Title of file for HTML: Supplementary Information

Description: Supplementary Figures and Supplementary Table

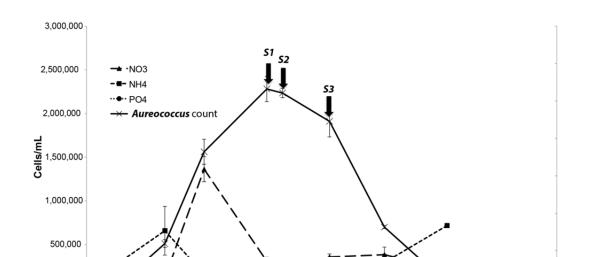
Title of file for HTML: Supplementary Dataset 1

Description: Mapping statistics of reads from the Quantuck Bay libraries to the genes of

Aureococcus anophagefferens virus (AaV).

Title of file for HTML: Supplementary Dataset 2

Description: Abbreviations and NCBI accession numbers of the reference sequences used to reconstruct the Eukaryotic RPB1, viral RdRP (+ssRNA virus) and viral replicase (ssDNA virus) phylogenies.



Supplementary figure 1: – *Aureococcus* and nutrient dynamics during different phases of the brown tide bloom. The samples collected for metatranscriptomic analysis are marked with black arrows.

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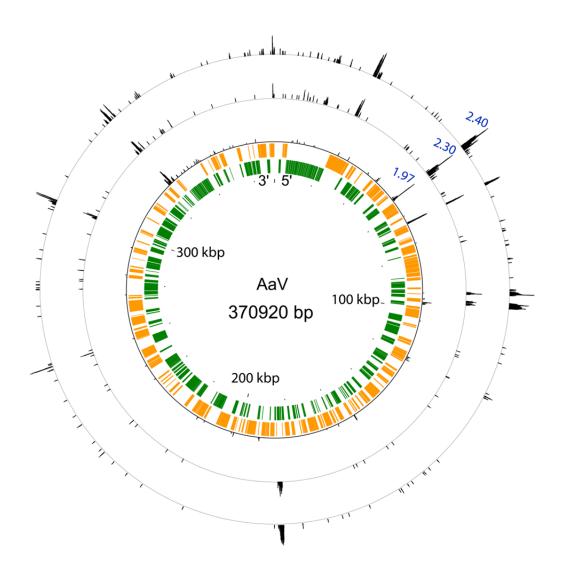
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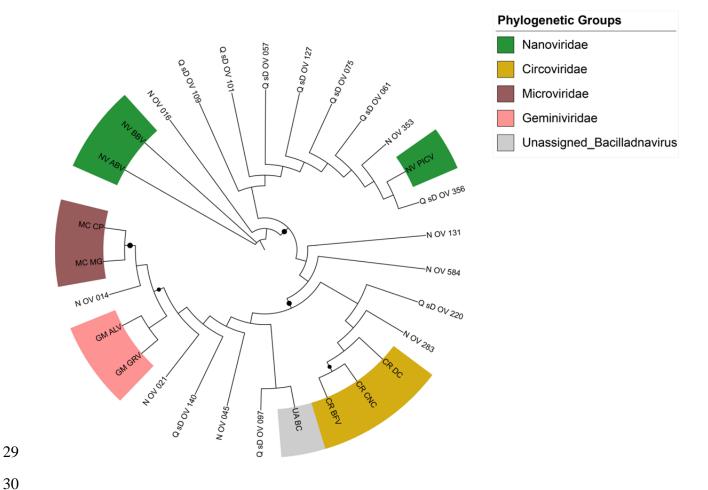
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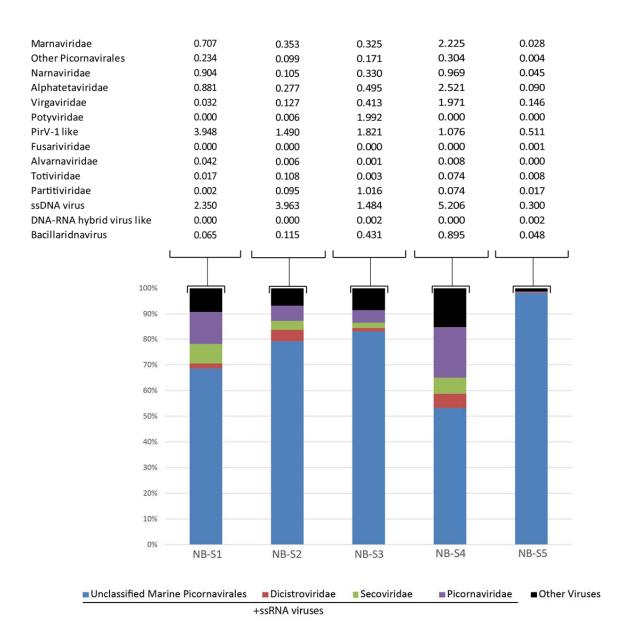
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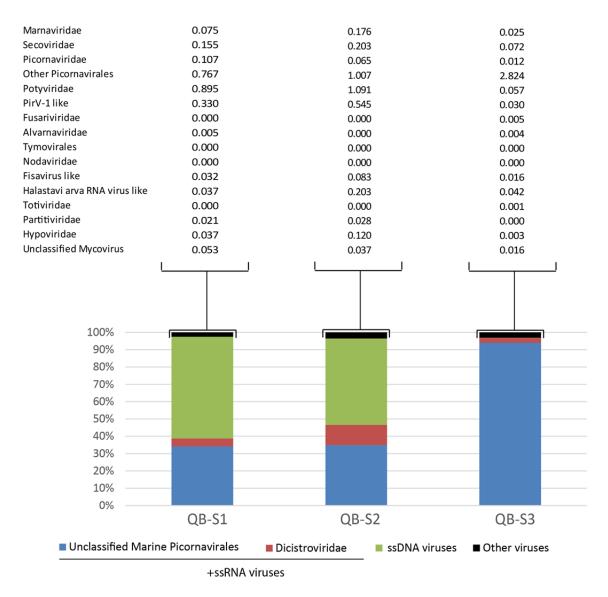
Supplementary Figure 2: Normalized read mapping statistics to the 370,920 bp AaV genome from the three Quantuck Bay samples. From outermost to innermost ring: Log converted number of reads mapped from QB-S1 (June 14), QB-S2 (June 16) and QB-S3 (June 22), respectively. Forward CDSs are in green while reverse CDSs are shown in orange. The value in blue on each ring represents the highest number of reads (log converted) mapped from the particular sample.



