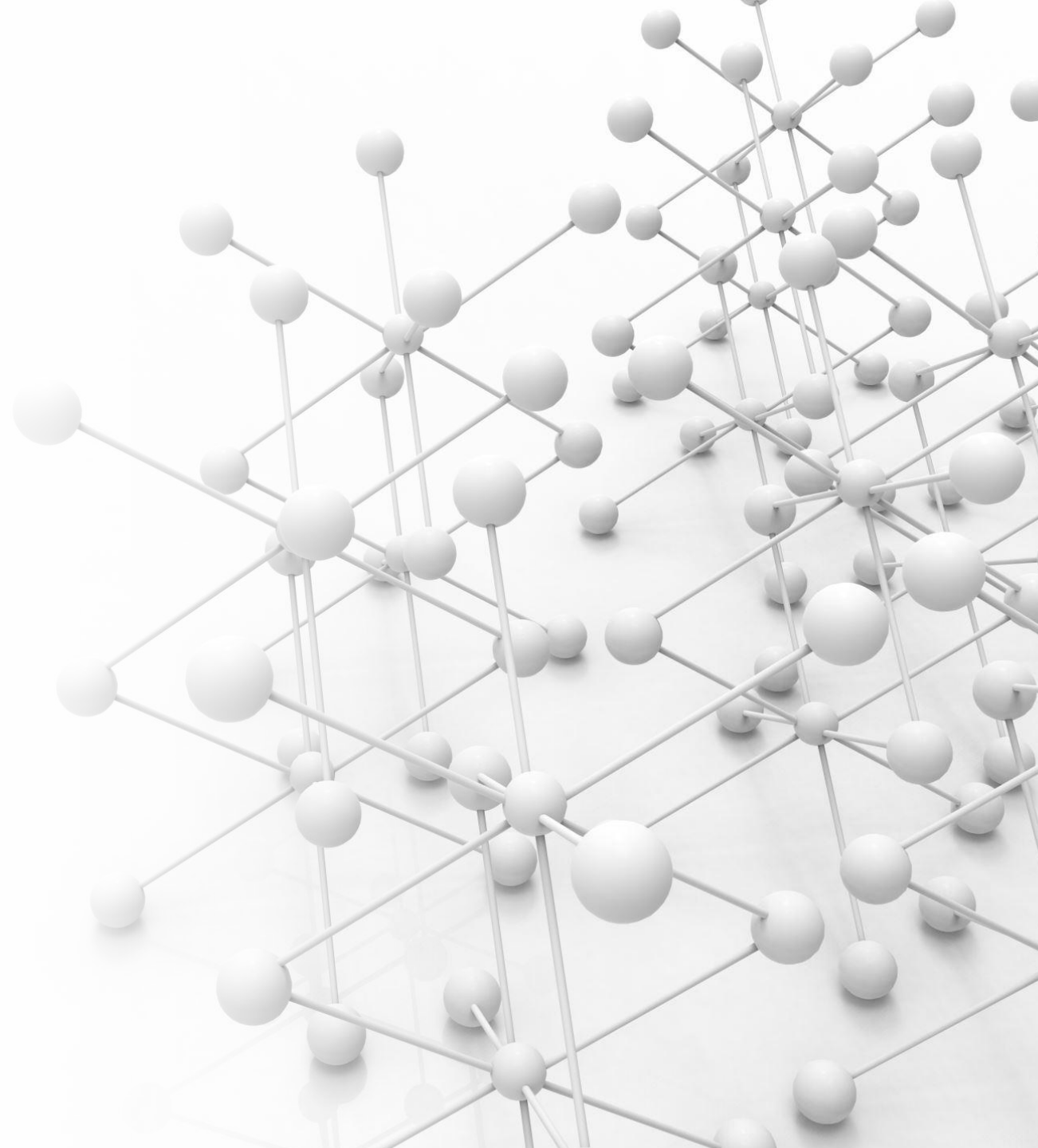




# Phylogenetic trees across algorithms

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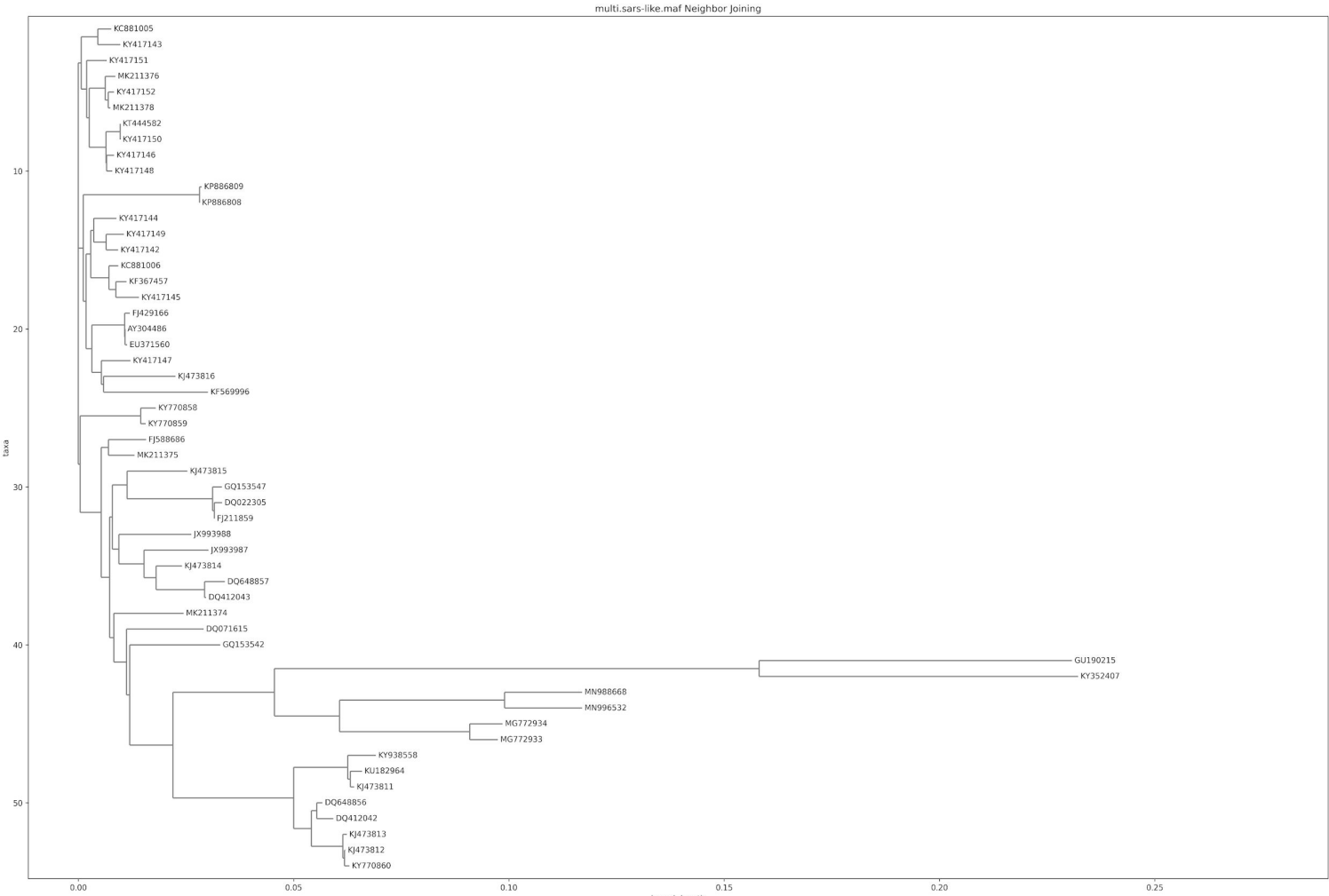
A presentation by Liz Wyman, Kleo  
Bano, Roberto Rivas, and Chris  
Troyer



