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Supplementary Information for

Seasonal and Diel Patterns of Abundance and Activity of Viruses in the Red Sea

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  Excel files can be download from https://doi.org/10.17605/osf.io/b74mt

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www.pnas.org/cgi/doi/10.1073/pnas.2010783117

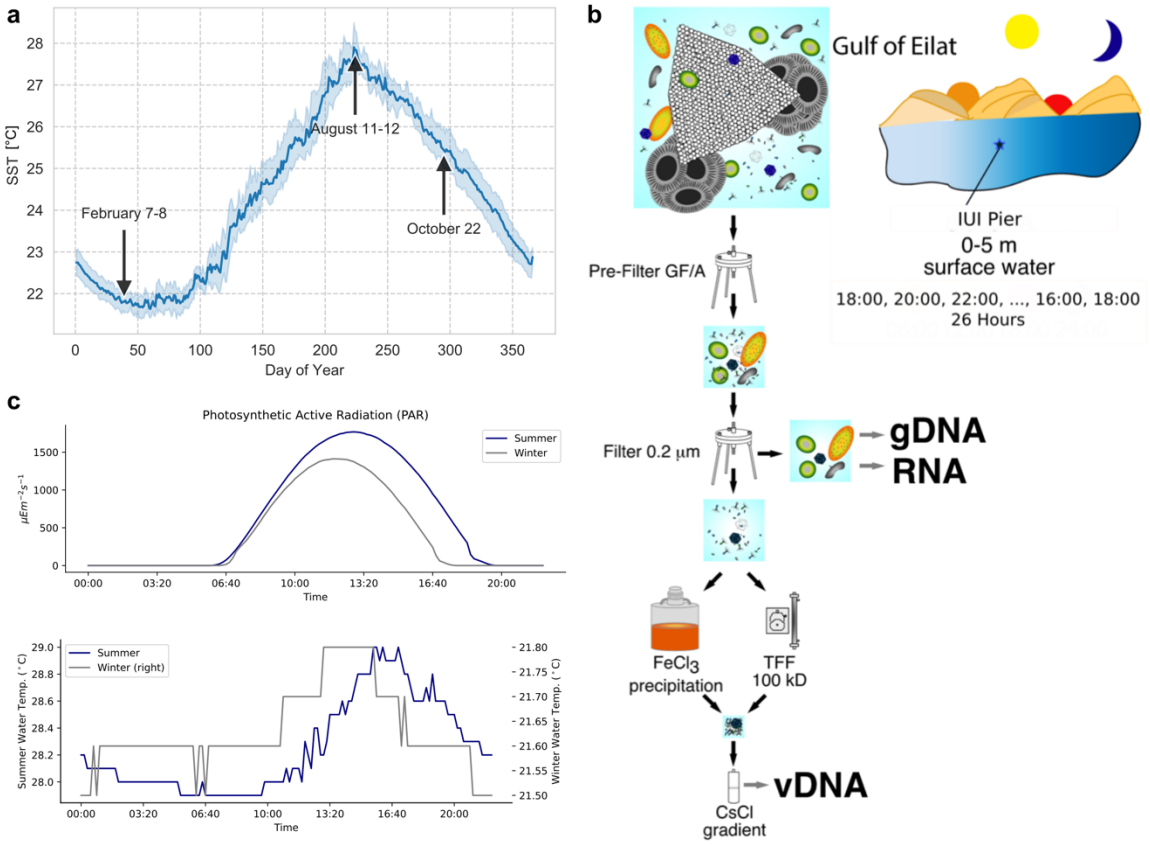

Fig. S1. Environmental parameters and experimental design. **(a)** Sea surface temperature (SST) measured at the IUI Pier from 2011-2019. x-axis: Day of Year, y-axis: mean SST with 95% confidence bands (1000 bootstraps). Arrows indicate day-of-year of samples mentioned in this study. **(b)** Sampling scheme. Sea water sampled every two hours, filtered and fractionated based on microorganismal size and nucleic acid content. **(c)** Photosynthetic Active Radiation (PAR) and water temperature recorded at the IUI pier during days of sampling in August 2015 (blue) and February 2016 (grey).

