

Supplemental material associated with Van Doorslaer et al., 2018

Supplemental Figure 1 Comparison of the eel associated viruses

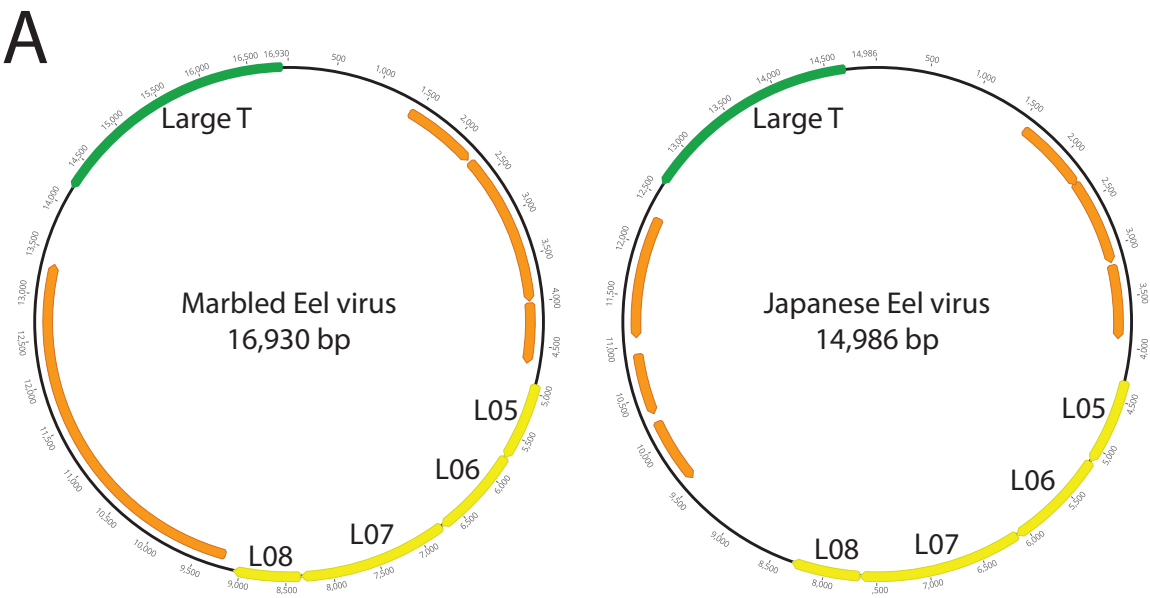
- (A) Genome cartoon of the Marbled and Japanese eel viruses. The T-Ag like ORF is highlighted in green. The conserved L05, L06, L07, and L08 ORFs are shown in yellow. ORFs (larger than 500 nt) unique to each virus are identified in orange.
- (B) graphical representation of the regions of similarity between the L05, L06, L07, and L08 proteins of the Japanese and Marbled eel viruses. Blots were generated using dotmatcher (EMBOSS 6.5.7 and [1,2]) as implemented in Geneious 10.2.2 [3]. The BLOSUM62 matrix with window size = 20, and Threshold = 23 was used.

