Additional figures

Endogenous virophages populate the genomes of a marine heterotrophic flagellate

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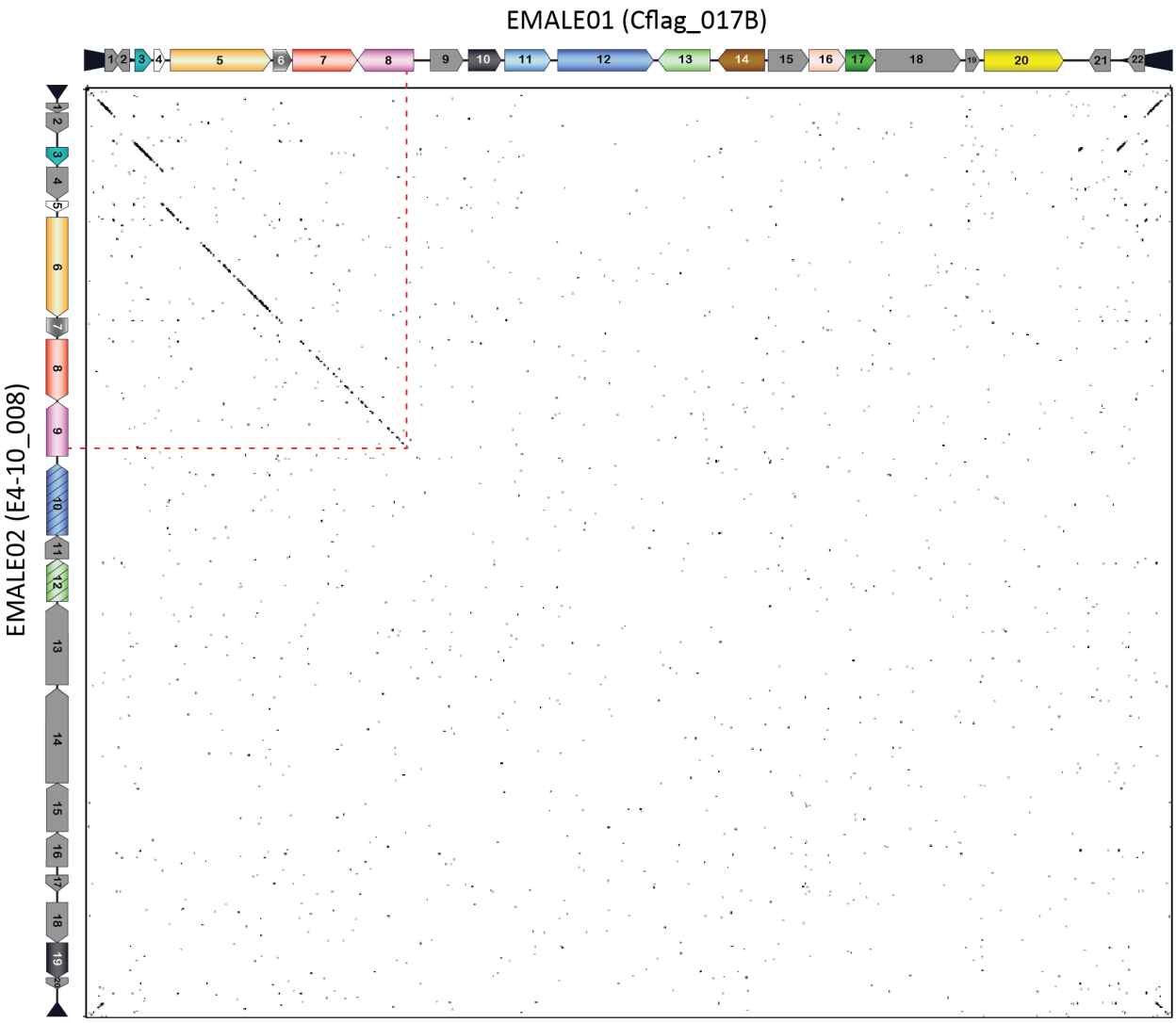
