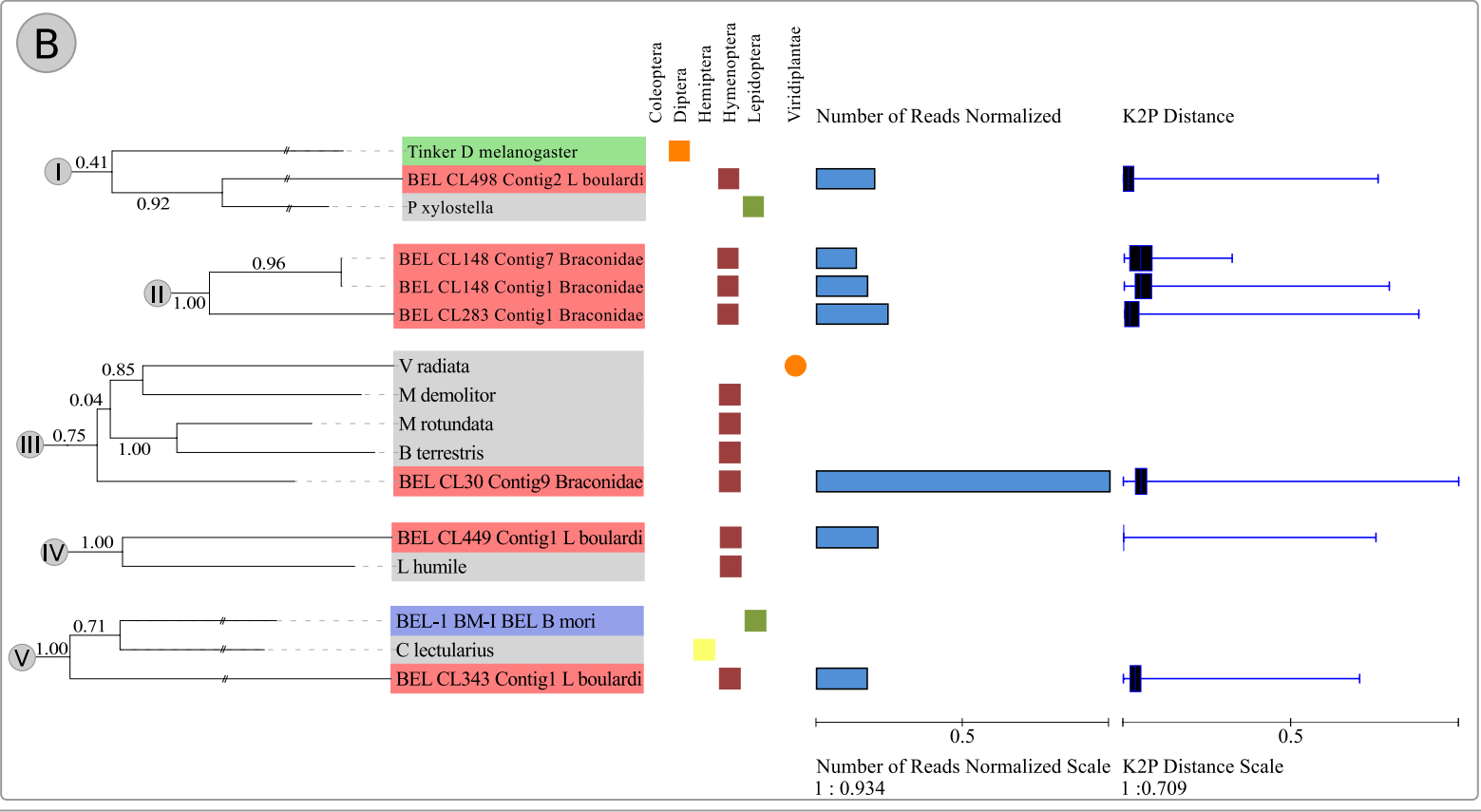
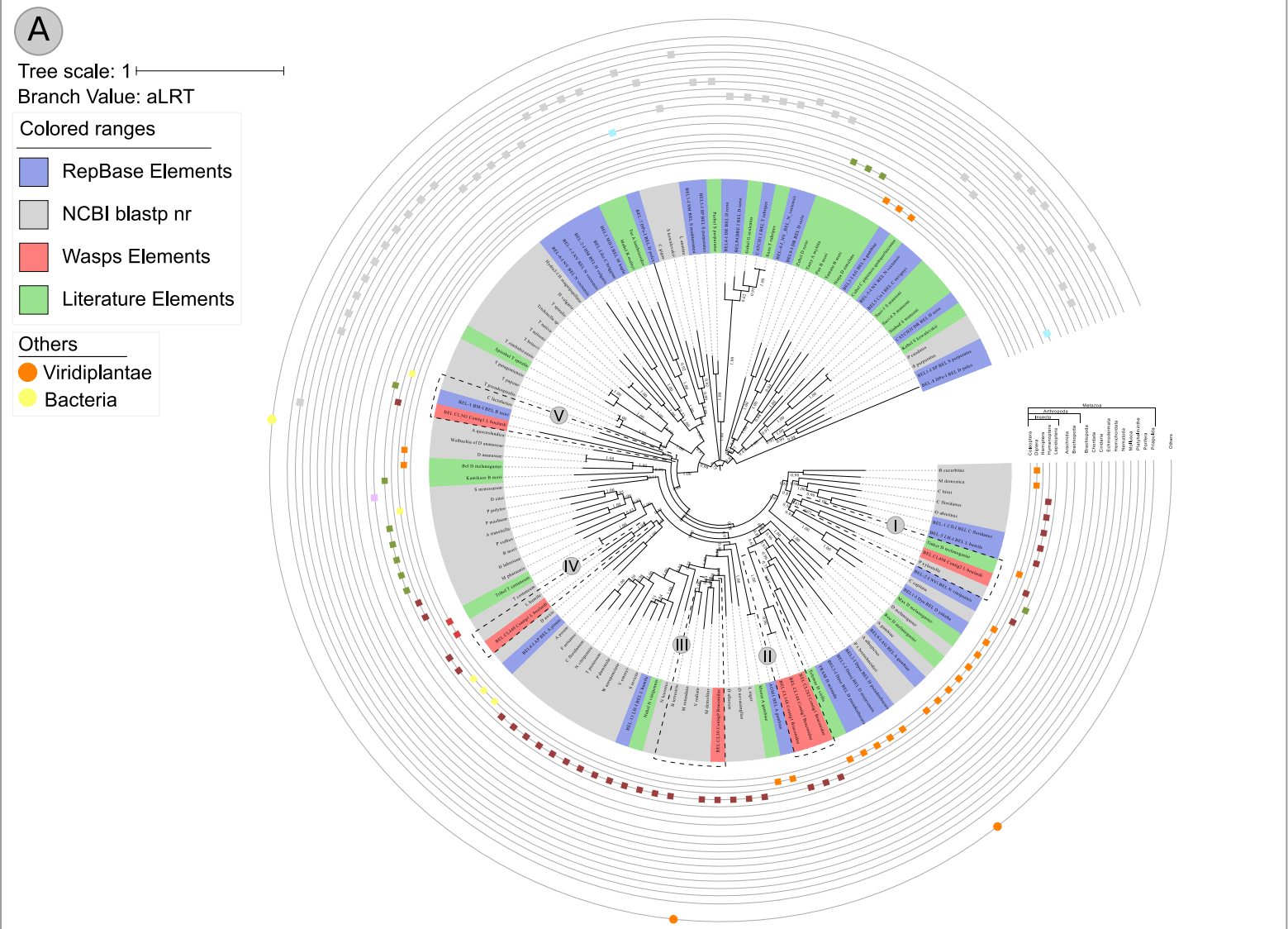
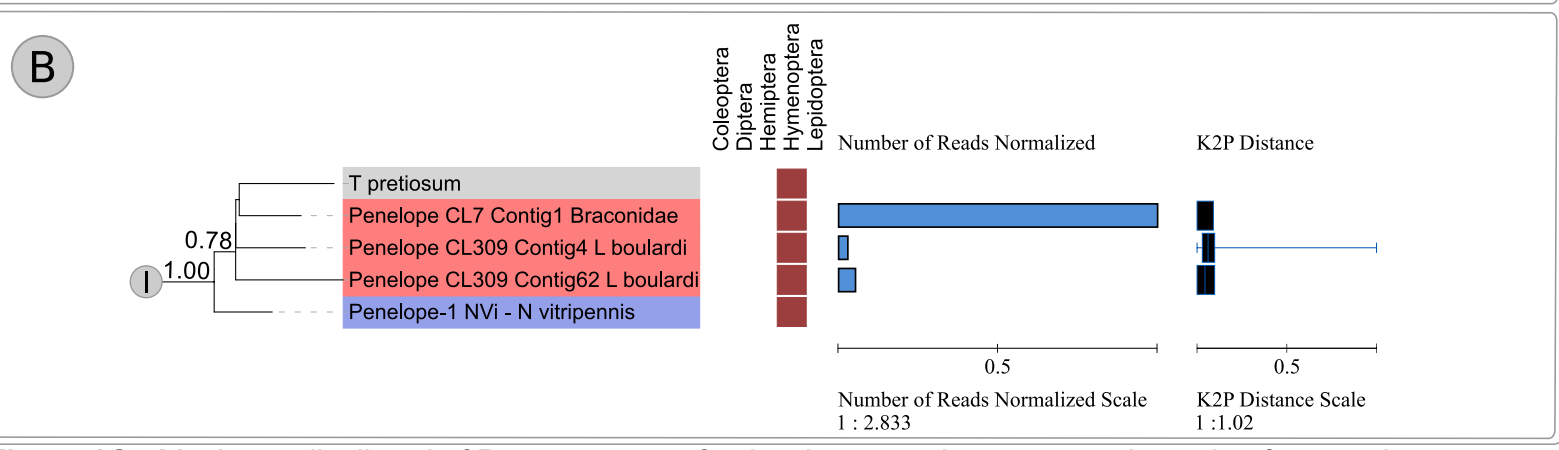
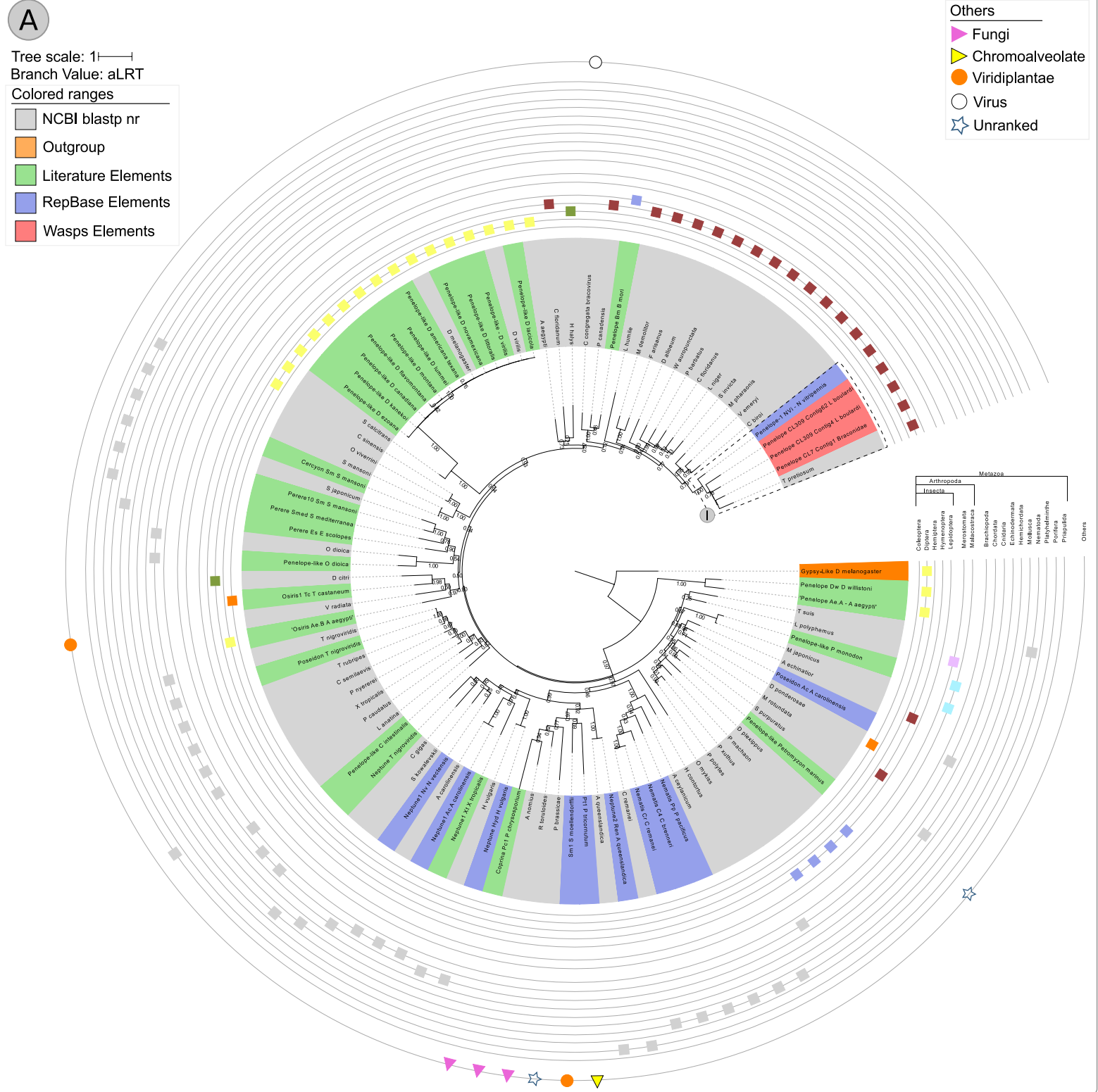


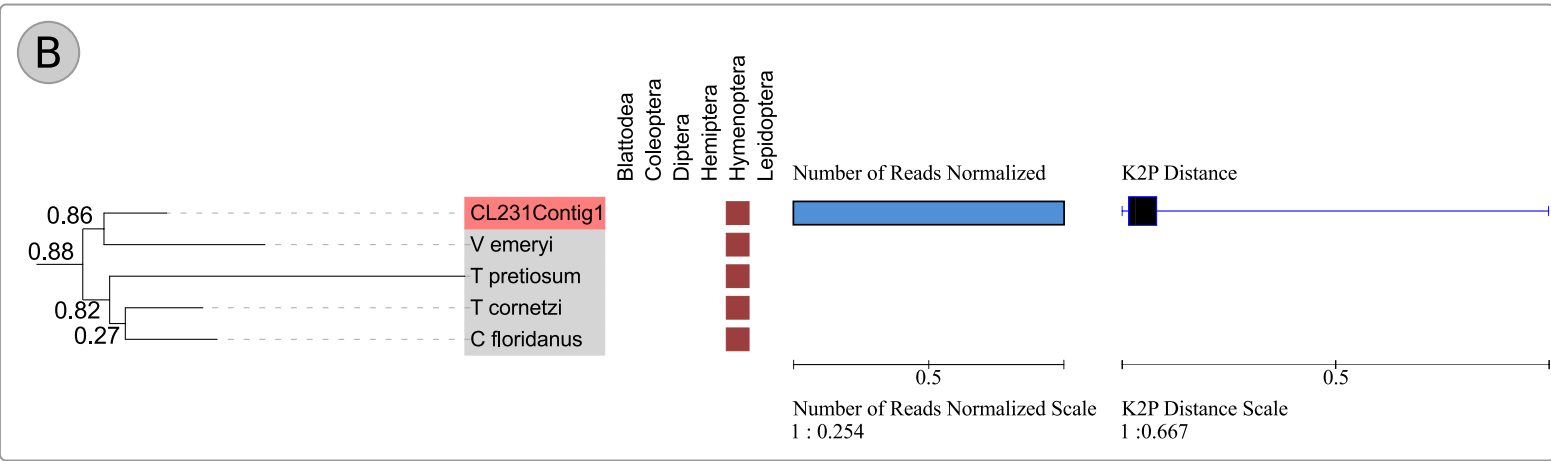
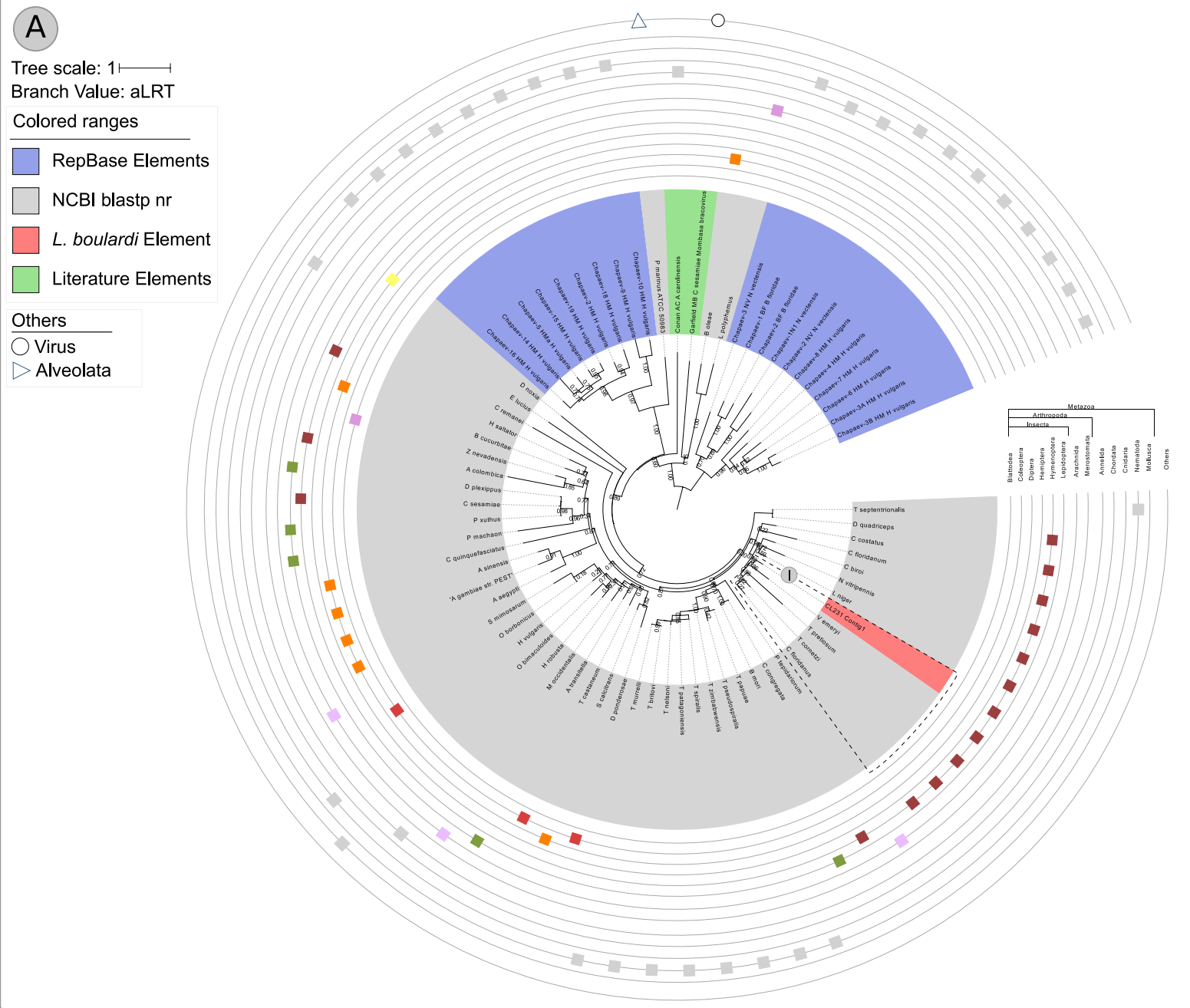
**Figure 1S** - Maximum likelihood of L2 superfamily phylogenetic reconstruction using full protein sequences from Repbase and NCBI search along with L2 sequence from both wasps. Tip colors represent sequences recovered from RepBase - blue