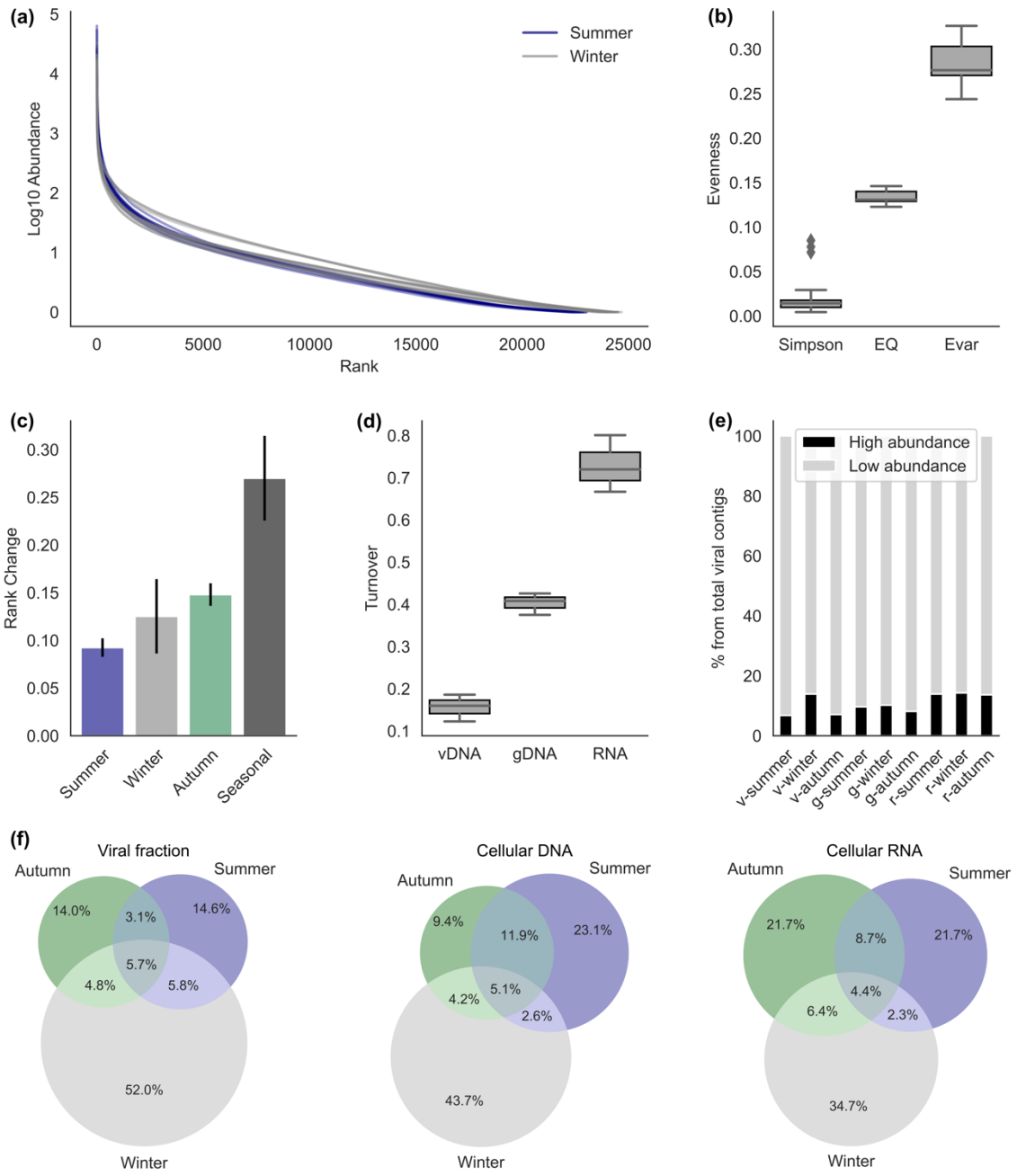

Fig. S2. Viral community structure. **(a)** Rank abundance curves of the viral contigs in the diel summer (blue) and winter (grey) samples. **(b)** *Simpsons, E_Q and E_{var}* evenness measures of viral contigs abundance in the diel summer and winter samples. **(c)** Scaled rank change, measuring how much the abundance of viral contigs changes over time relative to each other in the diel samples per season (summer, blue; winter, light grey; autumn, green), or between seasons (dark grey). The error bars represent the standard deviation of rank changes. **(d)** Viral contigs turnover between the three seasons, measured as the proportion of contigs either gained or lost relative to the total number of contigs observed across seasons. **(e)** The proportion of contigs that account for 80% of the viral abundance by sample (high abundance) from the total number of viral contigs. **(f)** Percentage of high abundance viral contigs shared and unshared between seasons in the viral fraction (n=6863), cellular DNA fraction (n=4944) and cellular RNA fraction (n=2544).

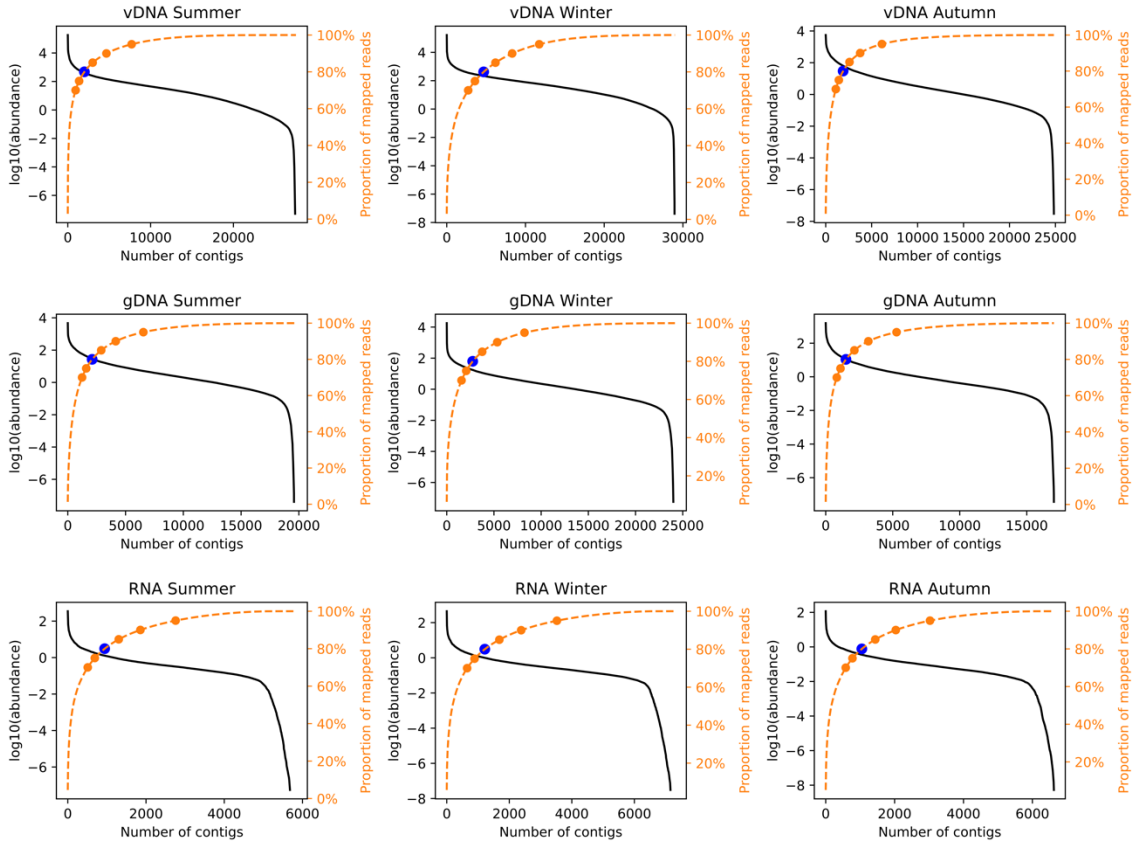

Fig. S3. Rank abundance curves of viral contigs in all samples (black) overlayed with cumulative percentage curve (orange). Cumulative percentage is calculated by dividing the cumulative sum of abundances by the sum abundance of each sample and multiplying by 100. Dots on the orange curve represent a range of cumulative percentage cutoffs (70-90%), where the blue dots represent the 80% cutoff used in this study.

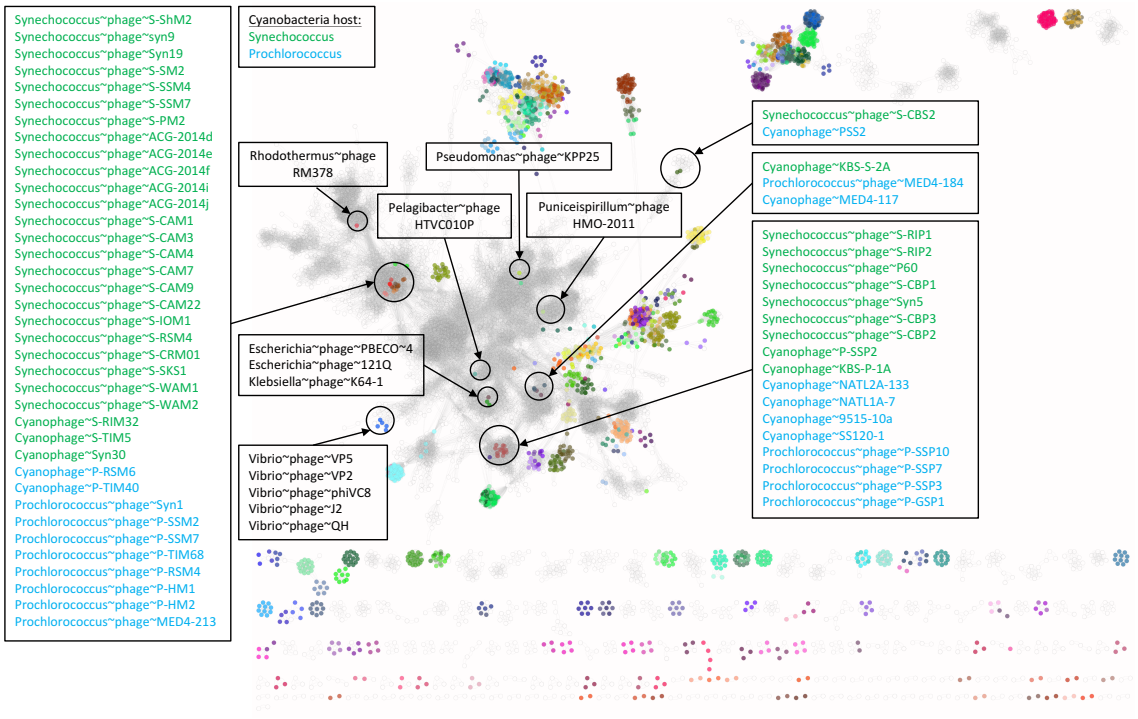

Fig. S4. Gene sharing network of Refseq viral genomes and Red Sea predicted viral contigs (2,239 and 7,047 genomes, respectively). Grey nodes represent Red Sea viral contigs. Colored nodes represent RefSeq viral genomes. Labeled clusters represent taxonomic annotation based on Refseq viral genomes that appear in a specific cluster.

