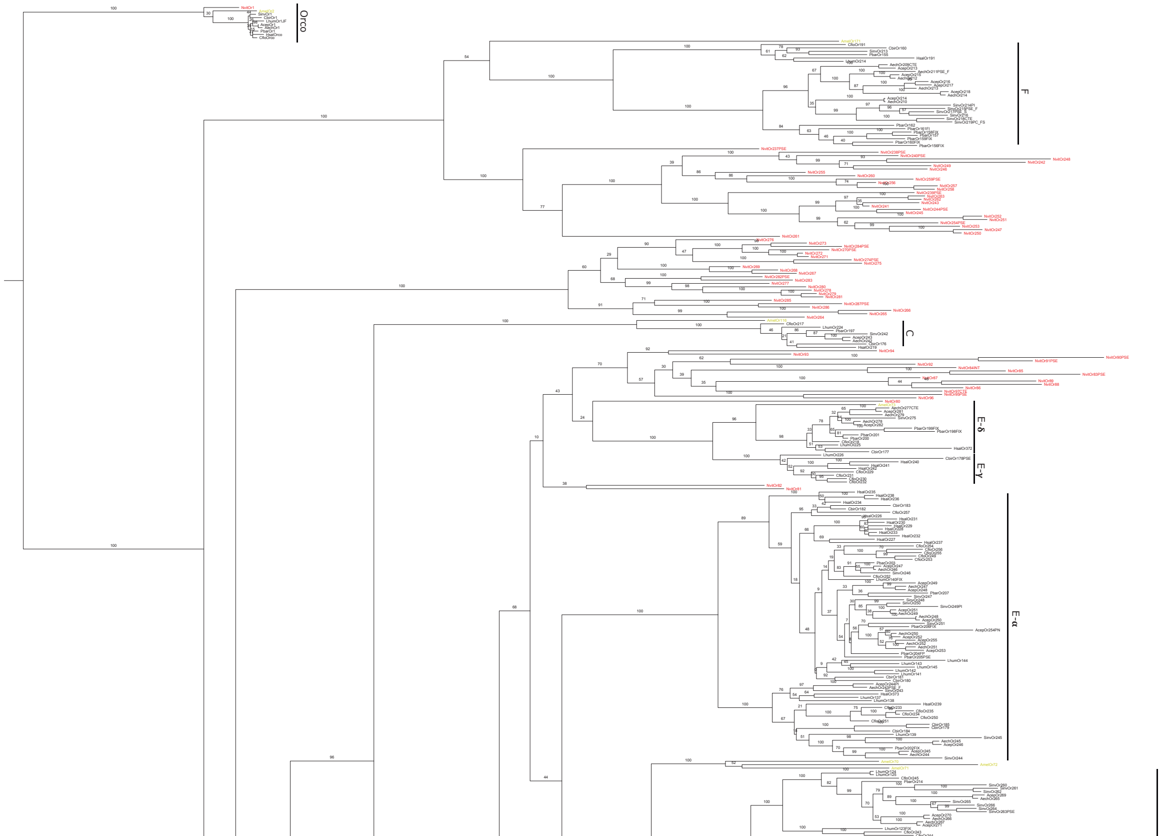
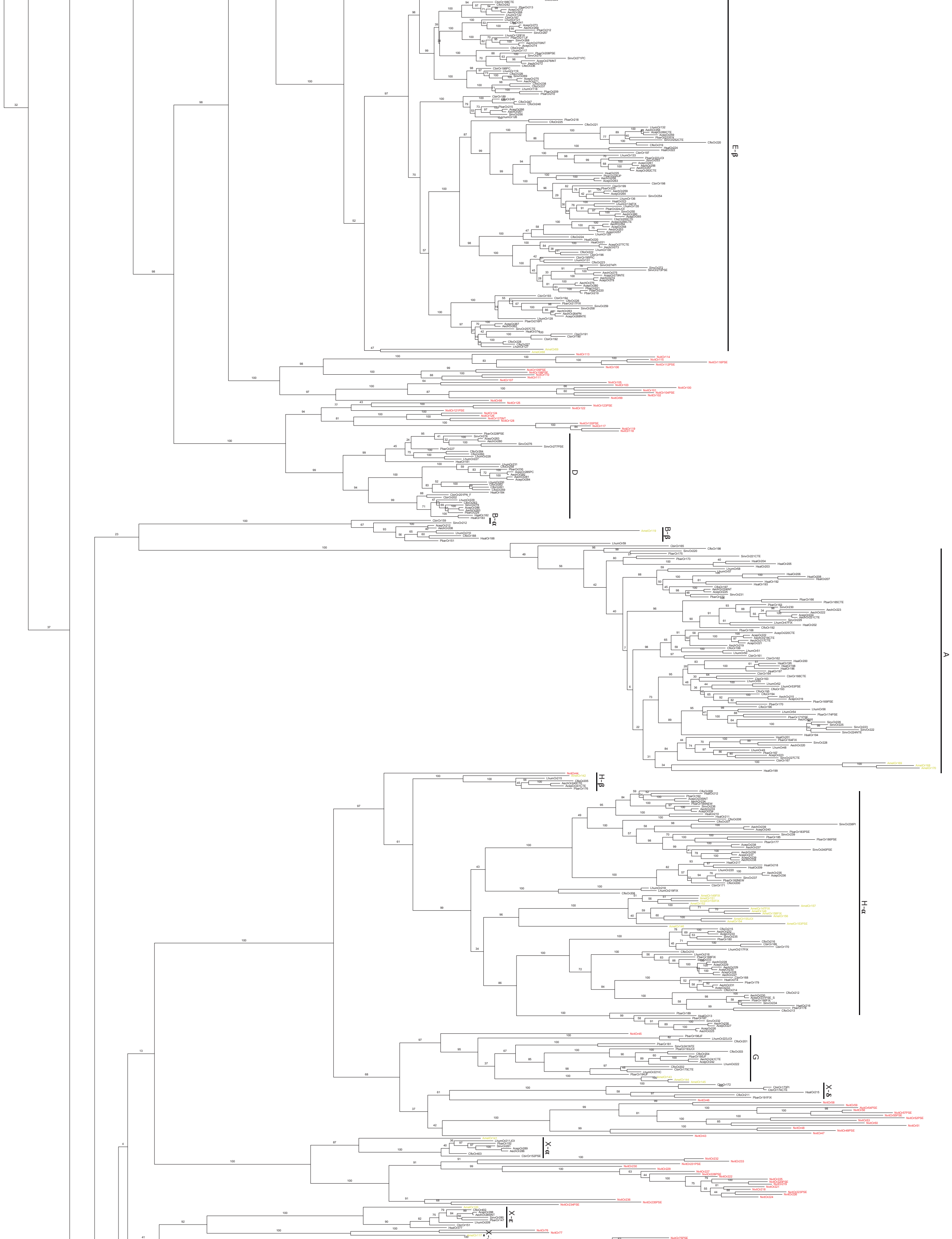
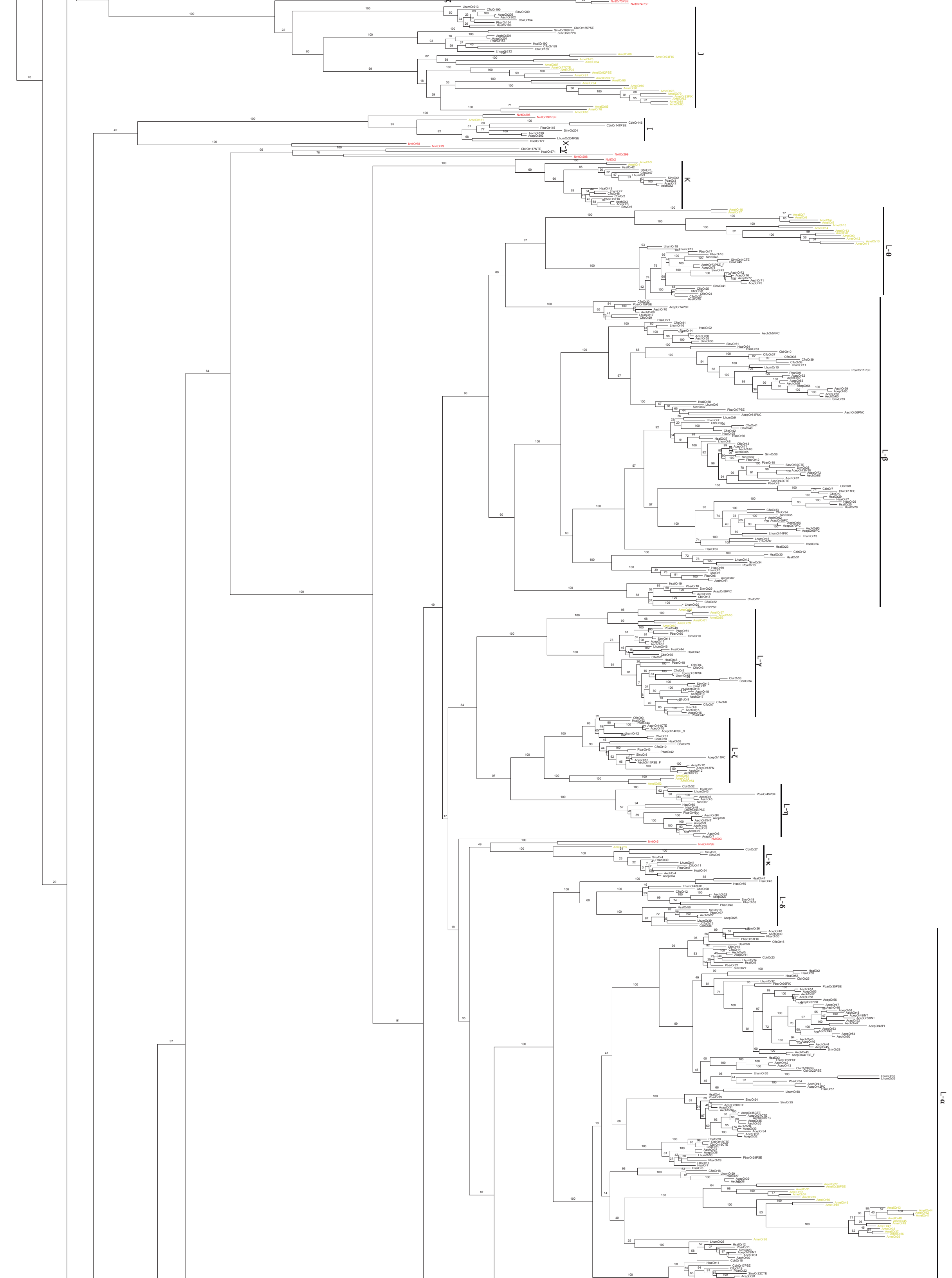
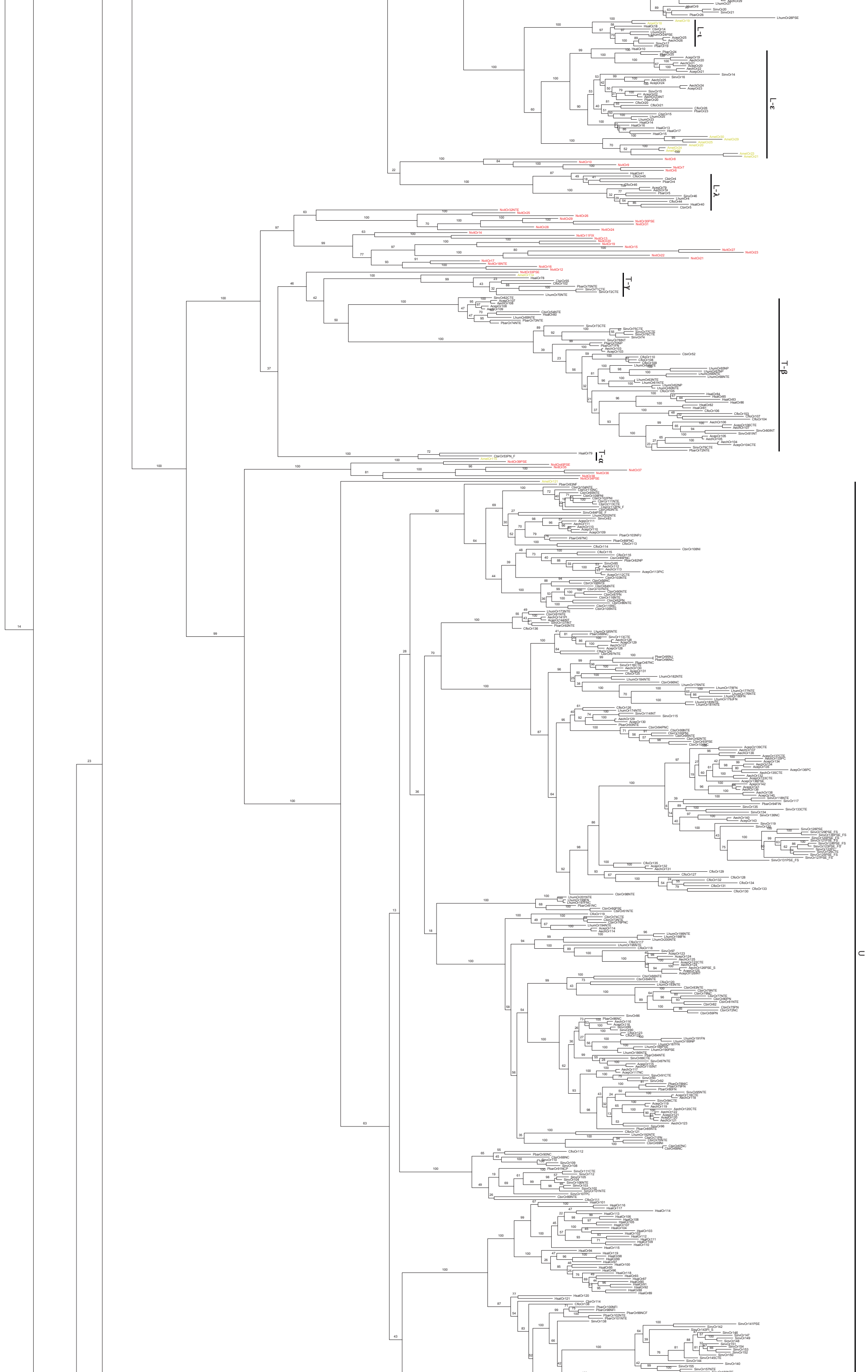
