

This Supplementary Information contains Supplementary Figures 1-7. The full legend for each tree is located beneath it.

Supplementary Figure 1: Maximum likelihood tree of  $\beta$ -PFTx sequences.

Supplementary Figure 2: Maximum likelihood tree of PCPDP sequences.

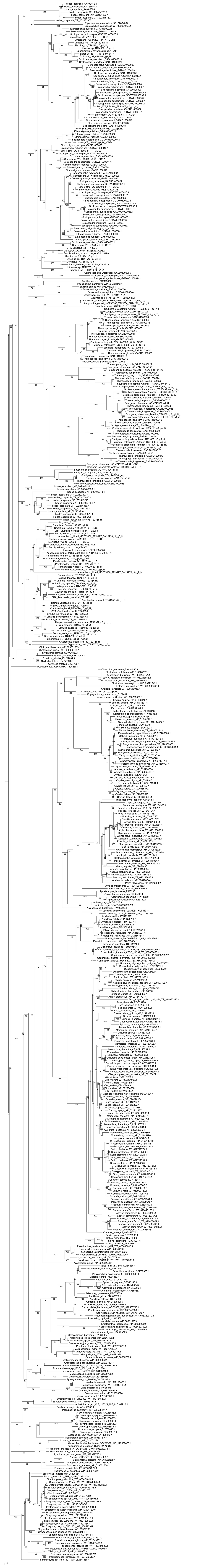
Supplementary Figure 3: Maximum likelihood tree of PAD sequences.

Supplementary Figure 4: Maximum likelihood tree of DUF3472 sequences.

Supplementary Figure 5: Maximum likelihood tree of GEOTX02 sequences.

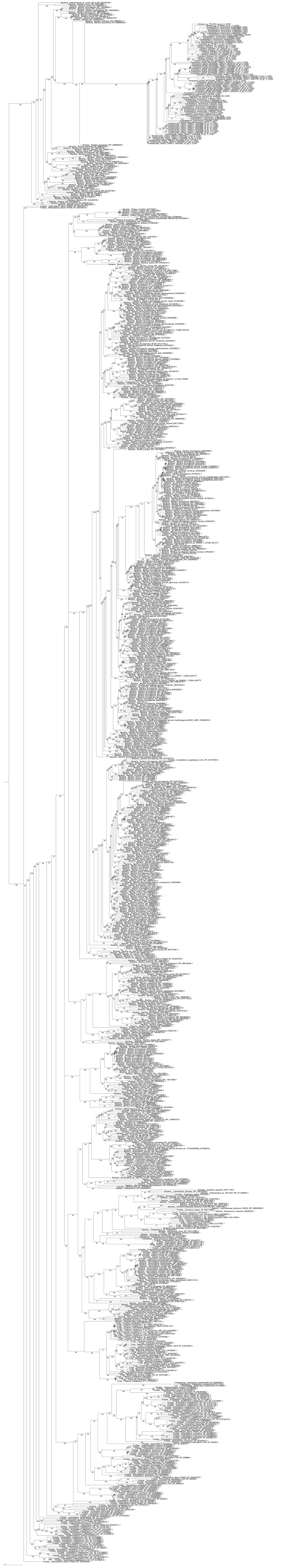
Supplementary Figure 6: Maximum likelihood tree of unchar05 sequences.

Supplementary Figure 7: Maximum likelihood tree of unchar16 sequences.



**Supplementary Fig. 1.** Maximum likelihood tree of  $\beta$ -PFTx sequences. The tree was reconstructed using the WAG+R7 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.