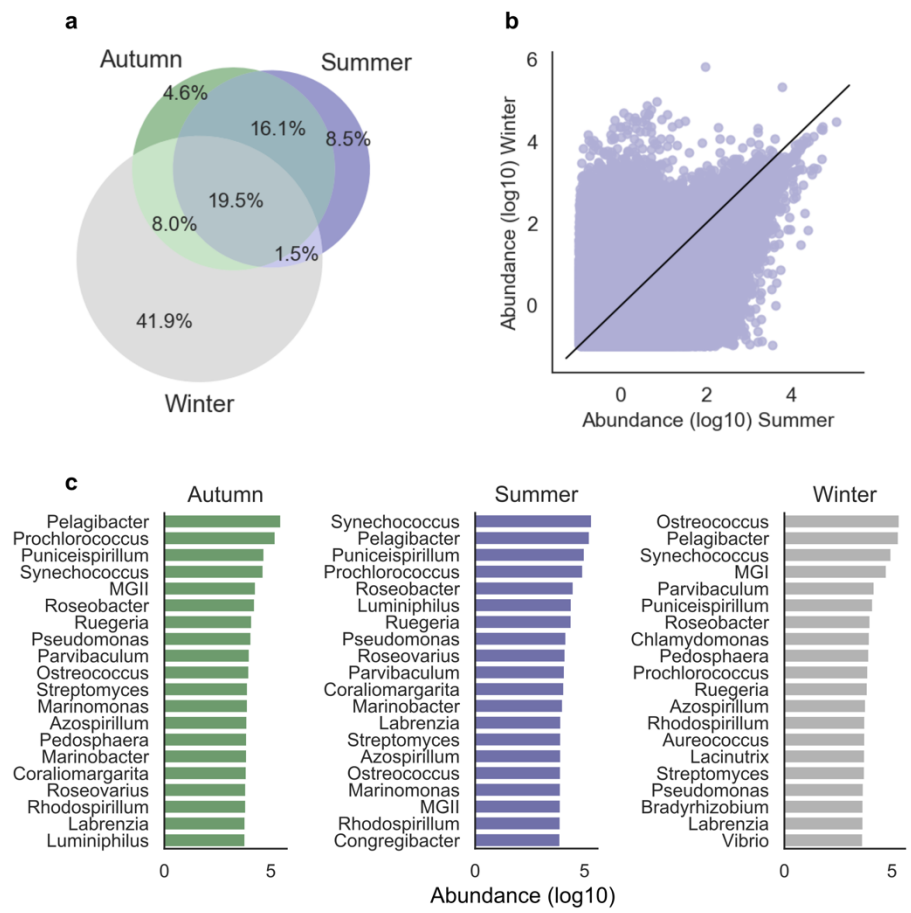

Fig. S5. Microbial community seasonal abundance. **(a)** Percentage of microbial contigs shared between seasons with count ≥ 1 RPKM in the metagenome samples. **(b)** Abundance of microbial contigs in the summer vs. winter cellular DNA samples. A 1:1 line is shown for reference. **(c)** Most abundant microbial genera by season: autumn (green), summer (blue) and winter (grey).

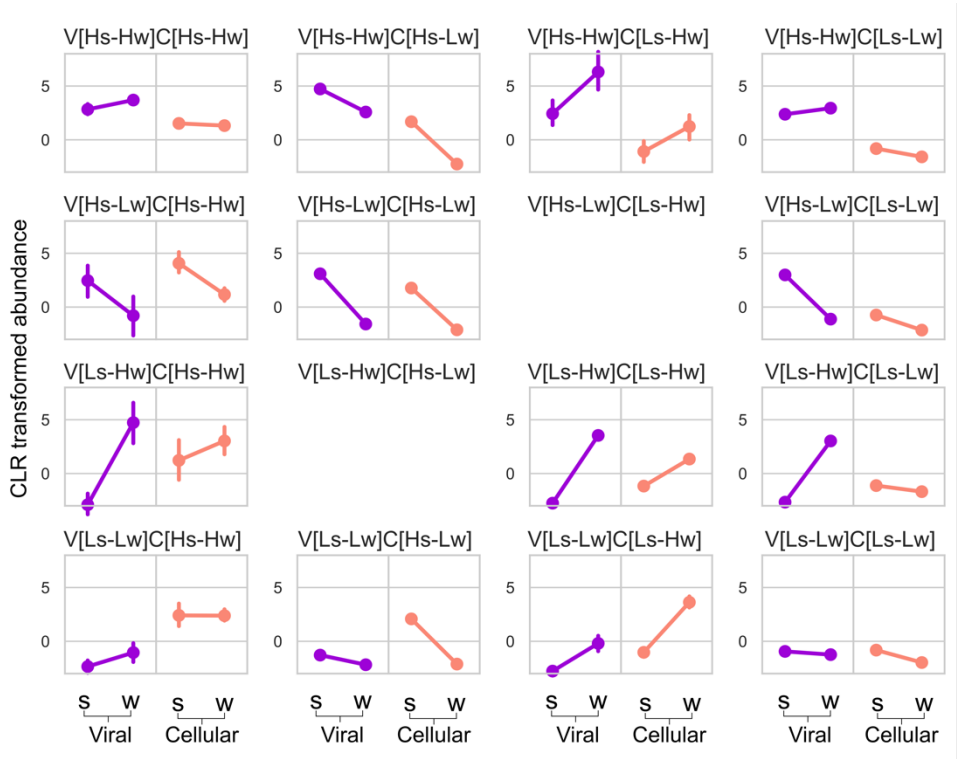

Fig. S6. The centered log ratio (CLR) transformed abundance (RPKM) of the rank-states patterns described in the paper. The CLR-based results show that these patterns are also detectable using methods that are insensitive to the biases associated with relative abundance measures in metagenomic data (1).