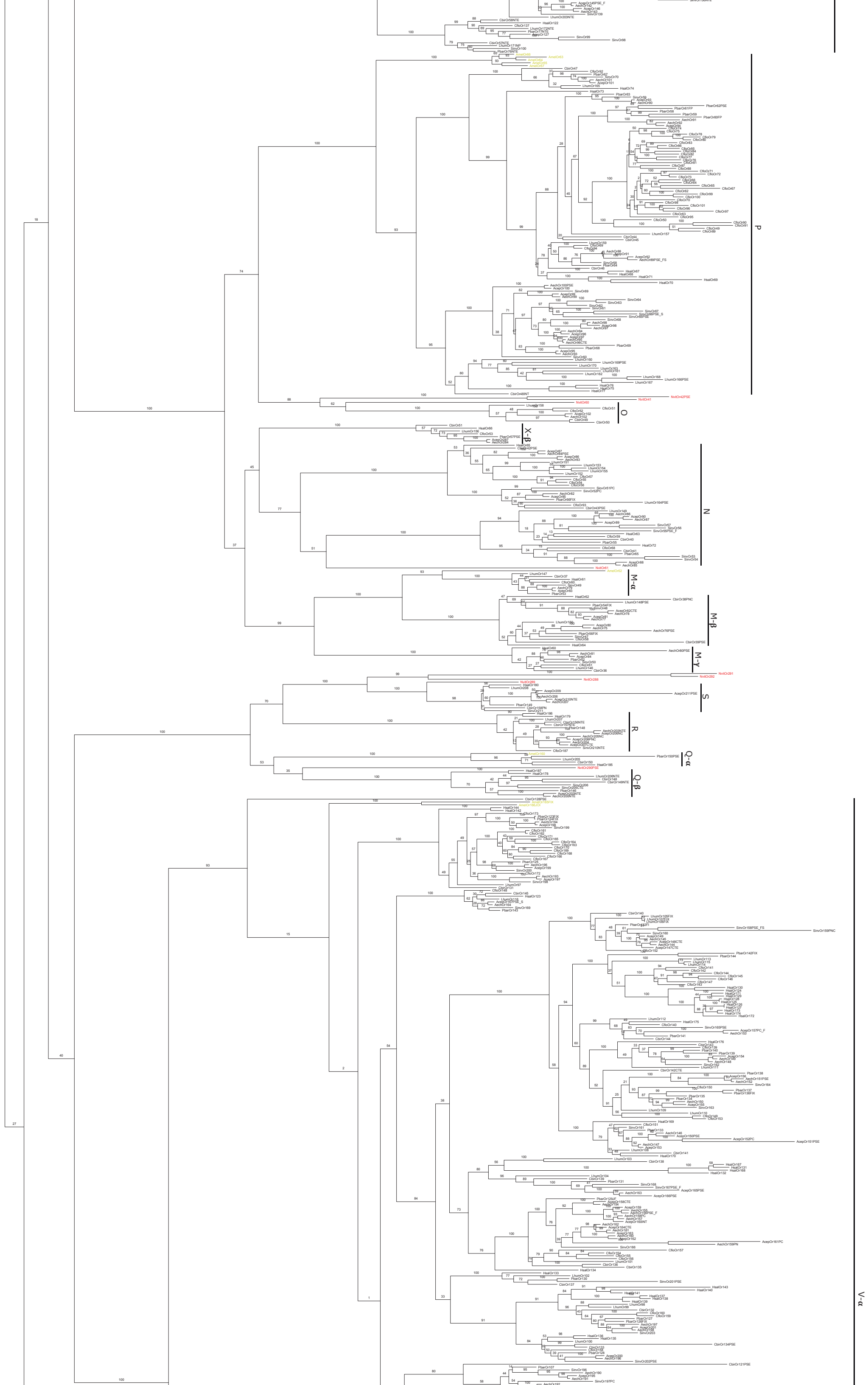
Dataset S1. Maximum likelihood phylogeny of odorant receptor genes in *Nasonia vitripennis*, *Apis mellifera*, and eight