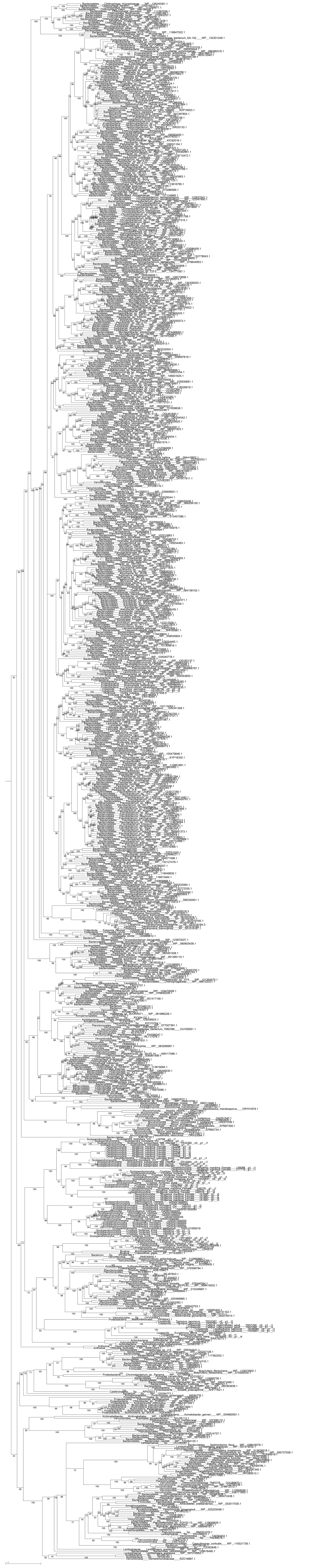






**Supplementary Fig. 2.** Maximum likelihood tree of PCPDP sequences. The tree was reconstructed using the VT+G4 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.

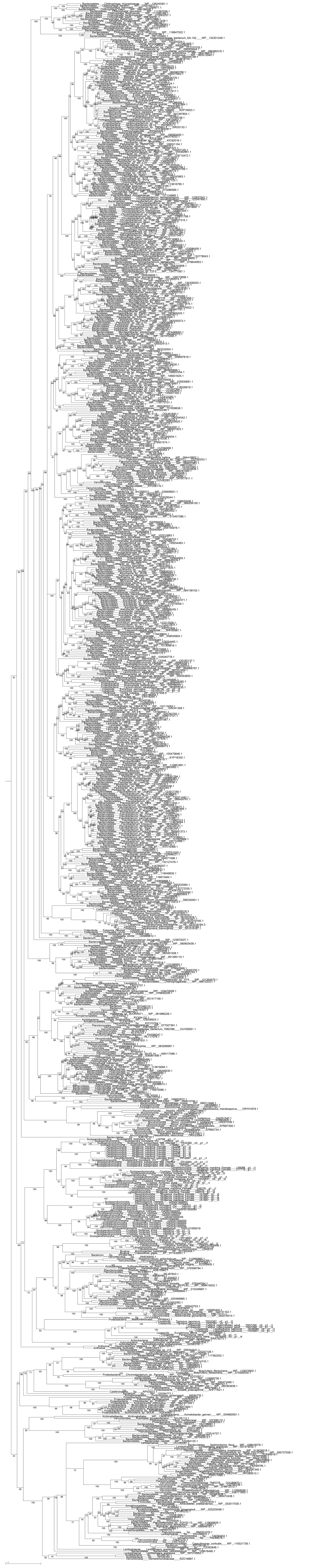






**Supplementary Fig. 3.** Maximum likelihood tree of PAD sequences. The tree was reconstructed using the WAG+G4 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.

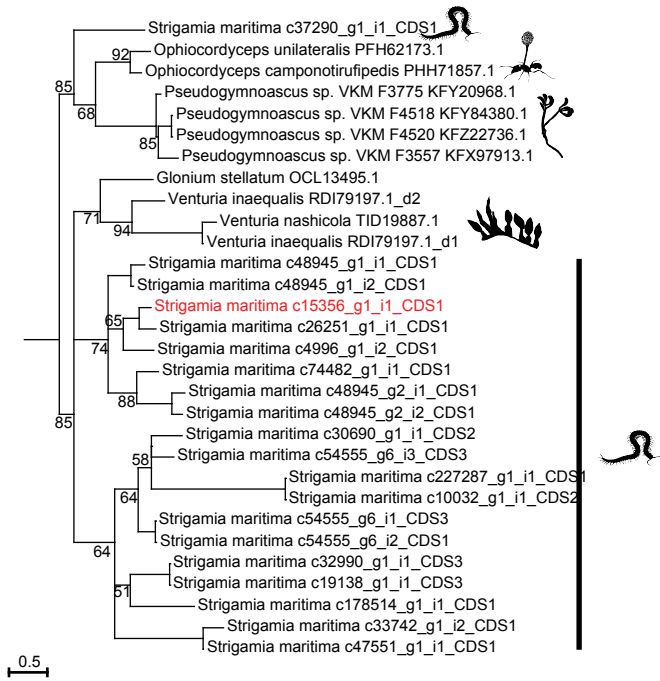






**Supplementary Fig. 4.** Maximum likelihood tree of DUF3472 sequences. The tree was reconstructed using the WAG+R10 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.







