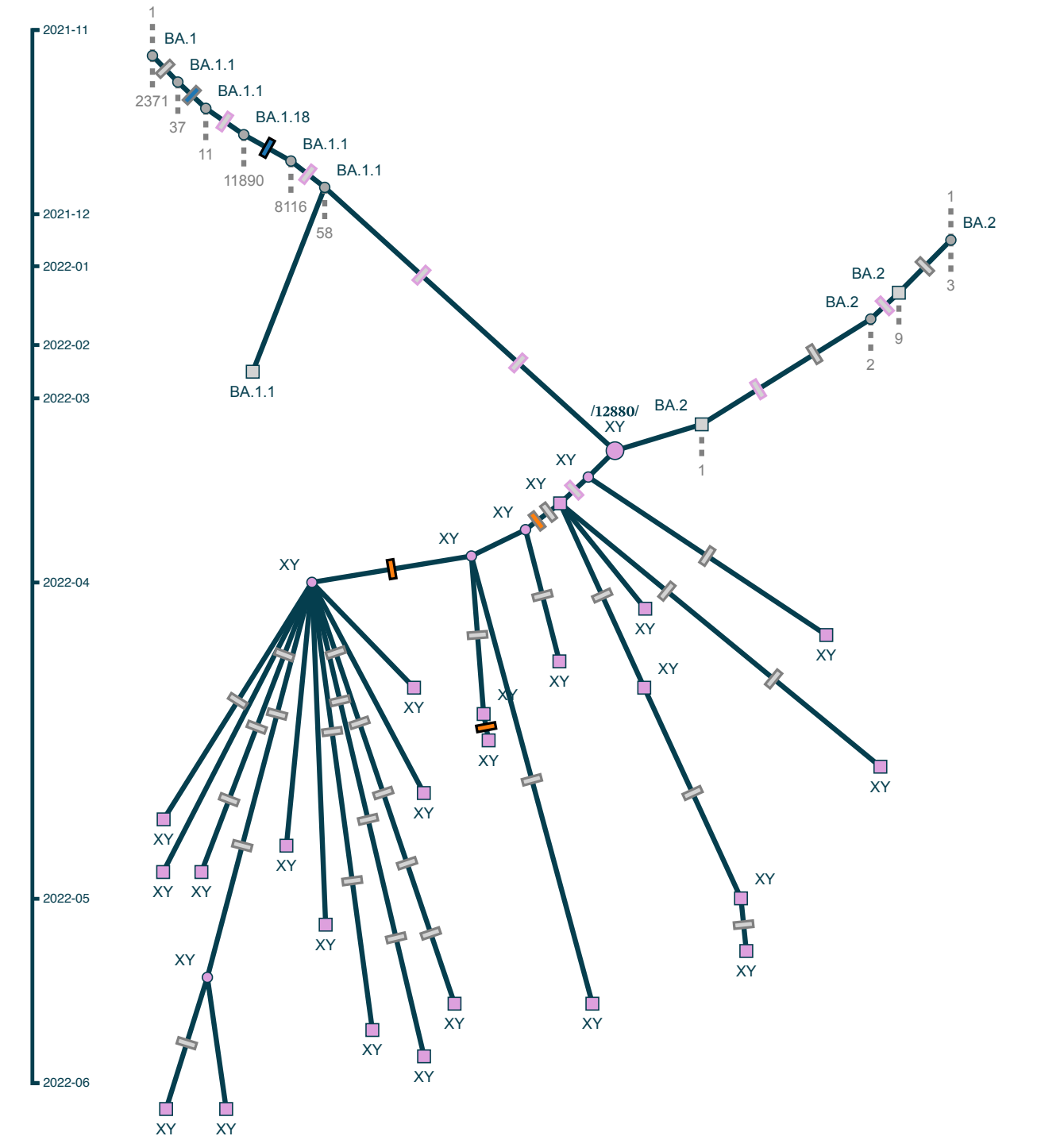
Subgraph of pango XS: (17 samples, 17 shown)



Subgraph of pango XW: (32 samples, 32 shown)

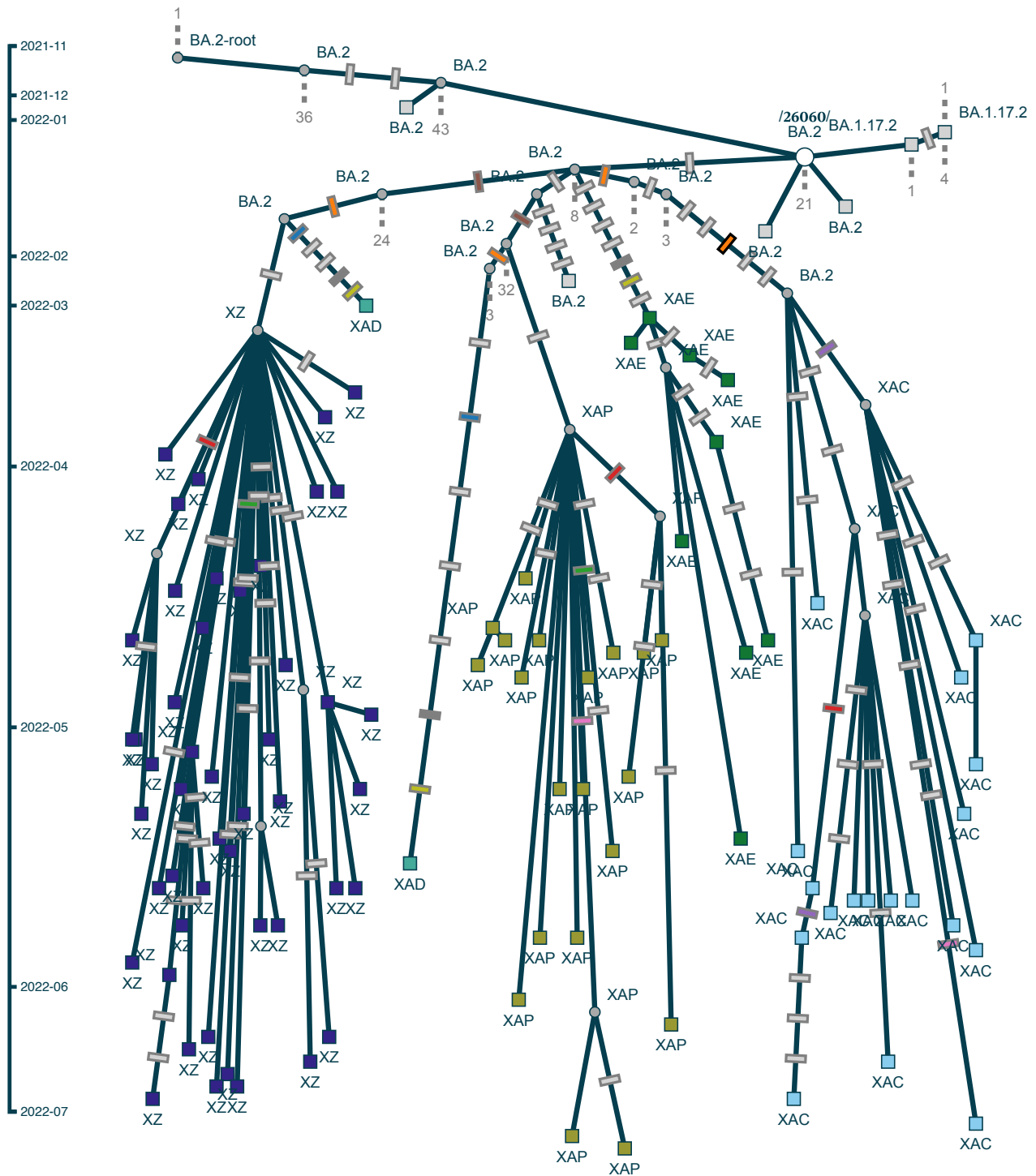


Subgraph of pango XY: (23 samples, 23 shown)

