SUPPLEMENTARY INFORMATION

New single-stranded DNA virus with a unique genomic structure that infects marine diatom *Chaetoceros setoensis*

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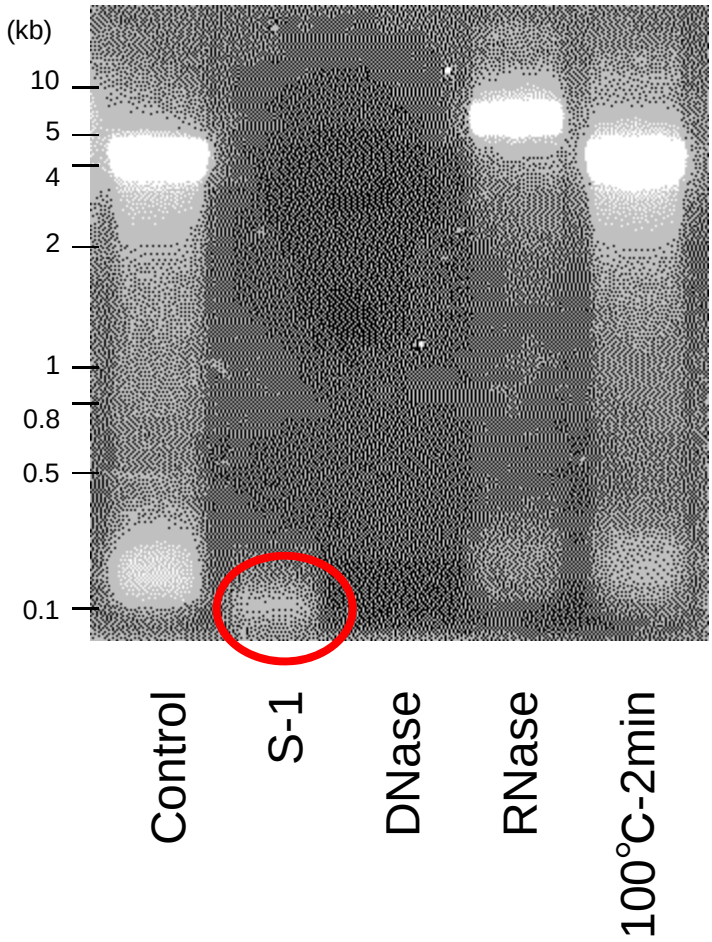
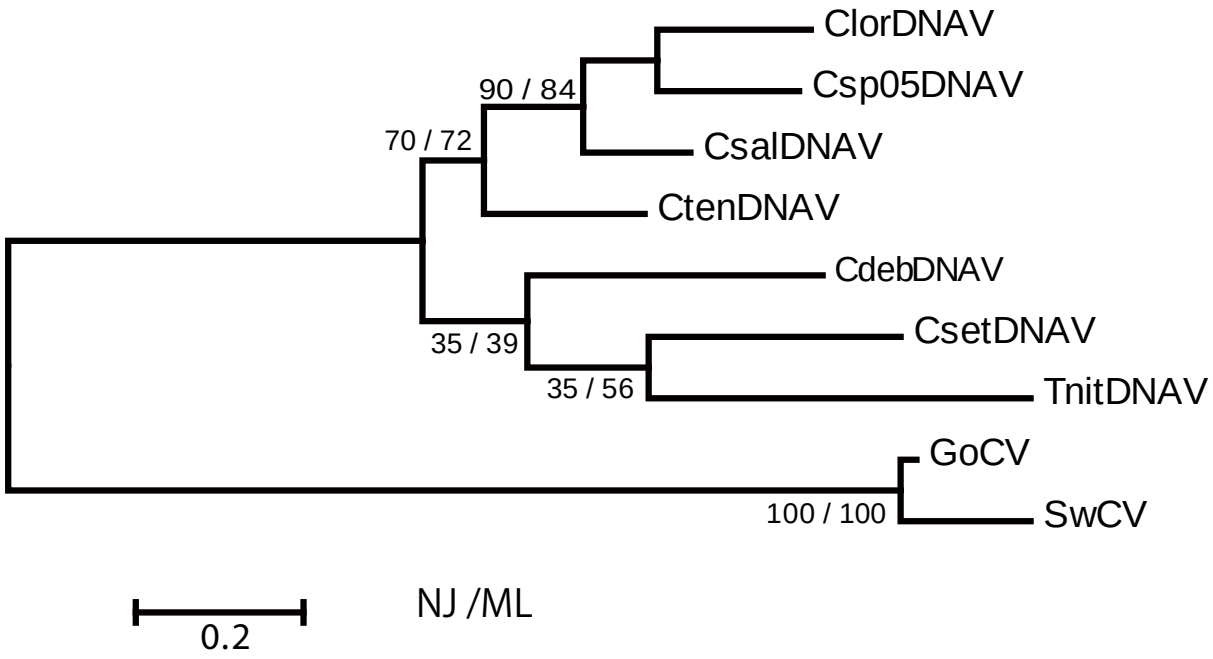