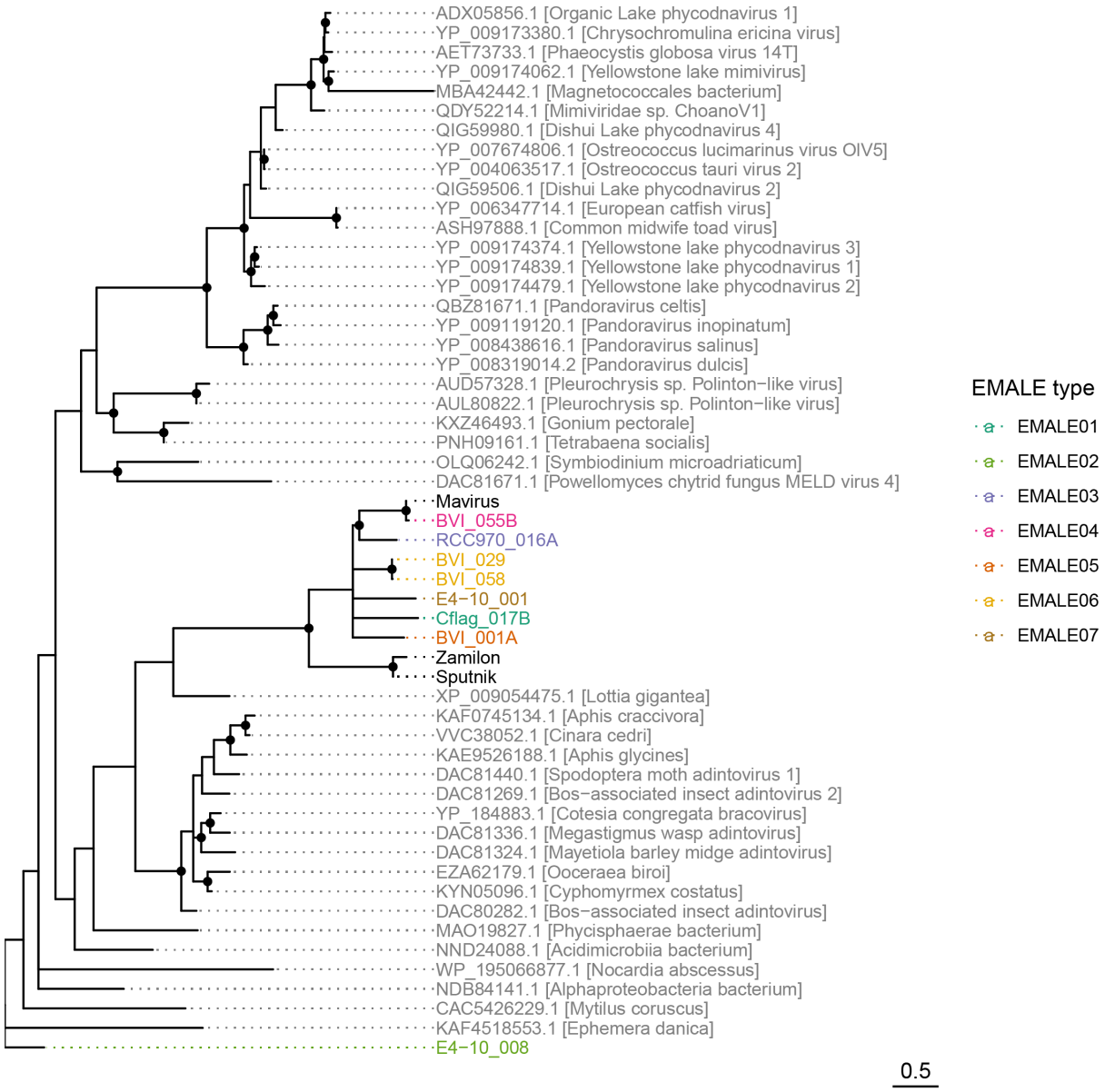
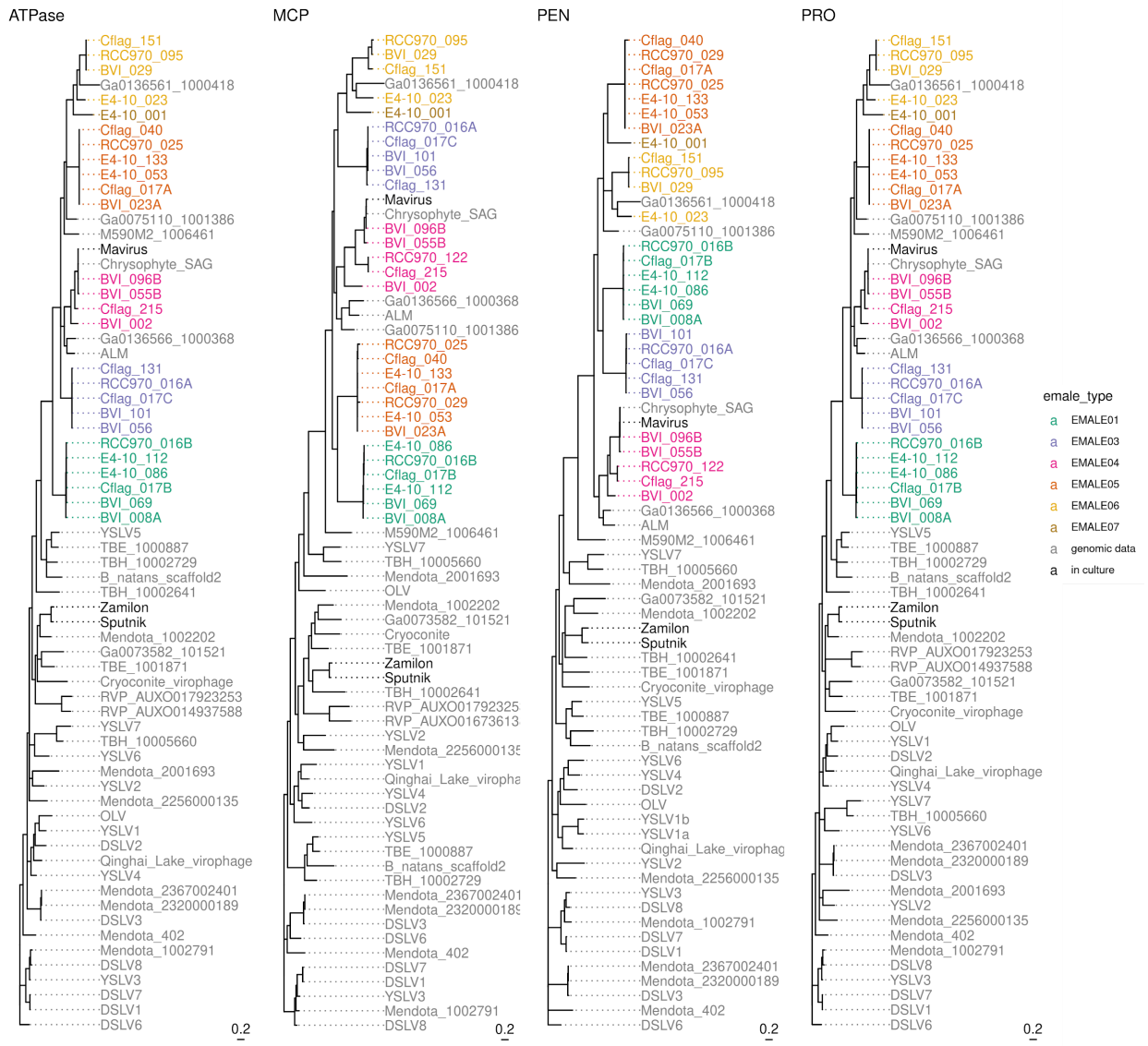


