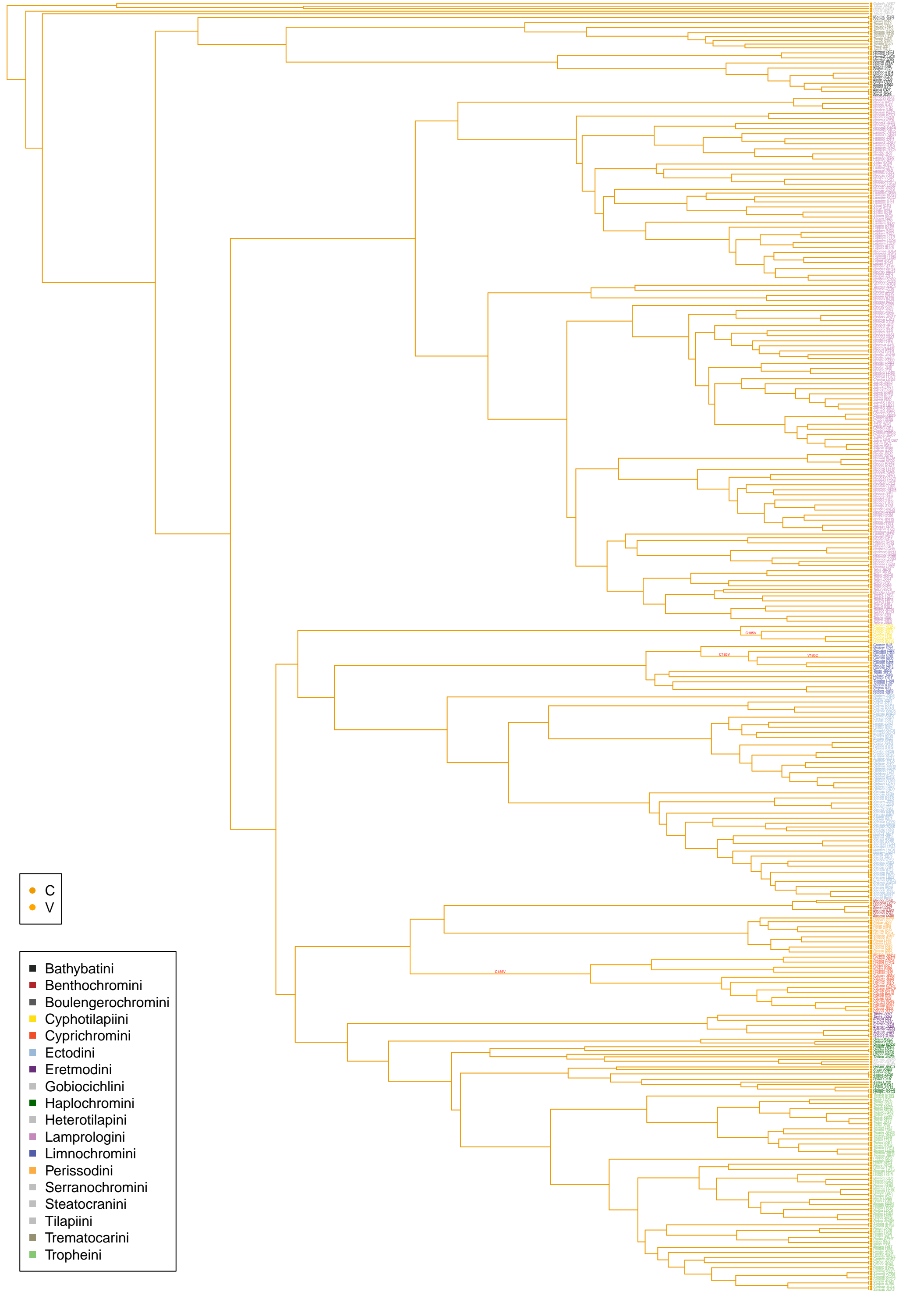


C  
V

- Bathybatini
- Benthochromini
- Boulengerochromini
- Cyphotilapiini
- Cyprichromini
- Ectodini
- Eretmodini
- Gobiocichlini
- Haplochromini
- Heterotilapini
- Lamprologini
- Limnochromini
- Perissodini
- Serranochromini
- Steatocranini
- Tilapiini
- Trematocarini
- Tropheini