ant species. Groups consistent with being descendants of a single copy in the most recent common ancestor of ants and bees are indicated on the right. Node labels indicate bootstrap supports. Nvit = *Nasonia vitripennis*, Amel = *Apis mellifera*, Hsal = *Harpegnathos saltator*, Cbir = *Ooceraea biroi* (gene designations are maintained as “Cbir” to match the official annotation), Lhum = *Linepithema humile*, Cflo = *Camponotus floridanus*, Pbar = *Pogonomyrmex barbatus*, Sinv = *Solenopsis invicta*, Aech = *Acromyrmex echinatior*, Acep = *Atta cephalotes*.

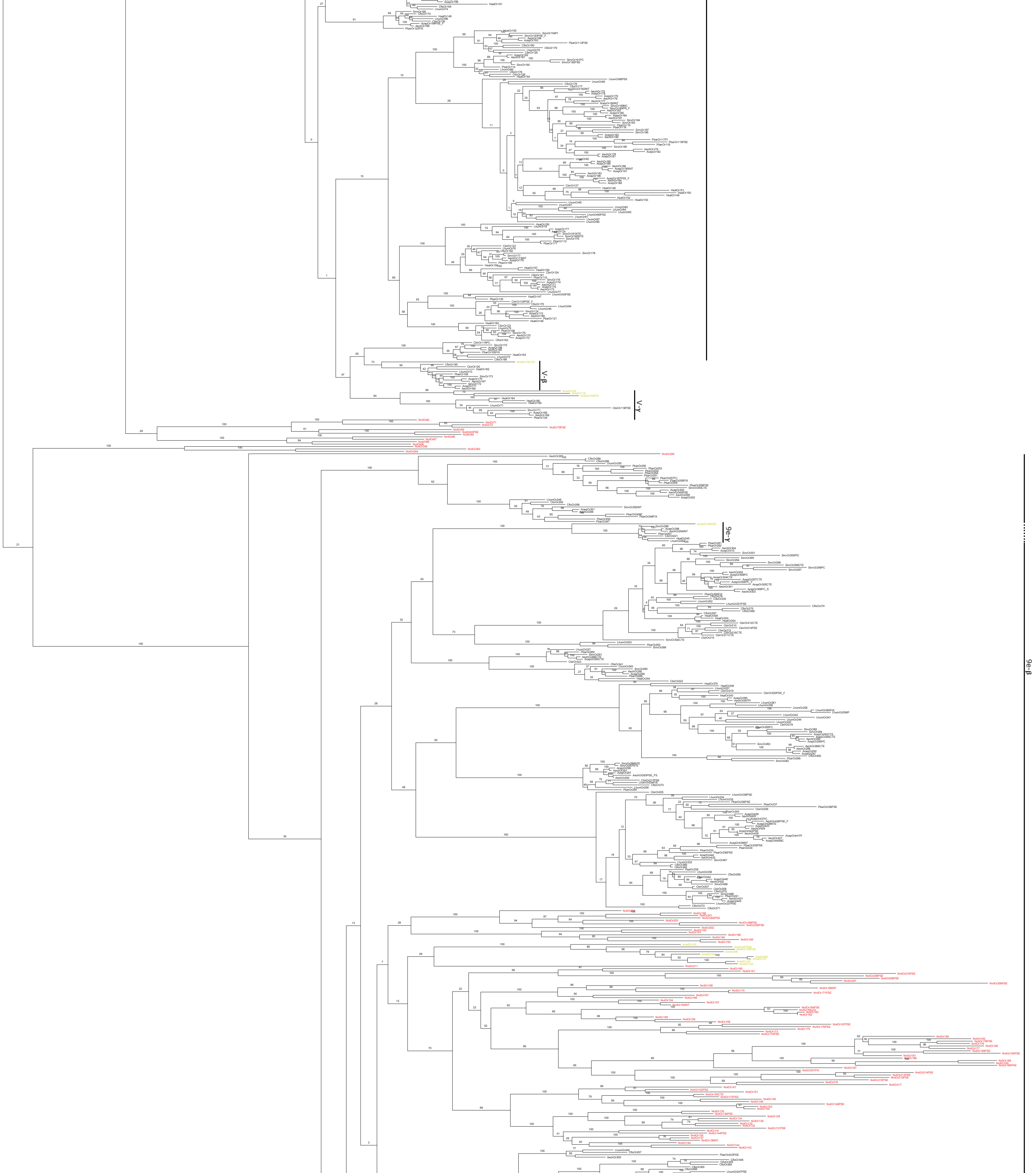

Orco
F
C
E-δ
E-γ
E-α

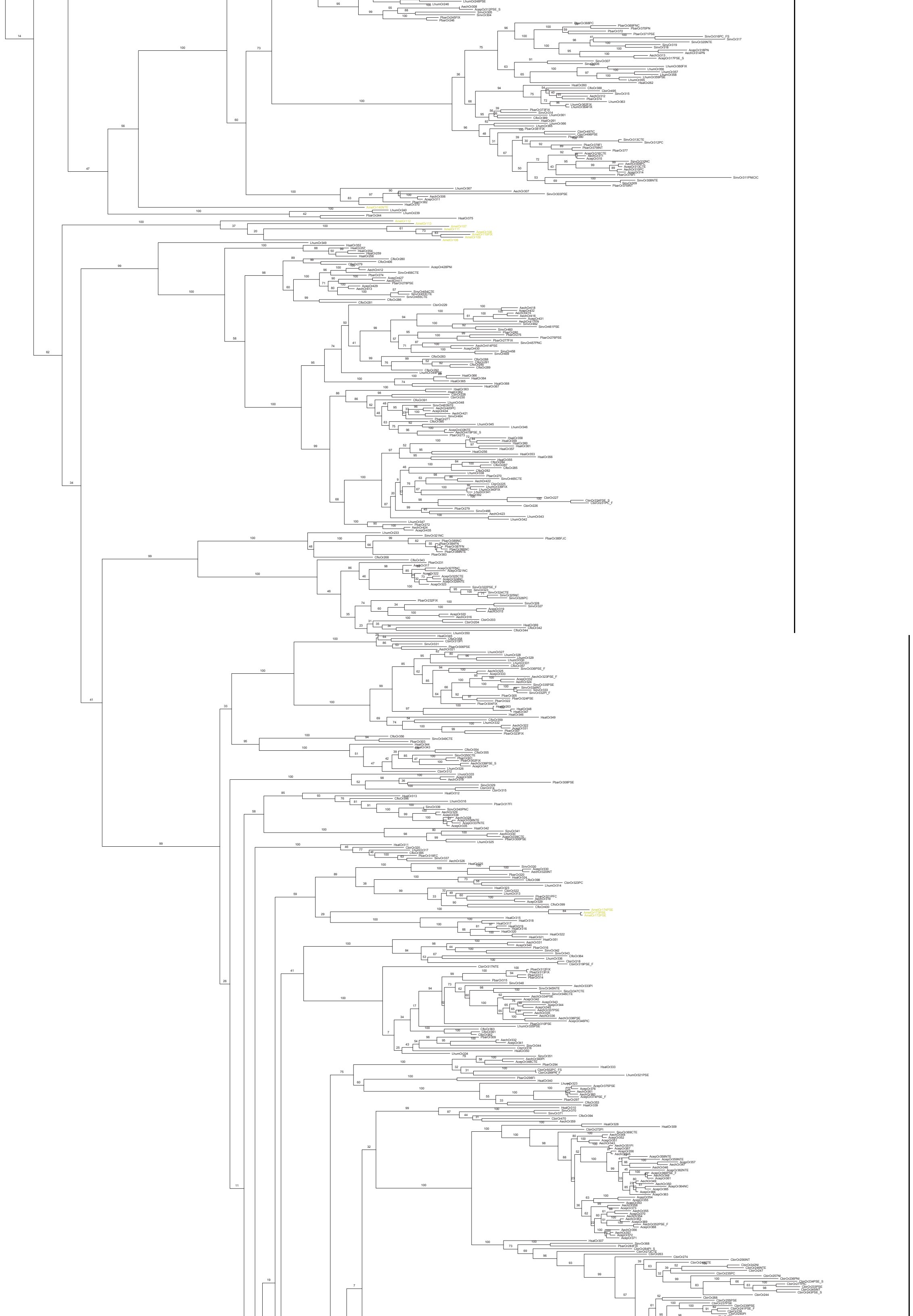

