

Phylogenetic trees based on the VETF, mRNA and DNA topoisomerase II proteins.

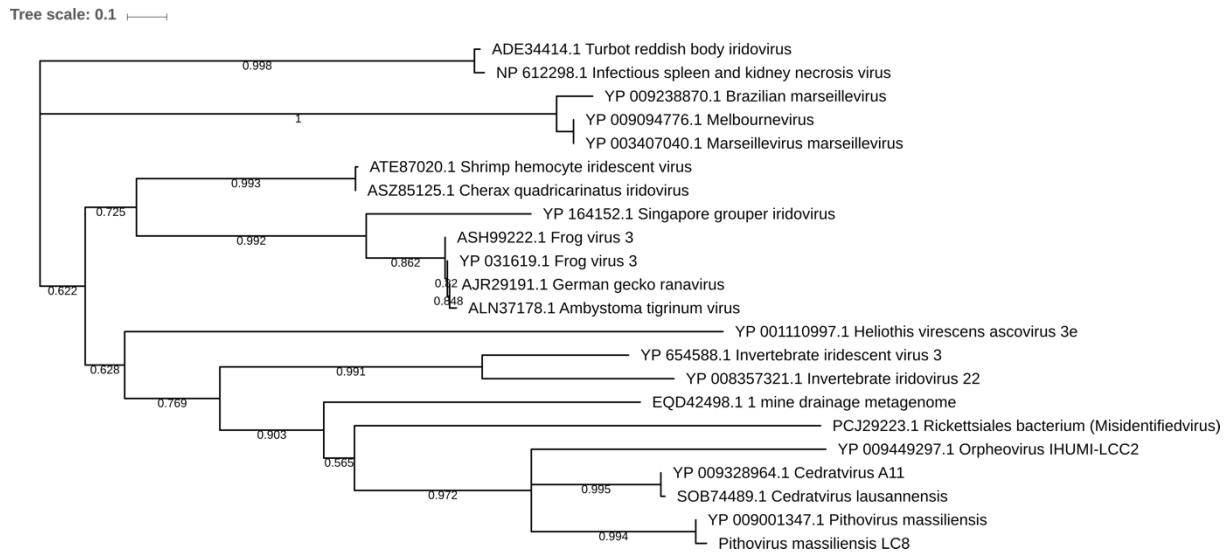


Figure S1: Phylogenetic tree based on the Very Early Transcription Factor protein.

Maximum-likelihood tree based on 454 positions. We deleted branches with a bootstrap value inferior at 0.5. Muscle program was used with standard parameter. The tree was built using FastTree program with JTT model.

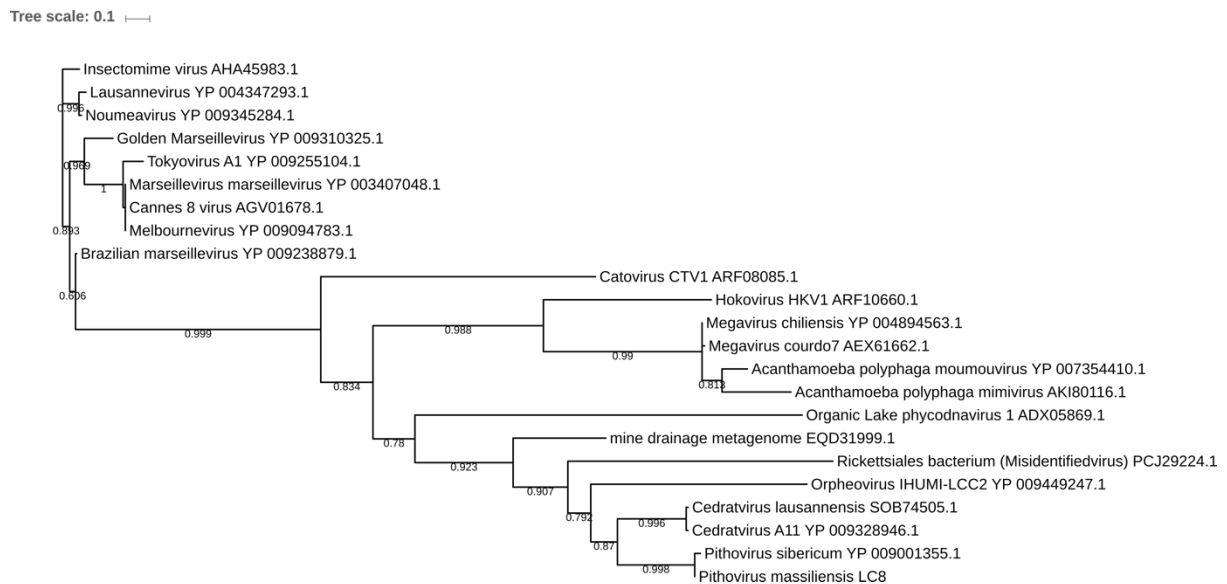


Figure S2: Phylogenetic tree based on the mRNA capping enzyme protein.

Maximum-likelihood tree based on 507 positions. We deleted branches with a bootstrap value inferior at 0.5. Muscle program was used with standard parameter. The tree was built using FastTree program with JTT model.

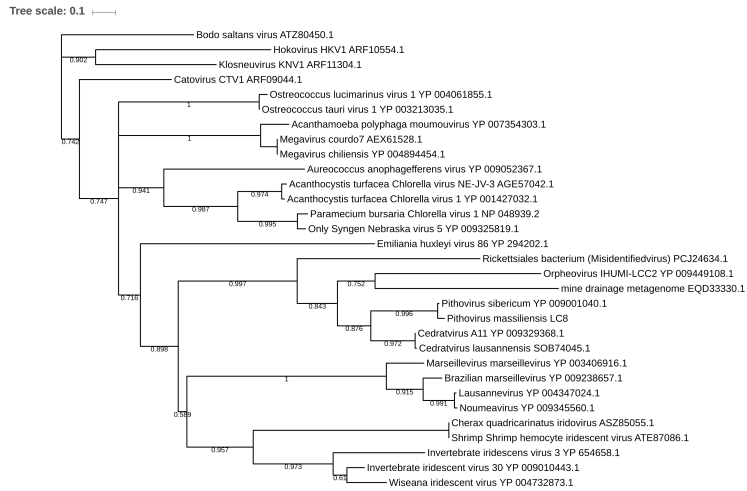


Figure S3: Phylogenetic tree based on the DNA topoisomerase IIA protein.

Maximum likelihood tree based on 280 positions. We deleted branches with a bootstrap value inferior at 0.5. Muscle program was used with standard parameter. The tree was built using FastTree program with JTT model.