and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outermost bars from part A. Online data about L2 phylogeny is available on: <https://itol.embl.de/tree/2001321431101691510857774>



**Figure 2S** - Maximum likelihood of Bel superfamily phylogenetic reconstruction using full protein sequences from Repbase, literature and NCBI search along with Bel sequence from both wasps. Tip colors represent sequences recovered from RepBase - blue, from the literature - green and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outermost bars from part A. Online data about Bel phylogeny is available on: <https://itol.embl.de/tree/200133261027121507571775>



**Figure 3S** - Maximum likelihood of Penelope superfamily phylogenetic reconstruction using full protein sequences from Repbase, literature and NCBI search along with Penelope sequence from both wasps. Tip colors represent sequences recovered from RepBase - blue, from the literature - green and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoozomed one clade highlighted in the outermost bars from part A. Online data about Penelope phylogeny is available on: <https://itol.embl.de/tree/200133261039931510144697>



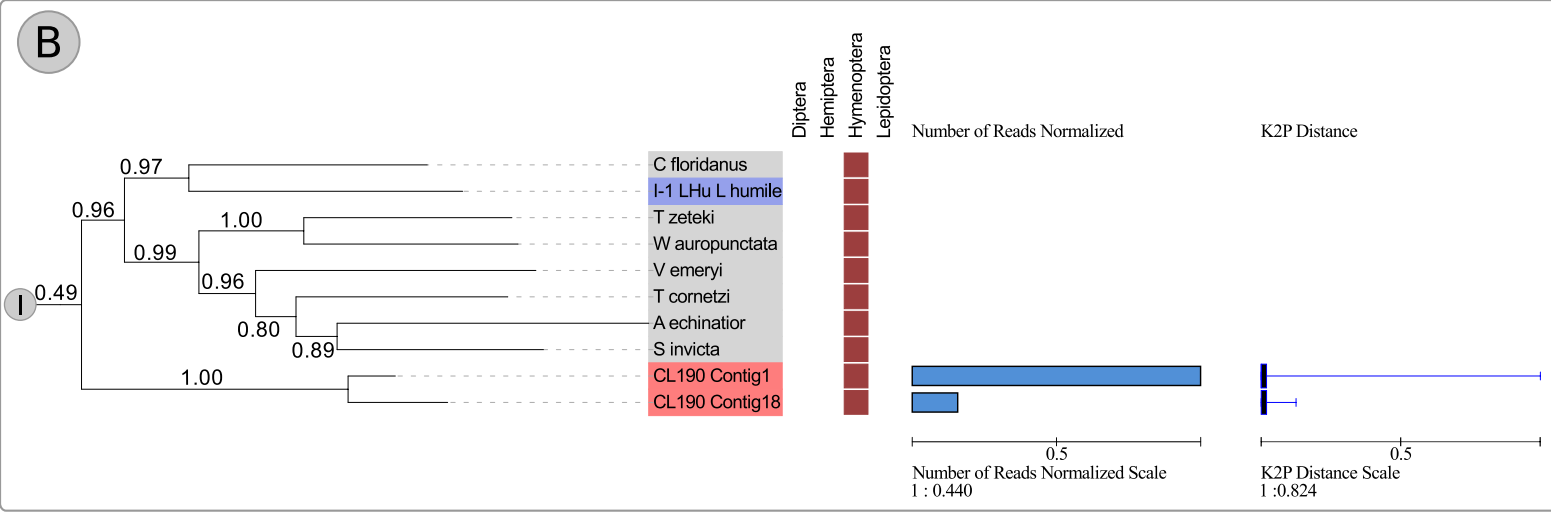
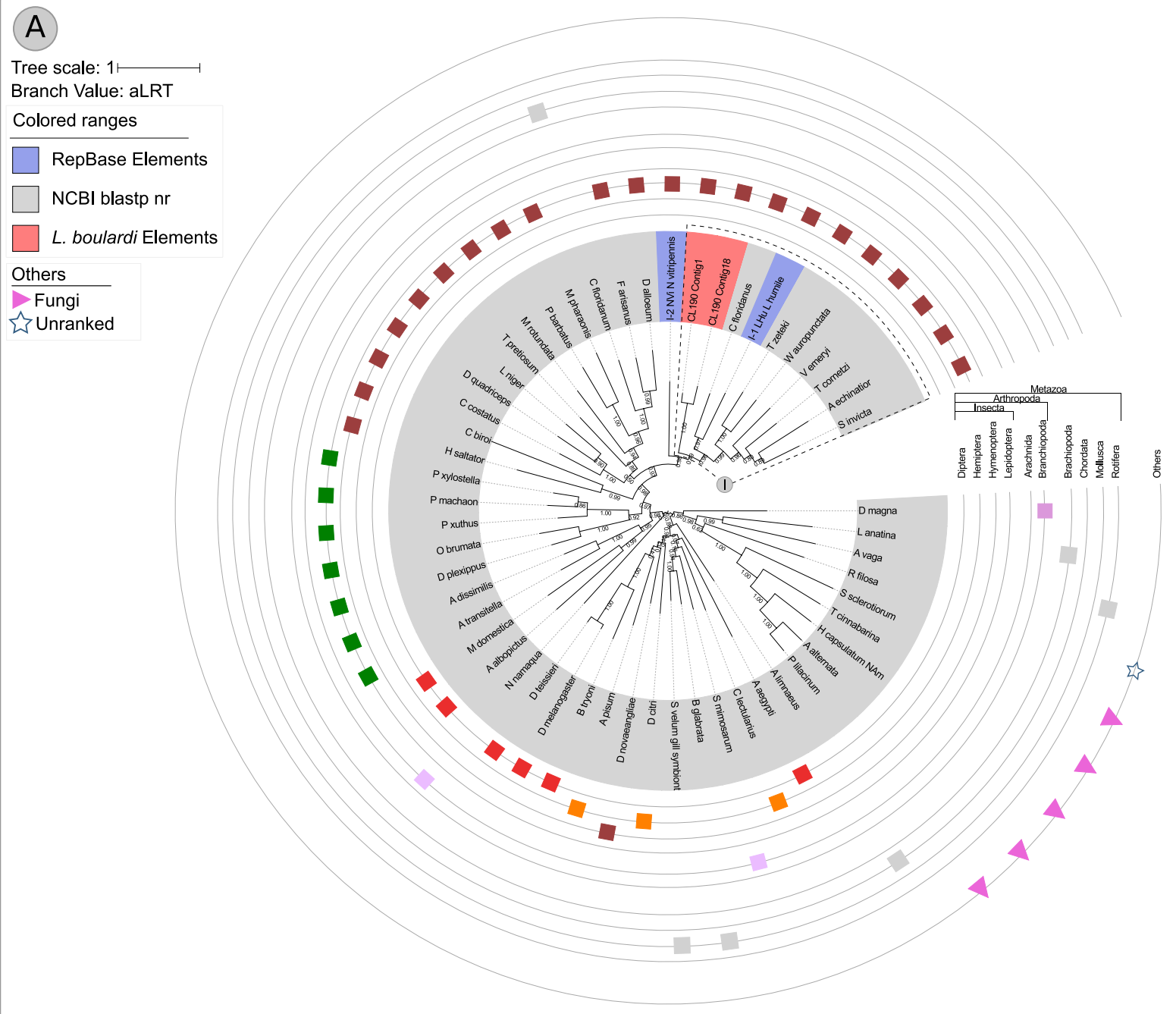
**Figure 4S** - Maximum likelihood of Chapaev superfamily phylogenetic reconstruction using full protein sequences from Repbase, literature and NCBI search along with Chapaev sequence from *Leptopilina bouvardi*. Tip colors