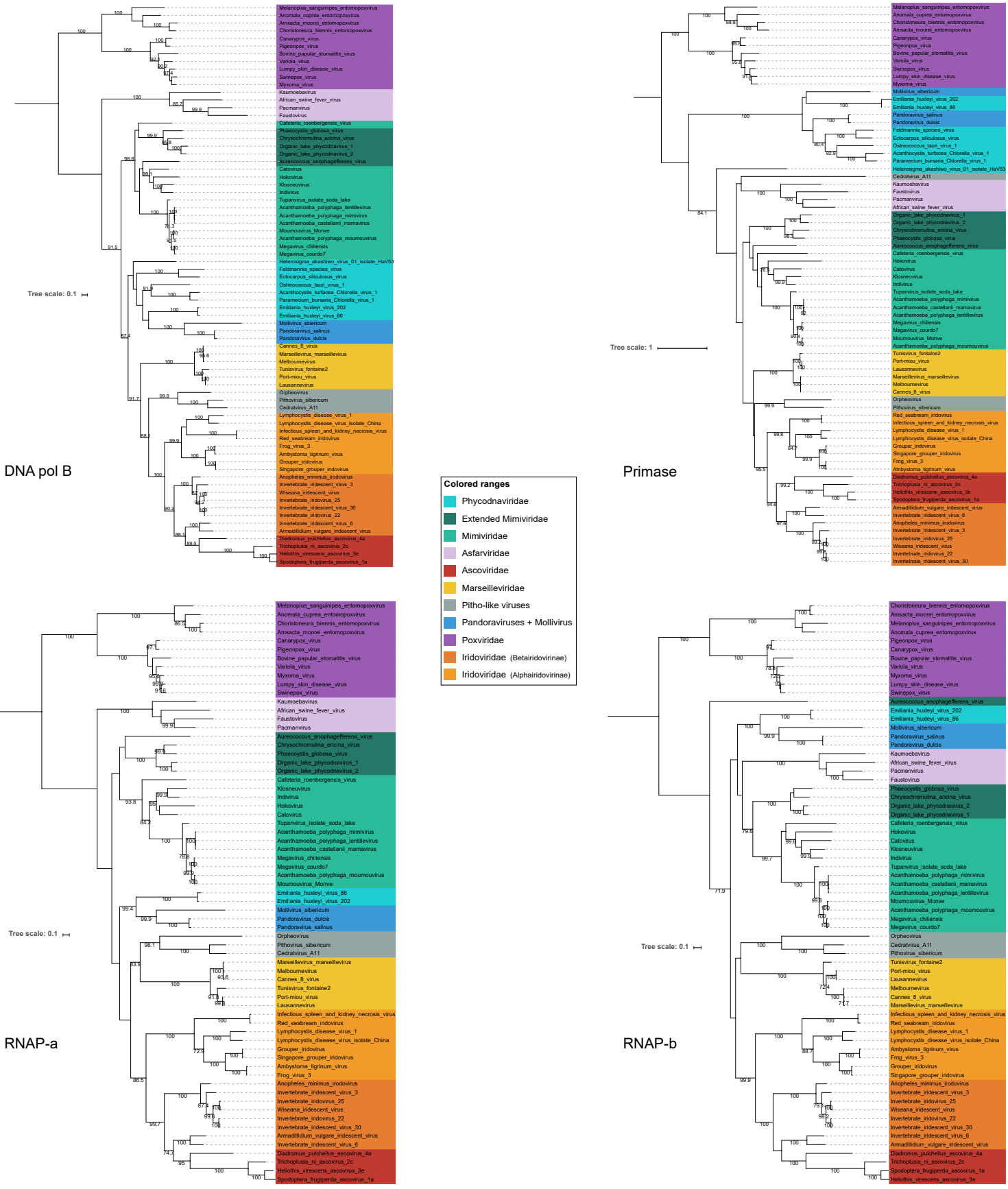
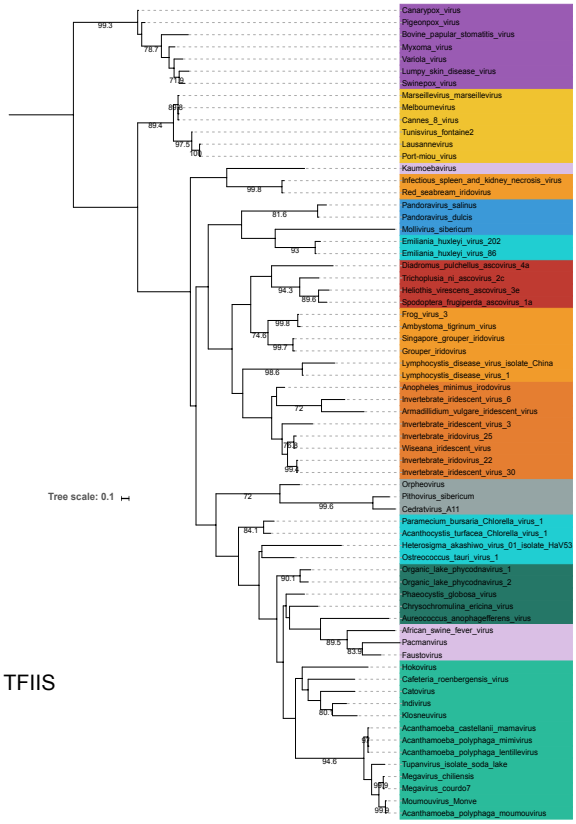
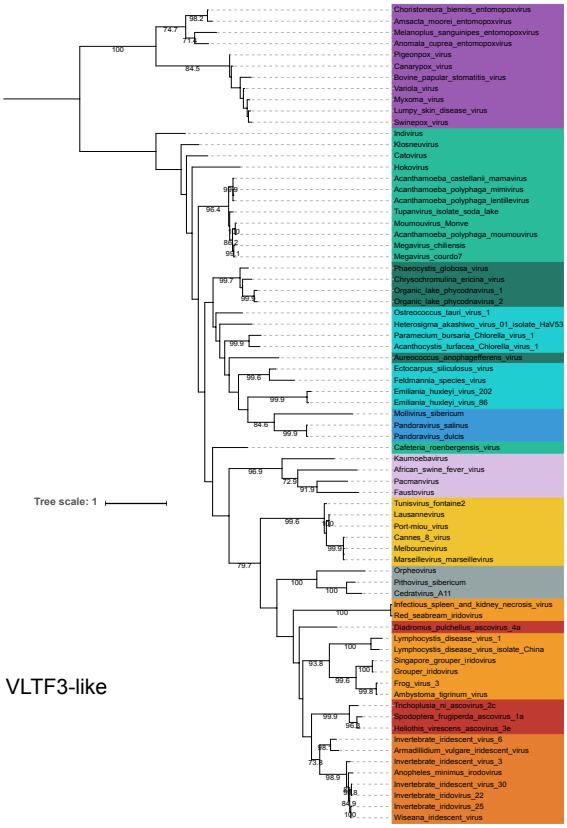


