Tables (provided as a separate file)

Table S1.

Summaries and major conclusions of research articles and reviews on environmental RNA viruses with specific focus on the ocean.

Table S2.

Protistan RNA virus isolates.

Table S3.

List of Tara Ocean studies related to this work.

Table S4.

List of RNA samples, their metadata, and their unique identifiers.

Table S5.

A full list of the RNA virus contigs identified in this study, along with their representative vOTU sequences, novelty and long-read matches, RdRp domain and genome completeness, and other statistics.

Table S6.

RdRp domain sequences across different datasets included in this study.

Table S7.

High-ranks taxonomic assignment for RNA viruses based on network-guided iterative clustering and phylogeny of the RdRp domains (pre-clustered at 50% identity and at least 90% complete; n=6,238).

Table S8.

Pairwise protein superfamily reliability scores calculated from experimentally resolved or predicted three-dimensional structures of RNA virus RdRps and other reverse transcriptases.

Table S9.

Domain annotations (section A) and enrichment analysis per megataxon (section B) for RNA vOTUs in this study (n=5,122 annotatable out of 5,504).

Table S10.

Detected RdRp domain motifs and their arrangement in the new megataxa discovered in this study.

Table S11.

Host prediction results for the RNA vOTUs identified in this study.

Table S12.

Inferring new RNA phages from prokaryotic Shine–Dalgarno sequences.