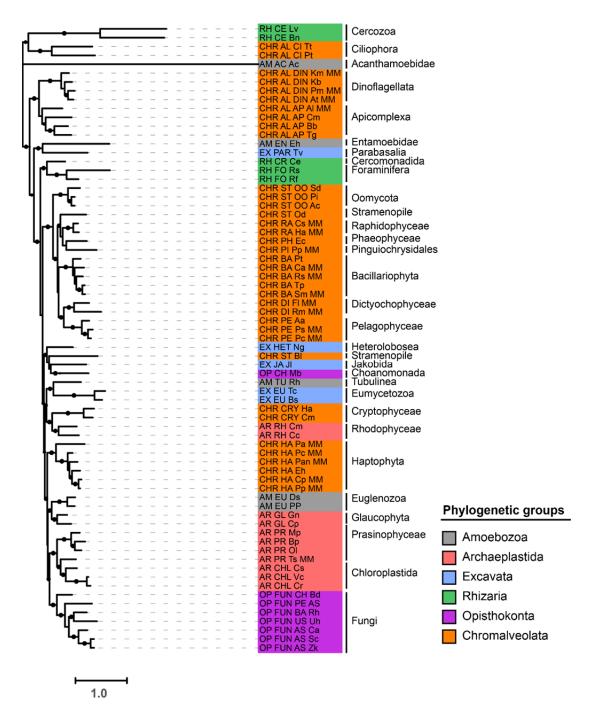
Supplementary Figure 3: Phylogenetic placement of ssDNA virus contigs (prefix: N_OV_ and Q_sR_OV_) harboring viral replicase motifs from Quantuck Bay and Narragansett Bay on a reference tree. Node support (aLRT-SH statistic) >50% are shown as dark circles. Contigs up to 225bp are shown. The reference sequences are shown in bold italic typeface. Complete name and other details of the reference sequences are presented in Supplementary Data 2.



Supplementary Figure 4: Proportional abundance of reads (in percentage) assigned to different viral groups in the Narragansett Bay study site over the five *in situ* samples. The 'other viruses' portion (in black) is further broken down into viral groups in the tables, which represent a minor contribution towards the diversity.



Supplementary Figure 5: Proportional abundance of reads (in percentage) assigned to different viral groups in the Quantuck Bay study site over the three *in situ* samples. The 'other viruses' portion (in black) is further broken down into viral groups in the tables, which represent a minor contribution towards the diversity.



Supplementary Figure 6: Maximum likelihood phylogenetic tree of eukaryotic RPB1 (RNA polymerase II large subunit) used as reference to classify the RPB1 contigs assisted by pplacer. Node support (>50%) values >50% are shown as dark circles. Complete names and other details of the reference sequences are provided in Supplementary Data 2.

Supplementary Table 1: RNA–seq library sizes after quality trimming. The Quantuck Bay samples were sequenced as single reads, while paired-end sequencing was carried out for the Narragansett Bay samples (denoted by X2). For Quantuck bay, the nutrient amendments were carried out in bottles filled with natural seawater from the bloom and amended with the following nutrients in triplicate: $25~\mu M$ ammonium only (+Nitrogen), $4~\mu M$ phosphate only (+Phosphorus), and $25~\mu M$ ammonium and $4~\mu M$ phosphate (+Nitrogen and +Phosphorus). Three additional bottles were filled and no nutrients were added (control). Similar amendments were conducted for the Narragansett Bay samples (see Alexander *et al.*, 2015).

	Sample	Number of reads
Quantuck Bay	June 14, 2011 (QB-S1)	43,755,618
	June 16, 2011 (QB-S2)	40,228,517
	June 22, 2011 (QB-S3)	214,681,748
	Nutrient amendment -control	41,156,535
	+Nitrogen	39,539,666
	+Phosphorus	36,797,290
	+Nitrogen and +Phosphorus	37,442,936
Narragansett Bay	16-05-2012 (NB-S1)	88,207,422 X2
	21-05-2012 (NB-S2)	53,911,567 X2
	30-05-2012 (NB-S3)	68,734,805 X2
	4-06-2012 (NB-S4)	45,344,970 X2
	8-06-2012 (NB-S5)	55,025,398 X2
	Nutrient amendment - control	38,713,917 X2
	-Phosphorus	45,764,698 X2
	+Phosphorus	37,528,376 X2
	-Nitrogen	36,671,310 X2
	+Nitrogen	49,217,942 X2