E-β
D
B-α
B-β
A
H-β
H-α
G
X-δ
X-α
X-ε

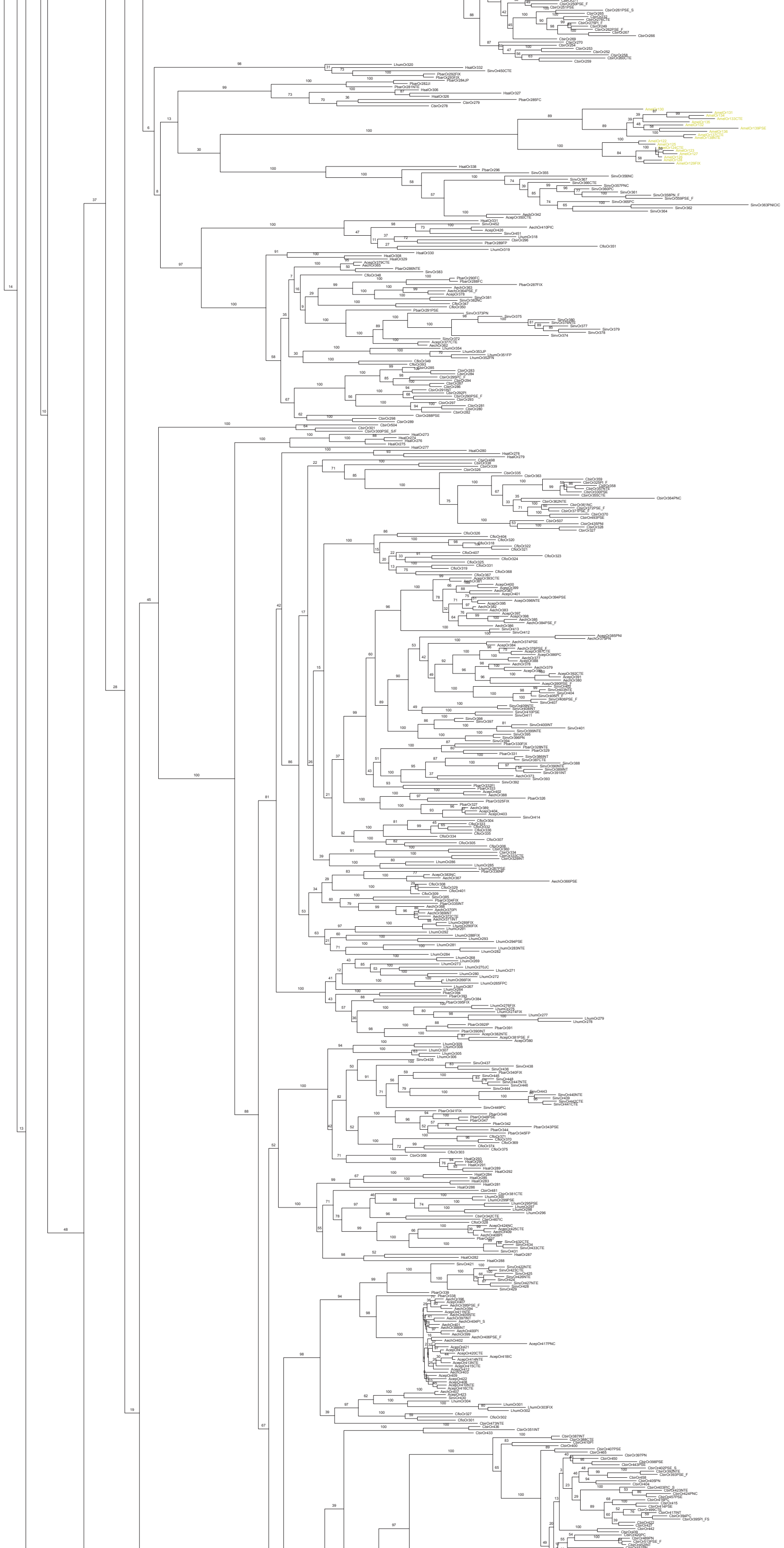

J
I
K
L-θ
L-β
L-γ
L-ζ
L-η
L-κ
L-δ
L-α


L-ι
L-ε
L-λ
T-γ
T-β
T-α
U