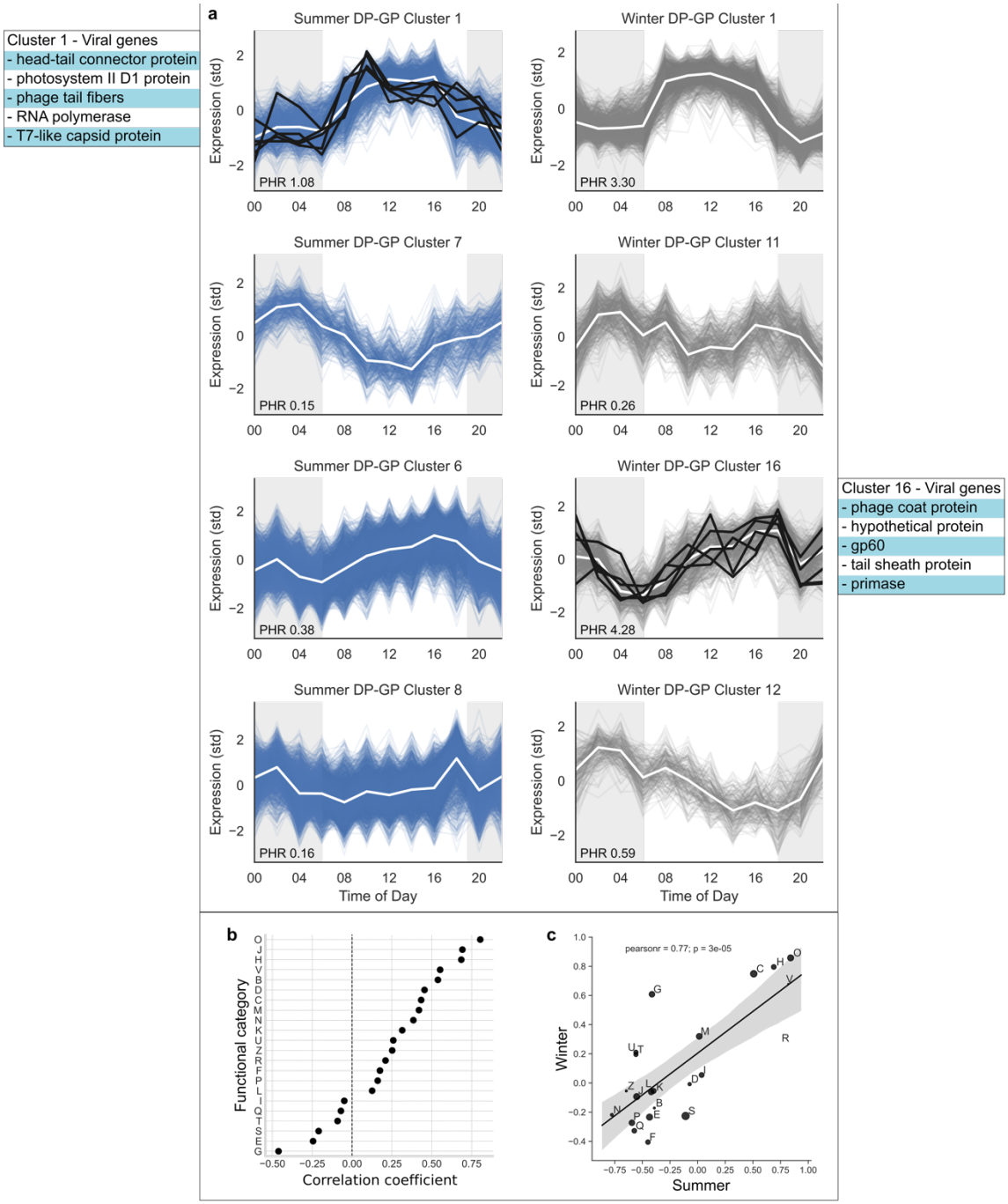

Fig. S7. Microbial community expression patterns. **(a)** Selected gene clusters of similar expression patterns in the summer (blue) and winter (grey) metatranscriptomic samples. The genes were clustered using Gaussian mixture models coupled with Dirichlet process (DP-GP)(2). The black lines in clusters 1 (summer) and 16 (winter) represent viral genes that were clustered together with the microbial genes. x-axis: time of day, y-axis: standard deviations from the mean, confidence bands (dashed lines) represent two standard deviations from the mean, horizontal bars: light (yellow) and dark (black) hours. **(b)** Correlation of the mean expression by functional category between seasons. x-axis: Spearman R correlation coefficient, y-axis: COG functional categories **(c)** Correlation of functional categories with diel light intensity. x-axis: Correlation coefficient of summer functional groups, y-axis: Correlation coefficient of winter functional groups. The fitted linear correlation line is shown for reference.

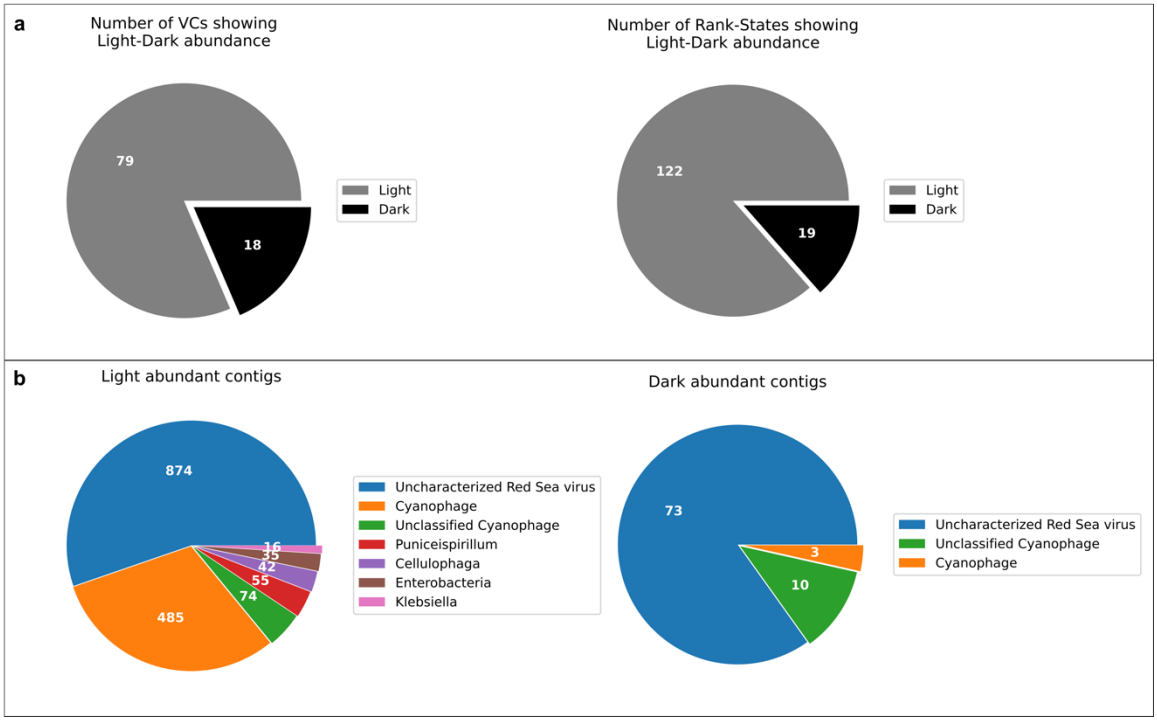

Fig. S8. Light-dependent virus-host interaction **(a)** Number of viral clusters (minimum of 10 ORFs in cluster and minimum counts > 0 RPKM by ORF in either the light or dark samples), with at least one rank-state that displayed differential light-dark abundance (Mann-Whitney test < 0.05). **(b)** Number of contigs from 16 viral clusters and 9 rank-states (grouped by predicted host genus) with significant light-dark differential abundance (Mann-Whitney test < 0.05).