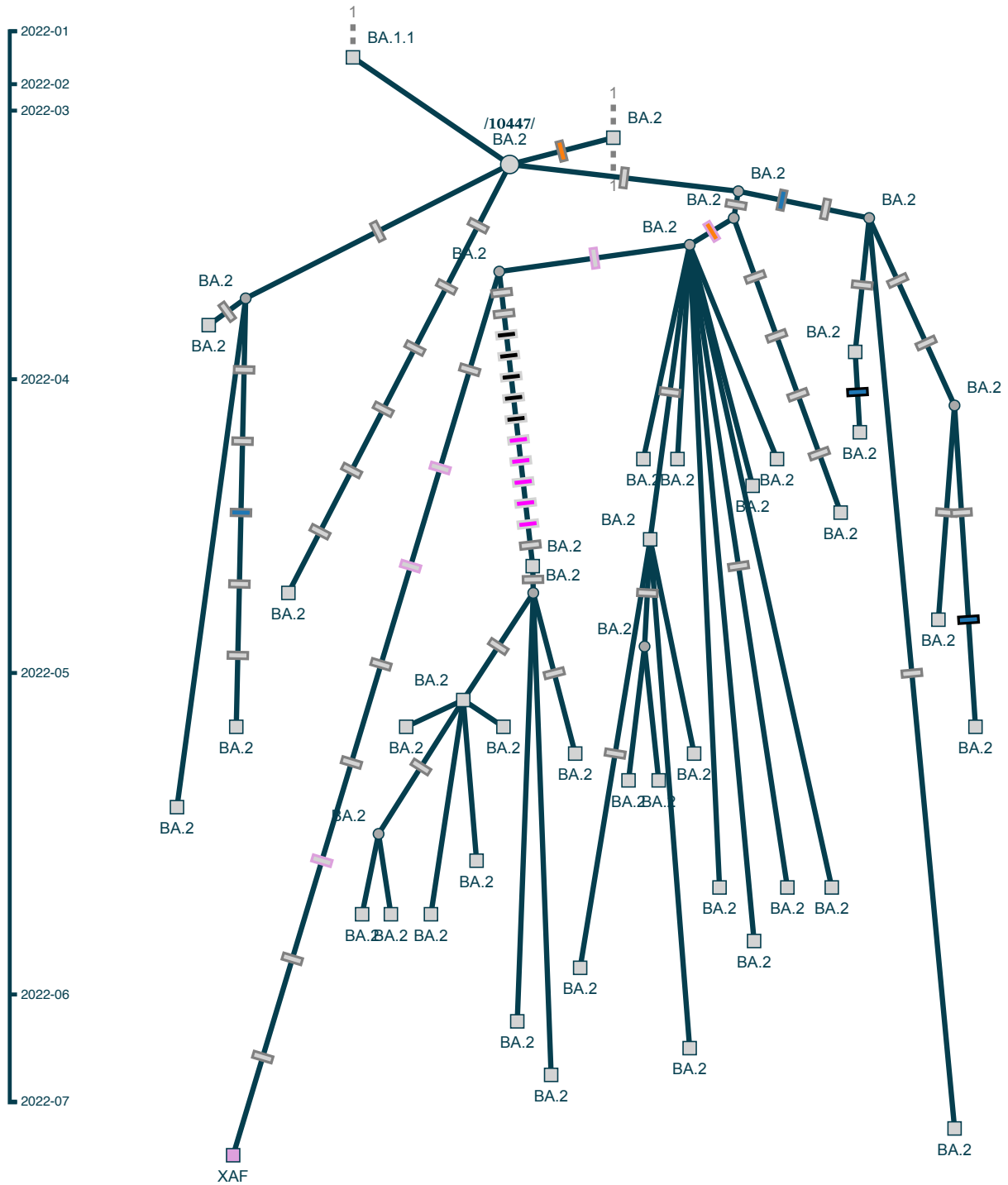




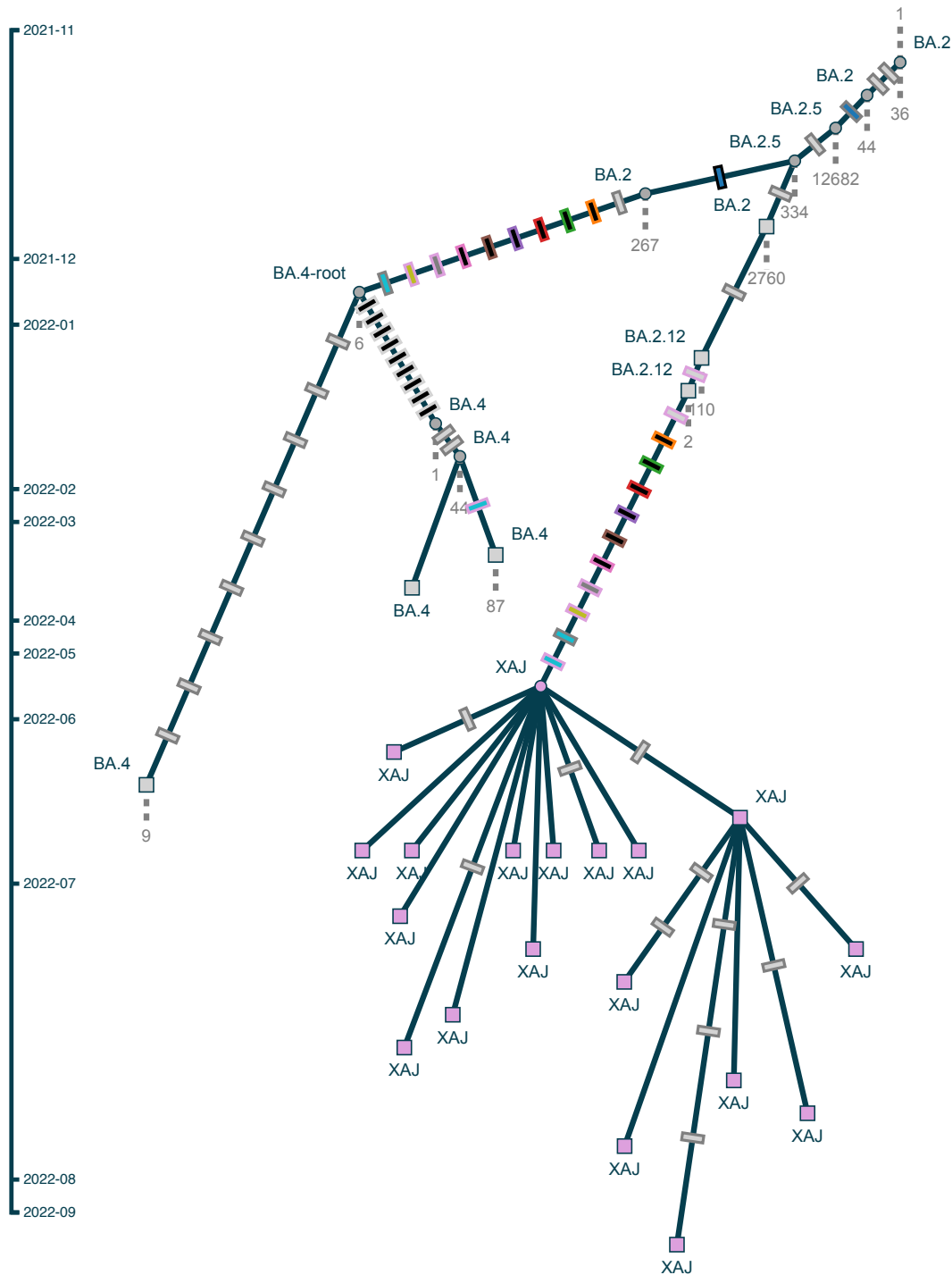
Subgraph of pango XZ/XAC/XAD/XAE/XAP: (97 samples, 97 shown)