# Algorithm differences

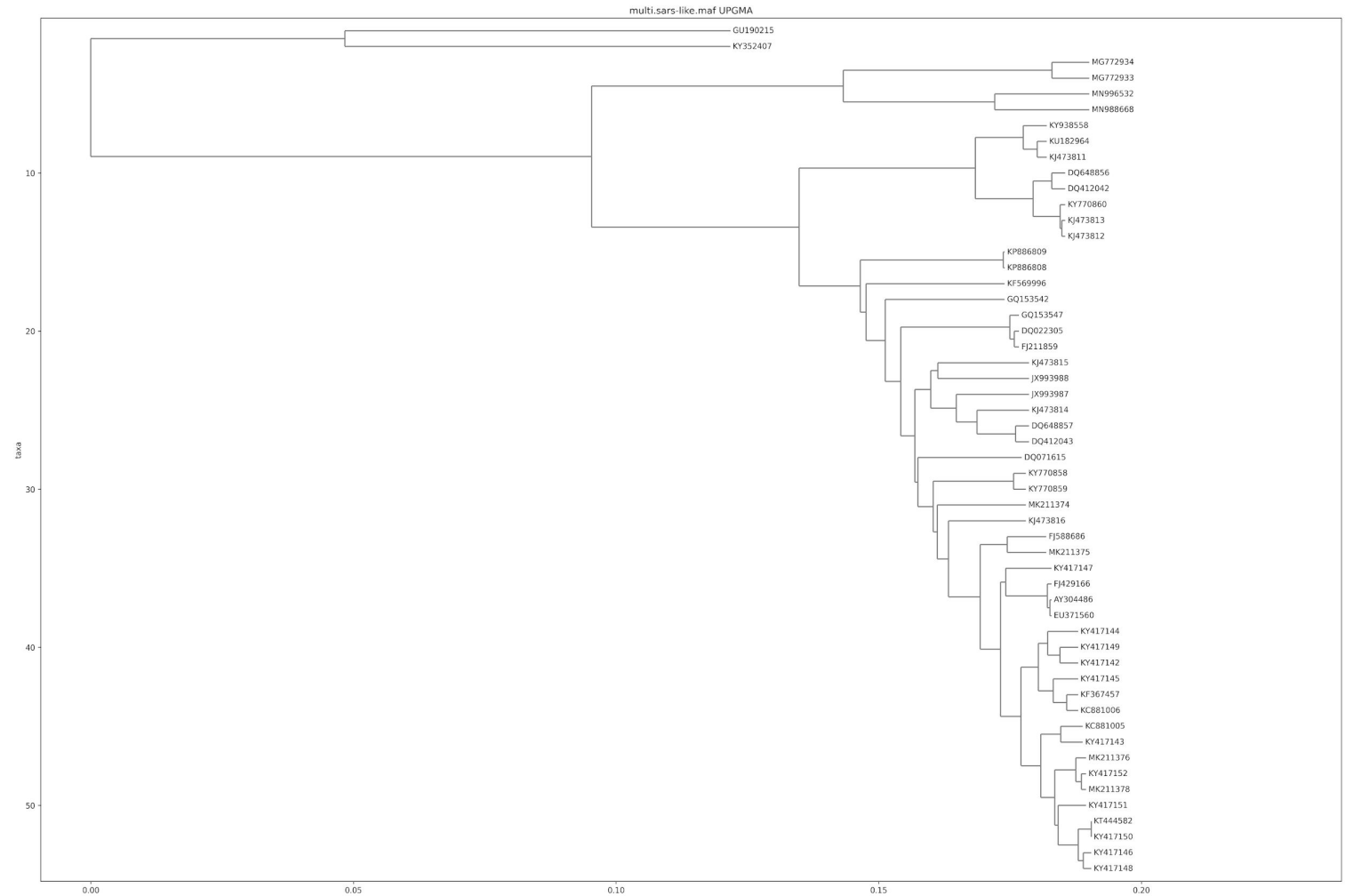
- **UPGMA** – Distance-based tree in which distances of leaves with same root are the same.
- **Neighbor-Joining** – Distance-based tree that finds a pair of leaves close to each other and far from other leaves.
- **Parsimony** – Character-based tree that seeks lowest number of mutations possible.