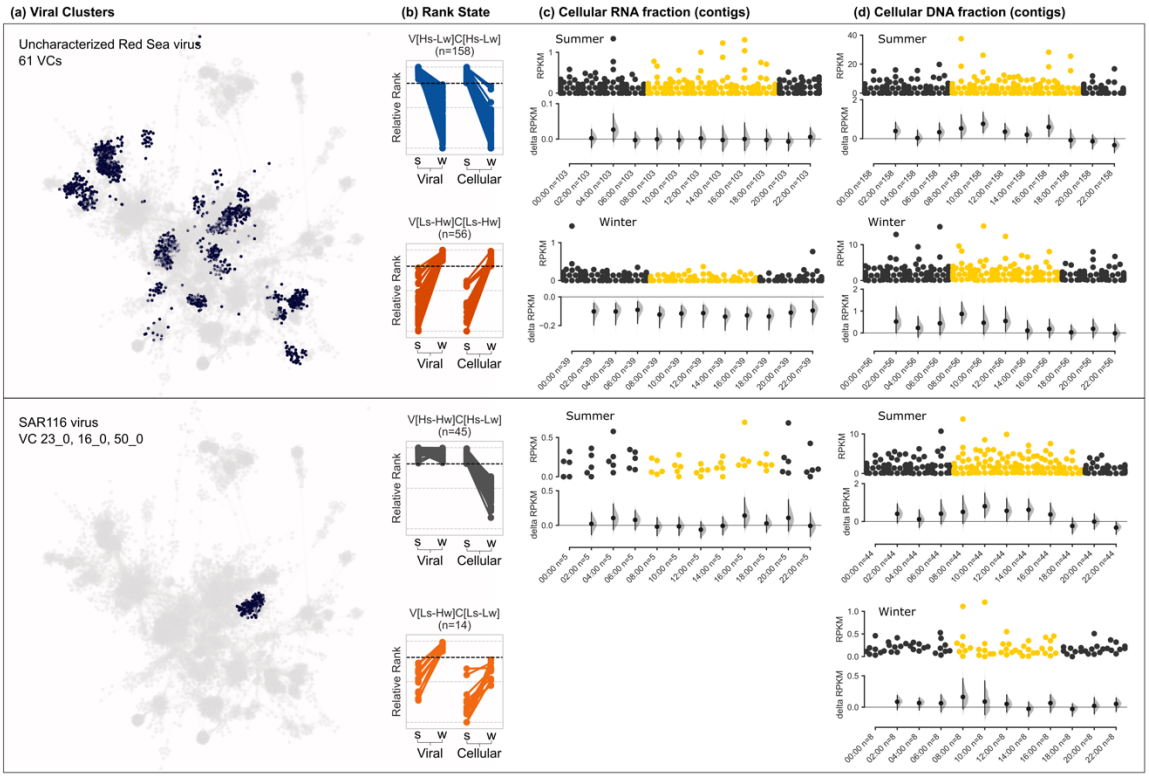

Fig. S9. Intracellular diel abundance patterns of uncharacterized Red Sea virus VCs (top) and SAR116 virus VCs (bottom). **(a)** Superclusters of selected VCs that displayed a differential light-dark signal (Mann-Whitney U test, $p < 0.05$). **(b)** VCs contigs that were classified into two rank-states with strong seasonal abundance pattern (V[Hs-Lw]C[Hs-Lw] and V[Ls-Hw]C[Ls-Hw]). **(c-d)** Diel distribution in the cellular RNA (c) and DNA (d) fractions of viral contigs from specific VCs and rank-state from (b); x-axis, hours of the day when a sample was collected and the number of viral contigs expressed; upper panel, abundance distribution of viral contigs by time point (each point represents a contig); point color represent samples collected in the dark (black) and light (yellow); y-axis, contig abundance (RPKM); lower panel, estimation plot (3) displaying the effect size as a 95% confidence interval (1,000 bootstraps) of the mean differences between each time point compared against midnight as a reference group.

Table S1. Distribution of rank-states for the viral contigs in the Active group. Top: number of contigs by rank-state. Bottom: Percentage of contigs by rank-state from total.

# Contigs by rank-state				
RankState	**C[Hs-Hw]**	**C[Hs-Lw]**	**C[Ls-Hw]**	**C[Ls-Lw]**
V[Hs-Hw]	75	212	8	1049
V[Hs-Lw]	5	679	0	461
V[Ls-Hw]	8	0	239	2017
V[Ls-Lw]	17	259	39	196

% Contigs by rank-state				
RankState	**C[Hs-Hw]**	**C[Hs-Lw]**	**C[Ls-Hw]**	**C[Ls-Lw]**
V[Hs-Hw]	1.42%	4.03%	0.15%	19.93%
V[Hs-Lw]	0.09%	12.90%	0.00%	8.76%
V[Ls-Hw]	0.15%	0.00%	4.54%	38.32%
V[Ls-Lw]	0.32%	4.92%	0.74%	3.72%

Table S2. Viral Clusters (VC) with significant Light-Dark differential abundance (Mann-Whitney) in the intracellular samples: gDNA, RNA. (a) Detailed list. (b) Summary of by samples and taxa groups of interest.

(a)