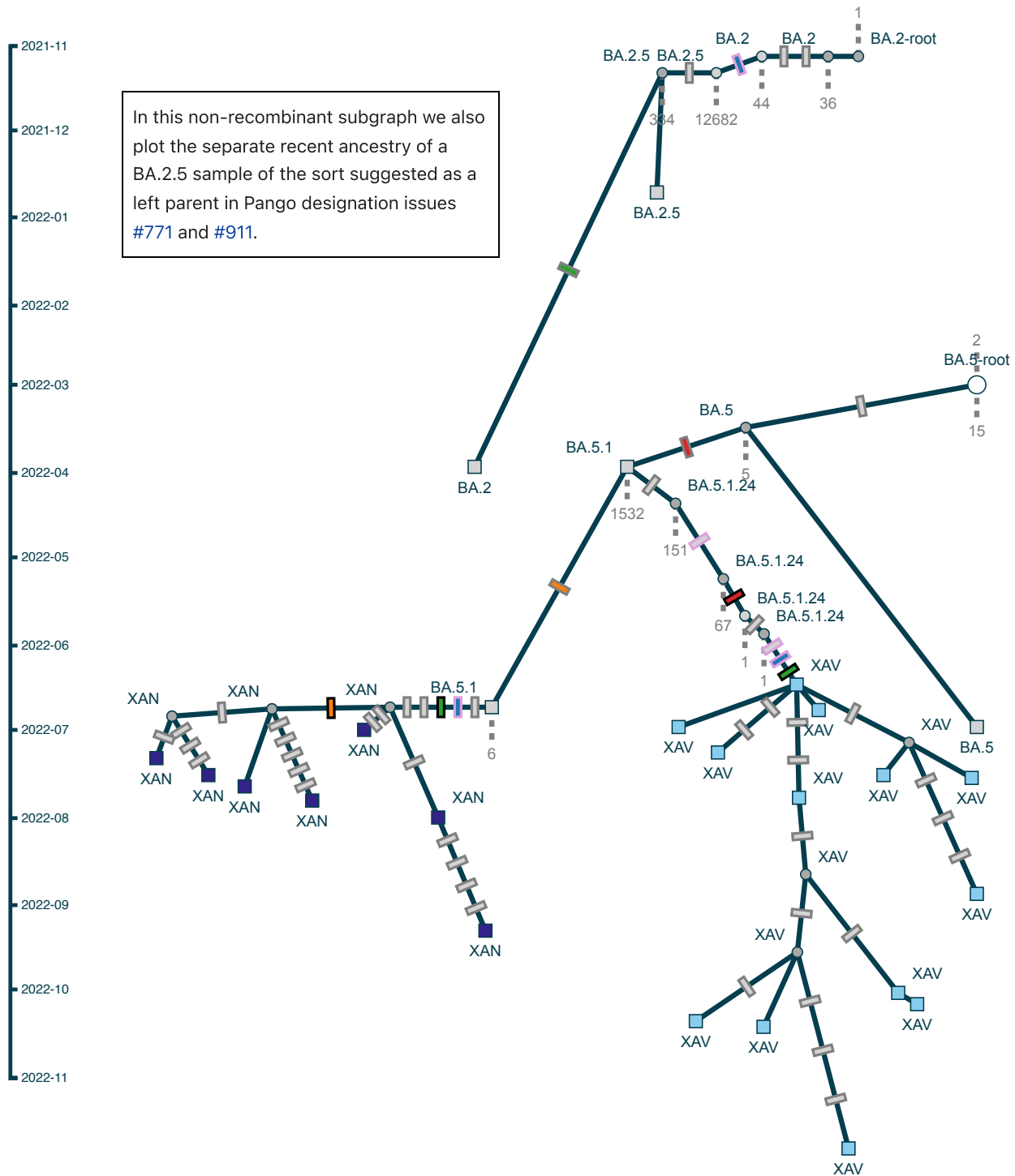
Subgraph of pango XAF: (1 sample, 1 shown)



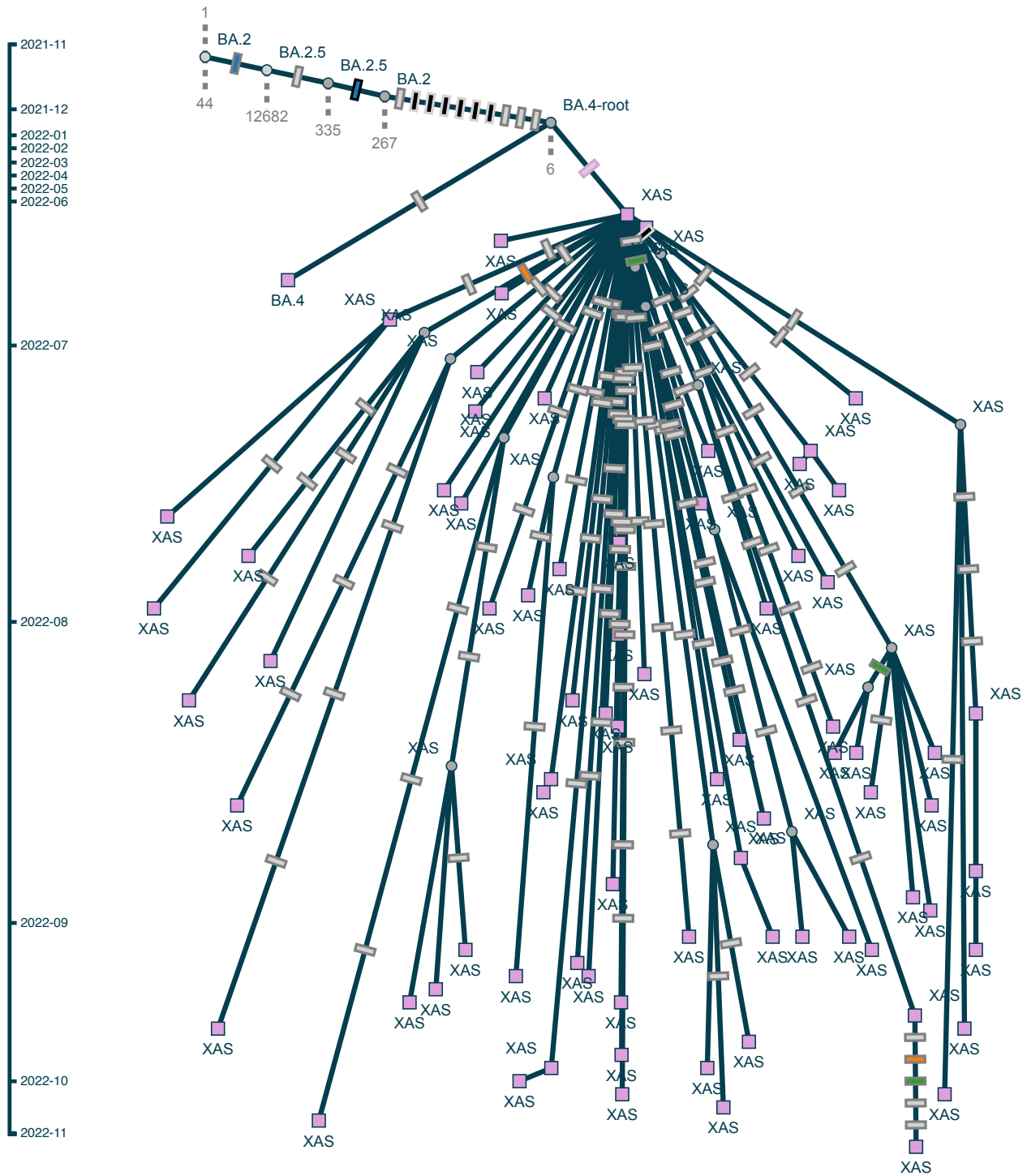
Subgraph of pango XAJ: (18 samples, 18 shown)