Supplemental Figure 2 Comparison of the eel associated viruses

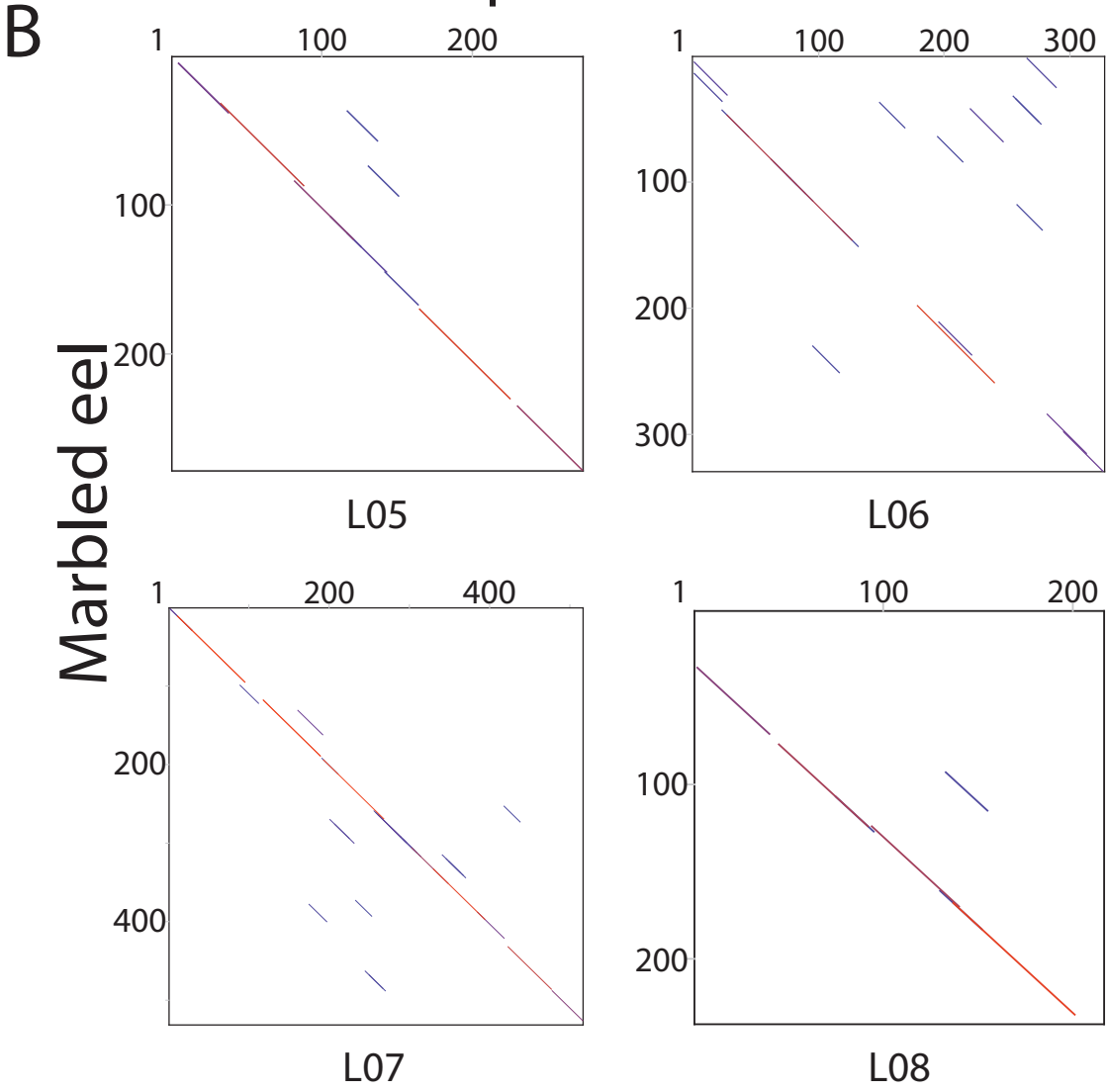
Maximum likelihood phylogenetic trees of individual protein trees (A) T-Ag, (B) VP1, and (C) VP2. The trees were rooted using the amniote PyV clade. These trees represent the unrooted, non-pruned versions of the trees in figure 2.

1. **Hancock JM, Bishop MJ.** EMBOSS (The European Molecular Biology Open Software Suite). In: *Dictionary of Bioinformatics and Computational Biology*. 2004.
2. **Rice P, Longden I, Bleasby A.** EMBOSS: the European Molecular Biology Open Software Suite. *Trends Genet* 2000;16:276–277.
3. **Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, et al.** Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* 2012;28:1647–1649.