Neighbor  
joining -  
SARS-like  
genomes

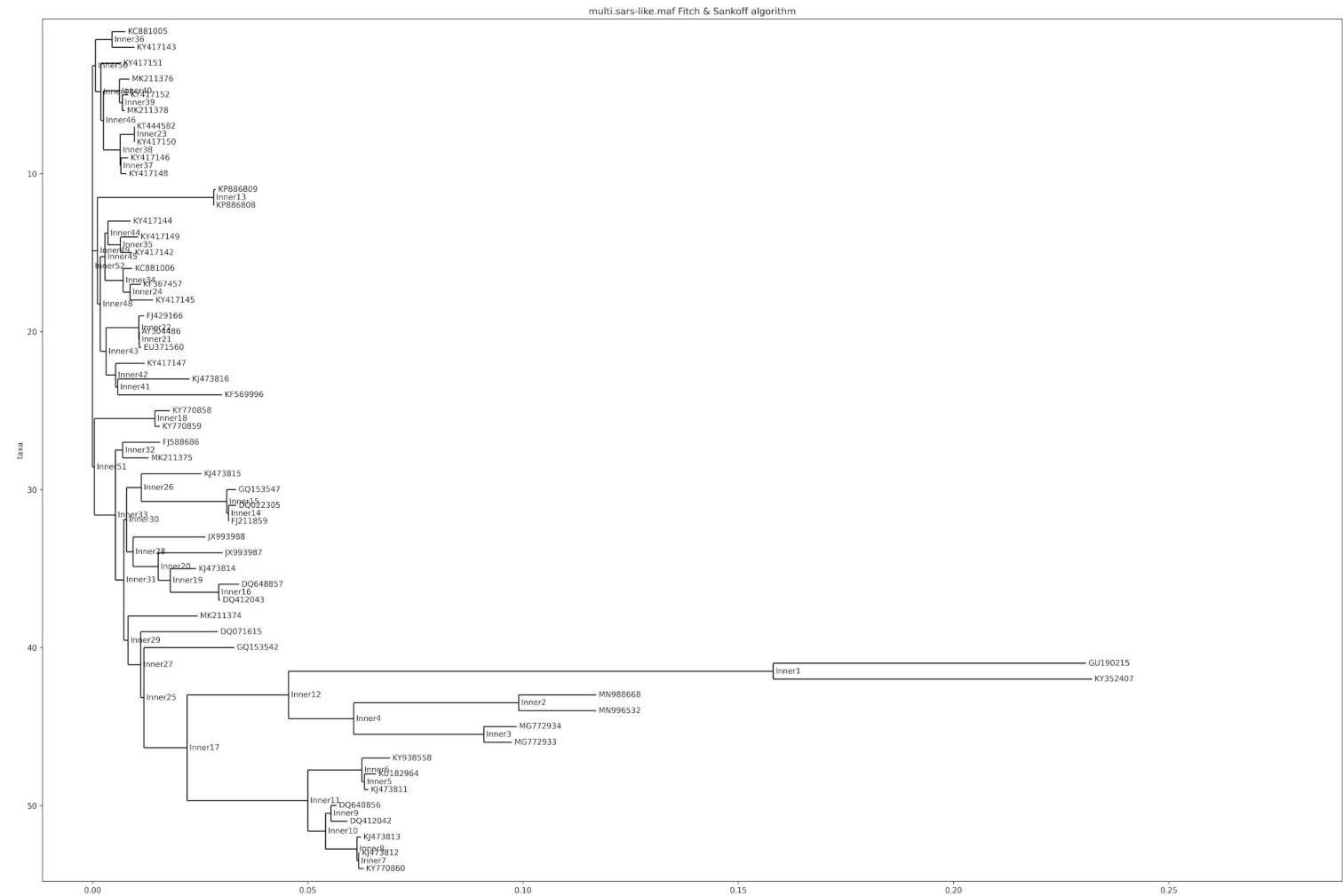


# UPGMA

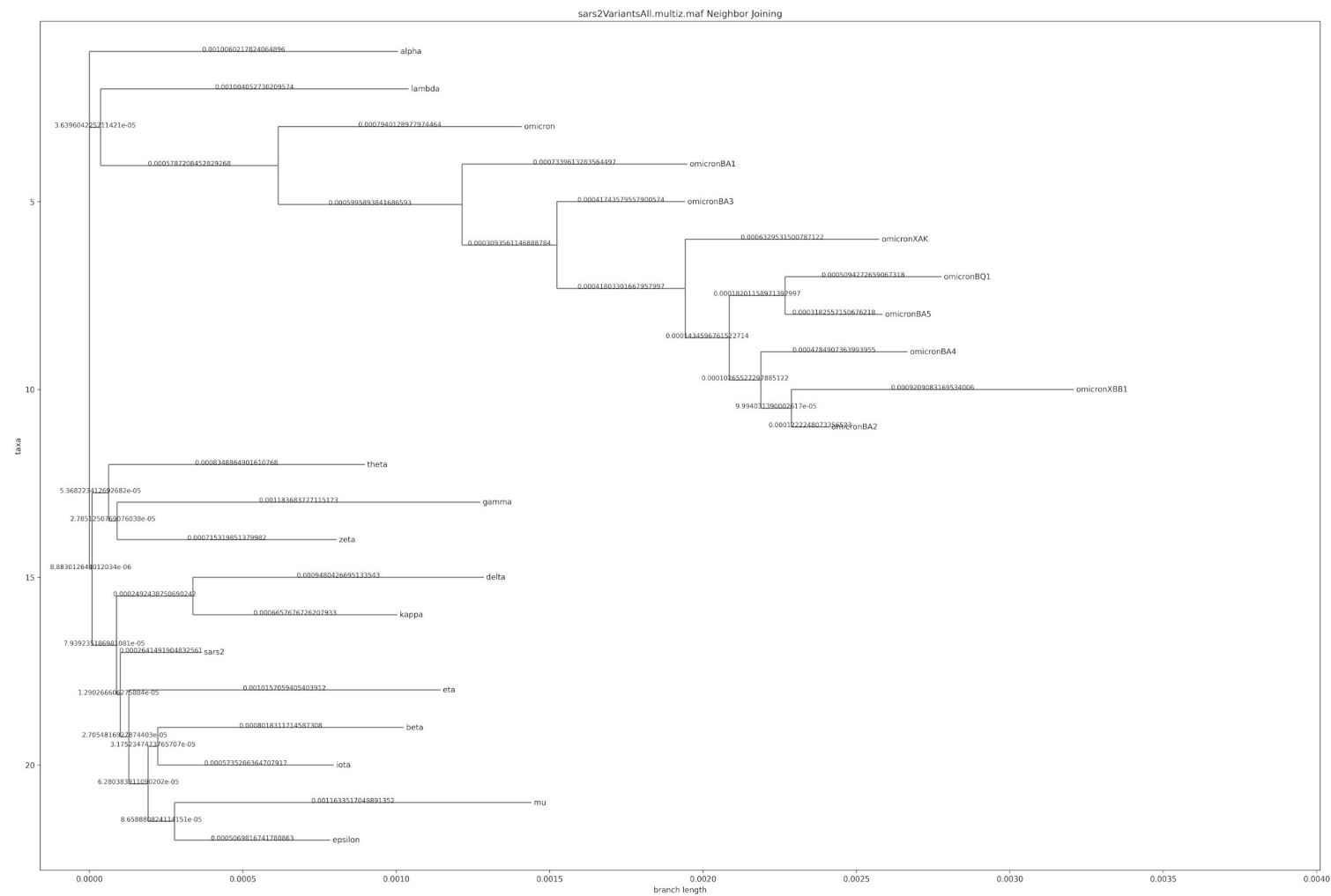