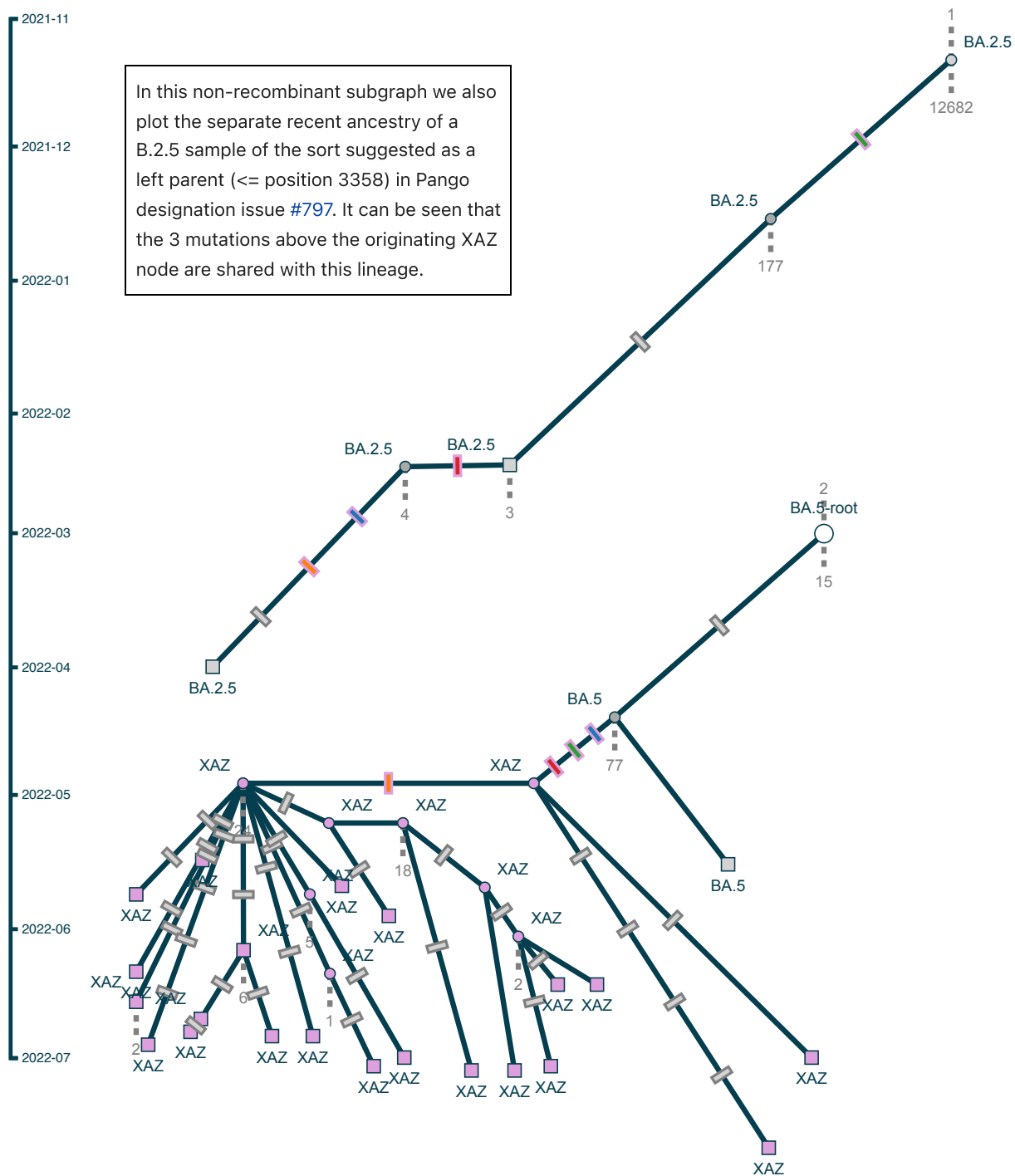
Subgraph of pango XAN/XAV: (20 samples, 20 shown)



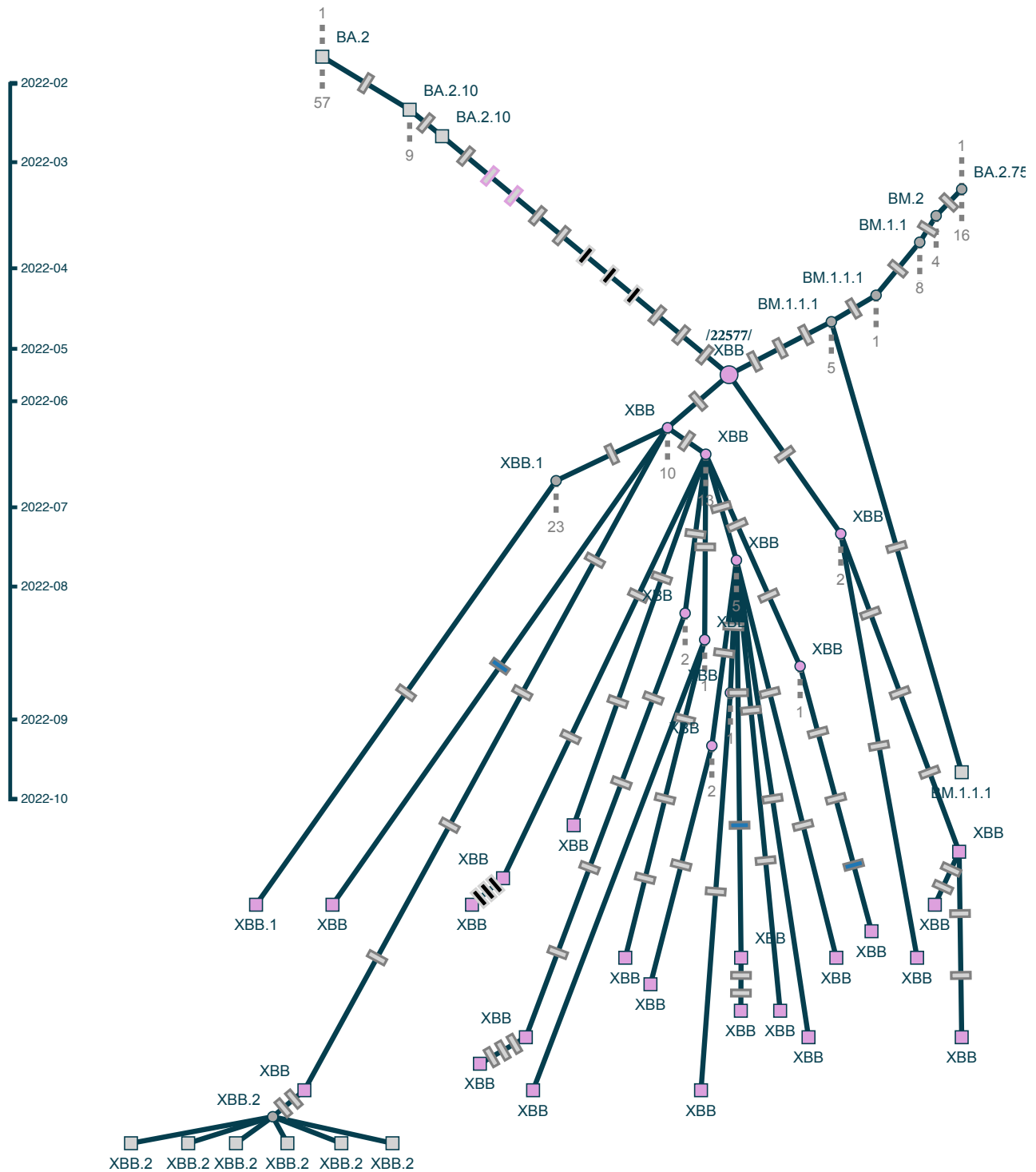
Subgraph of pango XAS: (77 samples, 77 shown)