VC	RankState	SampleType	Season	MannWhitney_pval	CorrelationCoefficient	Direction	NumberOfContigs	NumberOfFamily	Annotation
VC_161_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Summer	0.014121385	0.143512395	0.011229928	11	74	Unassigned	Uncultured
VC_29_0	V[Hs-Lw]C[Hs-Lw]	RNA	Summer	0.040583941		0.02939505	12	25	Siphoviridae	Cyanophage
VC_68_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Winter	0.019942127		-0.025345962	1	19	Unassigned	Uncultured
VC_374_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.002474698	0.284110903	0.012375842	9	56	Unassigned	Uncultured
VC_141_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.022812044	0.664159801	-0.032162012	11	64	Unassigned	Uncultured
VC_306_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.027059917	0.67484858	0.248946828	9	29	Myoviridae	Cyanophage
VC_6_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.012437569	0.806731829	0.04339917	83	498	Unassigned	Uncultured
VC_9_0	V[Hs-Lw]C[Hs-Lw]	RNA	Summer	0.009662683	0.706633825	0.193606662	25	109	Podoviridae	Cyanophage
VC_769_0	V[Ls-Lw]C[Ls-Lw]	gDNA	Winter	0.039976477		0.002231774	2	16	Unassigned	Uncultured
VC_69_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.024376379	0.770772375	0.671949177	18	140	Unassigned	Uncultured
VC_422_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	5.71E-07	0.546089492	-1.494605799	10	65	Unassigned	Uncultured
VC_29_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.005080041	0.607583176	0.041899638	26	88	Siphoviridae	Cyanophage
VC_61_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.000260879	0.719926819	5.668402468	12	55	Podoviridae	Cyanophage
VC_100_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.007431386	0.286757523	0.019027083	7	31	Unassigned	Uncultured
VC_291_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.000394304	0.919831956	2.08494472	12	84	Myoviridae	Cyanophage
VC_31_2	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.034000595	0.797372063	0.273888052	4	45	Myoviridae	Cyanophage
VC_676_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.039976477		0.003031003	2	16	Unassigned	Uncultured
VC_8_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.039815403	0.070783627	0.011401485	35	235	Unassigned	Uncultured
VC_29_0	V[Hs-Hw]C[Hs-Lw]	RNA	Summer	0.013330599	0.543373105	0.12629571	4	37	Siphoviridae	Cyanophage
VC_3_1	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.006839779	0.267374218	0.02237957	65	325	Unassigned	Uncultured
VC_246_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.003708743	0.605025204	0.900549651	15	102	Unassigned	Uncultured
VC_79_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.009474381	0.446284287	-0.033967748	2	26	Unassigned	Uncultured
VC_25_2	V[Hs-Hw]C[Hs-Lw]	gDNA	Winter	0.045016926	0.240969275	0.011094641	6	34	Unassigned	Uncultured
VC_29_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.040761486		0.006069761	8	30	Siphoviridae	Cyanophage
VC_393_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.001164771	0.86896183	2.942442468	8	33	Unassigned	Uncultured
VC_938_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Summer	0.026969943	0.338219078	0.033109319	2	26	Unassigned	Uncultured
VC_4_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Winter	0.015583383	0.373813913	0.00800543	8	50	Unassigned	Uncultured
VC_21_1	V[Hs-Lw]C[Ls-Lw]	gDNA	Summer	0.005793603	0.934905923	0.534146298	12	80	Unassigned	Uncultured
VC_492_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.024717133	0.847879161	-0.014923584	6	24	Unassigned	Uncultured
VC_419_0	V[Ls-Hw]C[Hs-Hw]	RNA	Winter	0.003630172	0.865529317	-0.225914749	1	25	Siphoviridae	Cyanophage
VC_13_2	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.028990998	0.826447195	0.040358526	51	377	Unassigned	Uncultured
VC_324_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.047945499	0.614991139	0.224145121	1	13	Unassigned	Uncultured
VC_78_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.018343721		0.019334386	2	12	Unassigned	Uncultured
VC_282_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.008909425	0.636663601	0.104330936	8	31	Unassigned	Uncultured
VC_11_15	V[Hs-Hw]C[Hs-Lw]	gDNA	Winter	5.96E-05	0.773915523	0.085175661	29	198	Myoviridae	Cyanophage
VC_29_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Winter	0.000568679	0.828128993	0.051024947	36	228	Siphoviridae	Cyanophage
VC_160_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.000745107	0.037585534	0.028408488	7	37	Unassigned	Uncultured
VC_96_1	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.039191558		-0.00926961	1	11	Unassigned	Uncultured
VC_16_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.040926944	0.88246832	0.242260523	21	174	Unassigned	Punicispirillum
VC_645_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.02974098	0.725114658	0.050363728	1	22	Unassigned	Uncultured
VC_67_0	V[Hs-Lw]C[Hs-Lw]	RNA	Summer	2.00E-05	0.720411541	0.320137024	25	65	Podoviridae	Cyanophage
VC_96_2	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.036191393	0.812279715	0.302639055	16	171	Myoviridae	Klebsiella
VC_18_0	V[Ls-Lw]C[Ls-Lw]	gDNA	Winter	0.042601945	0.710424964	0.005221722	14	69	Unassigned	Uncultured
VC_626_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.011306317	0.066692928	-0.042901268	1	25	Unassigned	Uncultured
VC_13_1	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.006063894	0.249024848	0.015457863	2	75	Unassigned	Uncultured
VC_9_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.046301345	0.488857791	0.001432451	11	43	Podoviridae	Cyanophage
VC_0_4	V[Hs-Hw]C[Hs-Hw]	RNA	Summer	0.002895916		0.029097981	5	33	Myoviridae	Cyanophage
VC_13_15	V[Hs-Hw]C[Hs-Hw]	RNA	Summer	0.000589233		0.130666201	2	25	Myoviridae	Cyanophage
VC_266_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.038521866	0.296662151	0.123971582	2	11	Unassigned	Uncultured
VC_84_1	V[Hs-Hw]C[Hs-Hw]	gDNA	Winter	0.030987136	0.940732021	0.37609387	1	23	Unassigned	Uncultured
VC_2_3	V[Hs-Lw]C[Ls-Hw]	gDNA	Winter	0.036920996	0.650271031	0.375571885	7	73	Unassigned	Uncultured
VC_6_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Winter	0.029310498	0.603251322	0.019331601	9	90	Unassigned	Uncultured
VC_559_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Winter	0.020609124		-0.002815016	8	25	Unassigned	Uncultured
VC_9_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.006194374	0.928531469	0.092959228	9	56	Podoviridae	Cyanophage
VC_610_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.011470668	0.373763013	1.78542406	3	14	Unassigned	Uncultured
VC_896_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.037830786	0.92371349	0.561474387	1	10	Unassigned	Uncultured
VC_0_4	V[Hs-Lw]C[Hs-Hw]	gDNA	Winter	0.023052555	0.77283196	0.517791413	2	19	Myoviridae	Cyanophage
VC_657_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.038936236		-0.040662396	2	10	Unassigned	Uncultured
VC_418_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.041664101	0.422816252	0.042063452	11	76	Unassigned	Uncultured
VC_558_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.000276382	0.914618781	4.511532703	3	24	Unassigned	Uncultured
VC_164_0	V[Hs-Hw]C[Hs-Hw]	RNA	Summer	0.039191558		0.104357768	1	11	Unassigned	Uncultured
VC_16_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.021288844	0.544200051	0.084741976	13	104	Unassigned	Punicispirillum
VC_11_15	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	1.66E-06	0.626412598	0.086879858	11	58	Myoviridae	Cyanophage
VC_29_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.039293993	0.393243274	0.021492416	4	27	Siphoviridae	Cyanophage
VC_158_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.014037692	0.956295236	5.938856479	5	24	Unassigned	Uncultured
VC_147_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.014433319	0.936200719	1.532909513	10	50	Myoviridae	Cyanophage
VC_291_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.020175723	0.845022717	4.118086744	2	20	Myoviridae	Cyanophage
VC_11_15	V[Hs-Hw]C[Hs-Hw]	gDNA	Summer	0.043591148	0.914405954	1.037209963	5	67	Myoviridae	Cyanophage
VC_26_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Winter	0.003457546	-0.060404023	0.171996451	2	14	Siphoviridae	Cyanophage
VC_14_1	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.000779082	0.575963582	0.019165086	40	276	Podoviridae	Cellulophaga
VC_51_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.041871682	0.834224667	0.128992255	6	41	Unassigned	Cyanophage
VC_173_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.038936236		-0.125447702	2	10	Unassigned	Uncultured
VC_91_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.036277903	0.684591654	0.028629815	3	38	Unassigned	Uncultured
VC_11_15	V[Hs-Hw]C[Hs-Lw]	RNA	Summer	0.009048307		0.33280125	2	15	Myoviridae	Cyanophage
VC_46_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.016449408	0.514537745	0.011743592	35	214	Podoviridae	Enterobacteria
VC_529_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.018267229	-0.044488889	0.11672949	2	12	Unassigned	Uncultured
VC_393_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.001050517	0.836987241	0.134431064	8	32	Unassigned	Uncultured
VC_281_0	V[Ls-Hw]C[Hs-Hw]	RNA	Winter	0.000774244	0.834425318	-0.076121853	2	34	Siphoviridae	Cyanophage
VC_491_0	V[Hs-Lw]C[Ls-Hw]	RNA	Winter	0.009590319	0.951774081	-0.061398533	1	21	Unassigned	Uncultured
VC_108_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.012750463	0.830791328	0.640370367	2	20	Unassigned	Uncultured
VC_322_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Summer	0.004564177		0.072039483	3	18	Unassigned	Uncultured
VC_535_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.030207362	0.870607341	0.01787665	7	60	Unassigned	Uncultured
VC_134_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Summer	0.030212645	0.393299119	-0.039730829	14	76	Unassigned	Uncultured
VC_21_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.041779277	0.937450065	0.885745963	2	59	Unassigned	Uncultured
VC_0_4	V[Hs-Hw]C[Hs-Hw]	gDNA	Summer	0.025085338	0.888840248	0.798473451	7	73	Myoviridae	Cyanophage
VC_62_1	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.011506667	0.966594155	0.003148288	65	392	Unassigned	Uncultured
VC_38_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.008393656	0.675114111	0.285427578	15	67	Myoviridae	Cyanophage
VC_11_15	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.012082432	0.89426926	0.858128935	29	328	Myoviridae	Cyanophage
VC_74_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.017681219	0.763605729	0.136536396	7	74	Unassigned	Uncultured
VC_291_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	4.48E-05	0.482725773	0.081954842	12	81	Myoviridae	Cyanophage
VC_61_0	V[Hs-Lw]C[Hs-Lw]	RNA	Summer	0.023945026	0.393433915	0.129026679	12	46	Podoviridae	Cyanophage
VC_545_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.005886689	0.63347	0.127574786	3	17	Myoviridae	Cyanophage
VC_104_0	V[Ls-Lw]C[Ls-Lw]	gDNA	Winter	0.020188003	0.929537856	0.074456982	25	131	Unassigned	Uncultured
VC_9_0	V[Ls-Hw]C[Ls-Hw]	gDNA	Winter	0.027144271	0.792669159	0.407670915	9	65	Podoviridae	Cyanophage
VC_13_2	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.01597595	0.830070711	0.101398873	5	83	Unassigned	Uncultured
VC_2_3	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.043576903	0.110608081	0.014020172	1	21	Unassigned	Uncultured
VC_22_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.003291268	0.81047258	0.045723416	53	324	Unassigned	Uncultured
VC_103_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.02358678	0.885187362	0.02346574	8	57	Unassigned	Uncultured
VC_152_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.027411513	0.77694463	0.014374807	7	37	Unassigned	Uncultured
VC_766_0	V[Ls-Lw]C[Ls-Lw]	RNA	Summer	0.034266612	0.737412031	-0.039172683	2	12	Unassigned	Uncultured
VC_275_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.000346064	0.587980346	0.044394894	16	287	Unassigned	Uncultured
VC_269_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.018560802	0.939454561	0.629736938	4	30	Unassigned	Uncultured
VC_6_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.025842936	0.917514756	0.405043041	5	54	Unassigned	Uncultured
VC_460_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.020520836		0.039202425	7	24	Unassigned	Uncultured
VC_31_2	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	2.10E-05	0.641062328	0.026674019	22	189	Myoviridae	Cyanophage
VC_279_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Summer	0.04787133	0.889940146	0.404886739	2	12	Siphoviridae	Cellulophaga
VC_68_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.0042902	0.819747102	0.575236097	1	22	Unassigned	Uncultured
VC_265_0	V[Hs-Hw]C[Hs-Lw]	RNA	Summer	0.024415435	0.55767441	0.027878865	3	32	Unassigned	Uncultured
VC_178_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Summer	0.017173962	0.348959555	0.142550084	1	24	Unassigned	Uncultured
VC_306_0	V[Ls-Lw]C[Ls-Lw]	gDNA	Summer	0.006727456	0.780615242	4.276932297	9	30	Myoviridae	Cyanophage
VC_120_0	V[Hs-Hw]C[Hs-Hw]	gDNA	Summer	0.049925554	0.667408041	0.103963201	2	78	Unassigned	Uncultured
VC_418_0	V[Ls-Hw]C[Ls-Lw]	RNA	Winter	0.019207162		-0.00162859	6	15	Unassigned	Uncultured
VC_158_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.002470739	0.807556377	0.294500774	5	25	Unassigned	Uncultured
VC_291_0	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.00795914	0.89261473	0.067252272	2	22	Myoviridae	Cyanophage
VC_25_2	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.013541749	0.839820745	0.257450619	9	102	Unassigned	Uncultured
VC_147_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.02150899	0.818227989	0.111865101	9	35	Myoviridae	Cyanophage
VC_61_0	V[Ls-Hw]C[Ls-Hw]	RNA	Winter	0.007465695		0.080696915	2	10	Podoviridae	Cyanophage
VC_323_0	V[Hs-Lw]C[Ls-Lw]	gDNA	Winter	0.027105783	0.5154362	0.03519663	6	35	Unassigned	Uncultured
VC_31_2	V[Hs-Lw]C[Hs-Lw]	gDNA	Winter	0.021929361	0.349244175	0.008578297	5	57	Myoviridae	Cyanophage
VC_78_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.048364423	0.927397861	0.577958239	5	39	Unassigned	Uncultured
VC_141_0	V[Ls-Hw]C[Ls-Hw]	gDNA	Winter	0.039222339	0.930056263	-0.548523537	11	80	Unassigned	Uncultured
VC_558_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.022514062	0.897125022	0.289889853	3	24	Unassigned	Uncultured
VC_29_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Summer	0.001893995	0.852019538	6.450479259	4	40	Siphoviridae	Cyanophage
VC_765_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.007465695		0.030563605	2	10	Unassigned	Uncultured
VC_67_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.01162492	0.891148073	10.76331223	26	68	Podoviridae	Cyanophage
VC_79_0	V[Ls-Hw]C[Ls-Hw]	gDNA	Winter	0.016365183	0.858284117	0.00604297	41	302	Unassigned	Uncultured
VC_621_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.004344999	0.564948943	0.203650018	4	17	Unassigned	Uncultured
VC_494_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.041066973	0.471939369	-0.074964058	2	49	Unassigned	Uncultured
VC_663_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.01370652	0.893156498	0.065339617	1	53	Unassigned	Uncultured
VC_330_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Winter	0.024618302	0.27595894	0.08141852	3	23	Unassigned	Uncultured
VC_29_0	V[Hs-Hw]C[Ls-Lw]	gDNA	Summer	0.04035931	0.321652979	0.023764368	33	124	Siphoviridae	Cyanophage
VC_31_4	V[Ls-Hw]C[Ls-Hw]	gDNA	Winter	0.000143406	0.903203936	0.101696749	1	61	Unassigned	Uncultured
VC_16_0	V[Hs-Hw]C[Hs-Lw]	gDNA	Winter	0.014378803	0.666758405	0.017939733	21	114	Unassigned	Punicispirillum
VC_547_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Winter	0.020508774	0.853432328	0.054973678	4	36	Unassigned	Uncultured
VC_215_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.015491775	0.823500103	0.070842125	8	59	Unassigned	Uncultured
VC_9_0	V[Ls-Lw]C[Hs-Lw]	gDNA	Summer	0.039330184	0.873025413	0.78190629	13	73	Podoviridae	Cyanophage
VC_163_0	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.010034764	0.607627899	0.037916888	5	24	Unassigned	Uncultured
VC_2_3	V[Ls-Hw]C[Ls-Lw]	gDNA	Winter	0.006022758	0.832721034	0.019220154	67	488	Unassigned	Uncultured