## –SARS-like genomes



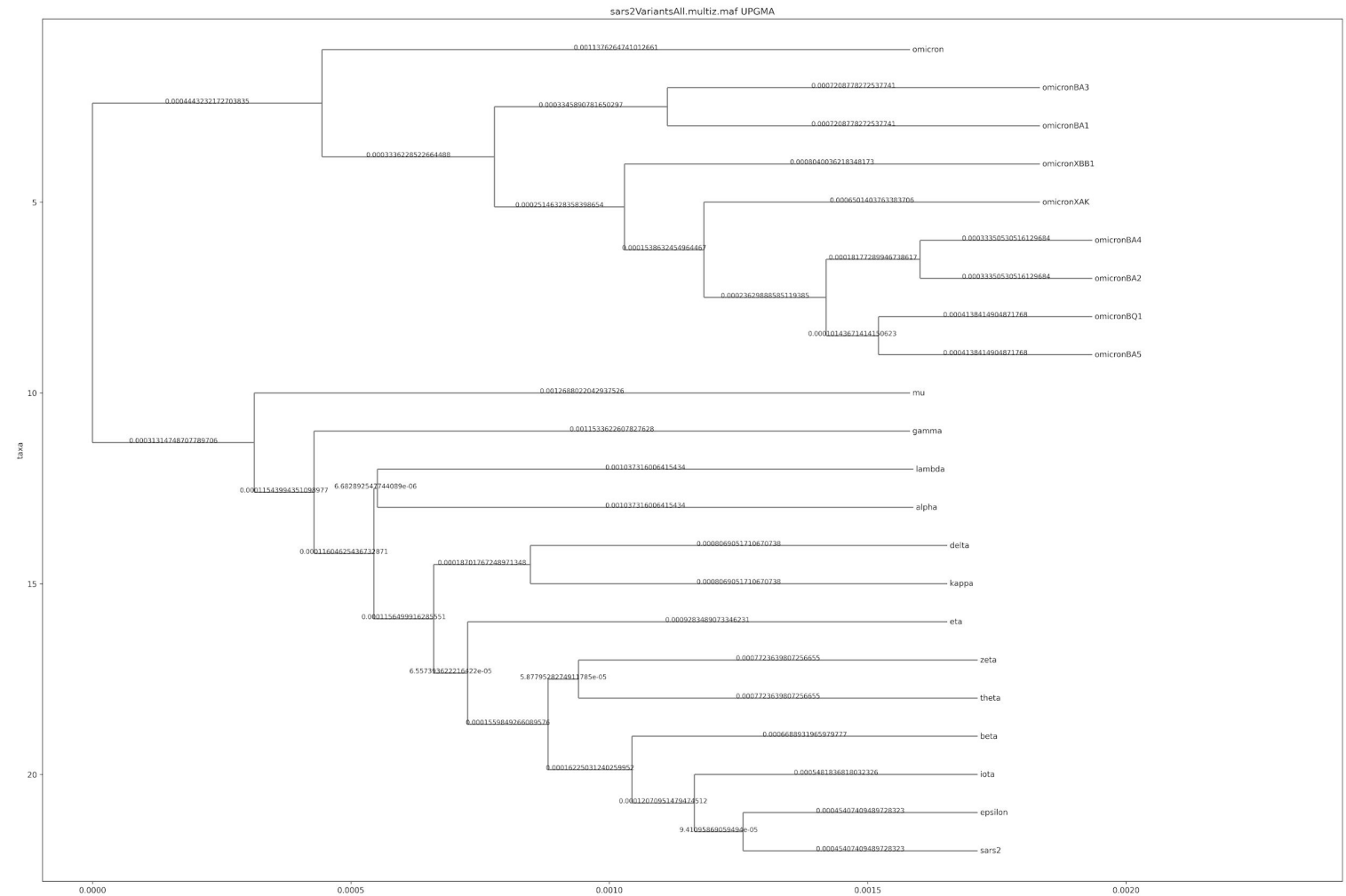
# Parsimony –SARS-like genomes



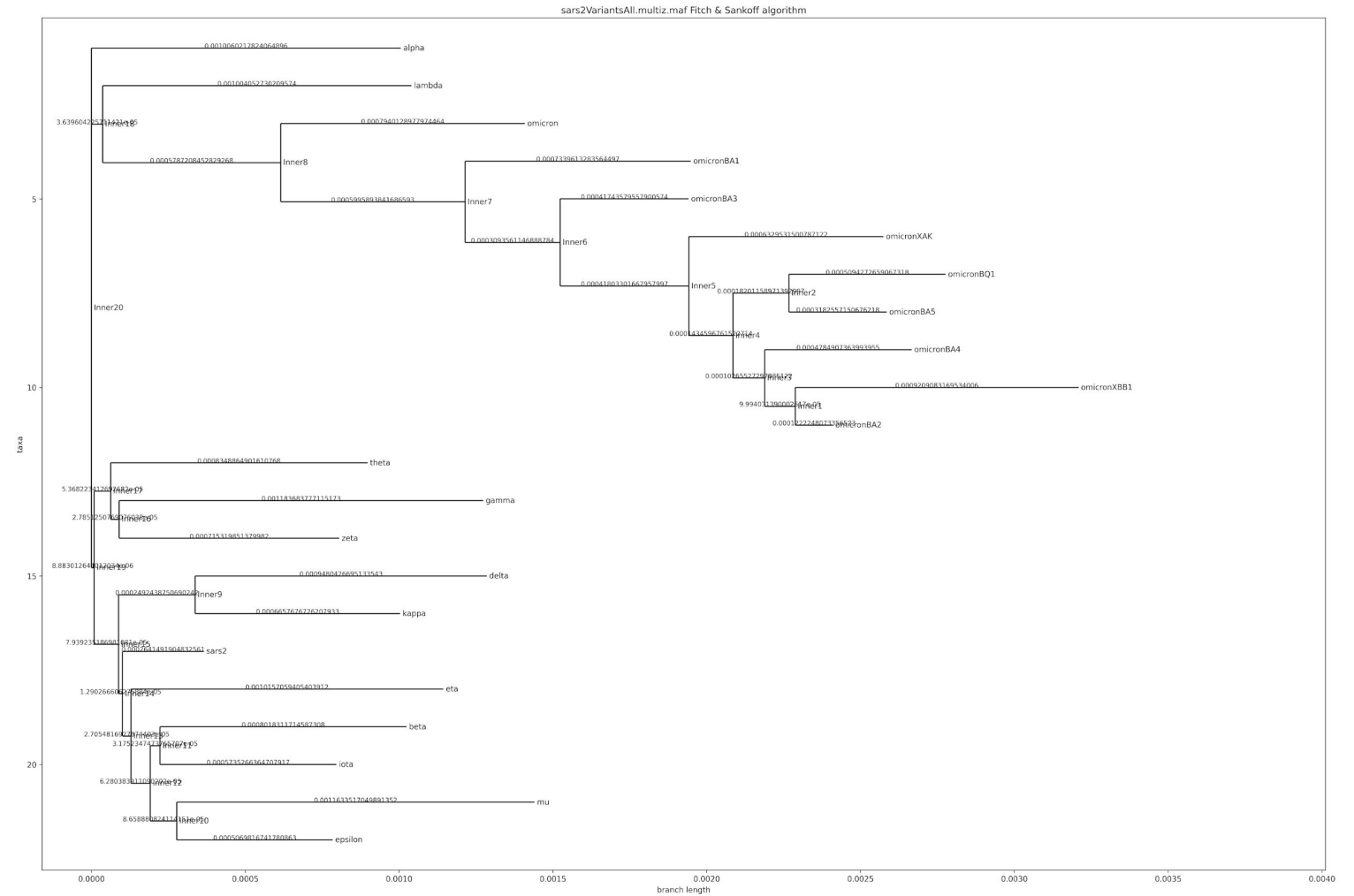
# Neighbor joining – SARS-COV-2 variants