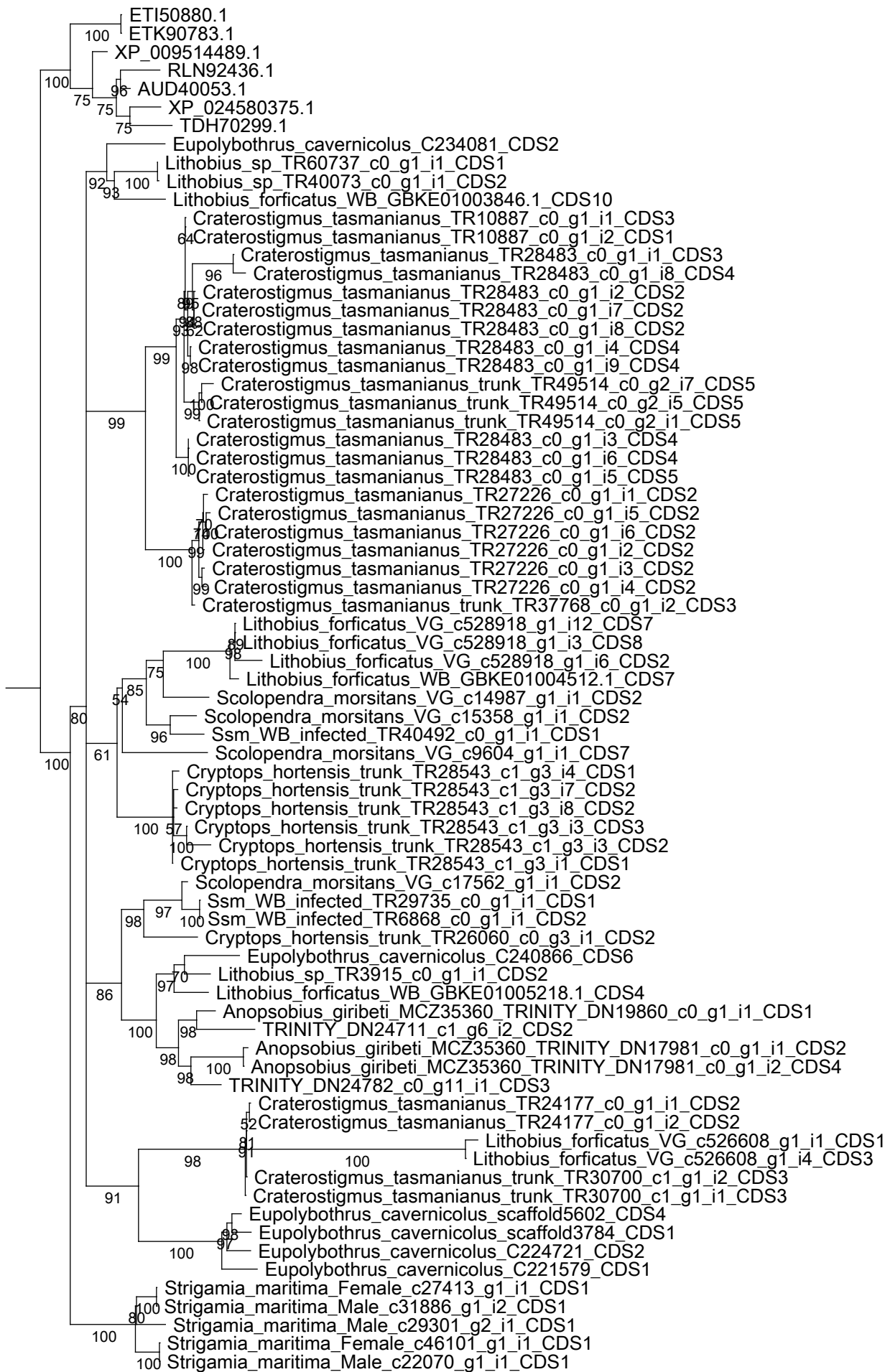
**Supplementary Fig. 5.** Maximum likelihood tree of GEOTX02 sequences. The sequence in red is present in both the venom gland transcriptome and venom proteome. The tree was reconstructed using the VT+I+G4 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.





**Supplementary Fig. 6.** Maximum likelihood tree of unchar05 sequences. The tree was reconstructed using the WAG+R5 model and is displayed as midpoint rooted. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.





1.0

**Supplementary Fig. 7.** Maximum likelihood tree of unchar16 sequences. The tree was reconstructed using the VT+R3 model and is rooted with the oomycete sequences. Bootstrap support values are shown at each node. Nodes with support <50% are collapsed into polytomies.