



Figure S4: Maps of contiguous sequences matching Nodamuravirales recovered in this survey of *Pisaster ochraceus*. Contigs were annotated based on BLASTx (e-value $< 1 \times 10^{-20}$) 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.