Technical Appendix

Figure. ClustalW alignment of sequences used to generate the phylogenetic tree in the Figure (see article text). Sequences were generated from RNA isolated from 50–100 mg of digestive gland or gill. Tissue was homogenized in 300 μL phosphate-buffered saline, and viral RNA was isolated by using a viral RNA kit (QIAGEN, Crawley, UK), and PCR was conducted by amplifying nucleotides.
6332–6476 as described (1). The nucleotide sequences were aligned and bootstrapped, and phylogenetic neighbor-joining trees were constructed by using the ClustalW software (www.ebi.ac.uk/Tools/msa/clustalw2).

Reference