**Supplementary Table S1.** Physicochemical properties of the water column and the correlation (Pearson correlation analysis) of these variables with sample depth.

| Depth (m) | Irradiance (µmol m\(^{-2}\) s\(^{-1}\)) | pH   | Temperature (°C) | Conductivity (mS m\(^{-1}\)) | Oxygen (%) | Dissolved Organic Carbon (mg l\(^{-1}\)) | Dissolved Inorganic Carbon (mg l\(^{-1}\)) | Total Nitrogen (µg l\(^{-1}\)) | Total Phosphorus (µg l\(^{-1}\)) | Correlation with Depth |
|-----------|----------------------------------------|------|------------------|-------------------------------|------------|----------------------------------------|----------------------------------------|-------------------------------|-------------------------------|------------------------|
| 2         | 153                                    | 6.96 | 1.07             | 0.40                          | 114.9      | 0.41                                   | 3.0                                    | 35.84                         | 20.40                        | -0.8                   |
| 9         | 1.55                                   | 7.10 | 0.20             | 9.21                          | 113.9      | 0.47                                   | 6.5                                    | 74.04                         | 19.54                        | 0.96                   |
| 13        | –                                      | 7.26 | -0.93            | 41.84                         | 90.4       | 0.95                                   | 21.4                                   | 235.89                        | 5.00                         | -0.95                  |
| 20        | –                                      | 7.75 | -1.15            | 43.07                         | 86.9       | 1.16                                   | 22.5                                   | 292.83                        | 12.01                        | 0.9                   |
| Correlation with Depth | -0.8 | 0.96 | -0.95 | 0.9 | -0.89 | 0.93 | 0.91 | 0.94 | -0.64 |
**Table S3.** Characteristics of putative Uncultivated Viral Genomes (UViGs), which have been identified as circular by VirSorter. Viral Family has been determined by VPF-Class, and Module is determined by WGCNA as described in the text. ‘*’ indicates UViGs that are shown in Figure 7A.

| Contig identifier | Viral Family | Module | Length (bp) | Open Reading Frames | Non-hypothetical proteins | Total Reads recruited to vOTU | Distribution          |
|-------------------|--------------|--------|-------------|---------------------|---------------------------|-----------------------------|-----------------------|
| NODE51_04         | Myoviridae   | Yellow | 37 365      | 50                  | 5                         | 43 595                      | Marine                |
| NODE34_03         | Myoviridae   | Yellow | 42 107      | 51                  | 10                        | 97 385                      | Marine                |
| NODE30_02         | Myoviridae   | Brown  | 39 941      | 58                  | 7                         | 27 174                      | Surface-Halocline     |
| NODE684_01        | Podoviridae  | Blue   | 31 966      | 44                  | 13                        | 139 816                     | Marine                |
| NODE62_02         | Siphoviridae | Yellow | 31 876      | 47                  | 8                         | 40 826                      | Marine                |
| NODE42_03         | Myoviridae   | Blue   | 38 599      | 52                  | 16                        | 30 391                      | Marine                |
| NODE72_04*        | Podoviridae  | Green  | 34 569      | 48                  | 9                         | 38 620                      | Surface-Halocline     |
| NODE2_01*         | Phycodnaviridae | Blue   | 110 748     | 116                 | 15                        | 37 163                      | Marine                |
| NODE24_03         | Podoviridae  | Blue   | 55 116      | 76                  | 13                        | 45 917                      | Marine                |
| NODE41_03*        | Podoviridae  | Blue   | 39 547      | 47                  | 20                        | 25 472                      | Marine                |
| NODE37_03*        | Podoviridae  | Yellow | 36 431      | 46                  | 9                         | 80 750                      | Marine                |
| NODE16_01*        | Siphoviridae | Brown  | 48 628      | 69                  | 13                        | 23 627                      | Surface-Halocline     |
| NODE41_02         | Podoviridae  | Blue   | 38 968      | 36                  | 17                        | 142 288                     | Marine                |
| NODE15_04*        | Podoviridae  | Blue   | 61 246      | 72                  | 15                        | 227 725                     | Marine                |
| NODE12_03         | Podoviridae  | Yellow | 68 348      | 88                  | 17                        | 41 845                      | Marine                |
Table S4. Number of reads obtained per library.

| Depth (m) | Replicate | Number of reads  |
|-----------|-----------|-----------------|
| 2         | A         | 19,666,448      |
|           | B         | 18,695,438      |
|           | C         | 15,932,910      |
| 9         | A         | 20,104,378      |
|           | B         | 9,513,168       |
|           | C         | 15,110,742      |
| 13        | A         | 19,860,086      |
|           | B         | 18,470,662      |
|           | C         | 19,974,192      |
| 20        | A         | 14,687,992      |
|           | B         | 18,000,044      |
|           | C         | 18,210,582      |
Figure S2. *Pelagibacter* (SAR11) clades detected by 16S rRNA genes in replicate samples from four depths.
Figure S3. Comparison of vOTU abundance and frequency between virus families. A flatter peak indicates fewer, and more abundant vOTUs. vOTUs were clustered at 95% identity over 85% of the sequence length. Gaussian kernel density estimation was plotted using a fast Fourier transform, with bandwidth value selected using Silverman’s rule of thumb, such that the bandwidth was the standard deviation of the smoothing kernels. Note that x axis is truncated.
Figure S4. Gene annotation from RefSeq, KEGG, and PFAM databases of selected vOTUs with ecological significance, representing genome fragments, (a) vsNODE54_01, (b) NODE170_03, and (c) NODE14_04. In (c), orthologs of genes with best hit to *Phycodnaviridae* genomes in GenBank are starred (*). The numbering of each Open Reading Frame is shown within the arrow. Abbreviations: DNA Pol, DNA polymerase; NUDIX, nucleoside diphosphate linked moiety X; WLM, Wss1p-like metalloprotease; PAP2_C, Type 2 phosphatidic acid phosphatase; SWIB, SWI/SNF (Switch/Sucrose non-fermentable) complex B; TBP, TATA-box binding protein; HRD1B, HMG-CoA reductase degradation ubiquitin ligase 1B.
Figure S5. Fraction of Open Reading Frames (ORFs) annotated with genes for (a) DNA polymerase A, (b) T7 primase/helicase, (c) RNA reductase, (d) tauD, (e) patatin-like phospholipid, and (f) integrase, by WGCNA module. Dashed line represents overall fraction of ORFs (modules pooled together). Note that a lower diversity of vOTUs in the modules purple, pink, and magenta contributes to less reliable values for these modules.