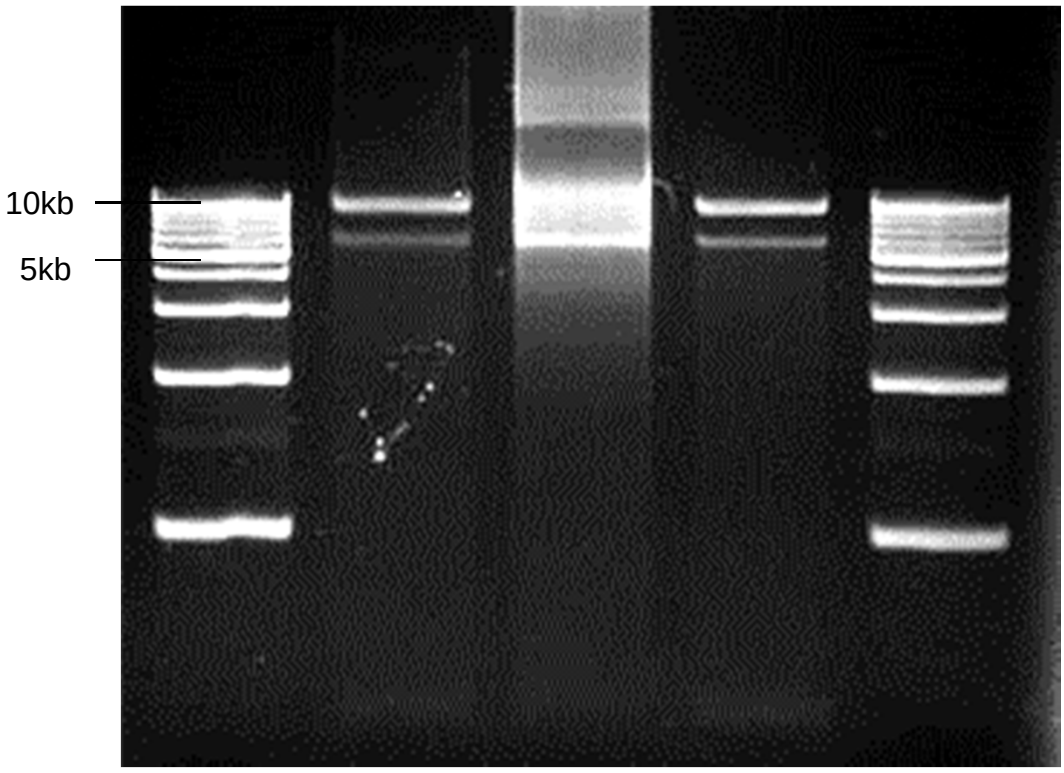
Supplementary Fig. S1

Supplementary Fig. S1. Figure 3 displayed with enhanced contrast.



Supplementary Fig. S2

Supplementary Fig. S2. ML tree based on deduced amino acid sequences of the putative replication region. NJ bootstrap values (%) from 1000 samples are shown at the nodes, followed by bootstrap values (%) based on the ML analysis of 1000 samples. The ML distance scale bar is shown. Amino acid sequences used for comparison in the analyses with database accession numbers were as follows: *Chaetoceros debilis* DNA virus (CdebDNAV), AB504376; *Chaetoceros lorenzianus* DNA virus (ClorDNAV), AB553581; *Chaetoceros salsugineum* DNA virus (CsalDNAV), AB193315; *Chaetoceros setoensis* DNA virus (CsetDNAV), AB781089; *Chaetoceros tenuissimus* DNA virus (CtenDNAV), AB597949; *Chaetoceros* sp. strain TG07-C28 DNA virus (Csp05DNAV), AB647334; *Thalassionema nitzschioides* DNA virus (TnitDNAV), AB781284; Goose circo virus (GoCV), ABA39169.1; swan circovirus (SwCV), ABU48445.1.



Supplementary Fig. S3

Supplementary Fig. S3. PCR amplification was conducted with 20 µL mixtures containing ~57 ng viral template DNA, 1X BlendTaq buffer, 200 nM of each dNTP, 10 pmol of each primer, and 1 U BlendTaq DNA polymerase, using a GeneAmp PCR System 9700 as follows: 25 rounds (denaturation at 94˚ C, 30 s; annealing at 52˚ C, 30 s; and extension at 72˚ C, 6 min). The PCR products were electrophoresed through 1% (w/v) agarose ME gels (WAKO Pure chemical Industries). Nucleic acids were visualised using ethidium bromide staining. Lane 1, viral genomic DNA incubated with the PCR reaction mixture but not cycled. Lane 2, PCR amplification of the viral genome. Lane 3, control.