(b)

All fractions

RankState	# of occurences	Proportion
V[Ls-Hw]C[Ls-Lw]	34	24.64%
V[Hs-Lw]C[Hs-Lw]	32	23.19%
V[Ls-Lw]C[Hs-Lw]	16	11.59%
V[Ls-Hw]C[Ls-Hw]	14	10.14%
V[Hs-Hw]C[Hs-Lw]	13	9.42%
V[Hs-Hw]C[Ls-Lw]	13	9.42%
V[Hs-Hw]C[Hs-Hw]	7	5.07%
V[Hs-Lw]C[Ls-Lw]	3	2.17%
V[Ls-Lw]C[Ls-Lw]	3	2.17%
V[Ls-Hw]C[Hs-Hw]	2	1.45%
V[Hs-Lw]C[Hs-Hw]	1	0.72%
V[Hs-Hw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Hs-Hw]	0	0.00%
V[Ls-Lw]C[Ls-Hw]	0	0.00%

Cellular DNA fraction

RankState	# of occurences	Proportion
V[Ls-Hw]C[Ls-Lw]	33	28.45%
V[Hs-Lw]C[Hs-Lw]	26	22.41%
V[Ls-Lw]C[Hs-Lw]	15	12.93%
V[Ls-Hw]C[Ls-Hw]	7	6.03%
V[Hs-Hw]C[Hs-Lw]	11	9.48%
V[Hs-Hw]C[Ls-Lw]	13	11.21%
V[Hs-Hw]C[Hs-Hw]	4	3.45%
V[Hs-Lw]C[Ls-Lw]	3	2.59%
V[Ls-Lw]C[Ls-Lw]	3	2.59%
V[Ls-Hw]C[Hs-Hw]	0	0.00%
V[Hs-Lw]C[Hs-Hw]	1	0.86%
V[Hs-Hw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Hs-Hw]	0	0.00%
V[Ls-Lw]C[Ls-Hw]	0	0.00%