# UPGMA – SARS-COV-2 variants

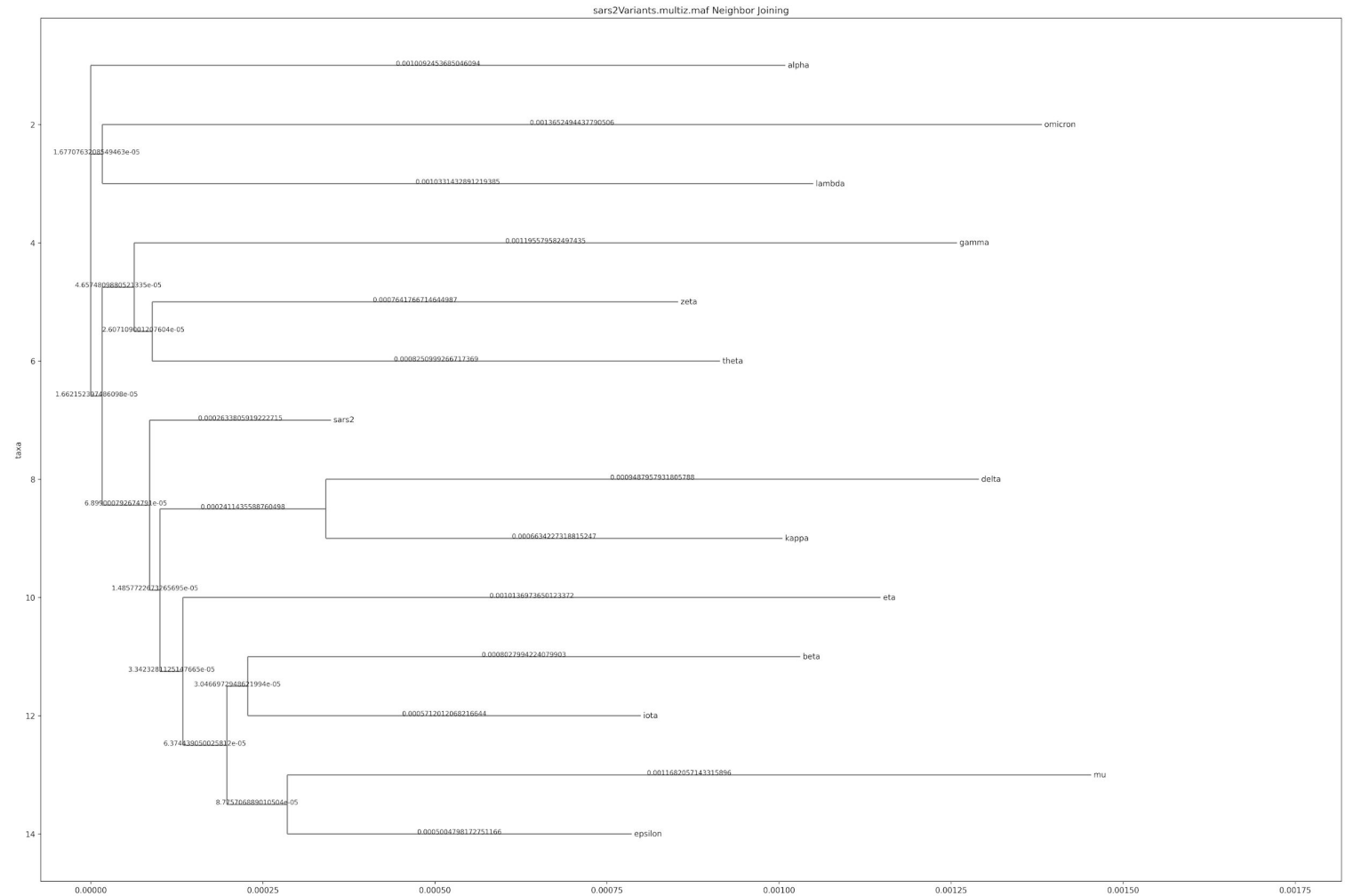


# Parsimony – SARS-COV-2 variants