Figure S1



Japanese eel



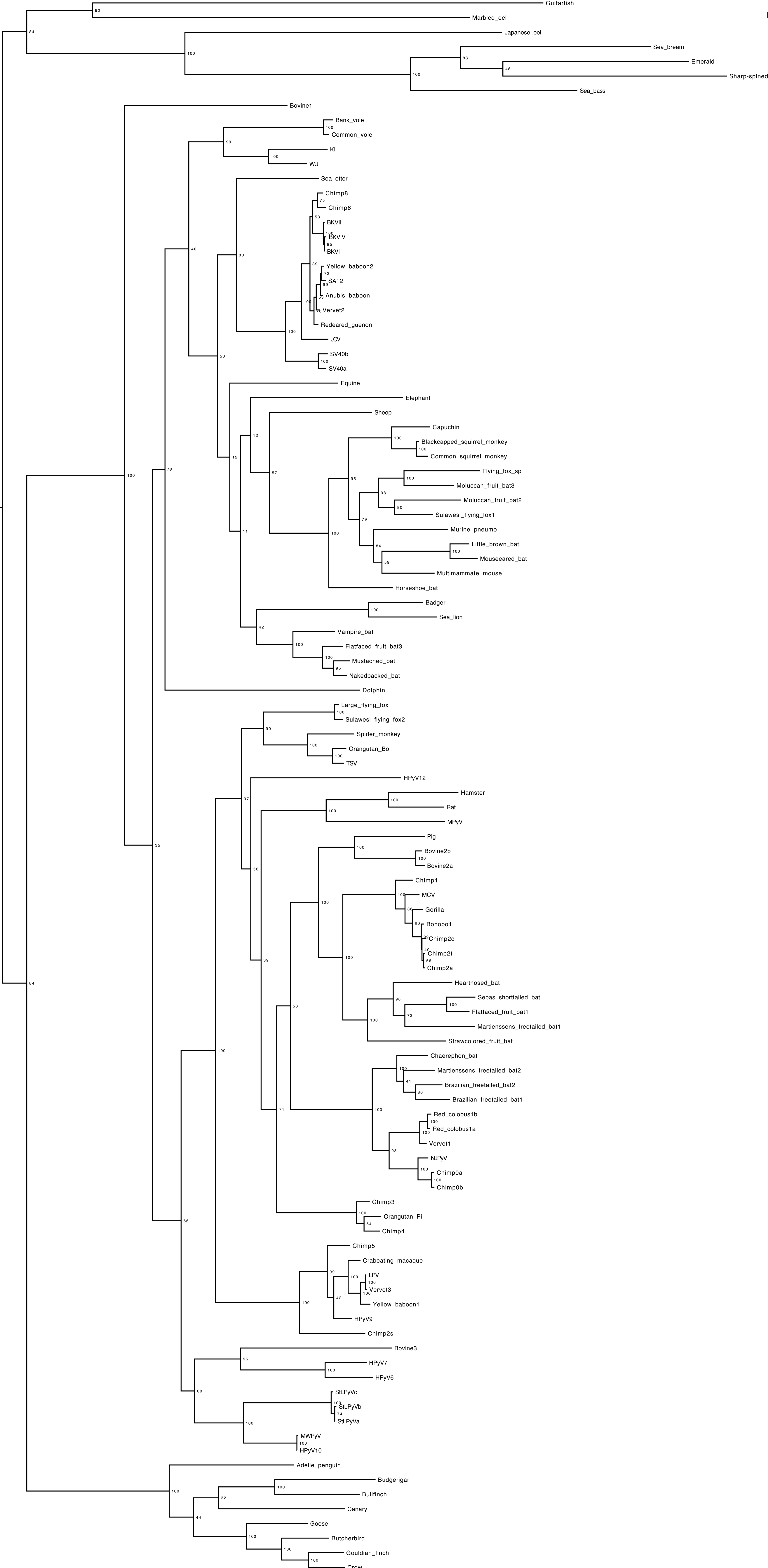


Figure S2B