Cellular RNA fraction

RankState	# of occurences	Proportion
V[Ls-Hw]C[Ls-Lw]	1	4.55%
V[Hs-Lw]C[Hs-Lw]	6	27.27%
V[Ls-Lw]C[Hs-Lw]	1	4.55%
V[Ls-Hw]C[Ls-Hw]	7	31.82%
V[Hs-Hw]C[Hs-Lw]	2	9.09%
V[Hs-Hw]C[Ls-Lw]	0	0.00%
V[Hs-Hw]C[Hs-Hw]	3	13.64%
V[Hs-Lw]C[Ls-Lw]	0	0.00%
V[Ls-Lw]C[Ls-Lw]	0	0.00%
V[Ls-Lw]C[Hs-Hw]	2	9.09%
V[Hs-Lw]C[Hs-Hw]	0	0.00%
V[Hs-Hw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Hs-Lw]	0	0.00%

Cyanophages - All cellular fractions

RankState	# of occurences	Proportion
V[Ls-Hw]C[Ls-Lw]	3	6.82%
V[Hs-Lw]C[Hs-Lw]	13	29.55%
V[Ls-Lw]C[Hs-Lw]	9	20.45%
V[Ls-Hw]C[Ls-Hw]	3	6.82%
V[Hs-Hw]C[Hs-Lw]	5	11.36%
V[Hs-Hw]C[Ls-Lw]	4	9.09%
V[Hs-Hw]C[Hs-Hw]	4	9.09%
V[Hs-Lw]C[Ls-Lw]	0	0.00%
V[Ls-Lw]C[Ls-Lw]	0	0.00%
V[Ls-Hw]C[Hs-Hw]	2	4.55%
V[Hs-Lw]C[Hs-Hw]	1	2.27%
V[Hs-Hw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Hs-Hw]	0	0.00%
V[Ls-Lw]C[Ls-Hw]	0	0.00%

Uncultured - All cellular fractions

RankState	# of occurences	Proportion
V[Ls-Hw]C[Ls-Lw]	29	33.33%
V[Hs-Lw]C[Hs-Lw]	17	19.54%
V[Ls-Lw]C[Hs-Lw]	7	8.05%
V[Ls-Hw]C[Ls-Hw]	11	12.64%
V[Hs-Hw]C[Hs-Lw]	6	6.90%
V[Hs-Hw]C[Ls-Lw]	8	9.20%
V[Hs-Hw]C[Hs-Hw]	3	3.45%
V[Hs-Lw]C[Ls-Lw]	3	3.45%
V[Ls-Lw]C[Ls-Lw]	3	3.45%
V[Ls-Hw]C[Hs-Hw]	0	0.00%
V[Hs-Lw]C[Hs-Hw]	0	0.00%
V[Hs-Hw]C[Ls-Hw]	0	0.00%
V[Ls-Lw]C[Hs-Hw]	0	0.00%
V[Ls-Lw]C[Ls-Hw]	0	0.00%

V[Hs-Lw]C[Ls-Lw]	RNA	Light-induced
Annotation	# of occurences	Proportion
Uncultured	2	33.33%
Cyanophage	4	66.67%
Punicispirillum	0	0.00%
Klebsiella	0	0.00%
Cellulophaga	0	0.00%
Enterobacteria	0	0.00%

V[Ls-Hw]C[Ls-Hw]	RNA	Light-induced
Annotation	# of occurences	Proportion
Uncultured	0	0.00%
Cyanophage	2	100.00%
Punicispirillum	0	0.00%
Klebsiella	0	0.00%
Cellulophaga	0	0.00%
Enterobacteria	0	0.00%

V[Hs-Lw]C[Hs-Lw]	gDNA	Light-induced
Annotation	# of occurences	Proportion
Uncultured	13	54.17%
Cyanophage	9	37.50%
Punicispirillum	0	0.00%
Klebsiella	1	4.17%
Cellulophaga	1	4.17%
Enterobacteria	0	0.00%

V[Ls-Hw]C[Ls-Hw]	gDNA	Light-induced
Annotation	# of occurences	Proportion
Uncultured	5	83.33%
Cyanophage	1	16.67%
Punicispirillum	0	0.00%
Klebsiella	0	0.00%
Cellulophaga	0	0.00%
Enterobacteria	0	0.00%

Table S3. DP-GP Clusrers (2) of the microbial community diel gene expression, with p-value of the Light-Dark differential abundantce (Mann-Whitney) by cluster, the effect size and correlation. PHR represents the photoautotrophs to heterotrophs in each cluster.

Season	Cluster	p-value of light-dark differential expression (Mann-Whitney)	Effect size (%)	Rank-biserial correlation (light +1, dark -1)	Photoautotroph to Heterotroph Ratio (PHR)
Summer	1	0.0E+00	100.00	1.00	1.08
Summer	2	8.0E-205	22.76	-0.54	0.26
Summer	3	3.7E-259	77.80	0.56	0.44
Summer	4	7.5E-214	21.21	-0.58	0.15
Summer	5	2.4E-82	1.00	-0.98	0.00
Summer	6	0.0E+00	99.61	0.99	0.38
Summer	7	6.5E-120	0.00	-1.00	0.15
Summer	8	1.7E-93	31.17	-0.38	0.16
Summer	9	3.0E-80	10.88	-0.78	0.24
Summer	10	5.5E-227	1.87	-0.96	0.29
Summer	11	3.9E-06	40.08	-0.20	0.57
Summer	12	1.2E-68	0.00	-1.00	1.12
Summer	13	4.8E-54	0.57	-0.99	0.95
Summer	14	4.7E-05	59.34	0.19	0.81
Summer	15	7.5E-70	99.96	1.00	1.67
Summer	16	3.5E-01	51.55	0.03	0.00
Summer	17	1.1E-30	7.40	-0.85	1.00
Summer	18	1.7E-06	100.00	1.00	
Winter	1	0.0E+00	100.00	1.00	3.30
Winter	2	3.2E-05	45.34	-0.09	0.47
Winter	3	4.2E-151	8.88	-0.82	0.13
Winter	4	6.4E-25	57.62	0.15	0.20
Winter	5	0.0E+00	98.41	0.97	0.31
Winter	6	0.0E+00	94.90	0.90	0.63
Winter	7	1.8E-199	100.00	1.00	2.58
Winter	8	0.0E+00	0.20	-1.00	0.09
Winter	9	4.0E-117	20.46	-0.59	0.49
Winter	10	1.9E-01	46.96	-0.06	0.83
Winter	11	1.3E-258	0.27	-0.99	0.26
Winter	12	2.1E-243	0.08	-1.00	0.59
Winter	13	1.1E-264	99.97	1.00	3.61
Winter	14	8.0E-196	94.57	0.89	0.48
Winter	15	9.0E-142	100.00	1.00	1.75
Winter	16	3.4E-79	84.74	0.69	4.28
Winter	17	9.3E-103	99.79	1.00	3.36
Winter	18	2.8E-31	98.35	0.97	0.00
Winter	19	1.4E-01	53.19	0.06	4.57
Winter	20	1.8E-22	100.00	1.00	2.29
Winter	21	2.6E-01	53.02	0.06	0.00
Winter	22	1.9E-48	0.66	-0.99	0.26
Winter	23	1.2E-04	94.44	0.89	

Table S4. Active contigs abundance in the winter and summer samples. Relative abundance, rank, rank-percentile and assigned rank-state for the contigs in the Active viral contigs group. Excel file can be downloaded from https://doi.org/10.17605/osf.io/b74mt

Table S5. Active viral contigs group viral cluster assignment (VC). Excel file can be downloaded from https://doi.org/10.17605/osf.io/b74mt

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