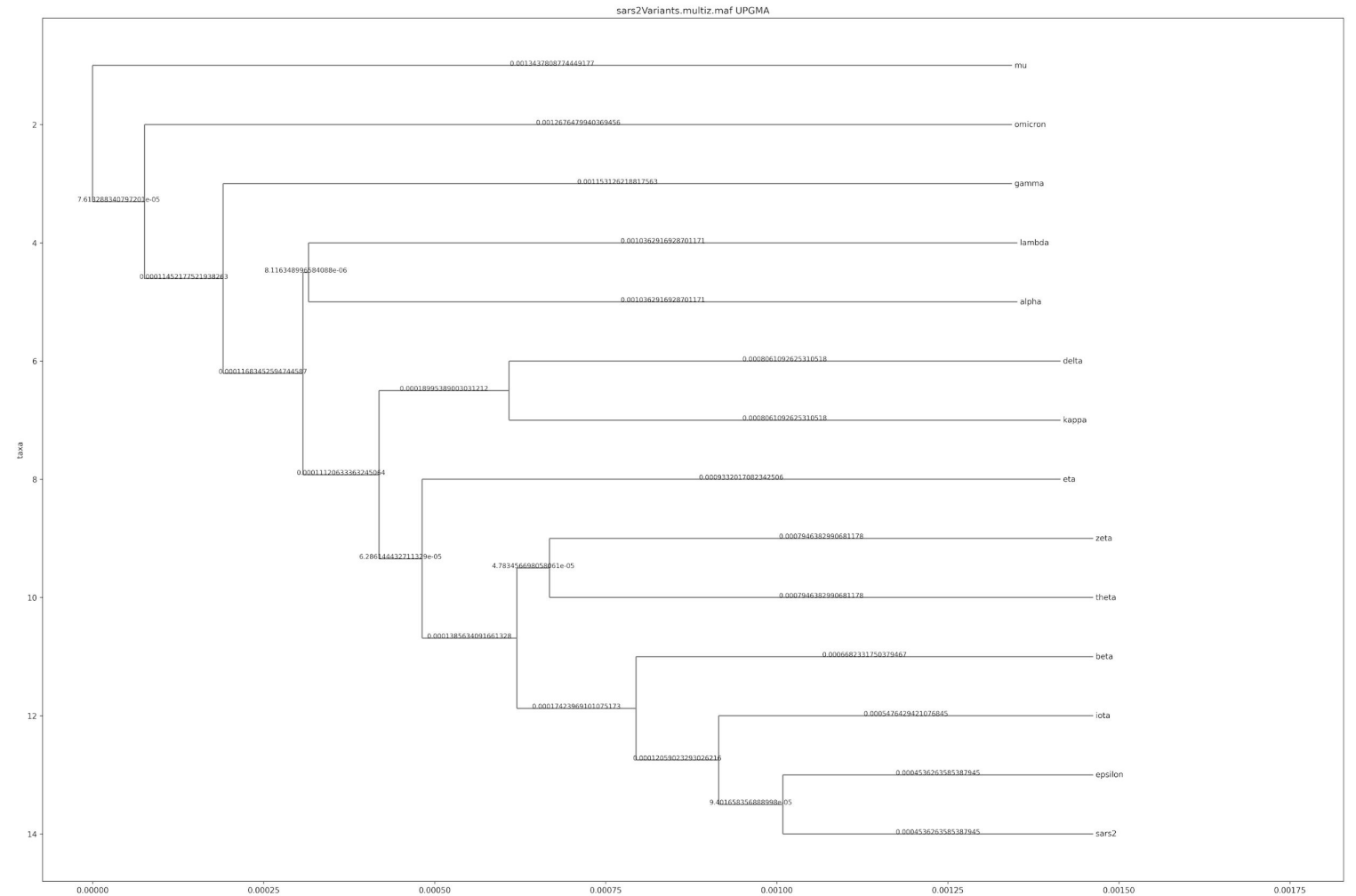




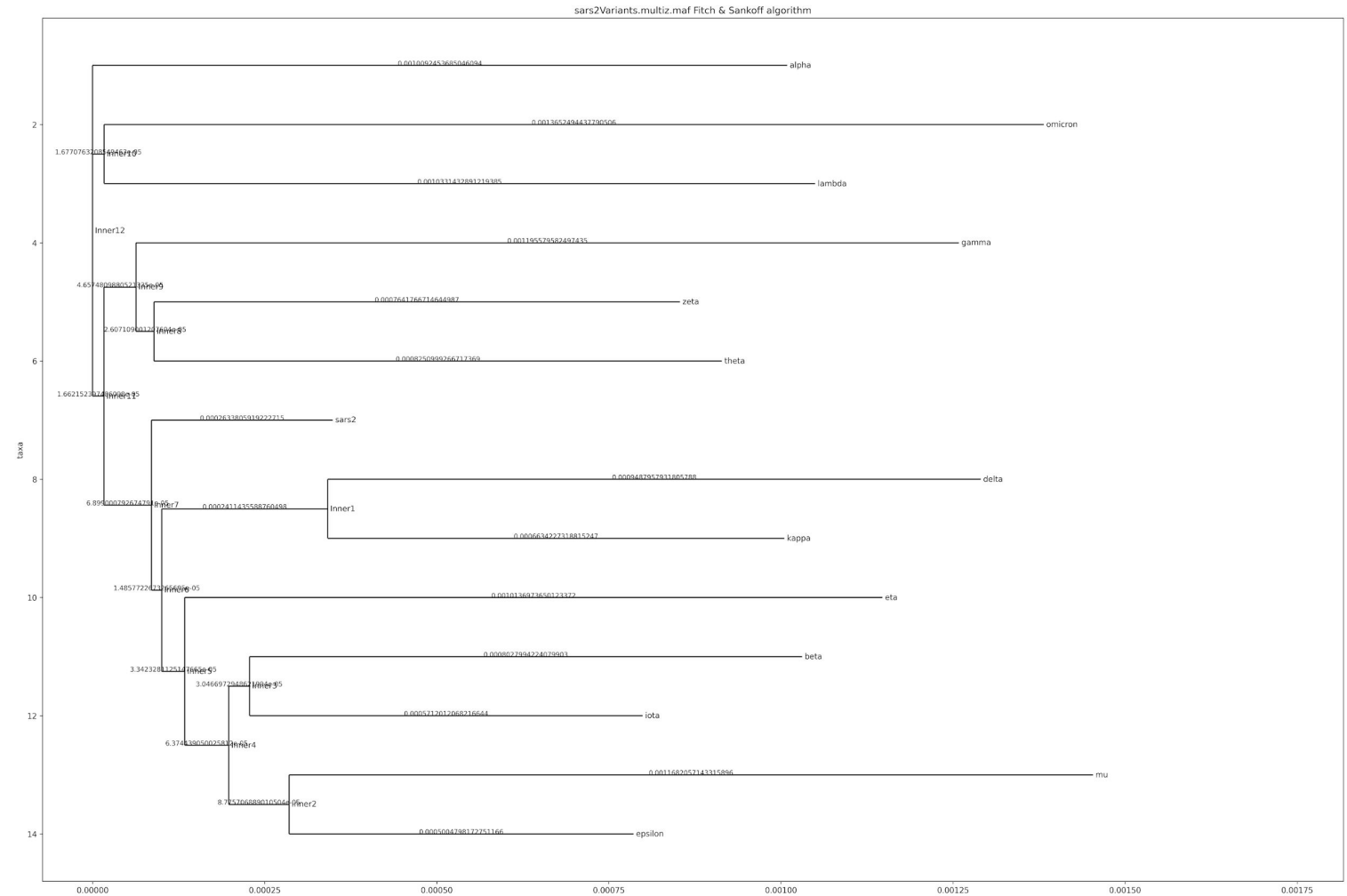
# Neighbor joining – SARS-COV-2 variants