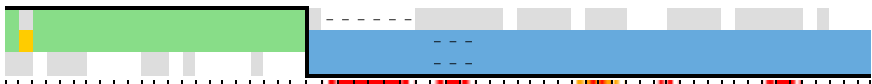
Subgraph of pango XAZ: (133 samples, 21 shown)



Subgraph of pango XBB: (72 samples, 20 shown)

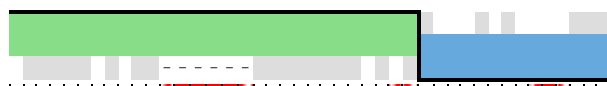
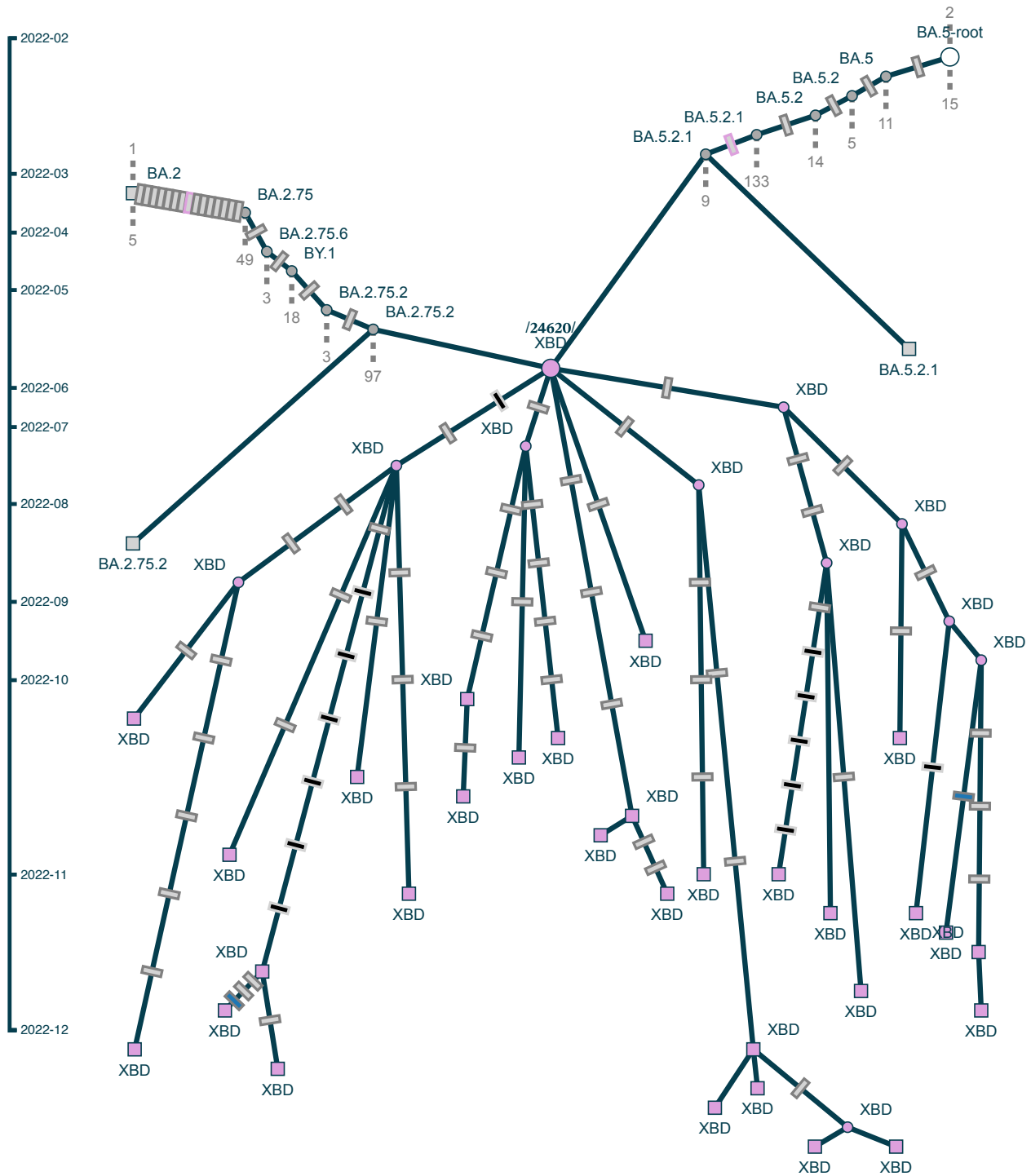


Subgraph of pango XBB.1: (525 samples, 22 shown)

