Supplemental Figure Legends

Figure S1: Maps of contiguous sequences matching *Nodamuravirales* recovered in this survey of *Pisaster ochraceus*. Contigs were annotated based on BLASTx (e-value < 1 x 10-20) against the non-redundant database at NCBI. All matches were to the RNA1 genome segment of nodaviruses. Numbers above the ORFs indicate the e-value of BLAST results. The total contig lengths are indicated by solid lines running through and between ORFs.

Figure S2: Phylogenetic representations of *Pisaster ochraceus* picornavirus-like genome fragments. The trees were constructed by performing alignments of overlapping regions with best BLASTx matches at NCBI using the CLC Sequence Viewer 8.0 native alignment algorithm. The trees are based on: a 98 amino acid (A) and 193 amino acid (D) alignment of the RNA dependent RNA polymerase gene; a 187 amino acid alignment of the rhv-like capsid domain (B) and a 160 amino acid alignment of the RNA helicase domain (C) . The tree was constructed by maximum likelihood with Poisson substitution and employing the Nearest-Neighbor-Interchange heuristic method in MEGA 6.0 [1].

Figure S3: Phylogenetic representations of *Pisaster ochraceus* nodavirus-like genome fragments. The trees were constructed by performing alignments of overlapping regions with best BLASTx matches at NCBI using the CLC Sequence Viewer 8.0 native alignment algorithm. The trees were constructed based on: a 234 amino acid alignment of the methyltransferase domain (A); and a 101 amino acid (B) and 559 amino acid (C) alignments of the RNA dependent RNA polymerase gene of the nodavirus RNA1 genome fragment including best matches at NCBI. The tree was constructed by maximum likelihood with Poisson substitution and employing the Nearest-Neighbor-Interchange heuristic method in MEGA 6.0 [1].

Figure S4: Phylogenetic representations of *Pisaster ochraceus* densovirus-like genome fragments. The trees were constructed based on: a 103 amino acid alignment of the structural (coat protein) gene; a 83 amino acid of the non-structural 1 (NS1) gene; a 112 amino acid of the NS2 gene; and a 111 amino acid of the NS3 gene. Phylogenetic representations include best matches by BLASTx against the non-redundant database at NCBI. The tree was constructed by maximum likelihood with Poisson substitution and employing the Nearest-Neighbor-Interchange heuristic method in MEGA 6.0 [1].