w/o omicron variants



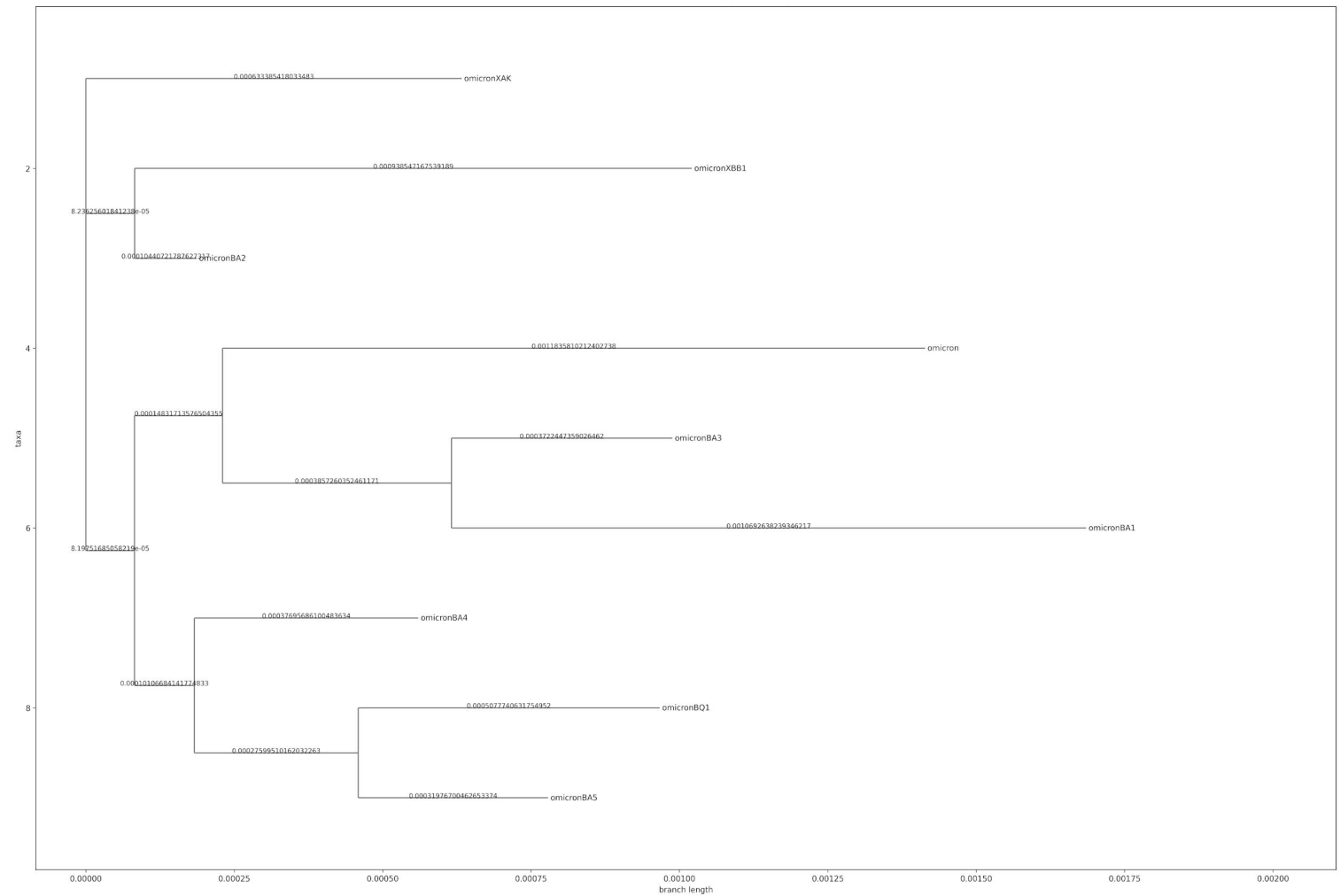
# UPGMA— SARS-COV-2 variants w/o omicron variants