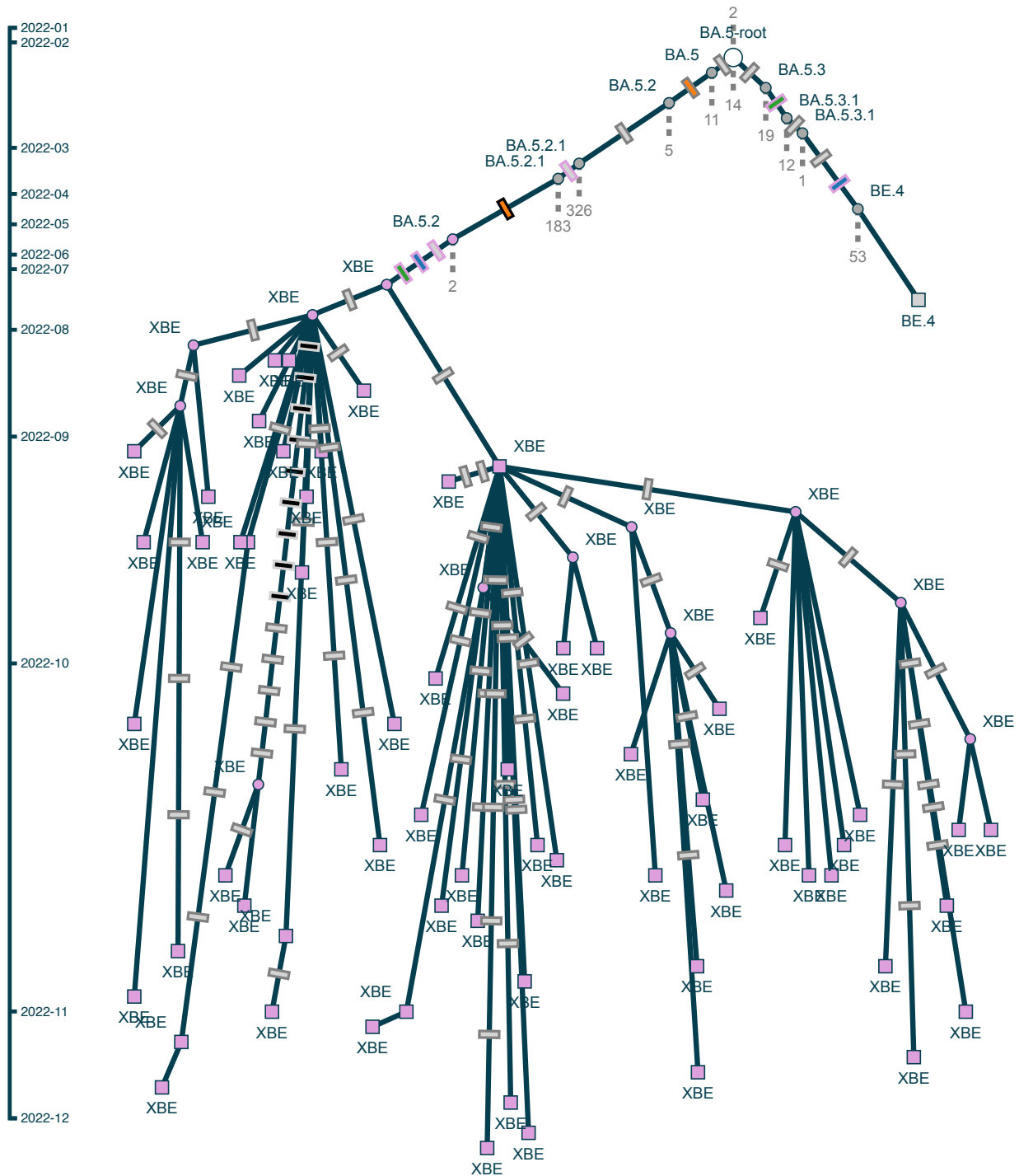




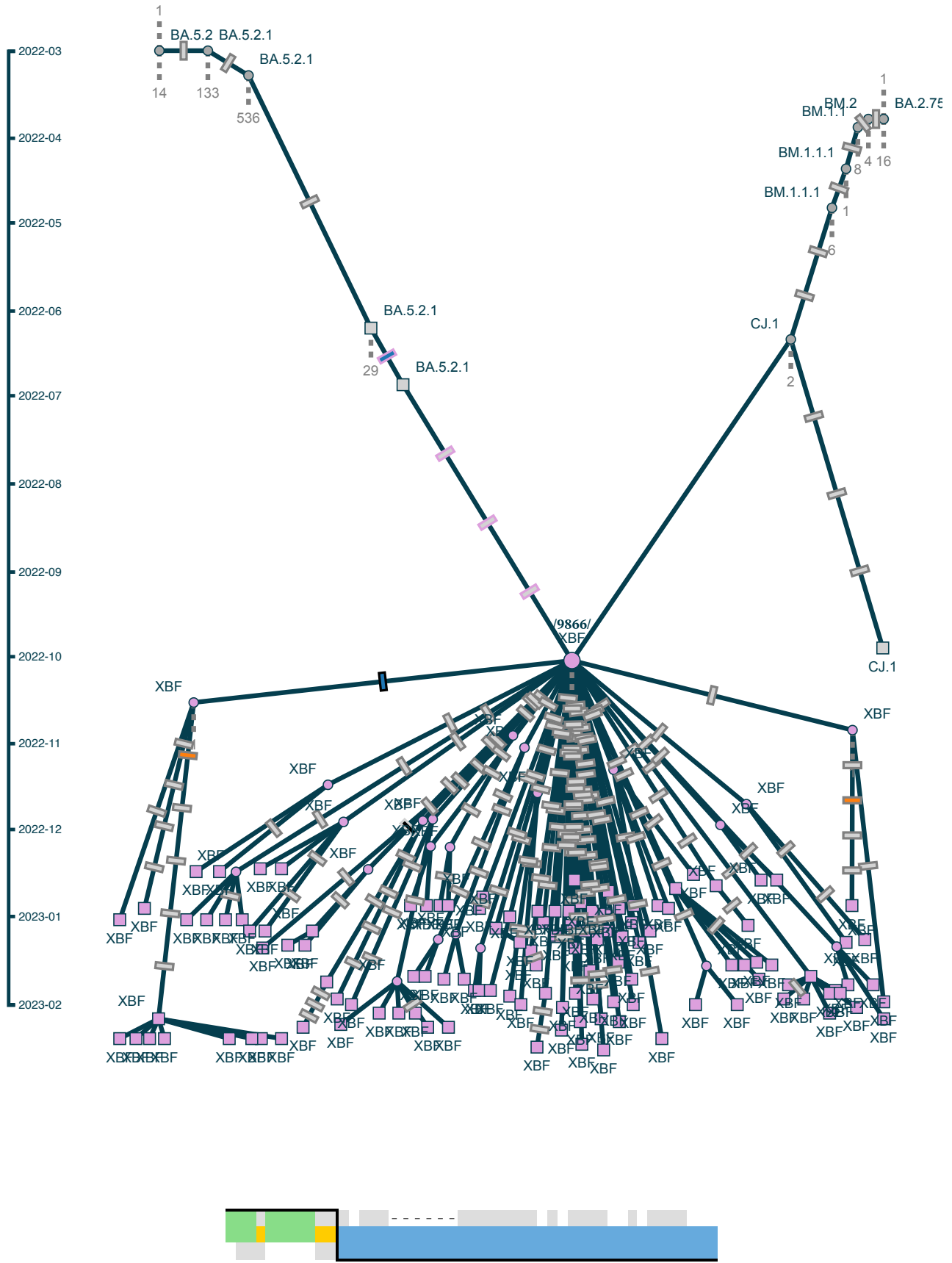
Subgraph of pango XBD: (30 samples, 30 shown)