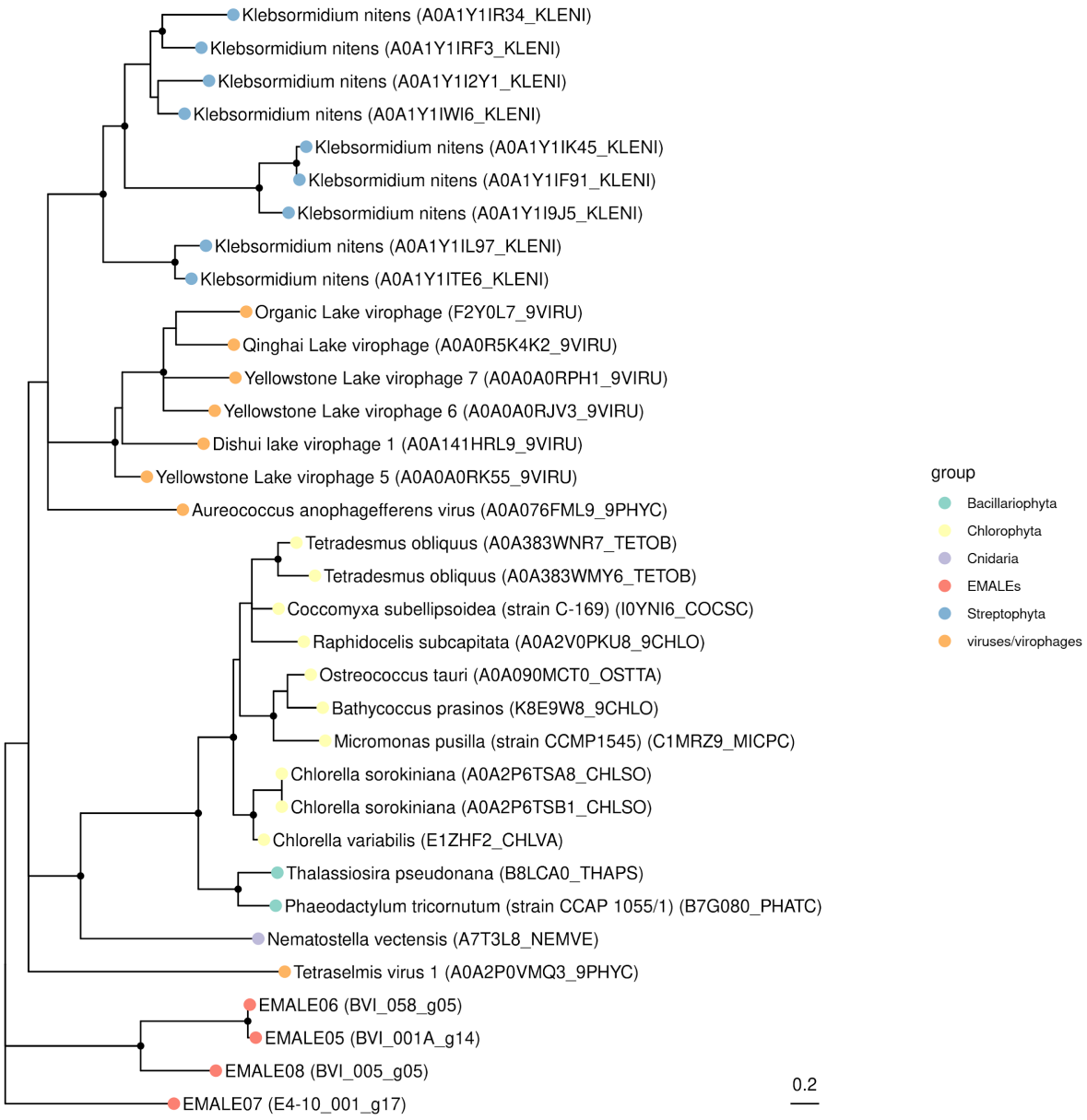
Partial synteny between EMALE01 and EMALE02.
DNA dot plot analysis of EMALE 01 Cflag_017B and EMALE02 E4-10_008 showing predicted genes along the axes. The synteny ends within the *rve-INT* gene, which represents the presumed recombination site (red dotted line). For the ORF color legend see Fig. 3 or Fig. S3.