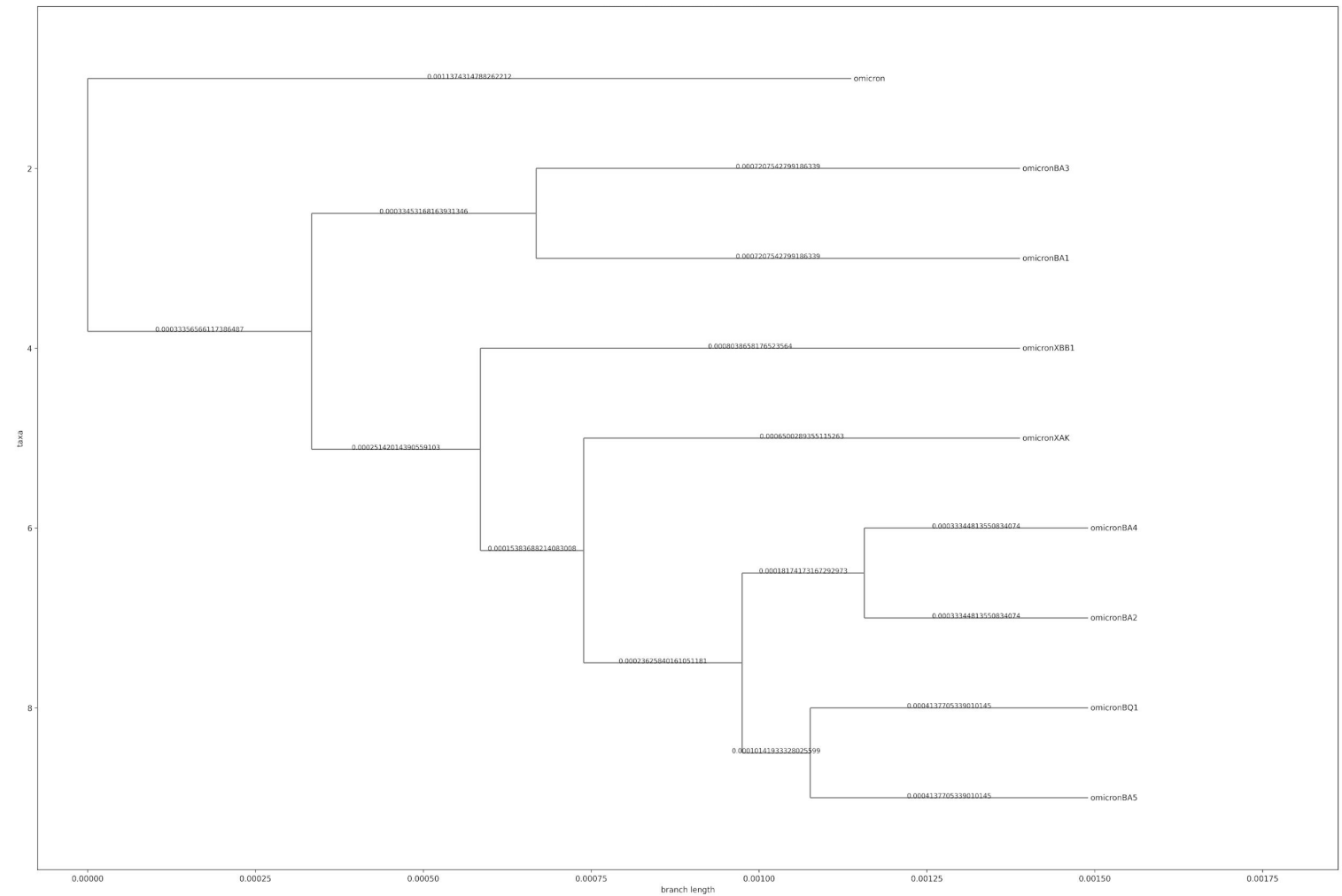
# Parsimony – SARS-COV-2 variants w/o omicron variants



# Neighbor joining – omicron variants only



# UPGMA – omicron variants only



# Parsimony – omicron variants only