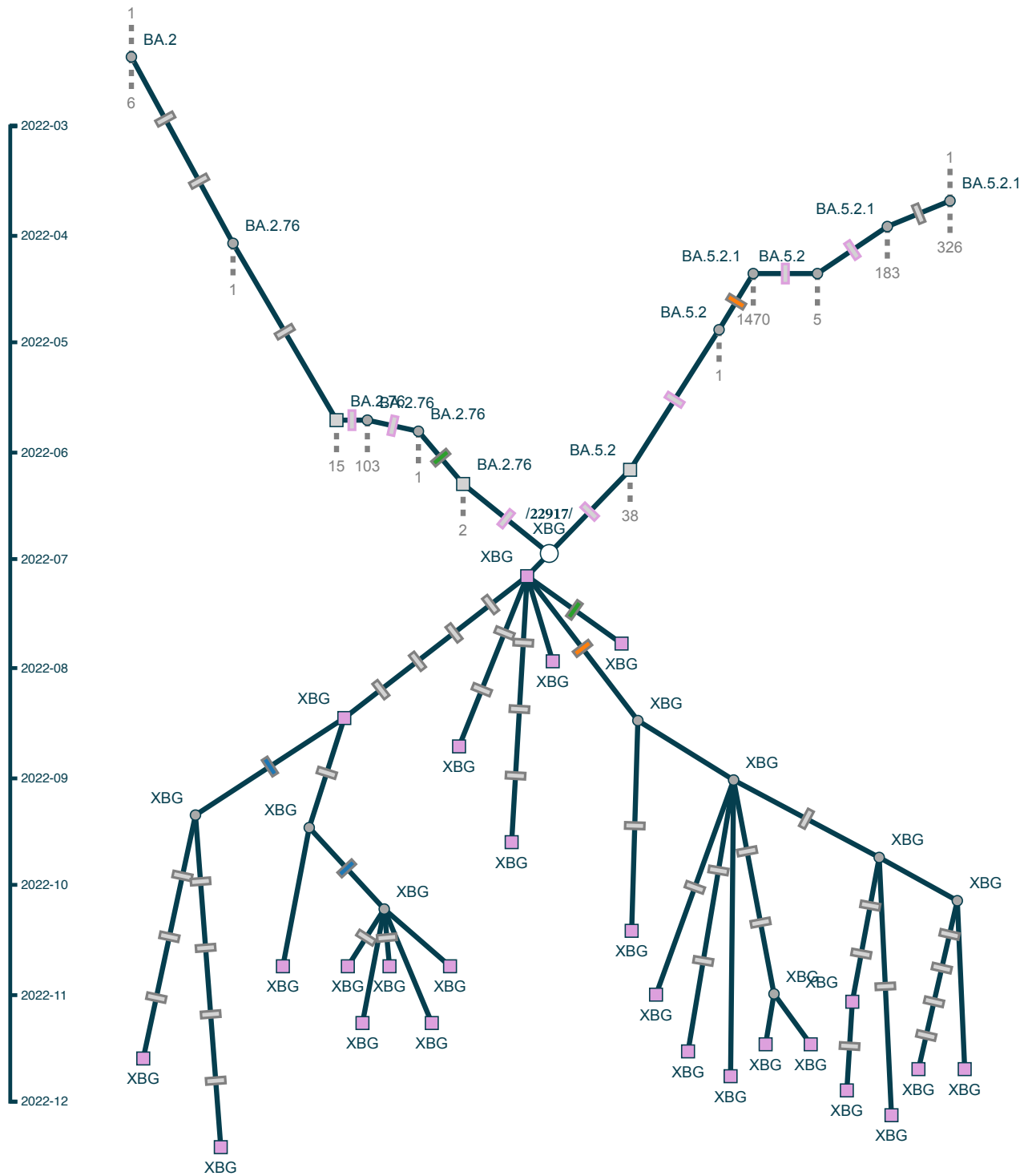
Subgraph of pango XBE: (65 samples, 65 shown)



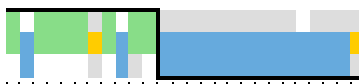
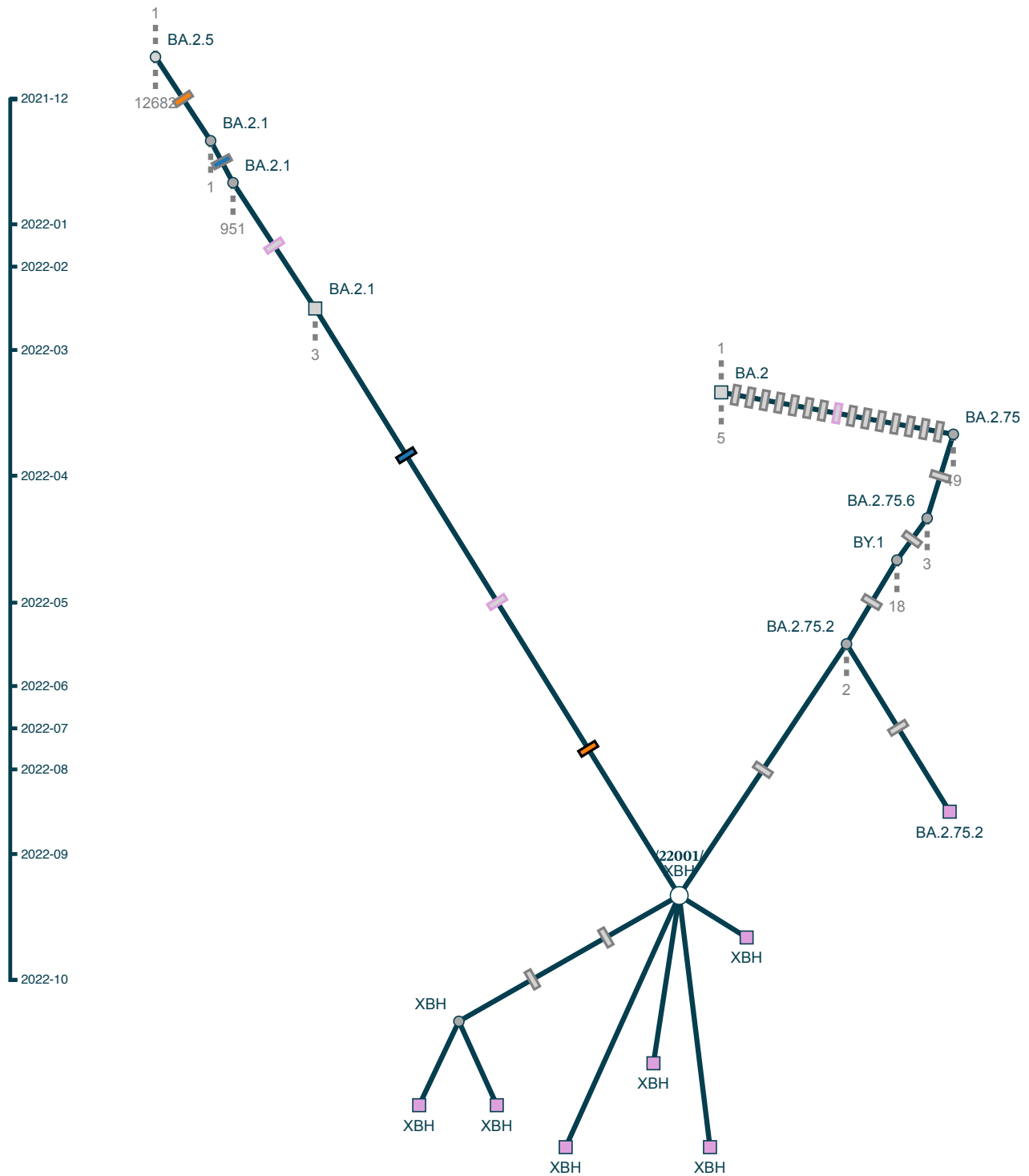
Subgraph of pango XBF: (124 samples, 124 shown)