Maximum likelihood (ML) single-protein trees of the 8 core genes from the NCLDVs. The *Poxviridae* have been used as the outgroup to root the trees. The scale-bars indicate the average number of substitutions per site. Values on branches represent support calculcated by nonparametric bootstrap; only supports superior to 70% are shown.



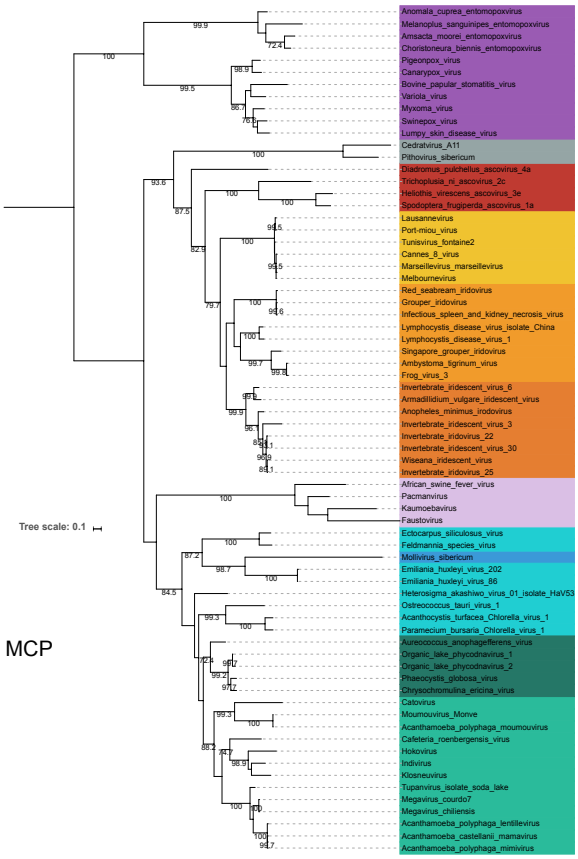
TFIIS



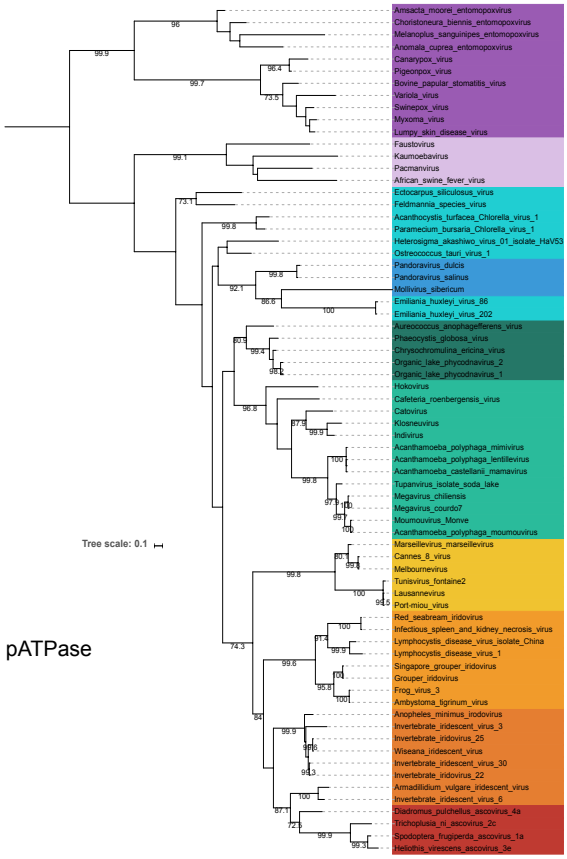
VLTF3-like

Colored ranges

- Phycodnaviridae
- Extended Mimiviridae
- Mimiviridae
- Asfarviridae
- Ascoviridae
- Marseilleviridae
- Pitho-like viruses
- Pandoraviruses + Mollivirus
- Poxviridae
- Iridoviridae (Betairidovirinae)
- Iridoviridae (Alphairidovirinae)



MCP



pATPase