represent sequences recovered from RepBase - blue, from the literature - green and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outermost bars from part A. Online data about Chapaev phylogeny is available on: <https://itol.embl.de/tree/2001332610128841509543832>

**A**

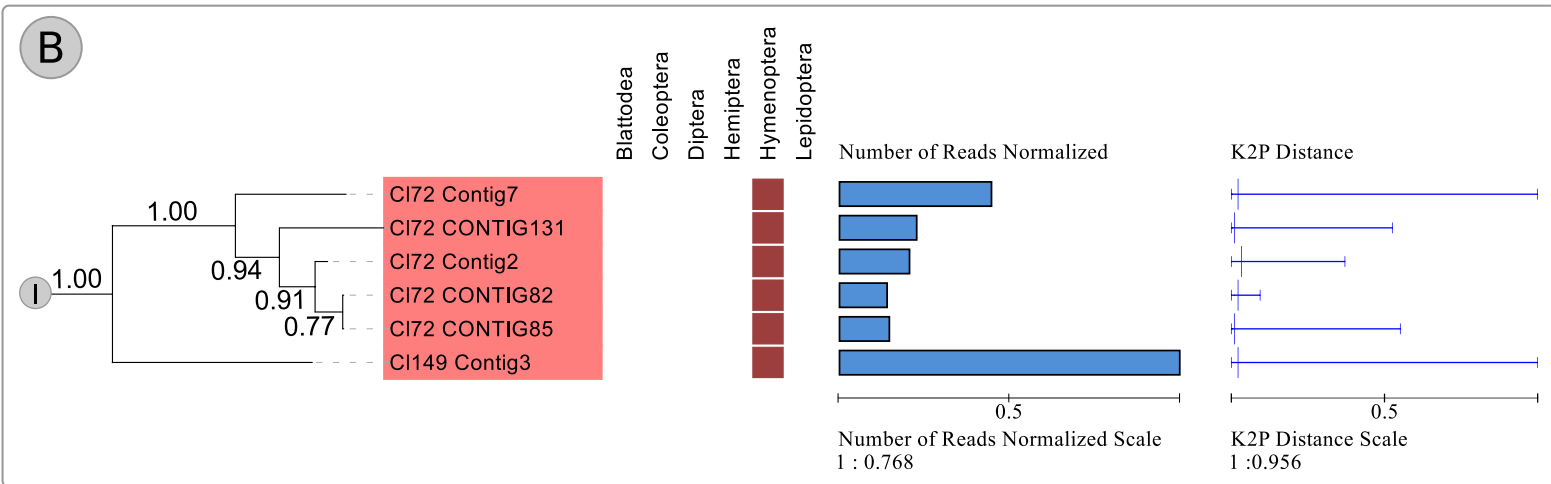
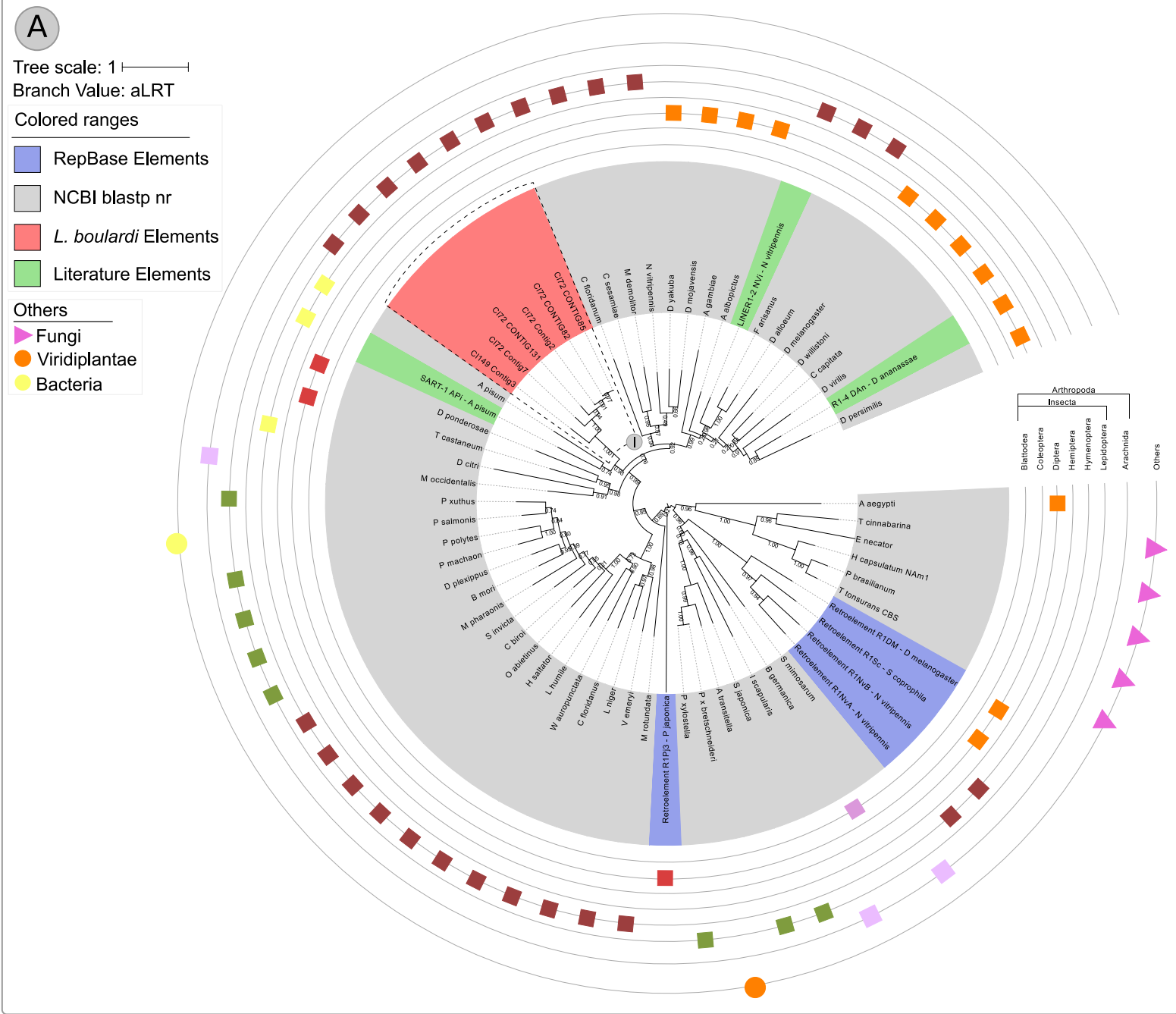
Tree scale: 1—  
 Branch Value: aLRT  
 Colored ranges  
 RepBase Element  
 NCBI blastp nr  
*L. boulandi* Element  
 Others  
 Fungi  