3 C185V, 1 V185C

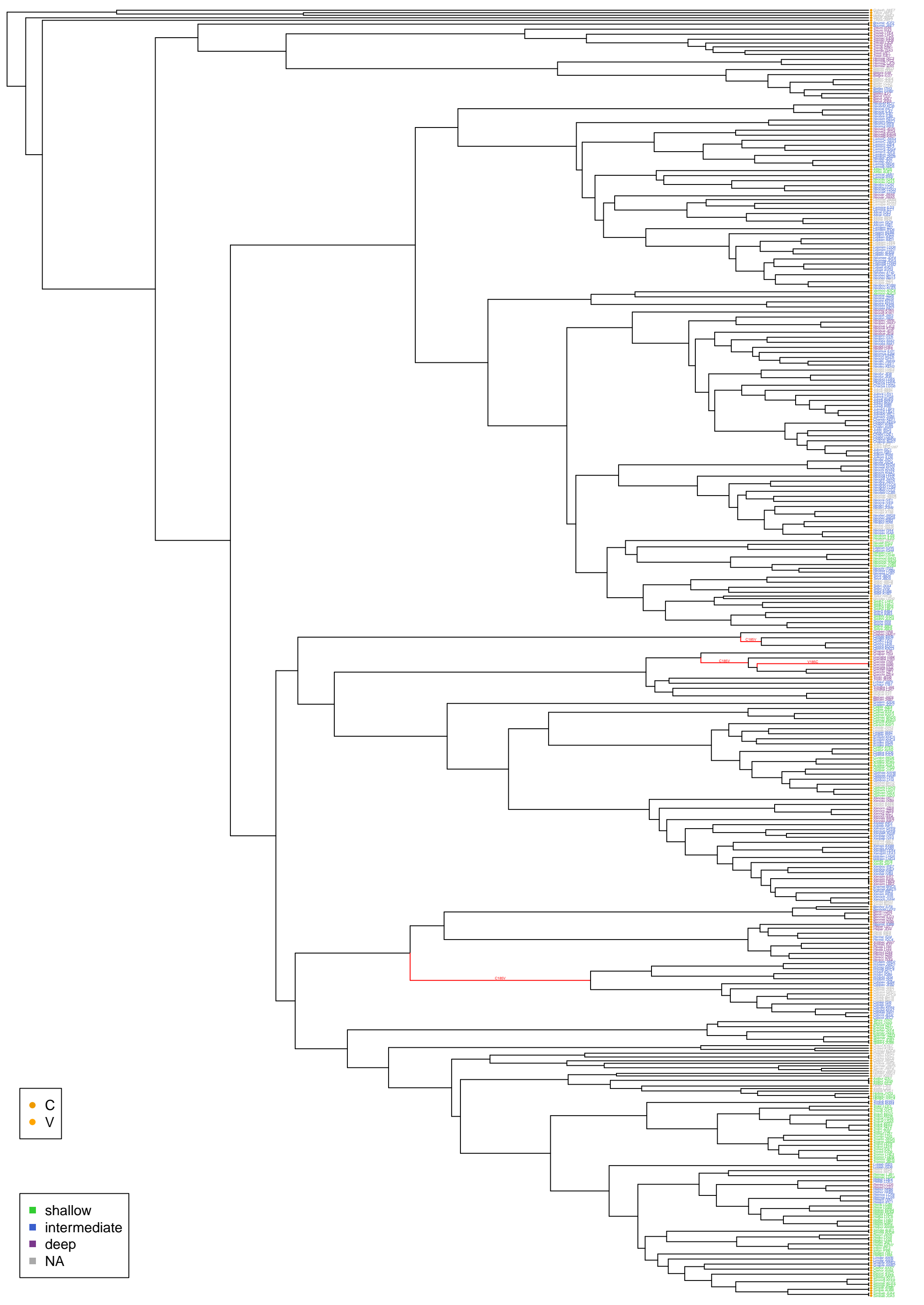


C  
V

- Bathybatini
- Benthochromini
- Boulengerochromini
- Cyphotilapiini
- Cyprichromini
- Ectodini
- Eretmodini
- Gobiocichlini
- Haplochromini
- Heterotilapini
- Lamprologini
- Limnochromini
- Perissodini
- Serranochromini
- Steatocranini
- Tilapiini
- Trematocarini
- Tropheini

0 2 4 6 8 10 12

3 C185V, 1 V185C



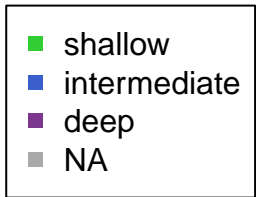
Phylogenetic tree showing the relationships between 185 SARS-CoV-2 sequences. The tree is rooted at the top left. The sequences are color-coded by geographic region: shallow (green), intermediate (blue), deep (purple), and NA (grey). The tree shows a clear separation between the NA clade and the other three regions. The NA clade is the largest and most diverse, while the other three regions are smaller and less diverse. The tree is rooted at the top left, with the root node labeled 'C' and 'V'.

Legend:

- shallow
- intermediate
- deep
- NA

Legend:

- C
- V



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