Maximum likelihood reconstruction of FtsK-HerA-type ATPases encoded by EMALEs.
Unrooted ML tree computed for the putative DNA-packaging ATPase encoded by EMALE02 with its best BLASTp hits and ATPases from other EMALE types and select virophages. The EMALE02 ATPase is not closely related to other virophage ATPases, suggesting acquisition by recombination from an unknown source (see Fig. S6). Nodes with <50% bootstrap support were collapsed; nodes with >80% support are marked by black dots.

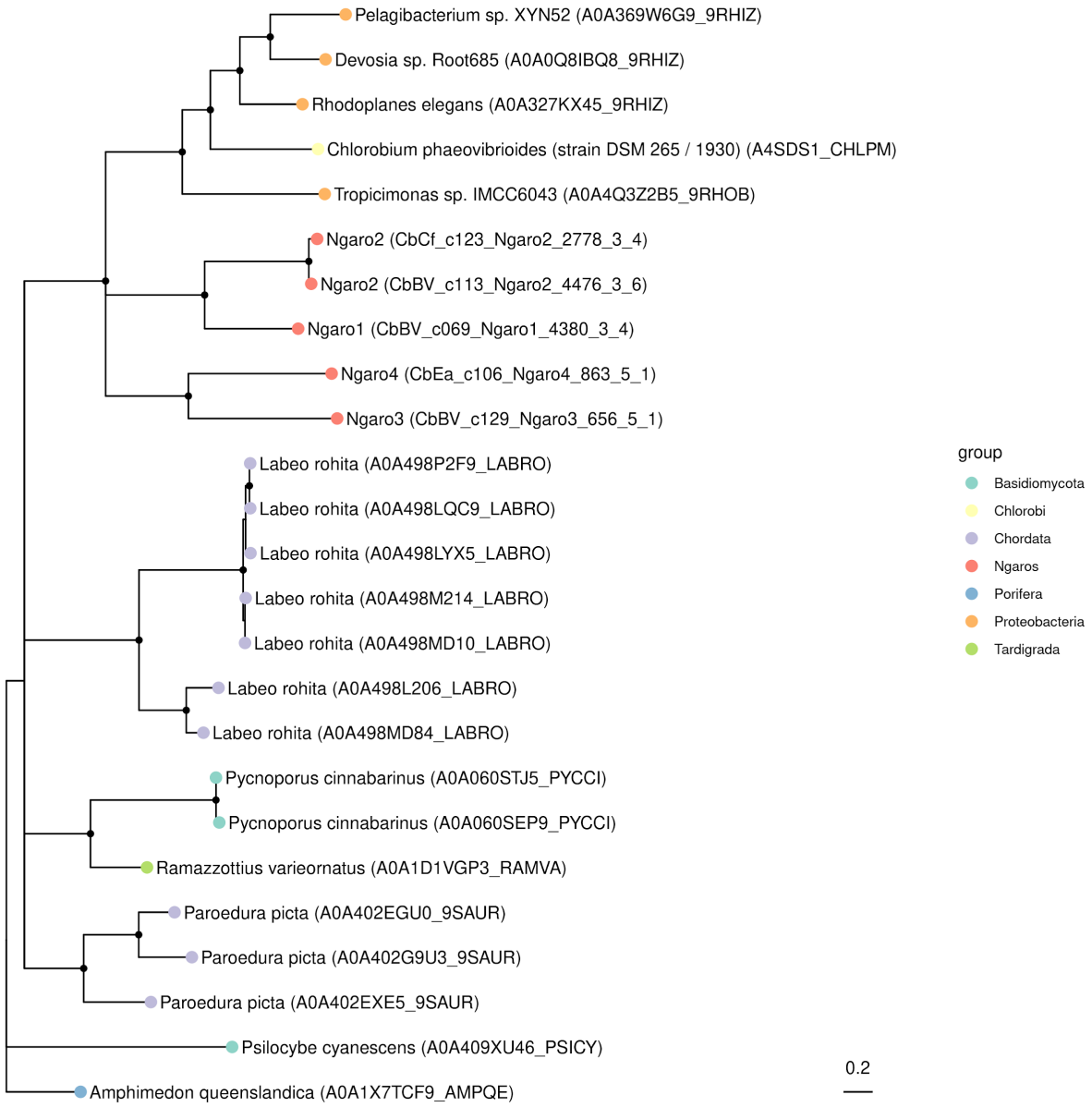


Bayesian reconstruction of EMALE morphogenesis proteins.
Unrooted phylogenetic trees for virophage core genes using the same multiple sequence alignments as for the ML phylogenies shown in Fig. 3, but computed with MrBayes (1 mio. generations). Nodes with <50% bootstrap support were collapsed.



Phylogenetic placement of EMALE tyrosine recombinases

An unrooted phylogenetic tree of tyrosine recombinases comparing those found in EMALEs (red dots) to their most similar sequences in UniProt (Color-coded at the phylum level). Splits with local support values >0.5 are collapsed, splits with local support values >0.8 are indicated by solid black dots.



Phylogenetic placement of Ngaro tyrosine recombinases

A phylogenetic tree of tyrosine recombinases comparing those found in Cafeteria Ngaros (red dots) to their most similar sequences in UniProt (Color-coded at the phylum level). Splits with local support values >0.5 are collapsed, splits with local support values >0.8 are indicated by solid black dots. The distribution across a very broad range of phyla (fish, fungi, sponges, tardigrades, and bacteria) indicates that this integrase is likely associated with highly mobile transposons with very broad host ranges, confirming previous studies on these type of elements (Poulter and Goodwin 2005).