 Unranked

**B**

**Figure 5S** - Maximum likelihood of *Loa* superfamily phylogenetic reconstruction using full protein sequences from Repbase and NCBI search along with *Loa* sequence from *Leptopilina boulandi*. Tip colors represent sequences recovered from RepBase - blue, and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outer-most bars from part A. Online data about *Loa* phylogeny is available on: <https://itol.embl.de/tree/2001321431256491510934880>



**Figure 6S** - Maximum likelihood of I superfamily phylogenetic reconstruction using full protein sequences from Repbase and NCBI search along with I sequence from *Leptopilina bouvardi*. Tip colors represent sequences recovered from RepBase - blue, and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outermost bars from part A. Online data about I phylogeny is available on: <https://itol.embl.de/tree/189354019179191511721260>



**Figure 7S** - Maximum likelihood of R1 superfamily phylogenetic reconstruction using full protein sequences from Repbase and NCBI search along with R1 sequence from *Leptopilina bouvardi*. Tip colors represent sequences recovered from RepBase - blue, Literature - green and NCBI database - black. Triangles over nodes are proportional to the node support accessed by aLRT estimates. A) Full phylogenetic tree and B) Zoomed one clade highlighted in the outermost bars from part A. Online data about R1 phylogeny is available on: <https://itol.embl.de/tree/189354019310111511728935t>