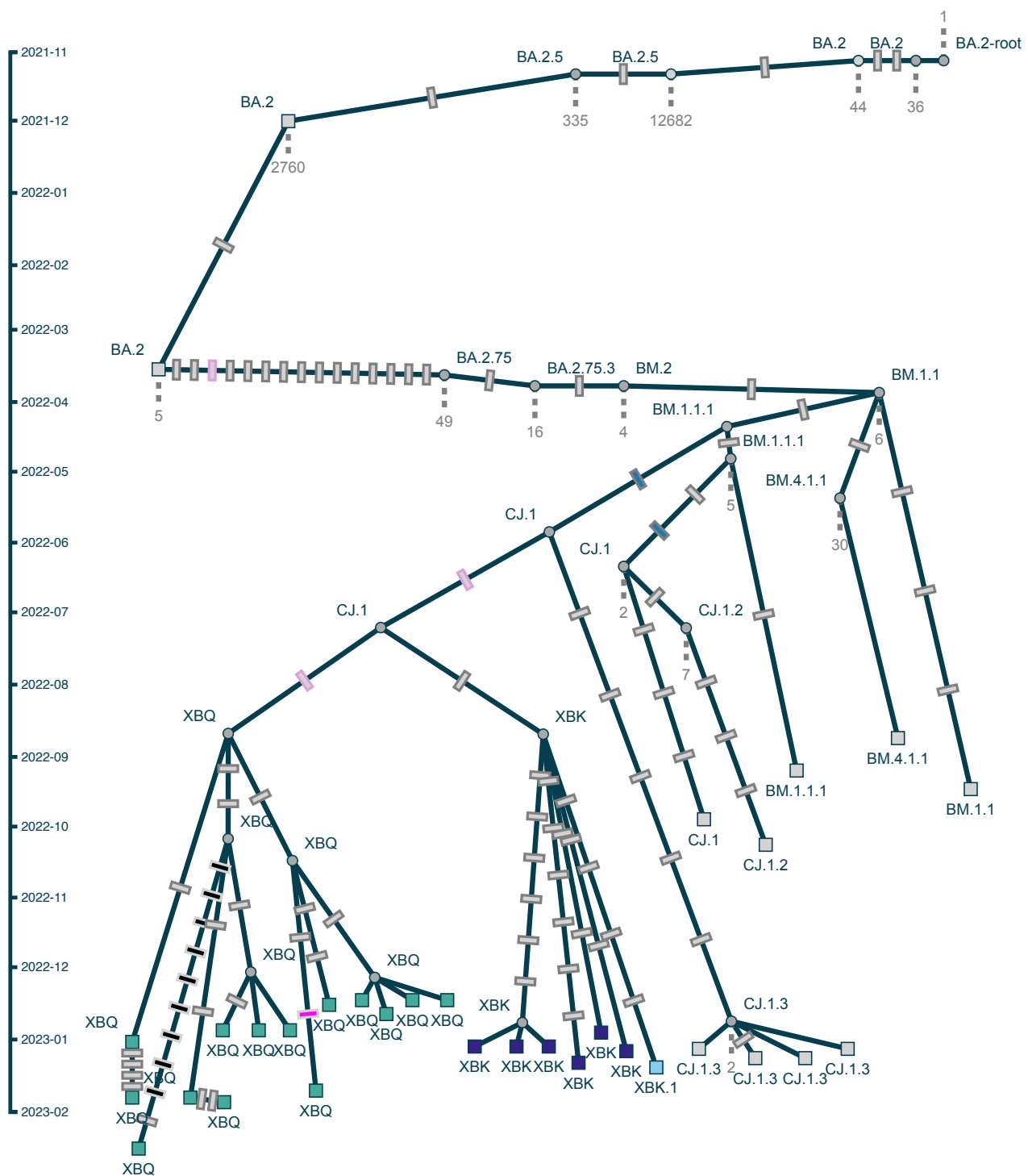
Subgraph of pango XBG: (25 samples, 25 shown)



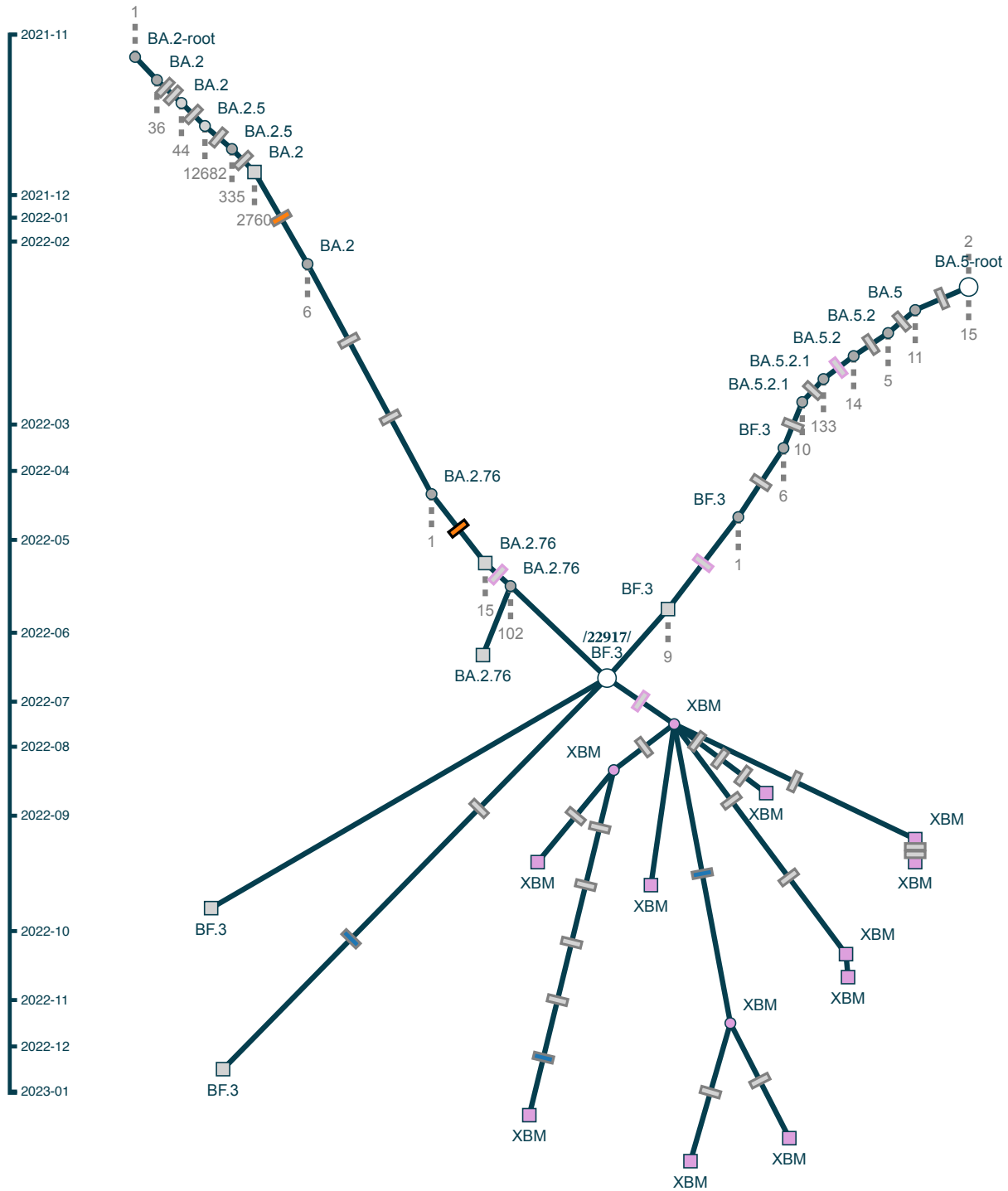
Subgraph of pango XBH: (6 samples, 6 shown)



Subgraph of panglo XBK/XBK.1/XBQ: (21 samples, 21 shown)



Subgraph of pango XBM: (10 samples, 10 shown)



Subgraph of pango XBR: (1 sample, 1 shown)