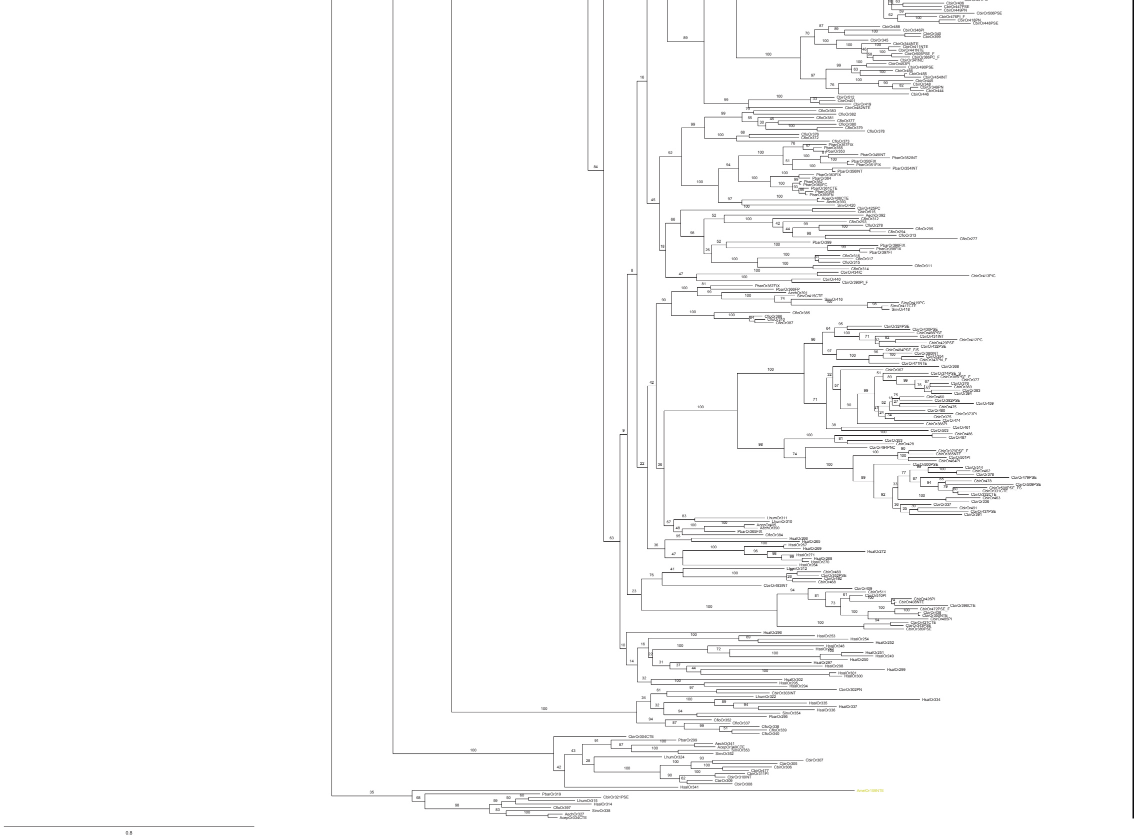

P
O
X-β
N
M-α
M-β
M-γ
S
R
Q-α
Q-β
V-α


V-β
V-γ
9e-γ
9e-β





9e-α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